

Disease modifying anti-rheumatic drug combination therapies

Field of the Invention

The present invention relates to combination therapies that can have reparative effects on a range of progressive and/or degenerative diseases. In particular instances, the combination therapies can be used for the treatment of autoimmune diseases such as arthritis, and in particular rheumatoid arthritis. In particular instances, the combination therapies comprise a disease modifying anti-rheumatic drug (DMARD) and a therapeutic agent which can act by binding mitochondrial Complex I. In particular instances, the DMARD is a conventional synthetic DMARD (csDMARD). The therapeutic agent which can act by binding mitochondrial Complex I are referred to herein as Mitochondrial Complex I Modulator compounds (or MCIM compounds).

Background

Mitochondrial Complex I (also known as NADH:ubiquinone oxidoreductase, Type I NADH dehydrogenase, respiratory Complex I, or simply 'Complex I') is the first enzyme complex of the respiratory chain (Yoga et al, 2021, which is hereby incorporated by reference in its entirety). Complex I is a very large protein complex comprising 45 subunits (Gutiérrez-Fernández, 2020) which is highly conserved in eukaryotes and prokaryotes. In eukaryotes, it couples the transfer of electrons from NADH to the coenzyme ubiquinone (Q) with the translocation of protons across the inner mitochondrial membrane, although the mechanism linking the spatially distinct proton translocation and electron transfer remains unknown (Gutiérrez-Fernández, 2020).

In humans, the most common form of ubiquinone is known as 'Q10' because it has ten isoprenyl subunits in its 'tail' region. Q10 is hydrophobic and it enters the Complex I enzyme from the mitochondrial inner membrane through a long binding channel (Bridges et al, 2020), which is often called the 'Q tunnel'. The Q-tunnel is long and heterogenous in nature. Various compounds are known to bind within the Q tunnel, but there is no single consensus site for compound binding. For example, piericidin A is reported to bind within the Q-tunnel as a 'short-form' ubiquinone, with interactions at multiple residues from the top of the Q-tunnel to its midway point (Gutiérrez-Fernández, 2020; Bridges et al, 2020; Chung et al, 2021, each of which is hereby incorporated by reference in its entirety). Aureothin and pyridaben, which are also quinone-like compounds, are also observed to bind at a similar site in *T. thermophilus* (Gutiérrez-Fernández, 2020; Chung et al, 2021). IACS-2858 and BAY-87-2243 act like a "cork in a bottle", binding a cluster of residues of subunits ND1 and NDUFS7 in the central charged region of the ubiquinone-binding pocket of mouse Complex I (Chung et al, 2021; Kurelac et al, 2022). Biguanides such as metformin are similarly thought to interact with Phe244 of ND1 and Arg77 of NDUFS7 in the Q-tunnel with a mode dependent on the active or inactive state of the enzyme. Furthermore, evidence indicates that the biguanides may be

non-selective in their binding, with a putative additional binding site on Complex IV, another subunit of the electron transport chain (LaMoia et al, 2021). Rotenone and CN-POBS are compounds that bind 'site Iq' of Complex I (Orr *et al*, 2013; Pereira *et al*, 2023) and act to alter superoxide production, the former increasing and the latter reducing or increasing superoxide production dependent on the source assessed. The binding sites of several Complex I inhibitors are reviewed by Schiller and Zickermann (2022).

Classical Complex I inhibitors, such as those mentioned above, often cause cytotoxicity and cell death. For instance, piericidin A is insecticidal and antibacterial, pyridaben is an acaricide (killing ticks and mites) and aureothin exhibits antitumor, antifungal and insecticidal activity. IACS-010579 and IM156 (also known as HL156A) have been reported to possess anti-tumour effects due to profound impacts on cancer cell viability (Tsogbadrakh et al, 2018 and Izreig et al, 2020). However, despite these properties, the known, classical, C1 inhibitors have not found use as approved therapeutics. Indeed, as well as showing mechanism-based toxicity (Yap, T et al, 2023), these agents have been used to elicit disease in mouse models of neurodegenerative conditions such as Parkinson disease (PD; Xiong et al, 2012, which is hereby incorporated by reference in its entirety) and Alzheimer's disease (AD; Joh et al, 2017, which is hereby incorporated by reference in its entirety). As such, for classical complex I inhibitors, identifying a suitable approach for therapeutic use that provides a benefit without toxicity has proved to be a challenge. An alternative approach which might elicit a benefit without adverse effects may have potential benefits for the treatment of a variety of progressive diseases.

The goal of therapeutic tissue repair is to restore the tissue to its original state of structure and function (Krafts, 2010 and Paul and Sharma, 2021). Attaining this goal has proved elusive, with the only effective examples being organ transplantation or surgical implants using natural or biomimetic structures such as aortic valves or joint replacement). Further, whilst there has been a significant increase in research into strategies to achieve repair in different organ systems, these approaches aim to remove the primary driver to tissue injury (e.g., the calcified heart valve) or to replace the dysfunctional matrix environment with an environment which favours homing of repair cells or local augmentation of soluble pro-repair factors (e.g., fibrin). Such examples include biomimetic scaffolds in orthopaedics, which simulate normal structural matrix for cell homing, and cellular products to simulate the soluble matrix microenvironment for cutaneous and ocular wound repair. As such, the identification of a therapeutic agent(s) which both attenuates the drive to tissue injury and concurrently promotes a pro-repair microenvironment, has proved elusive.

Tissue repair (healing) is a highly orchestrated and complex process involving a sequence of overlapping events that are precisely timed. The process has three broad phases which were first delineated in the 19th Century (Virchow, 1859) and have been since augmented by the addition of

data on their cellular genotypes, phenotypes, and molecular mediators (Liehn, 2011, Takeo, 2015, and Somer et al, 2021). However, there are limited, if any, data available regarding the mechanisms underpinning repair in most chronic disease settings (Peyrin-Biroulet, 2020) and current understanding of tissue repair processes has not led to substantial improvements in the clinical care of tissue damage (Eming et al, 2014).

As shown in Figure 1, the three phases of tissue repair are:

1. Inflammation
2. Proliferation (fibrogenesis and angiogenesis)
3. Tissue Remodelling (Lokmic et al, 2012.)

In the healthy, functional healing/repair process, these phases proceed in an overlapping sequence, with resolution of inflammation progressing alongside proliferation and matrix remodelling to restore tissue architecture. In conditions of chronic disease, this process is interrupted or dysregulated, resulting in persistent non-healing tissue damage.

Functional repair involves the resolution of the primary inflammatory response to injury and the simultaneous activation of the inflammatory response consequent upon repair. These phases show different qualitative and kinetic properties; the first phase induces a proliferative response in both infiltrating and resident cells whilst the second involves repolarisation of the infiltrating cells. Furthermore, the cells involved in the repair process show different responses to stress dependent on the progressing phase of repair. For example, immune cells of the myeloid lineage (short-lived cells with high bioenergetic demand) respond to stress by reducing proliferation and activating apoptosis pathways such that the overall phenotype of the myeloid lineage is anti-inflammatory, and in the context of repair, a reduced population showing immunomodulatory effects. By contrast, mesenchymal and epithelial cells respond to similar microenvironmental stressors by activating effector pathways. For example, mesenchymal cells typically respond to low oxygen tension (hypoxia) by the expansion and activation of a repair phenotype.

There is an urgent need for therapeutics which exert a dual pharmacology of reducing disease progression whilst supporting tissue repair in chronic progressive disease, medical conditions that worsen over time without medical intervention. Prominent examples are autoimmune diseases such as rheumatoid arthritis (RA), psoriasis and inflammatory bowel disease (IBD) and progressive fibrosis such as idiopathic pulmonary fibrosis (IPF), non-alcoholic fatty liver disease (NAFLD)/ non-alcoholic steatohepatitis (NASH) and chronic kidney disease. Without treatment these conditions typically progress in severity over time and may, as in the case of pulmonary fibrosis, be fatal.

The current treatments for these conditions inhibit the progression of the diseases. However, in general these agents typically fail to promote tissue repair by exerting a direct effector response on repair processes. Indeed, their suppression of the pro-inflammatory effector cell and molecular

response proceeds cyclically, perhaps for months or years. For example, in rheumatoid arthritis, persistent inflammation within the bone erosion prevents erosions from healing (Berardi et al, 2021) whilst a similar unresolved inflammation preventing repair is seen in chronic skin wounds (Li et al, 2021), ulcerative colitis and Crohn's disease. Examples of conditions where effective anti-

5 inflammatory effects by a therapeutic do not result in effective repair include:

- rheumatoid arthritis, in which suppression of synovitis and pannus formation does not result in complete suppression of erosions and bone loss;
- inflammatory bowel disease, in which suppression of mucosal inflammation does not result in complete suppression of ulceration;
- 10 • neurodegeneration, such as multiple sclerosis (MS), in which suppression of the inflammatory drive to de-myelination does not result in concomitant increase in oligodendrocyte or Schwann cell-induced re-myelination;
- pathology of the distal lungs, such as idiopathic pulmonary fibrosis, in which suppression of inflammation does not halt the drive to fibroblastic expansion and emphysematous
- 15 destruction, or result in the conservation of alveolar stem cells.

Furthermore, in other chronic diseases, the kinetic interplay between the drive to injury and sequential activation of repair, often results in 'futile' repair, i.e., creation of maladapted restitution of tissue remodelling to a normal state. Such futile repair is seen in settings such as osteoarthritis and fibrosis.

20 The result of either failure to repair or futile repair is that most patients with chronic disease experience ongoing symptoms, and disease progression despite treatment. As such, there is a pressing need for therapeutics with a dual pharmacology that can act on both the inflammatory and repair arms of a lesion. Such a therapeutic would:

- display a pharmacology-dependent, differential transduction of microenvironmental stress signals.
- 25 • mitigate the drive to injury and simultaneously, augment and capitalise upon the stressor events that constitute the inflammatory to proliferative phase of tissue repair.
- orchestrate repair, in an anatomically appropriate manner to restore key aspects of tissue function (Eming et al, 2014).

30 In addition, the pharmacological intervention might elicit cellular changes consistent with those required to orchestrate a controlled repair response. For example, the approach might elicit production of the key basement membrane collagen IV in a controlled manner, alongside production of growth factors important for angiogenesis, epithelialisation and matrix remodelling, such as VEGF, FGF21 and GDF15. Were this approach to be successful it would elicit repair in a pathology agnostic manner, i.e. the repair response would be seen in multiple settings regardless of the nature of the

original injury. In addition, it might alter the activation response of resident cells and de-sensitize' the microenvironment to the effects of a pro-inflammatory cell infiltrate, resulting in a 'permission' to repair.

One proposed approach to eliciting a tissue repair response has been to repair the cell first (Fu, 2021). The induction of an integrated stress response (ISR) may be an effective means of achieving this goal. The ISR is a cytoprotective mechanism that maintains cellular proteostasis (i.e., protein homeostasis) in response to stress conditions. The ISR is highly conserved across cell types, and is triggered in response to changes in mitochondrial function (Savu and Moiso, 2022). Activation of a controlled ISR has been shown to have beneficial effects in multiple disease settings. For example, in mouse models of multiple sclerosis the ISR can be harnessed to protect oligodendrocytes and myelin during inflammation (Way and Popko, 2016). In addition, the ISR has been shown to regulate the health of cardiac progenitor cells by removing unhealthy cells to prevent their differentiation and self-renewal (Searfoss et al, 2019), a property that may be shared across progenitor cells in other settings such as oligodendrocyte progenitors in the brain and spinal cord, alveolar type II epithelial cells (AT2) in the lung and mesenchymal stem cells and bone marrow progenitor cells. Roles for the ISR in obesity, neurodegeneration and heart failure have also been proposed. Importantly, to achieve these outcomes the ISR should be moderate and tightly regulated, like a rheostat, in order to avoid pushing cells towards apoptosis (Kaspar et al, 2021).

An agent which could both control symptoms and elicit tissue repair/healing may have greater benefits for patients than existing therapy and lead to improved treatment outcomes.

Disease-modifying antirheumatic drugs (DMARDs) are a class of drugs defined by their use in treating inflammatory arthritides, including rheumatoid arthritis (RA), psoriatic arthritis (PsA) and ankylosing spondylitis (AS). Particular DMARDs may also be used to treat a range of connective tissue diseases, inflammatory diseases and cancers. In particular, some DMARDs may be used to treat one or more of inflammatory bowel diseases (IBD), such as Crohn's disease and ulcerative colitis, systemic lupus erythematosus, psoriasis, gout, Sjögren syndrome, myasthenia gravis, and sarcoidosis.

DMARDs do not all share a related structure or mechanism of action and can be subdivided into categories. DMARDs include conventional synthetic DMARDs (csDMARDs), targeted synthetic DMARDs (tsDMARDs), biological DMARDs (bDMARDs).

csDMARDs are small molecule drugs which demonstrate anti-inflammatory function and include, for example, methotrexate, leflunomide, gold salts, hydroxychloroquine, and sulfasalazine. csDMARDs are so-called as they were not developed to specifically target a particular molecule. csDMARDs include methotrexate, azathioprine, chloroquine, D-penicillamine, ciclosporin, gold salts such as

- sodium aurothiomalate and auranofin, hydroxychloroquine, leflunomide, minocycline and sulfasalazine. Each of the aforementioned csDMARDs may be used, either alone or in combination with another DMARD, in the treatment of RA. Azathioprine, ciclosporin, methotrexate and sulfasalazine have also been used to treat inflammatory bowel diseases, such as Crohn's disease and ulcerative colitis. Azathioprine, chloroquine, hydroxychloroquine, and methotrexate have also been used to treat the autoimmune disease lupus erythematosus. Leflunomide, methotrexate and sulfasalazine have also been used to treat psoriatic arthritis, and methotrexate and sulfasalazine have been used to treat reactive arthritis.
- tsDMARDs are also small molecule drugs. In contrast to csDMARDs, however, tsDMARDs were and are developed to target particular molecular structures, such as particular protein targets. tsDMARDs include, for example, the Janus kinase (JAK) inhibitor compounds baricitinib, filgotinib, and tofacitinib, the Tyk2 inhibitor, deucravacitinib, and the phosphodiesterase 4 (PDE4) inhibitor apremilast.
- bDMARDs include monoclonal antibodies and receptor constructs which target either membrane bound or soluble proteins. For example, bDMARDs include the tumor necrosis factor (TNF) inhibitors adalimumab, certolizumab, etanercept (a decoy TNF receptor), golimumab, and infliximab. bDMARDs also include the CTLA4-Ig, abatacept, the IL-1 receptor antagonist, anakinra, the CD20 inhibitor, rituximab, the IL-6 inhibitors sarilumab and tocilizumab, the IL17A inhibitors, secukinumab, ixekizumab and bimekizumab, the IL23 inhibitors ustekinumab, risankizumab and guselkumab, and the BAFF inhibitor belimumab.

While there is a broad spectrum of DMARDs available, these are often associated with inadequate response and prominent side effects. For example, methotrexate is highly effective in suppressing the inflammation associated with rheumatoid arthritis, but it is a general cytotoxic and carries a corresponding toxicity burden. The biological disease-modifying anti-rheumatic drugs (bDMARDs) have been associated with rare but serious side-effects, including opportunistic infections such as tuberculosis and invasive fungal infections, and malignancies such as lymphoma. Furthermore, the small molecule, orally-available inhibitors of the Janus kinase (JAK)/signal transducer and activator of transcription (STAT) pathway (tsDMARDs), are associated with increased infections and CV events.

In addition to this spectrum of adverse effects, up to a third of patients fail to respond to therapy with the most commonly used bDMARDs, the anti-TNF α agents (Rubbert-Rotha, 2019). Although this may be addressed to an extent by switching between agents (Fleischmann, 2020), there is a pressing need for new agents with alternative mechanisms of action (Johnson, 2019), particularly since the available therapeutic options predominantly act as anti-inflammatory agents (Tanaka, 2019). In addition, although bDMARDs show evidence of slowing progression of underlying pathology in disease to a greater degree than methotrexate (Johnson, 2019), the tsDMARDs have not thus far demonstrated conclusive effects on underlying pathological progression (Chatzidionysiou, 2017) of

disease and patient QoL often remains poor despite treatment (Combe, 2015). For example, large proportions of patients require pain medication in addition to their normal treatment (Radawski, 2019). On top of these limitations, none of the available DMARDs directly address the mechanisms of structural and pathological damage (Tanaka, 2019). As such, there remains a need for new therapies that can both control inflammation but also support reparative processes in autoimmune and auto-inflammatory disease.

The inventors have previously discovered that compounds which can bind to and modulate the activity of mitochondrial complex I (see European patent application No. 23162131.9, which is incorporated herein by reference) are beneficial in the treatment of inflammatory and/or progressive diseases such as rheumatoid arthritis (RA), inflammatory bowel disease (IBD), interstitial lung disease or pulmonary fibrosis, and multiple sclerosis (MS). The inventors demonstrated that such compounds could slow down and even prevent disease progression in mice with the conditions. Even more surprisingly, however, was the observation that these compounds additionally promoted repair of affected tissues thereby reversing disease progression.

While this newly discovered class of compounds provides an exciting new avenue for treatment of inflammatory and/or progressive disease, there is still an ongoing need to improve the efficacy of these nascent drug treatment regimens to further improve patient quality of life.

The present invention has been devised in light of the above considerations.

Summary of the Invention

Current treatments for chronic, progressive conditions inhibit disease progression but fail to promote tissue repair. Consequently, patients with chronic disease experience ongoing symptoms and progression, and poor quality of life. Despite the attractiveness of restoring normal tissue architecture as a means to treat chronic disease, pharmacological interventions to achieve this have not been studied, and as a result practical applications of this approach do not yet exist. One potential approach to achieve pharmacological tissue repair is through changes in mitochondrial function. However, the literature currently teaches that eliciting changes in mitochondrial function suppresses repair and promotes inflammation (Cai *et al*, 2022), and indeed, alterations in mitochondrial function to alter disease progression through control of inflammation, or tissue remodelling, have not been extensively studied. The mitochondrial Complex I modulator (MCIM) compounds used disclosed herein, and disclosed in EP23162131.9, modulate the activity of mitochondrial Complex I in a manner that differs from that of conventional complex I inhibitors. This elicits an adaptive phase which directs cell fate choices and mimics a wound repair-like microenvironment. Phenotypically, this can control inflammation, alter the activation response of resident cells and desensitizes the microenvironment to the effects of a pro-inflammatory cell infiltrate, and concurrently initiate repair signals in affected

tissues, such as the lung and joint. In addition, the MCIM compounds can stimulate the production of key growth factors such as VEGF, and collagen I, and the basement collagen IV. Together, these mechanisms support a reduction in inflammation and restoration of tissue architecture in multiple organ/tissue settings.

- 5 In addition to the effects of MCIM compounds described in EP23162131.9, the inventors have further found that MCIM compounds can be used in combination with DMARDs to further improve treatment of inflammatory and/or progressive diseases. Such combinations lead to a surprising and synergistic improvement in the levels of protection against the progression of disease pathology, and tissue repair observed compared to when either an MCIM compound or DMARD is administered alone. For
- 10 example, a synergistic reduction in the mean change in bone pathology is observed in arthritic mouse models when mice are treated with an MCIM compound as disclosed herein and the DMARD etanercept. Similarly, synergy is observed in the change in the arthritic index of mice treated with a combination of an MCIM compound and the DMARD tofacitinib compared to mice treated with either alone. This decrease in bone pathology is also recapitulated in human subjects where a further
- 15 decrease in inflammatory biomarkers, and an increase in reparatory biomarkers, are observed in patients receiving a combination of the csDMARD methotrexate and an MCIM compound.

At its broadest, the invention provides a pharmaceutical combination comprising an MCIM compound and a DMARD. The pharmaceutical combination may be for use in medicine. The MCIM compound and the DMARD may be administered separately, sequentially, or simultaneously, and may be

20 administered in any order. The combination therapy can achieve reparative effects when used to treat inflammatory and/or progressive diseases. Preferably, the MCIM compounds bind complex I and are able to modulate complex I function.

Accordingly, in a first aspect, the disclosure provides a pharmaceutical combination comprising an MCIM compound and a DMARD. In some embodiments, the pharmaceutical combination comprises

25 the DMARD comprises methotrexate. In some embodiments, the pharmaceutical combination comprises the DMARD does not comprise methotrexate. In some embodiments, the pharmaceutical combination comprises the DMARD methotrexate and at least one other DMARD.

In a second aspect, the disclosure provides a pharmaceutical composition comprising an MCIM compound and a DMARD. In some embodiments, the pharmaceutical composition comprises the

30 DMARD methotrexate. In some embodiments, the pharmaceutical combination comprises the DMARD methotrexate and at least one other DMARD.

In a third aspect, the disclosure provides a pharmaceutical combination comprising an MCIM compound and a DMARD for use in medicine. In a related fourth aspect, the disclosure provides a pharmaceutical composition comprising an MCIM compound and a DMARD for use in medicine. In

35 some embodiments of the third and fourth aspects, the DMARD comprises methotrexate. In other

embodiments, the DMARD does not comprise methotrexate. In some embodiments, the pharmaceutical combination comprises the DMARD methotrexate and at least one other DMARD.

In a fifth aspect, the disclosure provides a pharmaceutical composition comprising an MCIM compound for use in a method of treating an inflammatory and/or progressive disease in a subject.

- 5 The method comprises the separate, sequential, or simultaneous administration of the pharmaceutical composition and a DMARD to the subject to achieve disease control, regression, or tissue repair, or any combination thereof. In some embodiments, the pharmaceutical combination comprises the DMARD comprises methotrexate. In some embodiments, the pharmaceutical combination comprises the DMARD does not comprise methotrexate. In some embodiments, the pharmaceutical
10 combination comprises the DMARD methotrexate and at least one other DMARD.

- In a sixth aspect, the disclosure further provides a pharmaceutical composition comprising a DMARD for use in a method of treating an inflammatory and/or progressive disease in a subject. The method comprises the separate, sequential, or simultaneous administration of the pharmaceutical composition and an MCIM compound to the subject to achieve disease control, regression, or tissue repair, or any
15 combination thereof. In some embodiments, the pharmaceutical combination comprises the DMARD comprises methotrexate. In some embodiments, the pharmaceutical combination comprises the DMARD does not comprise methotrexate. In some embodiments, the pharmaceutical combination comprises the DMARD methotrexate and at least one other DMARD.

- In a seventh aspect, the disclosure further provides a pharmaceutical composition comprising an
20 MCIM compound and a DMARD for use in a method of treating an inflammatory and/or progressive disease in a subject. The treatment achieves disease control, regression, or tissue repair, or any combination thereof. In some embodiments, the pharmaceutical combination comprises the DMARD comprises methotrexate. In some embodiments, the pharmaceutical combination comprises the DMARD methotrexate and at least one other DMARD.

- 25 In an eight aspect, the disclosure further provides a method of treating an inflammatory and/or progressive disease in a subject, wherein the method comprises administering a pharmaceutical composition comprising a MCIM compound to the subject. The method further comprises the separate, sequential, or simultaneous administration of a DMARD to the subject to achieve disease control, regression, or tissue repair, or any combination thereof. In some embodiments, the
30 pharmaceutical combination comprising the DMARD comprises methotrexate. In some embodiments, the pharmaceutical combination comprising the DMARD does not comprise methotrexate. In some embodiments, the pharmaceutical combination comprises the DMARD methotrexate and at least one other DMARD.

- In a ninth aspect, the disclosure further provides a method of treating an inflammatory and/or
35 progressive disease in a subject, wherein the method comprises administering a pharmaceutical composition comprising a DMARD to the subject. The treatment further comprises the separate,

sequential or simultaneous administration of a MCIM compound to the subject to achieve disease control, regression, or tissue repair, or any combination thereof. In some embodiments, the pharmaceutical combination comprising the DMARD comprises methotrexate. In some embodiments, the pharmaceutical combination comprising the DMARD does not comprise methotrexate. In some
5 embodiments, the pharmaceutical combination comprises the DMARD methotrexate and at least one other DMARD.

In a tenth aspect, the disclosure further provides a method of treating an inflammatory and/or progressive disease in a subject, wherein the method comprises administering a pharmaceutical composition comprising a MCIM compound and a DMARD to a subject to achieve disease control,
10 regression, or tissue repair, or any combination thereof.

In an eleventh aspect, the disclosure further provides a pharmaceutical combination comprising a MCIM compound and a DMARD. The pharmaceutical combination may be formulated as a single composition comprising the MCIM compound and the DMARD. The pharmaceutical combination may be formulated as two separate compositions, wherein each of the two separate compositions
15 comprises either a MCIM compound or a DMARD. In some embodiments, the combination may comprise two or more DMARDs. Where the combination comprises two or more DMARDs, the pharmaceutical combination may comprise a single composition comprising the two or more DMARDs or the two or more DMARDs may be comprised in separate compositions. In some embodiments, the pharmaceutical composition comprises HMC-C-01-A and methotrexate.

In some embodiments of the above aspects of the disclosure, the treatment elicits disease control, regression, or tissue repair, or any combination thereof. In some embodiments, the treatment achieves disease control, regression, or tissue repair, or any combination thereof. In some
20 embodiments, the treatment initiates an adaptive response in certain cell types that leads to pharmacodynamic evidence of disease control, regression, or tissue repair, or any combination thereof. In some embodiments, the adaptive response leads to tissue repair and/or disease regression. In some embodiments, the tissue repair and/or disease regression induces a restoration of tissue architecture towards its healthy state, which is characterised by anatomically normal architecture. In some embodiments, disease control comprises inhibition of disease progression. In some embodiments, inhibition of disease progression includes a prevention of disease progression.
25 In some embodiments, inhibition of disease progression includes a reduced rate of disease progression. In some embodiments, disease control comprises the prevention of a loss of anatomically normal tissue architecture, or a reduction in the speed of the loss of anatomically normal tissue architecture. In some embodiments, the tissue repair and/or disease regression is characterised by an increased clinical repair score and/or comprises increased wound healing.

In some embodiments, the inflammatory and/or progressive disease is an autoimmune or autoinflammatory disease. In some embodiments, the inflammatory and/or progressive disease is an

arthritis, inflammatory bowel disease (IBD), atopic dermatitis, psoriasis, or plaque psoriasis. In some embodiments, the disease or disorder may be an autoimmune disorder such as rheumatoid arthritis (RA), inflammatory bowel disease (IBD), ulcerative colitis, Crohn's disease, atopic dermatitis, eczema, alopecia areata, or a skeletal disorder such as osteoarthritis or osteoporosis. In some embodiments, the disease or disorder may be RA, psoriatic arthritis, inflammatory arthritis, ankylosing spondylitis, juvenile idiopathic arthritis, reactive arthritis, gout, septic arthritis, enteropathic arthritis, osteoarthritis, atopic dermatitis eczema, or alopecia areata. In some embodiments, the tissue repair and/or disease regression is characterised by an increased clinical repair score and/or comprises increased wound healing. In some embodiments, the inflammatory and/or progressive disease is RA, psoriatic arthritis, Crohn's disease, or ulcerative colitis.

Clinical repair scores can be used to objectively assess clinical repair in inflammatory and/or progressive diseases. Increased clinical repair score can be indicated by a decreased disease score. In some embodiments, disease control is characterised by a decreased rate of change in the disease score. In some embodiments, disease control is characterised by no change in disease score following treatment – that is, disease control may be characterised by an inhibition of disease progression associated with an increase in disease score. In some embodiments wherein the disease is an arthritis, tissue repair and/or disease regression may be characterised by a decrease in the average arthritic index score, ACR/EULAR score, DAS38 score, HAQ-DI score, CDAI score, SDAI score, ACR20/50/70 score, EULAR score, mTSS score, RAMRIS erosion score, or RAPID3 score, or any combination thereof, as described herein. In some embodiments, tissue repair and/or disease regression may be characterised by; i) a decrease in the serum concentration of C-reactive protein (CRP); ii) a decrease in serum concentration of Tartrate-resistant acid phosphatase 5 (TRAP5); iii) an increase in the serum concentration of procollagen 1 intact N-terminal (P1NP); iv) an increase in the serum concentration of osteocalcin; or v) any combination of i)-iv).

In some embodiments, the disease control, regression or tissue repair, or any combination thereof, comprises an increased cell count of reparative cells and/or a decreased cell count of pathology driving cells. In some embodiments, the disease control, regression, or tissue repair, or any combination thereof, comprises an increased count of mesenchymal and/or epithelial cells. In some embodiments, the adaptive response is characterised by an increased count of mesenchymal and/or epithelial cells. In some embodiments, the adaptive response is characterised by an increase in the differentiation of mesenchymal and/or epithelial cells. For instance, in the bone, an increase in the number and/or activity of osteoblasts, non-transformed fibroblasts or myeloid cells, or any combination thereof, may be seen. For example, an increase in the number and/or activity of M2 macrophages may be seen. In addition to, or alternatively, in the bone, a decrease in the number or activity of pathology driving cells such as osteoclasts, transformed fibroblasts, fibroblast-like synovocyte cells, proinflammatory macrophages, effector memory T-cells, plasmacytoid dendritic cells or transformed fibroblasts, or any combination thereof, may be seen. When the inflammatory

and/or progressive disease is an IBD, the reparative cells may comprise epithelial cells and/or mucus cells. For instance, in the gastrointestinal tract the cells may comprise fibroblasts or epithelial cells, or alternatively repair may be indicated by an increase in the overall number of mucus cells which indicate that epithelial differentiation is proceeding normally. In addition to, or alternatively, when the inflammatory and/or progressive disease is an IBD, the adaptive response is characterised by a decreased count of lymphocytes, macrophages or granulocytes, or any combination thereof.

In some embodiments, the tissue repair and/or disease regression comprises a decreased cell count and/or decreased function of activated immune cell subtypes. For instance, when the inflammatory and/or progressive disease is RA, the disease control, regression or tissue repair, or any combination thereof, may comprise a decrease in the number of myeloid cells such as macrophages, osteoclasts, lymphocytes such as T-, B-, or Th17 cells, or fibroblasts such as FLS cells, or any combination thereof. Preferably, the decrease in immune cell activity and/or activated immune cell numbers is not accompanied by a decrease in the activity, function or numbers of adapting mesenchymal or epithelial cells. In some embodiments, the adaptive response comprises a change in the function of mesenchymal and/or epithelial cells. For instance, in IBD the cells may comprise PAS positive cells, or surfactant producing epithelial cells.

In some embodiments, the tissue repair and/or disease regression induces a restoration of tissue architecture towards its healthy state, which is characterised by anatomically normal architecture. For example, in some embodiments, the inflammatory and/or progressive disease is an arthritis, such as RA, and the tissue repair and/or disease regression comprises increased bone formation and/or decreased bone resorption, optionally alongside reduced oedema and/or erythema. In some embodiments, disease control comprises decreased bone resorption and/or preventing further loss of anatomically normal architecture. In some embodiments, the disease control, tissue repair and/or disease regression comprises a reduction in inflammatory cytokine production from pro-inflammatory myeloid cells. In some embodiments, the disease control, tissue repair or disease regression, or any combination thereof, comprises an increase in growth factors that are important for angiogenesis, epithelialisation or matrix remodelling, or any combination thereof. For example, the disease control, tissue repair or disease regression, or any combination thereof, may comprise an increase in VEGF, FGF21 or GDF15, or any combination thereof. Cytokine and growth factor levels can be measured by any suitable method, e.g. via ELISA as described herein, or via ELISpot. In some embodiments, the disease control, tissue repair or disease regression, or any combination thereof, comprises an increase in basement collagen IV. Collagen IV levels can be measured by any suitable method, e.g. via ELISA as described herein and/or by immunohistochemical analysis.

Relatedly, the disclosure also provides a pharmaceutical composition comprising an MCIM compound for use in combination with a DMARD to increase reparative cells and/or decrease destructive cells in a subject with an inflammatory and/or progressive disease, to achieve disease control and/or tissue repair and, as a result, disease regression or resolution, or improved symptom control and quality of

life. Relatedly, the disclosure also provides a pharmaceutical composition comprising a DMARD for use in combination with an MCIM compound to increase reparative cells and/or decrease destructive cells in a subject with an inflammatory and/or progressive disease, to achieve disease control and/or tissue repair and, as a result, disease regression or resolution, or improved symptom control and quality of life. Relatedly, the disclosure also provides a pharmaceutical composition comprising an MCIM compound and a DMARD to increase reparative cells and/or decrease destructive cells in a subject with an inflammatory and/or progressive disease, to achieve disease control and/or tissue repair and, as a result, disease regression or resolution, or improved symptom control and quality of life. In some embodiments, the pharmaceutical compositions trigger an adaptive response in a subject with an inflammatory and/or progressive disease. The disclosure also provides methods for increasing reparative cells and/or decreasing destructive cells in a subject with an inflammatory and/or progressive disease, comprising administering the pharmaceutical composition to achieve disease control, tissue repair, disease regression, disease resolution, or improved symptom control and quality of life, or any combination thereof. In some embodiments, the method increases the adaptive response of mesenchymal and/or epithelial cells. In some embodiments, the method decreases the activation and/or numbers of pro-inflammatory cells, fibrotic cells, or erosive cells, or any combination thereof, in a subject with an inflammatory and/or progressive disease. Relatedly, the disclosure also provides pharmaceutical compositions for use in reducing cytokine production from pro-inflammatory myeloid cells in a subject with an inflammatory and/or progressive disease, to achieve disease control, tissue repair or disease regression, or any combination thereof. The disclosure also provides methods for reducing cytokine production from pro-inflammatory myeloid cells in a subject with an inflammatory and/or progressive disease, comprising administering the pharmaceutical composition to achieve disease control, tissue repair or disease regression, or any combination thereof. The compounds and inflammatory and/or progressive diseases are defined herein.

Preferably, the MCIM compound binds to Complex I and modulates Complex I activity. The modulation of Complex I activity may be determined by detecting a reduction in cellular O₂ consumption. In some embodiments, the reduction in cellular O₂ consumption is not associated with a reduction of cell viability. O₂ consumption may be measured by any standard technique known in the art, for example, using a real-time cell metabolic analyser (e.g. a Seahorse Analyzer). The modulation of Complex I activity may also lead to a reversible reduction of cell proliferation. The reversibility of the reduction of cell proliferation means that the reduction of proliferation is reversed when the compound is removed. This contrasts with the reduction of proliferation that is observed following treatment of the same cell type with a classical complex I binder, where reduced cell proliferation is not reversed by removal of the classical complex I binder. To assess the reversibility of the reduction of cell proliferation, an MCIM is applied to a cell culture, at a concentration to substantially reduce cell proliferation, for 24 hours at 37°C / 5% CO₂. After 24 hours, the cell culture

is washed and cultured under conditions conducive to cell growth and proliferation. Recovery of cell proliferation is measured after 24-hours incubation in these 'growth' conditions (37°C / 5% CO₂, without MCIM present). Recovery of cell proliferation is observed. This contrasts to observations made on the same cells that have undergone the same culture/wash/grow cycle with a classical

5 complex I binder in the culture step. The reversible reduction of cell proliferation may be assessed using human primary lung fibroblasts, e.g. as described in Example 4 (as illustrated in Figure 6).

Preferably, the compound interacts with Complex I at a binding site at the top of or outside the Q tunnel. In some embodiments, the binding site comprises one or more amino acid residues from NDUSF2 (SEQ ID NO: 1) and/or NDUSF7 (SEQ ID NO: 2). In some embodiments, the compound

10 interacts with at least one amino acid residues in NDUSF2 (SEQ ID NO: 1), for instance His92, Gly85, Tyr141, His88, Leu95, Asp193, or Phe458. In some embodiments, the compound interacts with one or more amino acid residues in NDUSF2 (SEQ ID NO: 1) selected from Tyr141, His92 and Asp193.

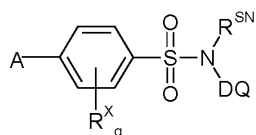
In some embodiments, the response may include promotion of a repair phenotype during the same time course as control of inflammation. The control of inflammation induced by the MCIM compounds

15 disclosed herein may be distinct from the control of inflammation induced by other anti-inflammatory drugs which rely on the suppression of inflammation before activation of tissue repair as a secondary effect.

In some embodiments, the compound comprises four or more of the pharmacophore features of the pharmacophore model represented in Figure 27. The three-dimensional arrangement of the

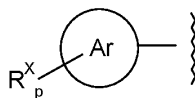
20 pharmacophore features may be as described in Tables 9-A, 9-B and 9-C.

In some embodiments, the compound is a compound, or a pharmaceutically acceptable salt, hydrate, or solvate thereof, of the following formula:



as defined in claim 1 of WO2010/032009, wherein:

-A is independently:



25

-Ar is independently phenyl, pyridinyl, or pyrimidinyl; and
p is independently an integer from 0 to 3;

and wherein:

30

q is independently an integer from 0 to 3;

and wherein:

$-R^{SN}$ is independently $-H$ or saturated aliphatic C_{1-4} alkyl;

and wherein:

5 $-DQ$ is independently $-D^1-Q^1$ or $-D^2=O$;

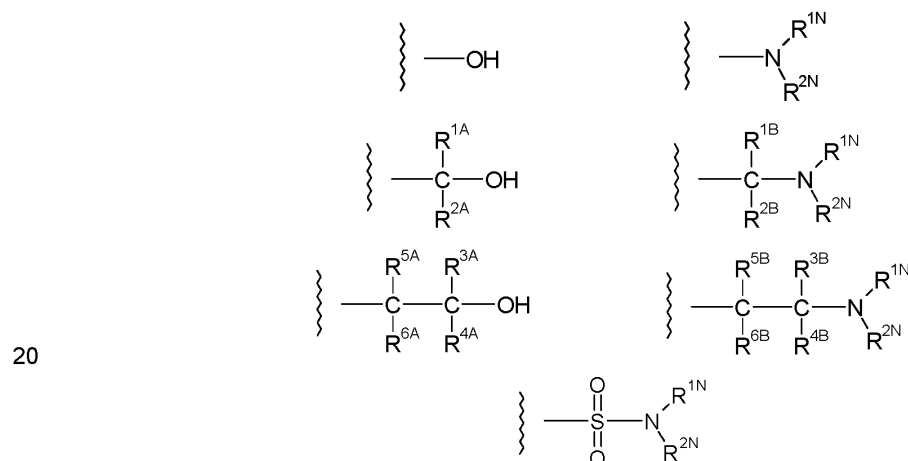
$-D^1-$ is independently cyclopentane-di-yl, cyclohexane-di-yl, cycloheptane-di-yl, bicyclo[3.1.1]heptane-di-yl, or bicyclo[3.2.1]octane-di-yl, and is optionally substituted with one or more groups $-R^D$;

10 $-D^2=$ is independently cyclopentane-yl-ylidene, cyclohexane-yl-ylidene, cycloheptane-yl-ylidene, bicyclo[3.1.1]heptane-yl-ylidene, or bicyclo[3.2.1]octane-yl-ylidene, and is optionally substituted with one or more groups $-R^D$;

each $-R^D$ is independently selected from $-F$, $-Cl$, $-Br$, $-I$, $-R^{DD}$, $-CF_3$, $-OH$, $-OR^{DD}$, $-NH_2$, $-NHR^{DD}$, and $-NR^{DD}_2$; and

15 each $-R^{DD}$ is independently saturated aliphatic C_{1-4} alkyl;

and wherein $-Q^1$ is independently selected from:



wherein:

25 each $-R^{1N}$ is independently $-H$, $-R^{CN}$, or $-R^{CF}$;

each $-R^{2N}$ is independently $-H$, $-R^{CN}$, or $-R^{CF}$;

each $-R^{CN}$ is independently saturated aliphatic C_{1-4} alkyl; and

each $-R^{CF}$, if present, is independently saturated aliphatic C_{1-4} fluoroalkyl;

or:

30 $-NR^{1N}R^{2N}$ is independently azetidino, pyrrolidino, imidazolidino, pyrazolidino, piperidino, piperazino, morpholino, thiomorpholino, azepino, or diazepino, each optionally substituted with one or more groups independently selected from saturated aliphatic C_{1-4} alkyl;

-R^{1A} is independently -H, -R^C, or -R^F; and
-R^{2A} is independently -H, -R^C, or -R^F;
or -R^{1A} and -R^{2A} together form a saturated aliphatic C₂₋₄alkylene group;

5 -R^{1B} is independently -H, -R^C, or -R^F; and
 -R^{2B} is independently -H, -R^C, or -R^F;
 or -R^{1B} and -R^{2B} together form a saturated aliphatic C₂₋₄alkylene group;
 or -R^{1B} and -R^{2B} together form =O;

10 -R^{3A} is independently -H, -R^C, or -R^F; and
 -R^{4A} is independently -H, -R^C, or -R^F;
 or -R^{3A} and -R^{4A} together form a saturated aliphatic C₂₋₄alkylene group;

 -R^{5A} is independently -H, -R^C, -R^F, or -R^J; and
15 -R^{6A} is independently -H, -R^C, or -R^F;
 or -R^{5A} and -R^{6A} together form a saturated aliphatic C₂₋₄alkylene group;

 -R^{3B} is independently -H, -R^C, or -R^F; and
 -R^{4B} is independently -H, -R^C, or -R^F;
20 or -R^{3B} and -R^{4B} together form a saturated aliphatic C₂₋₄alkylene group;

 -R^{5B} is independently -H, -R^C, -R^F, -OH, or -OR^O; and
 -R^{6B} is independently -H, -R^C, or -R^F;
 or -R^{5B} and -R^{6B} together form a saturated aliphatic C₂₋₄alkylene group;

25 each -R^C is independently saturated aliphatic C₁₋₄alkyl;
 each -R^F is independently saturated aliphatic C₁₋₄fluoroalkyl;
 -R^O is independently saturated aliphatic C₁₋₄alkyl;
 -R^J is independently -NH₂, -NHR^{JN1}, -NR^{JN1}₂, or -NR^{JN2}R^{JN3};
30 each -R^{JN1} is independently saturated aliphatic C₁₋₄alkyl; and
 -NR^{JN2}R^{JN3} is independently azetidino, pyrrolidino, imidazolidino, pyrazolidino,
piperidino, piperazino, morpholino, thiomorpholino, azepino, or diazepino, each
optionally substituted with one or more groups independently selected from saturated
aliphatic C₁₋₄alkyl;

35 and wherein each -R^X is independently:
 -F, -Cl, -Br, -I,

 -R^{XX},
 -OH, -OR^{XX},
40 -SH, -SR^{XX},
 -CF₃, -OCF₃, -SCF₃,

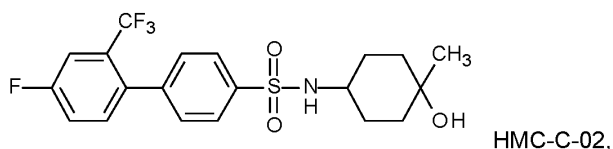
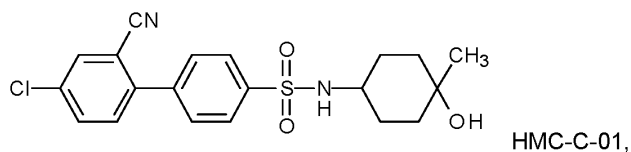
- NH₂, -NHR^{XX}, -NR^{XX}₂, -NR^{YY}R^{ZZ},
 -C(=O)R^{XX}, -OC(=O)R^{XX},
 -C(=O)OH, -C(=O)OR^{XX},
 -C(=O)NH₂, -C(=O)NHR^{XX}, -C(=O)NR^{XX}₂, -C(=O)NR^{YY}R^{ZZ},
 -OC(=O)NH₂, -OC(=O)NHR^{XX}, -OC(=O)NR^{XX}₂, -OC(=O)NR^{YY}R^{ZZ},
 -NHC(=O)R^{XX}, -NR^{XX}C(=O)R^{XX},
 -NHC(=O)OR^{XX}, -NR^{XX}C(=O)OR^{XX},
 -NHC(=O)NH₂, -NHC(=O)NHR^{XX}, -NHC(=O)NR^{XX}₂, -NHC(=O)NR^{YY}R^{ZZ},
 -NR^{XX}C(=O)NH₂, -NR^{XX}C(=O)NHR^{XX}, -NR^{XX}C(=O)NR^{XX}₂, -NR^{XX}C(=O)NR^{YY}R^{ZZ},
 -CN,
 -NO₂,
 -S(=O)₂NH₂, -S(=O)₂NHR^{XX}, -S(=O)₂NR^{XX}₂, -S(=O)₂NR^{YY}R^{ZZ},
 -S(=O)R^{XX}, -S(=O)₂R^{XX}, -OS(=O)₂R^{XX}, -S(=O)₂OH, or -S(=O)₂OR^{XX};

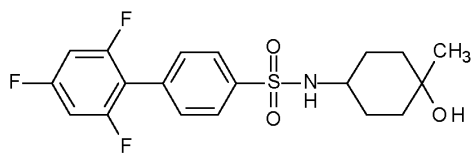
wherein:

- each -R^{XX} is independently saturated aliphatic C₁₋₆alkyl, phenyl, or benzyl,
 wherein said phenyl and benzyl are optionally substituted with one or more groups
 selected from: -F, -Cl, -Br, -I, -CF₃, -OCF₃, -R^{XXX}, -OH, -OR^{XXX}, or -SR^{XXX}, wherein
 each -R^{XXX} is independently saturated aliphatic C₁₋₄alkyl; and
 each -NR^{YY}R^{ZZ} is independently azetidino, pyrrolidino, imidazolidino,
 pyrazolidino, piperidino, piperazino, morpholino, thiomorpholino, azepino, or
 diazepino, each optionally substituted with one or more groups independently
 selected from saturated aliphatic C₁₋₄alkyl.

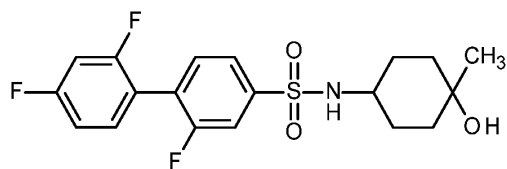
Claim 1 of WO2010/032009 is hereby incorporated by reference. Furthermore, WO2010/032009 is hereby incorporated by reference in its entirety.

- In one embodiment, the compound is a compound, or a pharmaceutically acceptable salt, hydrate, or
 solvate thereof as defined in WO2014/207445 A1, which is incorporated herein by reference in its
 entirety. For example, in some embodiments, the compound is a compound selected from
 compounds of the following formulae, or a pharmaceutically acceptable salt, hydrate, or solvate
 thereof:

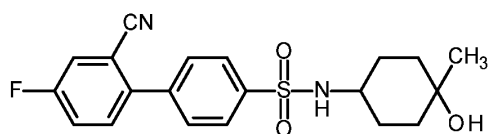




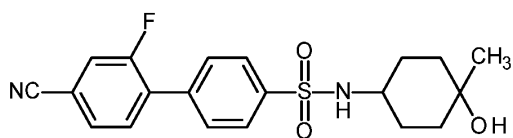
HMC-C-03,



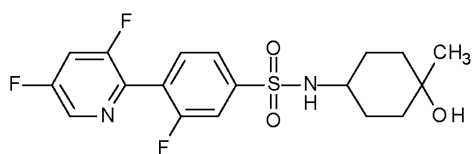
HMC-C-04,



HMC-C-05,

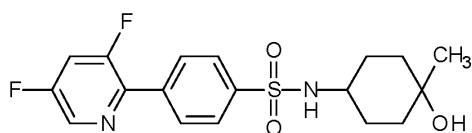


HMC-C-06,

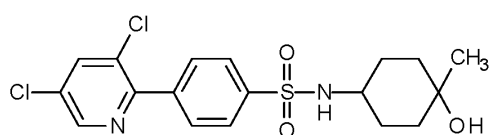


5

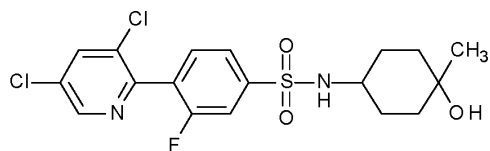
HMC-N-01,



HMC-N-02,

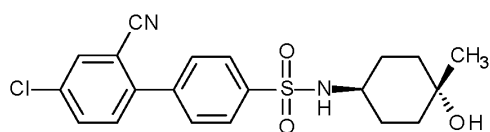


HMC-N-03, and



HMC-N-04.

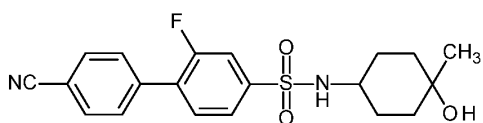
10 In some embodiments, the compound is a compound of the following formula, or a pharmaceutically acceptable salt, hydrate, or solvate thereof:



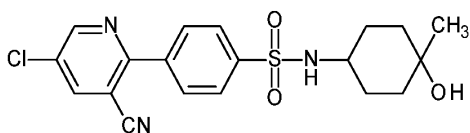
HMC-C-01-A.

In one embodiment, the compound is a compound, or a pharmaceutically acceptable salt, hydrate, or solvate thereof as defined in WO2016/097001 A1, which is incorporated herein by reference in its entirety. For example, in some embodiments, the compound is a compound selected from

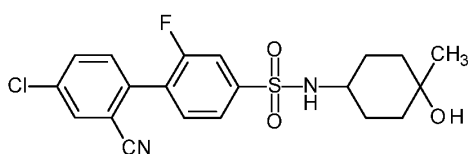
- 5 compounds of the following formulae, or a pharmaceutically acceptable salt, hydrate, or solvate thereof:



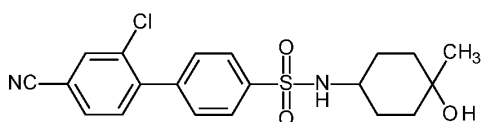
HMC-C-07.



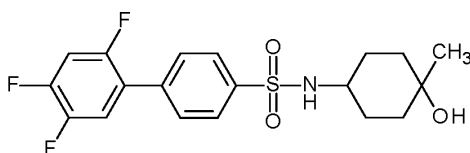
HMC-N-05,



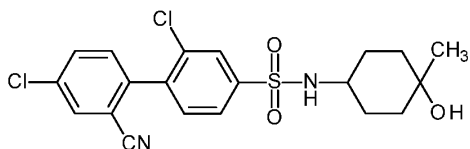
HMC-C-08,



HMC-C-09,



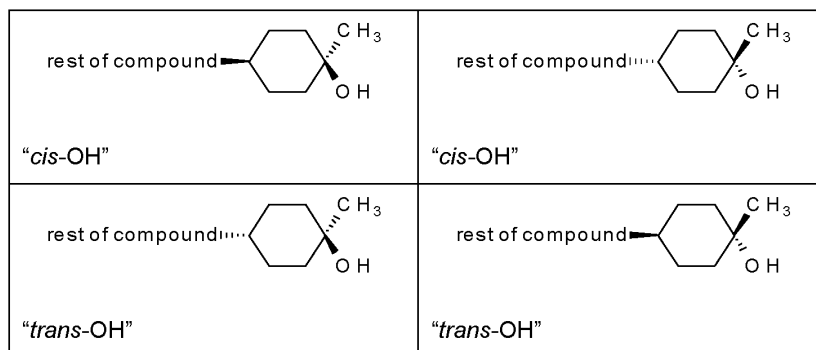
HMC-C-10, and



HMC-C-11.

Note for the "HMC" compounds as defined in WO2014/207445 A1 and WO2016/097001 A1, and as described above, the substituents on one side of the cyclohexyl ring (i.e., OH and CH₃ on the right-hand side) may be positioned "trans" / "cis" or "cis" / "trans" with respect to the rest of the molecule

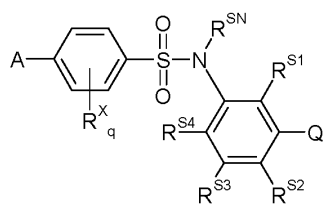
(that is, on the cyclohexyl ring to which they attached, with respect to the rest of the compound which is attached at the para position of the cyclohexyl ring).



Unless otherwise indicated, it is intended that all such conformations are encompassed by a

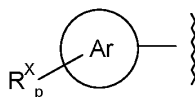
5 reference to a compound that does not specify a particular conformation.

In some embodiments, the compound is a compound, or a pharmaceutically acceptable salt, hydrate, or solvate thereof, of the following formula:



as defined in claim 1 of WO2010/032010, wherein:

-A is independently:



10

-Ar is independently phenyl, pyridinyl, or pyrimidinyl; and
p is independently an integer from 0 to 3;

and wherein:

15

q is independently an integer from 0 to 3;

and wherein:

-R^{SN} is independently -H or saturated aliphatic C₁₋₄alkyl;

20

and wherein:

-R^{S1} is independently -H or saturated aliphatic C₁₋₄alkyl;

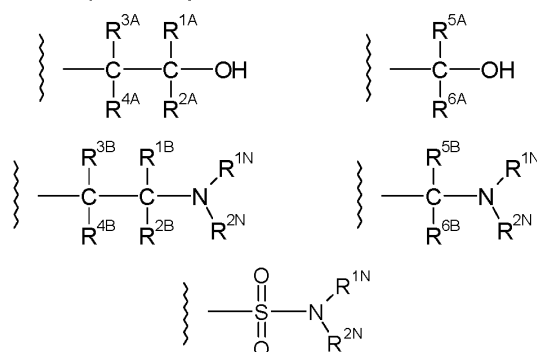
-R^{S2} is independently -H or saturated aliphatic C₁₋₄alkyl;

-R^{S3} is independently -H or saturated aliphatic C₁₋₄alkyl;

$-R^{S4}$ is independently -H or saturated aliphatic C_{1-4} alkyl;

and wherein -Q is independently selected from:

5



wherein:

10

each $-R^{1N}$ is independently -H or $-R^{CN}$;
 each $-R^{2N}$ is independently -H or $-R^{CN}$;
 each $-R^{CN}$ is independently saturated aliphatic C_{1-4} alkyl;
 or:

15

$-\text{NR}^{1N}\text{R}^{2N}$ is independently azetidino, pyrrolidino, imidazolidino, pyrazolidino, piperidino, piperazino, morpholino, thiomorpholino, azepino, or diazepino, each optionally substituted with one or more groups independently selected from saturated aliphatic C_{1-4} alkyl;

20

$-R^{1A}$ is independently -H, $-R^C$, or $-R^F$; and
 $-R^{2A}$ is independently -H, $-R^C$, or $-R^F$;
 or $-R^{1A}$ and $-R^{2A}$ together form a saturated aliphatic C_{2-4} alkylene group;

25

$-R^{3A}$ is independently $-R^C$, $-R^F$, or $-R^J$; and
 $-R^{4A}$ is independently -H, $-R^C$, or $-R^F$;
 or $-R^{3A}$ and $-R^{4A}$ together form a saturated aliphatic C_{2-4} alkylene group;

30

$-R^{5A}$ is independently $-R^C$ or $-R^F$; and
 $-R^{6A}$ is independently -H, $-R^C$, or $-R^F$;
 or $-R^{5A}$ and $-R^{6A}$ together form a saturated aliphatic C_{2-4} alkylene group;

35

$-R^{3B}$ is independently -H, $-R^C$, $-R^F$, -OH, or $-\text{OR}^O$; and

-R^{4B} is independently -H, -R^C, or -R^F;
or -R^{3B} and -R^{4B} together form a saturated aliphatic C₂₋₄alkylene group;

-R^{5B} is independently -H, -R^C, or -R^F; and
-R^{6B} is independently -H, -R^C, or -R^F;
or -R^{5B} and -R^{6B} together form a saturated aliphatic C₂₋₄alkylene group;

each -R^C is independently saturated aliphatic C₁₋₄alkyl;
each -R^F is independently saturated aliphatic C₁₋₄fluoroalkyl;
-R^O is independently saturated aliphatic C₁₋₄alkyl;
-R^J is independently -NH₂, -NHR^{JN1}, -NR^{JN1}₂, or -NR^{JN2}R^{JN3};
each -R^{JN1} is independently -R^{J1}, -R^{J2}-OH, -R^{J2}-O-R^{J1};
each -R^{J1} is independently saturated aliphatic C₁₋₄alkyl;
each -R^{J2}- is independently saturated aliphatic C₂₋₄alkylene;

-NR^{JN2}R^{JN3} is independently azetidino, pyrrolidino, imidazolidino, pyrazolidino,
piperidino, piperazino, morpholino, thiomorpholino, azepino, or diazepino, each
optionally substituted with one or more groups independently selected from saturated
aliphatic C₁₋₄alkyl;

and wherein each -R^X is independently:

-F, -Cl, -Br, -I,
-R^{XX},
-OH, -OR^{XX},
-SH, -SR^{XX},
-CF₃, -OCF₃, -SCF₃,
-NH₂, -NHR^{XX}, -NR^{XX}₂, -NR^{YY}R^{ZZ},
-C(=O)R^{XX}, -OC(=O)R^{XX},
-C(=O)OH, -C(=O)OR^{XX},
-C(=O)NH₂, -C(=O)NHR^{XX}, -C(=O)NR^{XX}₂, -C(=O)NR^{YY}R^{ZZ},
-OC(=O)NH₂, -OC(=O)NHR^{XX}, -OC(=O)NR^{XX}₂, -OC(=O)NR^{YY}R^{ZZ},
-NHC(=O)R^{XX}, -NR^{XX}C(=O)R^{XX},
-NHC(=O)OR^{XX}, -NR^{XX}C(=O)OR^{XX},
-NHC(=O)NH₂, -NHC(=O)NHR^{XX}, -NHC(=O)NR^{XX}₂, -NHC(=O)NR^{YY}R^{ZZ},
-NR^{XX}C(=O)NH₂, -NR^{XX}C(=O)NHR^{XX}, -NR^{XX}C(=O)NR^{XX}₂, -NR^{XX}C(=O)NR^{YY}R^{ZZ},
-CN,
-NO₂,
-S(=O)₂NH₂, -S(=O)₂NHR^{XX}, -S(=O)₂NR^{XX}₂, -S(=O)₂NR^{YY}R^{ZZ},
-S(=O)R^{XX}, -S(=O)₂R^{XX}, -OS(=O)₂R^{XX}, -S(=O)₂OH, or -S(=O)₂OR^{XX};
wherein:

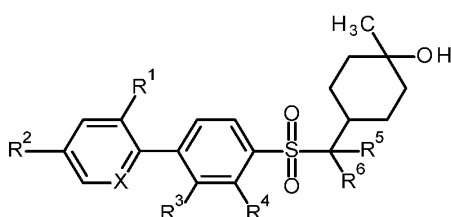
each -R^{XX} is independently saturated aliphatic C₁₋₆alkyl, phenyl, or benzyl,
wherein said phenyl and benzyl are optionally substituted with one or more groups

selected from: -F, -Cl, -Br, -I, -CF₃, -OCF₃, -R^{XXX}, -OH, -OR^{XXX}, or -SR^{XXX}, wherein each -R^{XXX} is independently saturated aliphatic C₁₋₄alkyl; and

- each -NR^{YY}R^{ZZ} is independently azetidino, pyrrolidino, imidazolidino, pyrazolidino, piperidino, piperazino, morpholino, thiomorpholino, azepino, or diazepino, each optionally substituted with one or more groups independently selected from saturated aliphatic C₁₋₄alkyl.

Claim 1 of WO2010/032010 is hereby incorporated by reference. Furthermore, WO2010/032010 is hereby incorporated by reference in its entirety.

- In some embodiments, the compound is a compound, or a pharmaceutically acceptable salt, hydrate, or solvate thereof, of the following formula:



as defined in claim 1 of WO2020/035560 A1, wherein:

=X- is independently -CH= or -N=;

- R¹ is independently -H or -R^{1X};
- R^{1X} is independently -F, -Cl, -R^{1C}, -R^{1F}, or -CN;
- R^{1C} is independently saturated linear or branched C₁₋₃alkyl;
- R^{1F} is independently saturated linear or branched C₁₋₃fluoroalkyl;
- R² is independently -H or -R^{2X};
- R^{2X} is independently -F, -Cl, -R^{2C}, -R^{2F}, or -CN;
- R^{2C} is independently saturated linear or branched C₁₋₃alkyl;
- R^{2F} is independently saturated linear or branched C₁₋₃fluoroalkyl;
- R³ is independently -H or -R^{3X};
- R^{3X} is independently -F, -Cl, -R^{3C}, -R^{3F}, or -CN;
- R^{3C} is independently saturated linear or branched C₁₋₃alkyl;
- R^{3F} is independently saturated linear or branched C₁₋₃fluoroalkyl;
- R⁴ is independently -H or -R^{4X};
- R^{4X} is independently -F, -Cl, -R^{4C}, -R^{4F}, or -CN;
- R^{4C} is independently saturated linear or branched C₁₋₃alkyl;
- R^{4F} is independently saturated linear or branched C₁₋₃fluoroalkyl;

- R⁵ is independently -H or -R^{5X};
- R^{5X} is independently -F, -R^{5C}, or -R^{5F};
- R^{5C} is independently saturated linear or branched C₁₋₃alkyl;
- R^{5F} is independently saturated linear or branched C₁₋₃fluoroalkyl;

5

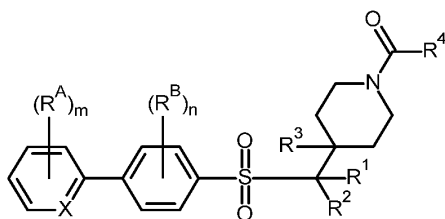
- R⁶ is independently -H or -R^{6X};
- R^{6X} is independently -F, -R^{6C}, or -R^{6F};
- R^{6C} is independently saturated linear or branched C₁₋₃alkyl; and
- R^{6F} is independently saturated linear or branched C₁₋₃fluoroalkyl;

10

or -R⁵ and -R⁶, taken together with the carbon atom to which they are attached, form saturated C₃₋₆cycloalkyl.

Claim 1 of WO2020/035560 A1 is hereby incorporated by reference. Furthermore, WO2020/035560 A1 is hereby incorporated by reference in its entirety.

- 15 In some embodiments, the compound is a compound, or a pharmaceutically acceptable salt, hydrate, or solvate thereof, of the following formula:



as defined in claim 1 of WO2020/212581 A1, wherein:

- X= is independently -CH= or -N=;
- "m" is independently 0, 1, 2, or 3;
- each -R^A is independently -F, -Cl, -R^{AC}, -R^{AF}, or -CN;
- R^{AC} is independently saturated linear or branched C₁₋₃alkyl;
- R^{AF} is independently saturated linear or branched C₁₋₃fluoroalkyl;
- "n" is independently 0, 1, or 2;
- each -R^B is independently -F, -Cl, -R^{BC}, -R^{BF}, or -CN;
- R^{BC} is independently saturated linear or branched C₁₋₃alkyl;
- R^{BF} is independently saturated linear or branched C₁₋₃fluoroalkyl;
- R¹ is independently -H or -R^{1X};
- R^{1X} is independently -F, -R^{1C}, or -R^{1F};
- R^{1C} is independently saturated linear or branched C₁₋₃alkyl;
- R^{1F} is independently saturated linear or branched C₁₋₃fluoroalkyl;

20

25

30

-R² is independently -H or -R^{2X};

-R^{2X} is independently -F, -R^{2C}, or -R^{2F};

-R^{2C} is independently saturated linear or branched C₁₋₃alkyl;

5 -R^{2F} is independently saturated linear or branched C₁₋₃fluoroalkyl;

or -R¹ and -R², taken together with the carbon atom to which they are attached, form saturated C₃₋₆cycloalkyl;

10 -R³ is independently -H or -R^{3X};

-R^{3X} is independently -R^{3C} or -R^{3F};

-R^{3C} is independently saturated linear or branched C₁₋₃alkyl;

-R^{3F} is independently saturated linear or branched C₁₋₃fluoroalkyl;

15 -R⁴ is independently -R^{4C}, -R^{4CC}, or -N(R^{4N1})(R^{4N2});

-R^{4C} is independently saturated linear or branched C₁₋₆alkyl;

-R^{4CC} is independently saturated C₃₋₆cycloalkyl;

-R^{4N1} is independently -H or -R^{4N1C};

-R^{4N1C} is independently saturated linear or branched C₁₋₄alkyl;

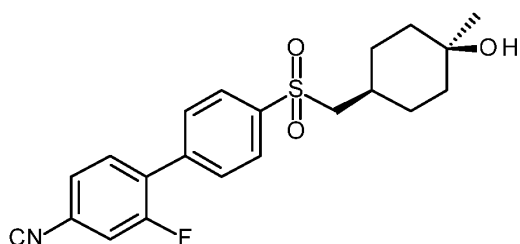
20 -R^{4N2} is independently -H or -R^{4N2C}; and

-R^{4N2C} is independently saturated linear or branched C₁₋₄alkyl,

or -N(R^{4N1})(R^{4N2}) is independently azetidiny, pyrrolidiny, piperidiny, piperaziny, or morpholiny, and is optionally substituted with one or more saturated linear or branched C₁₋₄alkyl groups.

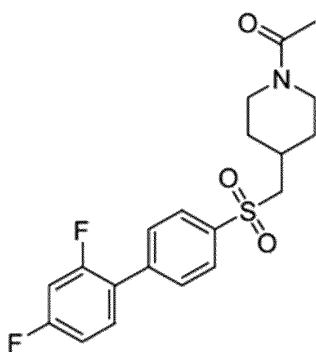
25 Claim 1 of WO2020/212581 A1 is hereby incorporated by reference. Furthermore, WO2020/212581 A1 is hereby incorporated by reference in its entirety.

In some embodiments, the compound is a compound of the following formula, or a pharmaceutically acceptable salt, hydrate, or solvate thereof:



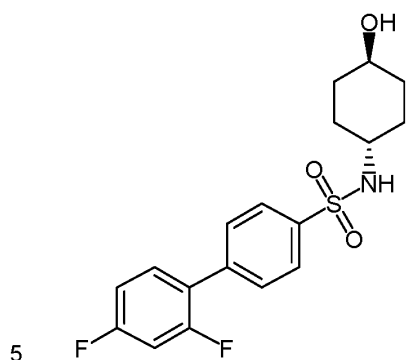
CHMSA-01-A.

30 In some embodiments, the compound is a compound of the following formula, or a pharmaceutically acceptable salt, hydrate, or solvate thereof:



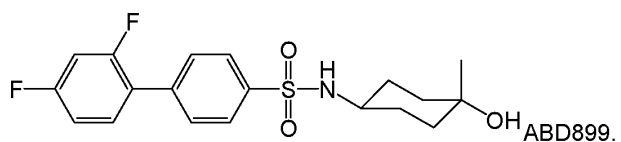
NASMP-01-A.

In some embodiments, the compound is a compound of the following formula, or a pharmaceutically acceptable salt, hydrate, or solvate thereof:



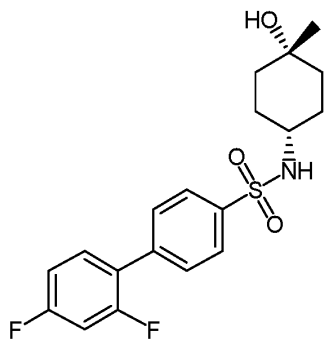
ABD599.

In some embodiments, the compound is a compound of the following formula, or a pharmaceutically acceptable salt, hydrate, or solvate thereof:



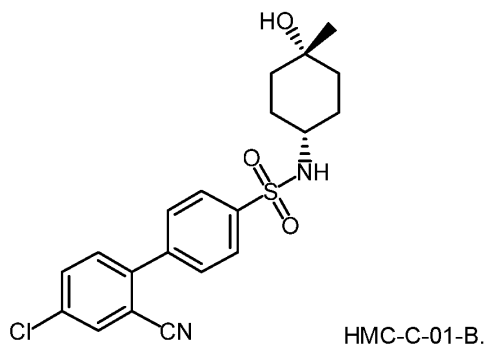
ABD899.

10 In some embodiments, the compound is a compound of the following formula, or a pharmaceutically acceptable salt, hydrate, or solvate thereof:

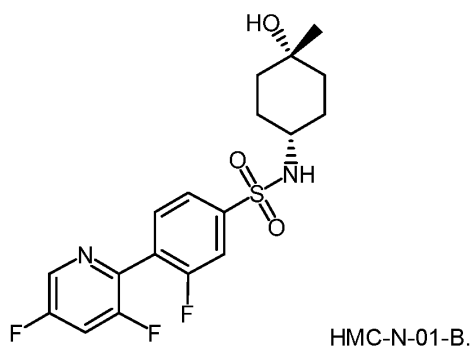


ABD900.

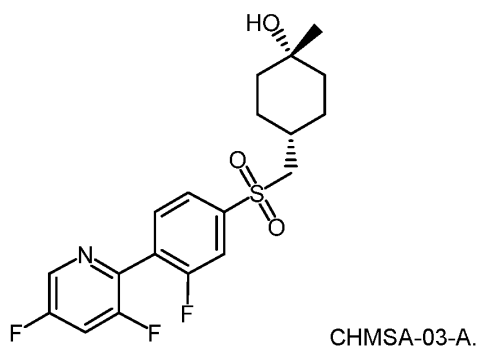
In some embodiments, the compound is a compound of the following formula, or a pharmaceutically acceptable salt, hydrate, or solvate thereof:



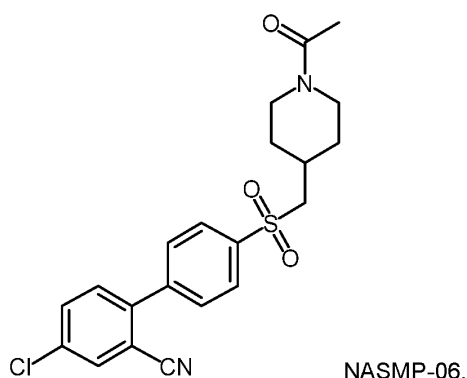
- 5 In some embodiments, the compound is a compound of the following formula, or a pharmaceutically acceptable salt, hydrate, or solvate thereof:



In some embodiments, the compound is a compound of the following formula, or a pharmaceutically acceptable salt, hydrate, or solvate thereof:



- 10 In some embodiments, the compound is a compound of the following formula, or a pharmaceutically acceptable salt, hydrate, or solvate thereof:



In some embodiments of the above aspects, the DMARD may comprise a conventional synthetic DMARD (csDMARD), targeted synthetic DMARD (tsDMARD), or a biological DMARD (bDMARD), or
5 a combination of any of the foregoing.

In some embodiments of the above aspects, the DMARD may comprise methotrexate, sulfasalazine, azathioprine, chloroquine, D-penicillamine, gold salts, sodium aurothiomalate, auranofin, hydroxychloroquine, leflunomide, minocycline, cyclosporin, abatacept, adalimumab, anakinra, certolizumab pegol, etanercept, golimumab, infliximab, rituximab, sarilumab, secukinumab,
10 tocilizumab, ustekinumab, apremilast, guselkumab, risankizumab, deucravacitinib, ixekizumab, bimekizumab, baricitinib, filgotinib, or tofacitinib, or any combination of the foregoing.

In preferred embodiments of the above aspects, the DMARD comprises a csDMARD. In some embodiments, the csDMARD comprises azathioprine, chloroquine, D-penicillamine, gold salts, sodium aurothiomalate, auranofin, hydroxychloroquine, leflunomide, methotrexate, minocycline,
15 sulfasalazine, or ciclosporin, or a combination of any of the foregoing. In preferred embodiments, the csDMARD comprises methotrexate, sulfasalazine, hydroxychloroquine, leflunomide, azathioprine, or any combination thereof.

In some embodiments of the above aspects, the pharmaceutical combinations, compositions or methods comprise two or more DMARDs. In some embodiments, combinations, compositions or
20 methods comprise a methotrexate and leflunomide. In some embodiments, combinations, compositions or methods comprise methotrexate and sulfasalazine. In some embodiments, the combinations, compositions or methods comprise a combination of methotrexate, sulfasalazine and hydroxychloroquine.

In some embodiments of the above aspects, the pharmaceutical combinations, compositions or
25 methods comprise the csDMARD methotrexate and a bDMARD, for example rituximab or abatacept, or tsDMARD.

The invention includes the combination of the aspects and preferred features described except where such a combination is clearly impermissible or expressly avoided.

Summary of the Figures

- 5 Embodiments and experiments illustrating the principles of the invention will now be discussed with reference to the accompanying figures in which:

Figure 1. A graph of response over time of each of the three phases of repair (Inflammation, proliferation and tissue remodelling) which are proposed to be broadly similar across tissues. Cell types and soluble factors involved in each phase are shown below the graph along with changes in
10 the extracellular matrix.

Figure 2. High throughput integrative biology platform (BioMAP®) profile of the effects of MCIM compounds on multiple disease-associated regulatory pathways identified that these compounds have the potential to regulate inflammatory responses and the tissue remodelling collagen, collagen type IV, for ABD599 (A) and HMC-C-01-A (B) and (C).

- 15 **Figure 3.** High throughput integrative biology platform (BioMAP®) profile of the effects of approved conventional disease modifying drugs (A) the csDMARD methotrexate (X) and the csDMARD sulfasalazine (●), (B) the tsDMARD tocilizumab (X) and the csDMARD prednisolone (●), (C) the bDMARD abatacept, and (D) HMC-C-01-A (X) and the tsDMARD apremilast (●), (E) the bDMARD etanercept (X) and the bDMARD adalimumab (●), (F) the tsDMARD tofacitinib (X) and the tsDMARD
20 baricitinib (●) and (G) the bDMARD ustekinumab on multiple disease-associated regulatory pathways identified that the compounds show specific and differentiated effects on inflammatory responses and on Type I collagen.

- Figure 4.** Electron micrographs of human primary myeloid cells (osteoclasts) treated with MCIM compounds show an adaptive response by changing mitochondrial morphology, with an increase in
25 mitochondrial area without an overt increase in mitochondrial mass.

- Figure 5.** A) Three graphs showing the change in intracellular ATP levels (top left), nuclei count (top middle) and ATP readout per cell (top right) in response to increasing MCIM compound dose in standard, glucose supplemented media (squares), media supplemented with glucose and L-glutamine (open circles) or media supplemented with glucose, L-glutamine, and pyruvate (close circles). B) A
30 graph showing the change in VEGF secretion in response to increasing MCIM compound concentration in standard, glucose and L-glutamine supplemented media containing pyruvate (closed circles), or medium containing glucose and L-glutamine but without pyruvate (open circles). MCIM compounds promote an adaptive response by increasing VEGF secretion in metabolically restricted human primary lung fibroblasts without a change in cell number.

Figure 6. Cell proliferation inhibition measured by BrdU incorporation (A) and nucleic count (B) as a function of increasing dosage of either Rotenone (squares), IACS-010759 (closed circles) or MCIM compound (open circles). Comparison of cells without washout vs washout of test compounds on cell proliferation measure by BrdU incorporation (C) and nuclei count (D). Non-washout and washout of rotenone are shown in grey and open grey, respectively. Non-washout and washout of IACS-010759 are shown in black and open black, respectively. Non-washout and washout of MCIM compound are shown in checkboard fill and open fill pattern, respectively. MCIM compounds reversibly inhibit cell proliferation whereas cells treated with typical Complex I inhibitors IACS-010759 and rotenone do not recover cell proliferative capacity after compound washing out.

Figure 7. Seven graphs each showing the average arthritic index as a function of time (dosing day) for test compound dosed at 10 mg/kg/day by oral gavage (open circles) and control (solid circles), for each of (A) HMC-C-02-A, (B) HMC-C-01-A, (C) HMC-N-02-A, (D) HMC-N-01-A, (E) NASMP-01-A, (F) CHMSA-01-A, (G) CHMSA-03-A.

Figure 8. Graphs showing the average bone resorption counts (A) and average bone resorption foci (B) in mice with collagen-induced arthritis treated with (A) vehicle control, 3 mg/kg/day etanercept (a bDMARD), or 10 mg/kg/day of either HMC-C-01-A, HMC-C-01-B, or HMC-N-01-B, and (B) vehicle control, or 10 mg/kg/day of either ABD900, NASMP-01, CHMSA-03-A, or NASMP-06. MCIM compounds protect against bone resorption in mice suffering from collagen-induced arthritis at levels comparable or exceeding the approved treatment etanercept. Data are mean $\pm$ s.e.m.. ** $p < 0.01$ *** $p < 0.005$ vs vehicle §§§ $p < 0.005$ vs etanercept.

Figure 9. Graphs showing the (A) average osteoid counts in mice with collagen-induced arthritis treated with vehicle control, 3 mg/kg/day etanercept, or 10 mg/kg/day of either HMC-C-01-A, HMC C 01 B, or HMC N 01 B, (B) average osteoid zones in mice with collagen-induced arthritis treated with vehicle control, or 10 mg/kg/day of either ABD900, NASMP-01, CHMSA-03-A, or NASMP-06, and (C) vehicle control or tofacitinib. MCIM compounds promote the formation of osteoid, an indicator of bone formation, in mice with established collagen-induced arthritis. The new bone formation in animals with existing bone erosion indicates a repair effect, occurring to a much greater extent than seen with the approved therapeutic drugs etanercept. Data are mean $\pm$ s.e.m.. ** $p < 0.01$ *** $p < 0.005$ vs vehicle §§§ $p < 0.005$ vs etanercept.

Figure 10. Histological sections (160x magnification, stained with toluidine blue) of limbs from mice with collagen-induced arthritis treated with either vehicle control (top panels), 10 mg/kg/day MCIM compound (middle panels) or 3 mg/kg/day etanercept (bottom panels). MCIM compounds promote bone formation in established arthritis, indicating an adaptive repair response. Top panel shows bone from collagen-induced arthritic mice treated with vehicle showing no clear signs of bone formation. Middle panel shows bone from collagen-induced arthritis mice which have clear indications of osteoid

(new bone) formation in a structured manner as indicated by the black arrows. In contrast, mice treated with etanercept show only low levels of reactive and sporadic new bone formation.

Figure 11. Graph showing the relative inflammatory (left two bars) and osteoid (right two bars) scores in mice with collagen-induced arthritis treated with either vehicle control or a very low dose MCIM compound at 0.03 mg/kg per day for 14 days. MCIM compounds promote adaptive responses leading to repair (osteoid formation) in mice with established collagen-induced arthritis at doses which don't control inflammation, showing that the response is not a consequence of control of inflammation, but an independent, adaptive response. Data are mean $\pm$ s.e.m.. *** $p < 0.005$ vs vehicle.

Figure 12. Graphs showing the mean change in (A) synovitis score (B) cartilage damage, (C) bone resorption and (D) bone pathology in mice with collagen-induced arthritis treated with either 1 mg/kg/day etanercept, 0.03 mg/kg/day MCIM compound or a combination of 1 mg/kg/day etanercept and 0.03 mg/kg/day MCIM compound. Mean changes were calculated relative to mice with collagen-induced arthritis treated with vehicle control. Data are mean $\pm$ s.e.m.. * $p < 0.05$ ** $p < 0.01$ vs vehicle.

Figure 13. Graph showing the mean change in osteoid score in mice with collagen-induced arthritis treated with either 3 mg/kg/day etanercept (black bar), 0.03 mg/kg/day MCIM compound (white bar) or a combination of 3 mg/kg/day etanercept and 0.03 mg/kg/day (grey bar). Mean changes were calculated relative to mice with collagen-induced arthritis treated with vehicle control. Data are mean fold increase above vehicle control.

Figure 14. Graphs showing the mean change in arthritic index (A), synovitis score (B), resorption score (C) and osteoid score (D) in mice with collagen-induced arthritis. Mice were treated with either tofacitinib (a tsDMARD) or MCIM compound, HMC-C-01-A, alone, or a combination of tofacitinib and MCIM compound. The doses were selected to show low effects on clinical signs of disease (arthritic index). The MCIM compound promotes osteoid formation to a greater degree than tofacitinib, despite equivalent effects on arthritic index and synovitis (joint inflammation). In addition, the combination of MCIM compounds and tofacitinib promotes osteoid formation, protects against bone resorption and synovitis and significantly reduces the overall arthritic score compared in mice suffering from collagen-induced arthritis at levels exceeding tofacitinib or MCIM compound alone. Data are mean $\pm$ s.e.m.. * $p < 0.05$, ** $p < 0.01$ *** $p < 0.005$ vs vehicle, § $p < 0.05$, §§ $p < 0.01$, §§§ $p < 0.005$ combination vs tofacitinib.

Figure 15. Graphs showing the (A) change in serum C-reactive protein (CRP) in mg/L, (B) percent change in Tartrate-resistant acid phosphatase (TRAP) 5, (C) percent change in procollagen 1 intact N-terminal (P1NP), and (D) osteocalcin in patients treated with HMC-C-01-A in combination with methotrexate.

Figure 16. A graph showing the mean change in the biomarkers CRP, TRAP5 and osteocalcin (A) and P1NP (B) in patients receiving a combination of HMC-C-01-A and methotrexate therapy.

Figure 17. A graph showing a comparison of disease activity index in mice with DSS-induced colitis treated with vehicle control, sulfasalazine, etanercept and MCIM compound. MCIM compounds reduce the severity of symptoms of mice with DSS-induced colitis compared to mice treated with vehicle control, sulfasalazine or etanercept. Data are mean $\pm$ s.e.m.. * $p < 0.05$, *** $p < 0.005$ vs vehicle, §§§ $p < 0.005$ vs sulfasalazine, ^{aaa} $p < 0.005$ vs etanercept.

Figure 18. Two graphs showing a comparison of mucosal erosion in mice with DSS-induced colitis treated with (A) vehicle control, sulfasalazine or ABD900 and (B) vehicle control, sulfasalazine or HMC-C-01-A. MCIM compounds inhibit mucosal erosion to a greater extent in mice with established DSS-induced colitis compared to mice treated with vehicle control, sulfasalazine (A), or etanercept (B). Data are mean $\pm$ s.e.m.. * $p < 0.05$ vs vehicle § $p < 0.05$ vs sulfasalazine.

Figure 19. Two graphs showing a comparison of glandular loss in mice with DSS-induced colitis treated with (A) vehicle control, sulfasalazine or ABD900 and (B) vehicle control, sulfasalazine or HMC-C-01-A. MCIM compounds reduce glandular loss to a greater extent in mice with established DSS-induced colitis compared to mice treated with vehicle control, sulfasalazine (A) or etanercept (B). Data are mean $\pm$ s.e.m.. ** $p < 0.01$ vs vehicle, § $p < 0.05$ vs sulfasalazine.

Figure 20. Two graphs showing a comparison of epithelial hyperplasia in mice with DSS-induced colitis treated with (A) vehicle control, sulfasalazine or ABD900 and (B) vehicle control, sulfasalazine or HMC-C-01-A. MCIM compounds can promote epithelial hyperplasia in mice with established DSS-induced colitis at a comparable level compared to mice treated with sulfasalazine (A) but to a greater extent than mice treated with etanercept (B). Data are mean $\pm$ s.e.m.. * $p < 0.05$ vs vehicle.

Figure 21. Two graphs showing a comparison of fibroplasia, which is indicative of tissue or wound repair, in mice with DSS-induced colitis treated with (A) vehicle control, sulfasalazine or ABD900 and (B) vehicle control, sulfasalazine or HMC-C-01-A. MCIM compounds promote increased 'healthy' fibroplasia in mice with established DSS-induced colitis compared to mice treated with vehicle control, sulfasalazine (A) or etanercept (B). Data are mean $\pm$ s.e.m.. *** $p < 0.005$ vs vehicle, §§§ $p < 0.005$ vs sulfasalazine, ^{aaa} $p < 0.005$ vs etanercept.

Figure 22. Histological sections from mice with DSS-induced colitis treated with either vehicle control (top panels), etanercept (middle panels) or an HMC-C-01-A (bottom panels). Ulceration, loss of architecture, oedema/inflammation and erosion is seen in the vehicle control (arrows). The positive control, etanercept, shows general conservation of tissue architecture but with underlying inflammation and oedema (arrows). Mice treated with MCIM compound show a general conservation of tissue architecture, with no inflammation or oedema and with radial distribution of repair (arrows).

Figure 23. Homology model of the complete Complex I constructed from publicly available structures for 5 different organisms. The putative targets were resolved in all 5 structures.

Figure 24. *In silico* homology model of NDUFS2. Druggability assessment was performed using SiteMap and identified two binding pockets in the Complex I subunit NDUFS2 (spheres).

Figure 25. *In silico* SiteFinder model of NDUFS2 when in Complex I. A narrow channel was identified for Q10 and drug-like compound binding in the Q-tunnel. Spheres are used to illustrate the space/channels around NDUFS2 when in the Complex I structure.

Figure 26. *In silico* model of a MCIM compound docked in the Q-site of Complex I. This model reveals interactions between a MCIM compound and NDUFS2 and additional interactions with the neighbouring Complex I subunit NDUFS7.

Figure 27. 3D representation of a pharmacophore model built from *in silico* modelling of drug docking in Complex I.

Figure 28. Overlay of a MCIM compound on the ligand-protein pharmacophore model illustrating successful docking of the MCIM compound in the Q-tunnel of Complex I.

Figure 29. Overlay of a MCIM compound, CHMSA-02-A, on the ligand-protein pharmacophore model (top panel) and the chemical structure of CHMSA-02-A (bottom panel). This illustrates successful docking of CHMSA-02-A in the Q-tunnel of Complex I.

Figure 30. Graph showing the quantitative structure-activity relationship (QSAR) model used to identify further MCIM compounds and to predict their activity *in vivo*. Predicted pAct of MCIM compounds correlate well with their experimentally validated pAct, with a coefficient of determination (R^2) value of 0.8322 demonstrating that this QSAR model can be used to accurately identify MCIM compounds.

Detailed Description of the Invention

Aspects and embodiments of the present invention will now be discussed with reference to the accompanying figures. Further aspects and embodiments will be apparent to those skilled in the art. All documents mentioned in this text are incorporated herein by reference.

The present disclosure provides a pharmaceutical combination and a pharmaceutical composition comprising an MCIM compound and a DMARD compound. The combination or composition may be for use as a medicament. The present disclosure also provides a pharmaceutical composition comprising an MCIM compound for use in a method of treatment, for example for use in treating or preventing an inflammatory and/or progressive disease, wherein the method further comprises administering a DMARD. Also provided is a pharmaceutical composition comprising a DMARD for use in a method of treatment, for example for use in treating or preventing an inflammatory and/or progressive disease, wherein the method further comprises administering an MCIM compound. Also provided is a pharmaceutical composition comprising an MCIM compound and a DMARD for use in a

method of treatment, for example for use in treating or preventing an inflammatory and/or progressive disease. Also provided is the use of an MCIM compound in the manufacture of a medicament for use in a method treatment, for example for use in of treating or preventing an inflammatory and/or progressive disease, wherein the method further comprises administering a DMARD. Also provided is

5 the use of a DMARD in the manufacture of a medicament for use in a method of treatment, for example for use in treating or preventing an inflammatory and/or progressive disease, wherein the method further comprises administering an MCIM compound.

Also provided is an MCIM compound in combination with a DMARD for use in a method of reducing arthritic index to a greater extent in a patient compared to administration of MCIM alone or DMARD

10 alone. Also provided is an MCIM compound for use in combination with a DMARD for use in a method of reducing arthritic index to a greater extent in a patient compared to administration of MCIM alone or DMARD alone. Also provided is a DMARD for use in combination with an MCIM compound for use in a method of reducing arthritic index to a greater extent in a patient compared to

15 administration of MCIM alone or DMARD alone. Administration of the MCIM compound and the DMARD may be separate, sequential, or simultaneous.

Further provided is a method of treating or preventing an inflammatory and/or progressive disease, the method comprising administering a therapeutically- or prophylactically-effective amount of (i) MCIM compound and (ii) a DMARD to a subject in need of treatment.

The present disclosure also provides an MCIM compound and DMARD (e.g. in the form of a

20 pharmaceutical combination or pharmaceutical composition comprising an MCIM compound and a DMARD) for use in a method of treating or preventing an inflammatory and/or progressive disease. Also provided is the use of an MCIM compound and a DMARD (e.g. in the form of a pharmaceutical combination or pharmaceutical composition comprising an MCIM compound and a DMARD) in the manufacture of a medicament for use in a method of treating or preventing an inflammatory and/or

25 progressive disease. Also provided is a method of treating or preventing an inflammatory and/or progressive disease, the method comprising administering a therapeutically- or prophylactically-effective amount of an MCIM compound and a DMARD (e.g. in the form of a pharmaceutical combination or pharmaceutical composition comprising an MCIM compound and DMARD) to a subject in need of treatment.

30 In some aspects and embodiments, the MCIM compound and the DMARD may be provided as a combination therapy. In some embodiments, the MCIM compound and the DMARD may be administered simultaneously or sequentially. Simultaneous administration refers to administration of the two or more agents together, for example as a pharmaceutical composition containing both agents (i.e. as a combined preparation), or immediately after one another (e.g. within 1, 4, 6, 8 or 12

35 hours), and optionally via the same route of administration, e.g. to the same artery, vein or other blood vessel. Sequential administration refers to administration of one of the agents followed after a given

time interval by separate administration of another agent. It is not required that the agents are administered by the same route, although this is the case in some embodiments. The time interval may be any time interval.

Also provided is the use of an MCIM compound in the manufacture of a medicament for use in
5 treating or preventing inflammatory and/or progressive disease, wherein treating or preventing the inflammatory and/or progressive disease further comprises administering a DMARD.

The present disclosure further provides a pharmaceutical composition comprising an MCIM as disclosed herein compound for use in a method of treatment, wherein the method further comprises administering a DMARD. The present disclosure further provides a pharmaceutical composition
10 comprising an MCIM compound as disclosed herein for use in a method of treatment, wherein the method further comprises administering a csDMARD. The present disclosure further provides a pharmaceutical composition comprising an MCIM compound for use in a method of treatment, wherein the method further comprises administering methotrexate. The present disclosure further provides a pharmaceutical composition comprising a DMARD for use in medicine, wherein the
15 method further comprises administering an MCIM compound as disclosed herein. The present disclosure further provides a pharmaceutical composition comprising a csDMARD for use in medicine, wherein the use further comprises administering an MCIM compound as disclosed herein. The present disclosure further provides a pharmaceutical composition comprising methotrexate for use in medicine, wherein the method further comprises administering an MCIM compound as disclosed
20 herein. The present disclosure further provides a pharmaceutical composition comprising an MCIM compound as disclosed herein and a DMARD for use in medicine. The present disclosure further provides a pharmaceutical composition comprising an MCIM compound and a csDMARD for use in medicine. The present disclosure further provides a pharmaceutical composition comprising an MCIM compound as disclosed herein and methotrexate for use in medicine.

25

Pharmacophores

The term "pharmacophore" is used herein as defined in Wermuth, C.G., Ganellin, C.R., Lindberg, P., Mitscher, L.A.; Glossary of Terms Used in Medicinal Chemistry (IUPAC Recommendations
1998); *Pure & Appl. Chem.* 70:5 (1998) 1129–1143: A pharmacophore is an ensemble of aromatic
30 steric and electronic features that is necessary to ensure the optimal supramolecular interactions with a specific biological target and to trigger (or block) its biological response. The ensemble of aromatic steric and electronic features represent so-called "pharmacophoric features". Typical pharmacophoric features include, for example, hydrogen bond donor, hydrogen bond acceptor, hydrophobic, aromatic, and positively and negatively ionized areas.

35 As used herein, the term "pharmacophore model" relates to a pharmacophore hypothesis for the binding interactions in a particular active site. A pharmacophore model is made up of a set of

annotation points which are interrelated in 3D space. The annotation points show the location and type of biologically important atoms and groups, i.e., each annotation point relates to a pharmacophore feature of the model. Each annotation point is associated with a radius that describes the permissible variation in 3D space for the location of the given pharmacophoric feature.

- 5 As used herein, the phrase “conform to a pharmacophore model” means that a compound described herein binds to the target binding site (i.e., the NDUSF2 and/or NDUSF7 binding site) in a 3D conformation (i.e., “pose”) whereby, 4 or more of the annotation points of the pharmacophore model described herein are occupied by corresponding features of the MCIM compound described herein, as determined the unified annotation scheme in *Molecular Operating Environment (MOE)*, 2022.02
- 10 Chemical Computing Group ULC, 1010 Sherbooke St. West, Suite #910, Montreal, QC, Canada, H3A 2R7, 2022. In some embodiments, four or more of the annotation points of the pharmacophore model described herein are occupied by corresponding features of the MCIM compound described herein. In some embodiments, five or more, six or more, seven or more, eight or more, or all nine of the
- 15 annotation points of the pharmacophore model described herein are occupied by corresponding features of the MCIM compound described herein. The conformance of a compound described herein with the pharmacophore features is as determined using the unified annotation scheme in *Molecular Operating Environment (MOE)*, 2022.02 Chemical Computing Group ULC, 1010 Sherbooke St. West, Suite #910, Montreal, QC, Canada, H3A 2R7, 2022

Annotation points can be broadly divided into three categories: *atom*, *projected*, and *centroid*.

- 20 Annotation points are determined for a given compound by the unified annotation scheme in *Molecular Operating Environment (MOE)*, 2022.02 Chemical Computing Group ULC, 1010 Sherbooke St. West, Suite #910, Montreal, QC, Canada, H3A 2R7, 2022.

The annotation points used herein are described below.

25

Atom

Don: H-bond Donor

Acc: H-bond Acceptor

- 30 *Atom* annotations are located directly on an atom of a molecule and typically indicate a function related to protein-ligand binding.

Don annotates an H-bond donor heavy atom. A **Don** annotation is added to all oxygen and nitrogen atoms with at least one (possibly implicit) hydrogen attached.

35

Acc annotates an H-bond acceptor heavy atom. O, S, and N elements can be hydrogen bond acceptors provided that they conform to the following rules:

1. Sulfur atoms are not acceptors except that sulfur in S=C groups and anionic sulfurs are acceptors and are given **Acc** annotations.

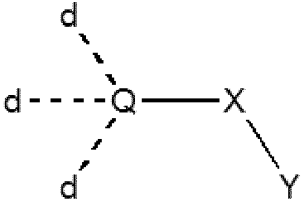
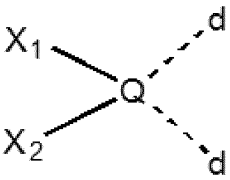
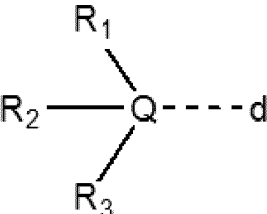
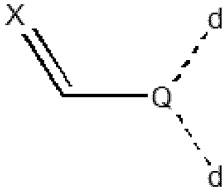
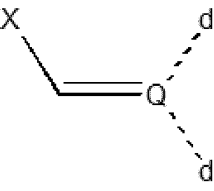
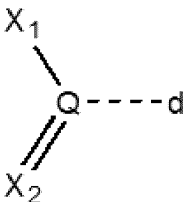
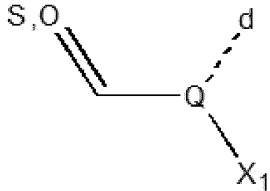
2. Nitrogen atoms are acceptors and given **Acc** annotations provided that they are not buried. A buried nitrogen is one of $\{=N=, -N\#, >N=, >N<\}$ or a non-3-ring conjugated nitrogen of the form $\{>N-\pi, >N-[C+], >N-B, >N-S=O, >N-P=O\}$.
3. Oxygen atoms are acceptors and are given **Acc** annotations provided that they are not buried and provided that they are not in certain exception groups. A buried oxygen is one of $\{=O=, -O\#, >O=, >O<\}$ or a non-3-ring conjugated oxygen of the form $\{>O-\pi, >O-B, >O-[C+]\}$. Non-buried oxygen atoms are acceptors unless they are part of the following exception groups:

not Acc; $X_i = \text{any}$	not Acc if any $X_i = \text{het}$; $Y \neq H$
not Acc if $Y \neq H$, $E = \{C\#N, N\#C, >[N,S,P]=O, Q+, CF_3\}$	not Acc if both $\{Q1, Q2\}$ are π not Acc if both $\{X1, X2\} = \text{het}$

Projected**Don2:** Projected Donor**Acc2:** Projected Acceptor

- 5 *Projected* annotations are (typically) located along implicit lone pair or implicit hydrogen directions and are used to annotate the location of possible hydrogen bond or metal ligation partners, or possible R-group atom locations.

Projected **Don2** annotations are added according to the hybridization and the heavy atom coordination of the donor. In the following table the **d** denotes a **Don2** feature.

Table 1 Projected donors		
 $Q = 1^\circ sp^3, X > 1\text{-coord}, Y \neq H$	 $Q = 2^\circ sp^3$	 $Q = 3^\circ sp^3$
 $Q = 1^\circ sp^2$	 $Q = 1^\circ sp^2, X \neq H$	 $Q = 2^\circ sp^2$
 $Q : 2^\circ sp^2$	 $Q = 1^\circ sp$	

Hydrogen bond **Acc2** projected annotations are added to those heavy atoms that qualify as H-bond acceptors (see above) and are given **Acc** annotations. The **Acc2** projected annotations are added in the same locations as those for the **Don2** projected annotations and according to the same rules.

- 5 (That is, the donors and the acceptors are projected using the same angles and the same distances.)
An atom that is both a **Don** and an **Acc** will be annotated with “Don2&Acc2” projected annotations.

- Projected annotations such as **Don2**, and **Acc2** are located at potential heavy atom positions. For example, **Don2** indicates a potential hydrogen bond partner heavy atom. Realistically, this partner atom cannot have too much overlap with any of the atoms of the molecule generating the projected annotation. This condition depends on the particular conformation of a molecule and cannot be reliably predicted by topological means. Consequently, a *solvent exposure test* must be applied to validate any hits resulting from a Pharmacophore Search, *i.e.*, a test to verify that applicable projected features are not covered by other parts of the conformation (that would prevent the putative projection atom from occupying the intended position).

Centroid

Aro Aromatic

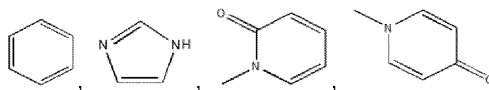
Hyd Hydrophobic

20

Centroid annotations (Aro, Hyd) are located at the geometric center of a subset of the atoms of a molecule.

- Aro** annotation centroids are used for aromatic and pseudo aromatic rings. The **Aro** annotation centroid is placed at the centroid of each aromatic ring (e.g. two centroids in naphthalene).

- The definition of aromaticity is generous (a Daylight-style definition) in which each ring is treated in isolation and a Hückel $4n+2$ rule is applied. C=O carbons count 0 electrons, otherwise C=R count as 1; N=X nitrogens count 1 and >N- nitrogens and -O- oxygens count 2 electrons. Thus, the following are treated as (pseudo) aromatic and are given an **Aro** annotation centroid in the center of the ring:



Hydrophobic atoms are annotated with **HydA** and hydrophobic centroids are annotated with **Hyd**. Hydrophobic groups are determined by graph theoretic algorithms.

35

The fundamental rules for deciding whether an atom is hydrophobic are summarized below:

1. Nitro nitrogen atoms (not in nitrate anions) are hydrophobic.

2. Divalent sulfur atoms with two heavy neighbors bonded only to carbon or sulfur are hydrophobic.

3. Halogens are hydrophobic.

4. Carbon atoms are hydrophobic except

- 5 a) aliphatic carbons π bonded to non-carbon atoms; or
b) π carbon atoms adjacent to univalent oxygen; or
c) aromatic carbon adjacent to aromatic oxygen in 5-rings; or
d) carbon atoms adjacent to two or more {N,O} atoms; or
e) anionic carbons in c1cccc1;

10

The assignment of hydrophobic annotations proceeds by first applying the preceding hydrophobic atom typing rules but leaving out fluorine atoms on the grounds that they are small and should not affect annotation placement.

- 15 The Unified scheme provides an atom-centered hydrophobic annotation, **HydA** and a centroid hydrophobic feature **Hyd**. The **HydA** annotation is used for hydrophobic atoms that are deemed to have sufficiently high (potential) exposure to a potential receptor. This means that, for example, *sp*³ carbons with 4 heavy neighbors are not marked (since they are buried) and aromatic carbons with two heavy neighbors and two *ortho* substituents are not annotated.

20

The **Hyd** annotations are assigned by a procedure that groups connected hydrophobic atoms and assigns centroids weighted by an estimate of the likely exposed surface area of each hydrophobic atom; that is, the **Hyd** centroid will be placed closer to more exposed hydrophobic atoms in a hydrophobic group.

25

The following grouping algorithm is used:

1. **Strip Fluorines.** Remove all fluorines that are not bonded to {H,F} from further consideration. Note that estimates of exposed surface area use a fluorine suppressed molecule.
2. **Rings.** Find all 5-, 6-, 7-, and 8-member rings that are not composed of smaller rings. For
30 each such ring, extract each contiguous stretch of hydrophobic atoms with at least three atoms that have a sufficiently high total exposed surface area, and generate a surface area weighted centroid annotation. Remove all annotated ring atoms from further consideration.
3. **Components.** Find all connected components (single-linkage clusters) among the remaining hydrophobes and remove from consideration those clusters with an exposed surface area sum
35 deemed too small (less than a -CH₂- group).
4. **Small Components.** For the remaining hydrophobic components with three or fewer atoms, generate an exposed surface area weighted centroid annotation.
5. **Large Components.** Identify the center of the component graph and generate a weighted centroid at the center including its neighbors. Remove the annotated atoms, splitting the component

and apply the Small Components step and/or the Large Components step (recursively) to group the hydrophobes.

The MCIM compounds described herein conform to a pharmacophore model as described herein.

- 5 That is, the MCIM compound as annotated by *Molecular Operating Environment (MOE) 2022* unified annotation scheme comprises 4 or more pharmacophore features which conform to the pharmacophore model represented in Figure 27, and Tables 9-A, 9-B and 9-C. Compounds which do not conform to the pharmacophore model, e.g. rotenone, IACS-010579, are not MCIM compounds.

The MCIM compounds for use in combination with a DMARD (e.g. methotrexate, sulfasalazine)

- 10 described herein conform to a pharmacophore model as described herein.

DMARDs

DMARDS which find use in the pharmaceutical compositions for use in treatment, pharmaceutical combinations, and methods of treatment disclosed herein include conventional synthetic DMARDS (csDMARDS), targeted synthetic DMARDS (tsDMARDS), biological DMARDS (bDMARDS). Any

15 DMARD may be used in the combination with an MCIM compound to treat an inflammatory and/or progressive disease, for example an arthritic disease.

- In some embodiments, the DMARD is a csDMARD. In some embodiments, the csDMARD is selected from methotrexate, azathioprine, chloroquine, D-penicillamine, ciclosporin, gold salts such as sodium aurothiomalate and auranofin, hydroxychloroquine, leflunomide, minocycline and sulfasalazine, or a
- 20 combination of any of the foregoing.

- In some embodiments, the DMARD is a tsDMARD. In some embodiments, the tsDMARD is selected from a JAK inhibitor or a PDE4 inhibitor, or a combination of a JAK inhibitor and a PDE4 inhibitor. In some embodiments, the tsDMARD is selected from baricitinib, filgotinib, tofacitinib, deucravacitinib, and apremilast, or a combination of any of the foregoing. In some embodiments, the DMARD is not a
- 25 tsDMARD. In some embodiments, the DMARD does not comprise baricitinib, filgotinib, or tofacitinib.

- In some embodiments, the DMARD is a bDMARD. In some embodiments, the bDMARD is selected from a TNF inhibitor, a TNF decoy receptor, a CTLA4-Ig fusion protein, a CD20 inhibitor, an IL-6 inhibitor, an IL17A inhibitor, an IL23 inhibitor, and a BAFF inhibitor, or a combination of any of the foregoing. In some embodiments, the bDMARD is selected from etanercept, adalimumab,
- 30 certolizumab, certolizumab pegol, golimumab, infliximab, abatacept, anakinra, rituximab, sarilumab, secukinumab, ixekizumab, bimekizumab, tocilizumab, ustekinumab, guselkumab, and belimumab or a combination of any of the foregoing. In some embodiments, the DMARD does not comprise adalimumab, certolizumab, certolizumab pegol, etanercept, golimumab, infliximab, sarilumab, tocilizumab, or ustekinumab.

- 35 In some embodiments, the combination therapy includes two or more DMARDS selected from methotrexate, azathioprine, chloroquine, D-penicillamine, ciclosporin, gold salts such as sodium

aurothiomalate and auranofin, hydroxychloroquine, leflunomide, minocycline, sulfasalazine, baricitinib, filgotinib, tofacitinib, deucravacitinib, apremilast, guselkumab, deucravacitinib, ixekizumab, bimekizumab, belimumab, adalimumab, certolizumab, etanercept, golimumab, infliximab, abatacept, anakinra, rituximab, sarilumab, secukinumab, tocilizumab, and ustekinumab. In particular, the
 5 combination therapy may include a combination of methotrexate and one or more of sulfasalazine, hydroxychloroquine, cyclosporine, leflunomide and azathioprine. In some embodiments the combination therapy comprises a combination of methotrexate and leflunomide. In some
 10 embodiments the combination therapy comprises a combination of methotrexate and sulfasalazine. In some embodiments, the combination therapy comprises a combination of methotrexate, sulfasalazine and hydroxychloroquine.

In some embodiments, the DMARD is a csDMARD. For example, the DMARD may comprise methotrexate, sulfasalazine, and hydroxychloroquine, or any combination thereof.

In preferred embodiments, the DMARD is a csDMARD and the compositions disclosed here are for use in the treatment of an arthritic disease. For example, the arthritic disease is rheumatoid arthritis,
 15 psoriatic arthritis, or reactive arthritis. In more preferred embodiments, the csDMARD is selected from methotrexate, sulfasalazine, and hydroxychloroquine, or any combination thereof.

Inflammatory and/or progressive diseases

As described herein, a combination of the mitochondrial Complex I modulator (MCIM) compound with a DMARD is suitable for use in treating inflammatory and/or progressive diseases.

20 The disease may be a chronic progressive disease associated with fibrosis of the affected tissue(s), such as: interstitial lung disease (ILD), idiopathic pulmonary fibrosis (IPF); pulmonary fibrosis; liver fibrosis; nonalcoholic steatohepatitis (NASH), nonalcoholic fatty liver disease (NAFLD); kidney fibrosis; chronic kidney disease (CKD); cardiac fibrosis; ischaemia reperfusion injury; heart failure with reduced ejection fraction, heart failure with preserved ejection fraction; myelofibrosis; retroperitoneal
 25 fibrosis; atherosclerosis; myocardial infarction; stroke; neurodegenerative disease; multiple sclerosis; fronto-temporal dementia (FTD); amyotrophic lateral sclerosis (ALS), Alzheimer's disease (AD); osteoporosis, osteopenia; osteoarthritis; endometriosis; bone loss associated with endometriosis; neoplasia of bones (including, e.g., as a primary tumour or as metastases and including, e.g., bone cancer; osteosarcoma; or osteoma); cancer associated bone disease (including, e.g., metastatic bone
 30 disease associated with, e.g., breast cancer, lung cancer, prostate cancer, or multiple myeloma; changes in bone mineralisation and density associated with cancer, including, e.g., hypercalcaemia associated with cancer); and bone metastases (including, e.g., osteolytic bone metastases).

The disease may be an autoimmune disease, such as: rheumatoid arthritis (RA); psoriatic arthritis; ankylosing spondylitis; spondyloarthritis; reactive arthritis; infectious arthritis; systemic lupus
 35 erythematosus; scleroderma; juvenile idiopathic arthritis; psoriasis; systemic lupus erythematosus; lupus nephritis; uveitis; systemic sclerosis; scleroderma; hepatitis; Sjogren's syndrome; inflammatory

- bowel disease; ulcerative colitis; Crohn's disease; multiple sclerosis; atherosclerosis; chronic obstructive pulmonary disease (COPD); uveitis; allergic disease (including, e.g., atopy, allergic rhinitis, atopic dermatitis, anaphylaxis, allergic bronchopulmonary aspergillosis, allergic gastroenteritis, hypersensitivity pneumonitis); type I diabetes; celiac disease; oophoritis; primary
- 5 biliary cirrhosis; insulin-resistant diabetes; Behçet's disease; myasthenia gravis; autoimmune polyneuritis; pemphigus; rheumatic carditis; Goodpasture's syndrome; postcardiotomy syndrome; polymyositis; dermatomyositis; irritable bowel syndrome; pancreatitis; gastritis, chronic pulmonary inflammation; pulmonary alveolitis; polycystic kidney disease; cryopyrin-associated periodic syndrome (CAPS); Muckle-Wells Syndrome; Guillain-Barre syndrome; chronic inflammatory demyelinating
- 10 polyneuropathy; dermatitis; atopic dermatomyositis; Graves' disease; autoimmune (Hashimoto's) thyroiditis; bronchitis; cystic fibrosis; pulmonary embolism; sarcoidosis; emphysema; respiratory failure; acute respiratory distress syndrome; BENTA disease; or polymyositis; SSC-ILD, hidradenitis suppurative, alopecia areata, atopic dermatitis. The disease may be an autoinflammatory disease, such as: Chron's disease, gout, Behçet's disease, or Muckle-Wells Syndrome.
- 15 In some embodiments, tissue repair, disease regression, disease control (which includes, for example, preventing or slowing disease progression), increase in reparative cells, decrease in destructive cells and/or reduction in cytokine production from peripheral mononuclear cells or lymphoid cells (such as T-, B- or NK-cells) can be determined as defined herein. For instance, in some embodiments, the MCIM compound reduces the levels of inflammatory mediators such as
- 20 $\text{TNF}\alpha$, eSEL, CD38, CD40, CD69, sIgG, sIL-17A, sIL-17F, sIL-2 and/or sIL-6 that are produced by a target cell. In some embodiments, the MCIM compound reduces the levels of collagen type I and/or MMP1, and/or increases collagen type IV production. In some embodiments, the MCIM compound increases ETC efficiency, without an increase in biomass. In some embodiments, the MCIM compound decreases ETC efficiency. In some embodiments, the MCIM compound reduces cellular
- 25 proliferation without reducing ATP concentration/cell and viability, dependent on the environmental composition such as in the absence of pyruvate. In some embodiments, the MCIM compound induces an adaptive/repair response under conditions of metabolic stress conditions. For instance, the MCIM compound modulates Complex I activity and attenuates high energy processes such as proliferation and/or differentiation and concurrently induces an adaptive/repair response by increasing
- 30 the production of pro-angiogenic/repair factors such as VEGF to restore tissue metabolic homeostasis, particularly under metabolic stress conditions. In some embodiments, the MCIM compound reduced cell viability, particularly in cell types which are heavily dependent on Complex I metabolism and lack the metabolic flexibility to adapt. Each of these effects on tissue repair, disease control, disease regression, increase in reparative cells, decrease in destructive cells and/or reduction
- 35 in cytokine production from pro-inflammatory myeloid cells can be determined by comparing the effect in the presence and absence of the MCIM compound.

In some embodiments, lung fibroblasts are used as a target cell to determine the effect of the MCIM compound. For example, cellular adaptation may be determined in human primary lung fibroblasts, e.g. by measuring vascular endothelial growth factor (VEGF) secretion. (VEGF can be induced in a cell that is not receiving enough oxygen or nutrients to support ATP production. This can indicate how metabolic signalling pathways interact and integrate with angiogenic signalling events and repair). In some embodiments, VEGF secretion can be measured by plating primary human lung fibroblasts at 2×10^3 cells/well in 96-well plates in 100 μ L DMEM complete medium with: 1 g/L glucose and 110 mg/L pyruvate; or 1 g/L glucose without pyruvate (each supplemented with 1% penicillin-streptomycin and 10% heat inactivated foetal bovine serum), and incubating in a humidified 37°C incubator with 5% CO₂ for 24 hours. The test compound is prepared as a 10x final concentration solution in culture medium and added to final concentrations before further incubating the cells at 37°C / 5% CO₂ for 24 hours. VEGF secretion is measured in the cell supernatants using Quantikine® ELISA Human VEGF kits according to the manufacturer's instructions. Absorbance at 450 nm is measured on a BMG Plate reader (CLARIOstar plus) using pathlength correction. Background absorbance is measured at 540 nm. Preferably, treatment with the test compound results in an increase in VEGF secretion in the absence of pyruvate, but not in the presence of pyruvate as a metabolic substrate for the cell. This indicates the induction of an adaptive/repair response under conditions of metabolic stress conditions via the attenuation of highly energy-consuming processes such as proliferation and concurrent production of pro-angiogenic/repair factors such as VEGF to restore tissue metabolic homeostasis.

Disease control may be achieved by treatment with the compositions of the invention. Disease control can comprise inhibition of disease progression and/or control of disease symptoms. Inhibition of disease progression includes prevention of disease progression and slowing down disease progression. Standard methods in the art may be employed to determine disease progression.

25

Evaluating disease repair in humans

Chronic autoimmune diseases are amenable to treatment with a combination of the Complex I modulator (MCIM) compound as described herein with a DMARD. Such diseases include RA, IBD, Ulcerative colitis (UC), Psoriatic arthritis (PsA), and psoriasis. As described herein, the MCIM compound can elicit tissue repair and disease regression.

In some embodiments, a histopathological assessment can be used to determine the effect of the MCIM compound and the MCIM compound in combination with a DMARD on arthritis. For this assessment of arthritis, the following signs are monitored in digits or limbs of each subject three times per week and summed to generate the Arthritic Index (AI). (The maximum AI for one animal is 16):

0: no visible effects of arthritis. 1: oedema and/or erythema of 1 digit. 2: oedema and/or erythema of 2 digits. 3: oedema and/or erythema of more than 2 digits. 4: severe arthritis of entire paw and digits.

In some embodiments, the MCIM compound in combination with a DMARD reduces the average score compared with subject treated with a negative control, MCIM compound alone and/or a DMARD alone.

In a subject suffering from arthritis, inhibition of disease progression may be indicated by a stable
5 Arthritic Index (AI) score, or any other suitable method known in the art. Other suitable clinical
scoring methods known in the art include the ACR/EULAR 2010 scoring criteria (ACR/EULAR score),
“disease activity score at 28 joints” criteria (DAS28 score), “health assessment questionnaire disability
index” (HAQ-DI score), “clinical disease activity index” (CDAI score), “simplified disease activity index”
(SDAI score), “American College of Rheumatology response criteria” (also known as “ACR20/50/70
10 response”; ACR20/50/70 score), European league against rheumatism response criteria (EULAR
score), “Modified total Sharp/van der Heijde score” (mTSS score), and/or the “routine assessment of
patient index data 3 score” (RAPID3 score), the DAS28-CRP (DAS28 calculated with CRP), the
DAS28-ESR (DAS28 calculated with ESR), Pain Visual Analogue Scale (Pain VAS), EULAR-RA
Impact of Disease (EULAR-RAID), patient global assessment of health (PGAH), Patient global
15 assessment of disease (PGAD), EQ-5D, EQ-5D-3L, EQ-5D-5L, EQ-5D VAS, and/or EQ-5D-Y-3L.
Other suitable scoring methods include the ATHLOS scale, the SAGE scale, the disability index, and
the SF-36 survey (Sanchez-Niubo et al, 2020; Spence et al, 2021; Zhang et al, 2023; Brazier et al,
1992; each of which is hereby incorporated by reference in their entirety). Other questionnaires that
assess activities of daily living and instrumental activities of daily living which may be used to assess
20 patient outcomes following treatment with the MCIM and DMARD disclosed herein are the Barthel
Index (BI), Groningen Activity Restriction Scale (GARS), and Lawton and Brody Instrumental
Activities of Daily Living Scale (LB-IADL) and the elderly mobility scale (version 2, June 2012). For
example, inhibition of disease progression may be determined by comparing the AI score,
ACR/EULAR score, DAS44 score, HAQ-DI score, CDAI score, SDAI score, ACR20/50/70 score,
25 EULAR score, mTSS score, and/or RAPID3 score of a subject before, during and/or after receiving
treatment with an MCIM compound and a DMARD. Inhibition of disease progression may be
indicated by the AI score, ACR/EULAR score, DAS38 score, HAQ-DI score, CDAI score, SDAI score,
ACR20/50/70 score, EULAR score, mTSS score, and/or RAPID3 score being stable (i.e. not
changing) over time following treatment. Inhibition of disease progression may be indicated by the AI
30 score, ACR/EULAR score, DAS38 score, HAQ-DI score, CDAI score, SDAI score, ACR20/50/70
score, EULAR score, mTSS score, and/or RAPID3 score progressing or increasing at a slower rate
following treatment. Disease control in Arthritis may be determined by any suitable method known in
the art. In some embodiments, the MCIM compound in combination with the DMARD is for use in the
treatment of arthritis to reduce the average arthritic score (e.g, AI score, ACR/EULAR score, DAS38
35 score, HAQ-DI score, CDAI score, SDAI score, ACR20/50/70 score, EULAR score, mTSS score,
and/or RAPID3 score) compared to administration of MCIM compound or DMARD alone. In some
embodiments, the MCIM compound in combination with a DMARD reduces the AI score, ACR/EULAR

score, DAS38 score, HAQ-DI score, CDAI score, SDAI score, ACR20/50/70 score, EULAR score, mTSS score, and/or RAPID3 score in a subject by at least 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100%.

5 HAQ-DI

The Health Assessment Questionnaire (HAQ) Disability Index (DI) may be carried out as described in Wolfe F et al (1994) and "THE HEALTH ASSESSMENT QUESTIONNAIRE (HAQ) DISABILITY INDEX (DI) OF THE CLINICAL HEALTH ASSESSMENT QUESTIONNAIRE (VERSION 96.4)", both of which is hereby incorporated by reference in their entirety. Briefly, the HAQ comprises 8 sections relating to dressing, arising, eating, walking, hygiene, reach, grip, and activities. Each section comprises 2 or 3 questions, with scoring for each section being given on a scale of 0 (without any difficulty) to 3 (unable to do). The score given to each section is the highest score given for any given question in each section. The 8 scores of the 8 sections are summed and divided by 8 (or if, for example, only 7 sections are completed by a subject divided by 7). A score of ≤ 1 indicates mild disability, a score of 1-2 indicates moderate disability and a score of ≥ 2 indicates severe disability (Krishnan et al., 2004). Scores indicative of a minimally important difference, critical important difference, functional remission and population normative are described in Table 1, below. Subjects treated with an MCIM and DMARD as described herein, may demonstrate a decrease in the HAQ-DI score of ≥ 0.22 , indicating the subject has achieved a MCID. Subjects treated with an MCIM and DMARD as described herein, may also demonstrate a decrease in the HAQ-DI score of ≥ 0.68 , indicating the subject has achieved a critical difference (i.e. the minimum change that can be reliably discriminated from random long-term variations). Subjects treated with an MCIM and DMARD as described herein may achieve functional remission, indicated by a HAQ-DI score of ≤ 0.5 , and in some cases a subject may achieve a population normative score of ≤ 0.25 .

25

EULAR-RAID score

The Rheumatoid Arthritis Impact of Disease (RAID) score is a global composite measure of the impact of RA that takes into account seven "domains" of impact of RA considered of utmost relevance by patients: pain, physical disability (functional), fatigue, sleep disturbances, coping, physical wellbeing and emotional well-being. The EULAR-RAID score may be determined as described in Gossec et al (2011), which is hereby incorporated by reference in its entirety. Briefly, each domain is evaluated by patients using a single 0 (no symptom) to 10 numeric rating scale and has a specific weight used to calculate a single composite RAID score using an online calculator (<https://rheumcalc.com/raid/>). A score of ≤ 2 indicates mild impairment, a score of 3-6 indicates moderate impairment and a score of ≥ 7 indicates severe impairment (Mistry et al., 2020). Following treatment with an MCIM and DMARD as described herein, one or more of the domain scores selected

from pain, physical disability (functional), fatigue, sleep disturbances, coping, physical wellbeing and emotional well-being may decrease by ≥ 23 points, for example by at least 2, 3, 4, 5, 6, 7, 8, 9 or 10 points compared to the respective domain score prior to treatment with an MCIM and DMARD. Or the patient may achieve a score of ≤ 2 , reflecting a patient acceptable state (PAS), as discussed in

- 5 Dougados et al (2012) which is hereby incorporated in its entirety by reference.

Following treatment with an MCIM and DMARD compound as described herein, a subject's composite RAID score may decrease by ≥ 2 , for example at least 2, 3, 4, 5, 6, 7, 8, 9 or 10 points compared to the RAID score prior to treatment with an MCIM and DMARD.

EQ-5D-5L

- 10 The EQ-5D-5L is a standardised measure of health status which provides a simple, generic measure of health for clinical and economic appraisal (The EuroQol Group, 1990) and may be carried out as described in the EQ-5D-5L User Guide, version 2 (Oemar and Janssen, 2013) which is hereby incorporated by reference in its entirety. The EQ-5D-5L consists of two components, a descriptive system and a visual analogue scale (EQ VAS). The descriptive component comprises 5 "dimensions"
- 15 to be measured (mobility, self-care, usual activities, pain/discomfort, anxiety/depression), with each dimension being scored on a 5-level scale (1 = no problem, 2 = slight problems, 3 = moderate problems, 4 = severe problems, 5 = extreme problems). Following treatment with an MCIM and DMARD as disclosed herein, one or more of the EQ-5D-5L dimensions (mobility, self-care, usual activities, pain/discomfort, and anxiety/depression) may be decreased by 1, 2, 3, or 4 points
- 20 compared to the score prior to treatment with an MCIM and DMARD.

The EQ-VAS component records a subjects self-rated health on a vertical, visual analogue scale with endpoints labelled "the best health you can imagine" (100) and "the worst health you can imagine" (0). EQ-VAS is measured at the time the test is administered (i.e. on the day of clinical visit). Following treatment with an MCIM and DMARD as described herein, a subject may have a higher EQ-VAS

25 score compared to their EQ-VAS score prior to treatment with an MCIM and DMARD. For example, the subject may have an increase in EQ-VAS of ≥ 5 points or ≥ 7.5 .

OMERACT RAMRIS

- The OMERACT RAMRIS system is a validated, MRI imaging-based scoring system for evaluating
- 30 bone erosion, bone marrow edema (osteitis), synovitis, and joint space narrowing. The OMERACT RAMRIS system assessment can be performed, and patients scored, as described in Østergaard (2017) and version 2.1 of The OMERACT Handbook (Beaton et al, 2021), each of which are hereby incorporated by reference in their entirety, and as discussed below. Figure 1 of Østergaard (2017), shows the areas, joint and bone regions assessed in the OMERACT RAMRIS scoring system.

Briefly, bone erosion is scored separately for each joint assessed. Joints assessment may include the distal radius, distal ulna, carpal bones, metacarpal bases, metacarpal heads, and phalangeal bases. Bone erosion is scored on a scale of 0-10, based on the proportion of eroded bone compared to the "assessed bone volume" judged on all available images: 0 = no erosion; 1 = 1-10% of bone eroded; 2 = 11-20%, 3 = 21-30%, 4 = 31-40%, 5 = 41-50%, 6 = 51-60%, 7 = 31-70%, 8 = 71-80, 9 = 81-90%, 10 = 91-100%. In case a bone is fused with another bone, bone erosion is scored as 10 in the bone. For long bones, the "assessed bone volume" is from the articular surface (or its best estimated position if absent) to a depth of 1 cm, while in carpal bones it is the whole bone. In subjects treated with MCIM and DMARD as disclosed herein, subjects may have a RAMRIS erosion score of 0%, indicating no erosion progression. In some subjects, bone erosion progression may be less than 0%, indicating potential erosion repair due to osteogenesis/ossification.

Osteitis/bone marrow edema is scored on a scale of 0-3 based on the proportion of bone with osteitis: 0 = no osteitis; 1 = 1-33% of bone with osteitis; 2 = 34-66%; 3 = 67-100%. Each bone is scored separately as for bone erosion. In patients treated with and MCIM and DMARD as described herein, osteitis score may decrease compared to osteitis score prior to treatment. For example, following treatment with an MCIM and DMARD, osteitis score may decrease from 3 to 2, 1 or 0, or osteitis score may decrease from 2 to 1 or 0, or osteitis score may decrease from 1 to 0.

Synovitis may be assessed in 3 wrist regions (e.g., the distal radioulnar joint; the radiocarpal joint; and the intercarpal and carpometacarpal joints) and in each MCP joint. The degree of synovitis is scored on a scale of 0-3. Score 0 is normal. A score of 1 (mild) is an increase of the presumed maximum volume of the synovial compartment by up to 33%. A score of 2 (moderate) is an increase of the presumed maximum volume of the synovial compartment by 34-66%. A score of 3 (severe) is an increase of the presumed maximum volume of the synovial compartment by 66%.

25 Cartilage loss and joint space narrowing (JSN)

Cartilage Loss/joint space narrowing is assessed at 17 locations in the wrist, between distal radius and carpal bones (2 sites), between the carpal bones (except the pisiform; 10 sites), and between carpal bones and each metacarpal bone (5 sites), and in each MCP joint. The degree of narrowing is classified on a scale of 0-4, as follows: 0.0, no cartilage loss or JSN; 0.5, equivocal cartilage loss or JSN; 1.0, minimal (< 10%) but definitive cartilage loss or JSN; 1.5, mild (10% to 25%) cartilage loss or JSN; 2.0, moderate cartilage loss or JSN (26% to 75%, including unilaterally denuded areas but no bilaterally denuded areas or bone-on-bone contact); 2.5, moderate-severe cartilage loss or JSN (> 75%, including focal denuding or focal bone-on-bone contact); 3.0, complete cartilage denuding or diffuse bone-on-bone contact; 3.5, partial ankylosis; 4.0, complete ankylosis. Following treatment with an MCIM and DMARD as described herein, joint space narrowing may be alleviated and/or cartilage loss may be reduced or reversed. For example, following treatment with an MCIM and

DMARD, the joint space narrowing score may decrease from 4 to 3, 2, 1, or 0, or the joint space narrowing score may decrease from 3 to 2, 1, or 0, or the joint space narrowing score may decrease from 2 to 1 or 0, or the joint space narrowing score may decrease from 1 to 0.

5 C-reactive protein

In addition to, or in place of one or more of the clinical scoring methods which can be used to determine effectiveness of a treatment for RA, biomarkers indicative of arthritis can be used to assess effectiveness of treatment, for example C-reactive protein (CRP). C-reactive protein (CRP) is an acute phase reactant which is increased during systemic inflammation. It is a well-recognised biomarker of inflammation and forms a key component of clinical assessments of arthritis such as the ACR score and the disease activity score (DAS28)-CRP. A concentration of CRP of greater than 0.3 mg/dL is considered to be above the upper limit of normal (Nehring et al., 2023; hereby incorporated in its entirety by reference). Following treatment, a decrease in serum CRP may be observed in subjects treated with an MCIM and DMARD as disclosed herein. For example, following treatment with an MCIM and DMARD the serum concentration of CRP in a subject may be decrease by $\geq 20\%$ compared to the serum CRP concentration prior to treatment. For example, the serum CRP concentration of a subject may be decreased by at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90% after treatment with an MCIM and DMARD compared to the serum concentration prior to treatment.

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In IBD, repair/healing can be clinically assessed using gut transit time, occult blood, endoscopy, histopathology, electrolytes and/or by measuring biomarkers such as pANCA, ASCA, GP2, CUZD1, CHI3L1, GM-CSF, ACA, PS/PT, ALCA, ACCA, AMCA, OmpC, I2, CBir1, Laminarin, Chitin, IFI16, IL-1 β , IL-6, IL-8, IL-9, IFN- γ , TNF, CCL2, IL-22, IL-2, and/or IL-6, as disclosed in Chen et al (2020) which is incorporated herein in its entirety by reference. Repair/healing can also be clinically assessed using ultrasound elastography, diffusion weighted MRI, or cross-sectional imaging (by ultrasonography, computed tomography, magnetic resonance or enterography) as disclosed in Sousa and Magro (2023) which is incorporated by reference in its entirety. In some embodiments, repair/healing is characterised by a 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 100% reduction in total lesion area.

In some embodiments, a histopathological assessment can be used to determine the effect of the MCIM compound and the MCIM compound in combination with a DMARD on IBD: Ileo-caecal tissue sections can be stained with Haematoxylin and Eosin (H&E) and parameters of inflammation, mucosal erosion, epithelial hyperplasia, epithelial metaplasia, mucus cell metaplasia, and fibroplasia are assessed on a scale of 0-5 as follows:

35

0: normal. 1: minimal, focal. 2: moderate, focal. 3: moderate, multi-focal or diffuse. 4: marked, focal. 5: marked, multi-focal or diffuse. In some embodiments, the MCIM compound in combination with the DMARD reduces the average score compared with a subject treated with a negative control, MCIM compound alone and/or a DMARD alone. In some embodiments, the MCIM compound in combination with the DMARD is for use in the treatment of IBD to reduce the average IBD score compared to administration of MCIM or DMARD alone. In some embodiments, the average score is reduced by at least 1, at least 2, at least 3, at least 4, or 5.

Disease control may be achieved by treatment with an MCIM compound and a DMARD. Disease control can comprise inhibition of disease progression, control of disease symptoms and/or supporting tissue repair. Inhibition of disease progression includes prevention of disease progression and slowing down disease progression. Standard methods in the art may be employed to determine disease progression.

Inhibition of disease progression, for example in subjects suffering from IBD, may be determined by the histopathological methods described above, or any other suitable method known in the art. For example, inhibition of disease progression may be determined by comparing histopathological results from a subject before and after treatment with the compositions disclosed herein. Inhibition of disease progression may be indicated by the histopathological score being stable (i.e. not changing) over time following treatment. Inhibition of disease progression may be indicated by the histopathological score progressing at a slower rate following treatment compared to disease progression before treatment.

In some embodiments, the csDMARD comprises methotrexate, azathioprine, chloroquine, D-penicillamine, ciclosporin, gold salts such as sodium aurothiomalate and auranofin, hydroxychloroquine, leflunomide, minocycline or sulfasalazine, or a combination of any of the foregoing, and the inflammatory and/or progressive disease is RA. In some embodiments, the csDMARD comprises azathioprine, ciclosporin, methotrexate or sulfasalazine, or any combination of the foregoing, and the inflammatory and/or progressive disease is an inflammatory bowel disease, such as Crohn's disease and ulcerative colitis. In some embodiments, the csDMARD comprises azathioprine, chloroquine, hydroxychloroquine, or methotrexate, or a combination of any of the foregoing, and the inflammatory and/or progressive disease is lupus erythematosus. In some embodiments, the csDMARD comprises leflunomide, methotrexate, or sulfasalazine, or a combination of any of the foregoing, and the inflammatory and/or progressive disease is psoriatic arthritis. In some embodiments, the csDMARD comprises methotrexate or sulfasalazine, or a combination thereof, and the inflammatory and/or progressive disease is reactive arthritis.

In some embodiments, tissue repair, disease regression, disease control, increase in reparative cells, decrease in destructive cells and/or reduction in cytokine production from pro-inflammatory myeloid

cells can be determined as defined herein. For instance, in some embodiments, the combination therapy reduces the levels of inflammatory mediators such as $\text{TNF}\alpha$, eSEL, CD38, CD40, CD69, sIgG, sIL-17A, sIL-17F, sIL-2 and/or sIL-6 that are produced by a target cell. In some embodiments, the combination therapy increases Coll IV expression. In some embodiments, the combination therapy increases ETC efficiency, without an increase in biomass. In some embodiments, the combination therapy reduces cellular proliferation without reducing ATP concentration/cell and viability, in the absence of pyruvate. In some embodiments, the combination therapy induces an adaptive/repair response under conditions of metabolic stress conditions, reducing cell death. For instance, the MCIMs compound modulates Complex I activity and attenuates high energy processes such as proliferation and concurrently induces an adaptive/repair response by increasing the production of pro-angiogenic/repair factors such as VEGF to restore tissue metabolic homeostasis, particularly under metabolic stress conditions. Each of these effects on tissue repair, disease regression, increase in reparative cells, decrease in destructive cells and/or reduction in cytokine production from pro-inflammatory myeloid cells can be determined by comparing the effect in the presence and absence of the combination therapy.

Pharmaceutical combinations

A pharmaceutical combination as disclosed herein refers to a combination comprising two or more active compounds. A pharmaceutical combination may comprise two or more compositions each comprising at least one active compound. In such embodiments, the two or more compositions may be administered separately, sequentially or simultaneously. For example, the pharmaceutical combination may comprise a first composition comprising an MCIM compound, such as HMC-C-01-A, and a second composition comprising a DMARD, such as methotrexate, azathioprine, chloroquine, hydroxychloroquine, ciclosporin, D-penicillamine, gold salt, sodium aurothiomalate, auranofin, leflunomide, or sulfasalazine, minocycline, or any combination of the foregoing. The first and second composition may be administered separately, sequentially or simultaneously.

Alternatively, a pharmaceutical combination may comprise a single composition comprising two or more active compounds. For example, the combination may comprise a single composition comprising an MCIM compound and a DMARD. In some embodiments, the MCIM compound comprises HMC-C-01-A. In some embodiments, the DMARD comprises one or more compounds selected from methotrexate, azathioprine, chloroquine, hydroxychloroquine, ciclosporin, D-penicillamine, gold salt, sodium aurothiomalate, auranofin, leflunomide, or sulfasalazine, minocycline, or any combination of the foregoing. In some embodiments, the composition comprises the MCIM compound HMC-C-01-A and a DMARD selected from methotrexate, sulfasalazine, hydroxychloroquine, leflunomide, azathioprine, or a combination thereof. In some embodiments, the

composition comprises the MCIM compound HMC-C-01-A and a bDMARD, for example rituximab or abatacept.

Pharmaceutical compositions

Medicaments and pharmaceutical compositions according to the aspects disclosed herein may be formulated for administration by a number of routes, including but not limited to, parenteral i.e. non-oral route (for example, by injection: sub-cutaneous, intravenous, intra-arterial, intramuscular, or intratumoural; by topical or intradermal; by inhalation or intranasal; or by rectal), and peroral i.e. oral route. The medicaments and compositions may be formulated in a solid, semi-solid, or liquid dosage form. The pharmaceutical compositions according to this invention may be delivered by a route which facilitates exposure in the systemic circulation or by a route or method which gives rise to localised, targeted, delivery of the active compounds to a selected region in the body. The pharmaceutical compositions according to this invention may also be administered to humans or animals.

Administration is preferably in a "therapeutically effective amount", this being sufficient to show benefit to the individual. The actual amount administered, and rate and time-course of administration, will depend on the nature and severity of the disease being treated. For example, the rate of release of the active compounds from the pharmaceutical composition may be immediate, sustained, extended, controlled, pulsatile or follow a pattern that is optimal for the intended therapeutic application. The frequency of dosing can be fixed or variable depending on the rate of drug release, the required level in the systemic circulation or at the target site to provide the desired therapeutic effect. Prescription of treatment, e.g. decisions on dosage etc., is within the responsibility of physicians and other medical doctors, and typically takes account of the disorder to be treated, the condition of the individual patient, the site of delivery, the method of administration and other factors known to practitioners. Examples of the techniques and protocols mentioned above can be found in Remington's Pharmaceutical Sciences, 23rd Edition, 2020, pub. Lippincott, Williams & Wilkins. The disclosure provides pharmaceutical combinations comprising a MCIM compound and a DMARD. In some embodiments, the combination may comprise a single composition comprising the MCIM compound and the DMARD. In other embodiments, the pharmaceutical combination may comprise a first composition comprising a MCIM compound and a second composition comprising a DMARD. In other embodiments, the combination comprises a first composition comprising a MCIM compound and a second compositions comprising two or more DMARDs. In embodiments wherein the combination comprises two or more DMARDs, the two or more DMARDs may be formulated as individual compositions comprising a single DMARD.

Pharmaceutical compositions may be prepared using a pharmaceutically acceptable "carrier" composed of materials, also known as excipients, that are generally considered safe and pharmacologically inert. "Pharmaceutically acceptable" refers to molecular entities and compositions that are "generally regarded as safe - GRAS", e.g., that are physiologically tolerable and do not

typically produce adverse or untoward effects when administered to a human. In some embodiments, this term refers to molecular entities and compositions approved by a regulatory agency of the US federal or a state government, as the GRAS list under section 204(s) and 409 of the Federal Food, Drug and Cosmetic Act, that is subject to premarket review and approval by the FDA or similar lists, the U.S. Pharmacopeia or another generally recognised pharmacopeia for use in animals, and more particularly in humans.

The term "carrier" refers to excipients that serve one or more functions in the pharmaceutical compositions, for example, as diluents, binders, lubricants, glidants, disintegrants, solubilisers or solubility enhancers, stabilisers, preservatives, taste-masking or taste-modifying agents, flavourant, and/or colourant. The pharmaceutical compositions, when formulated as a solid dosage form, may further be uncoated or coated with an outer layer to impart aesthetic features, physical protection, enhance the physical and/or chemical stability of the active compounds or other constituents of the pharmaceutical compositions, and/or alter the rate of dissolution and release of the active compounds from the pharmaceutical compositions. The pharmaceutical compositions, when formulated as a parenteral injectable dosage form, may additionally contain aqueous or non-aqueous solvents, co-solvent mixtures, buffering agents, surfactants, tonicity modifying agents, chelating agents, pH modifiers, viscosity modifiers, and/or suspending agents. The pharmaceutical compositions, when formulated as a parenteral dosage form for inhalation, may additionally contain particle carriers for the pulmonary delivery of the active compounds, absorption penetration enhancers, and/or propellants, dependent on the inhalation delivery device to be used. Those with skill in the art are familiar with such pharmaceutical carriers, excipients therein, and methods of compounding these excipients into pharmaceutical compositions. Suitable excipients for use in the pharmaceutical compositions can be found in standard pharmaceutical texts, for example, Handbook of Pharmaceutical Excipients, 9th edition, Pharmaceutical Press, American Pharmaceutical Association, 2020.

The choice of the pharmaceutical carrier is dependent on the dosage form type, the dose, intended route of delivery, the physicochemical properties of the active compounds, and the required bioavailability and/or exposure profile. When used, the excipients of the pharmaceutical compositions should not adversely affect the stability, bioavailability, safety, and/or therapeutic efficacy of the active compounds, i.e. the MCIM compound and/or the DMARD compound used in the pharmaceutical compositions. Thus, the skilled person will appreciate that pharmaceutical compositions are provided wherein there is no significant incompatibility between any of the components of the dosage form.

The pharmaceutical compositions provided herein may include one or more excipients, e.g., solvents, solubility enhancers, suspending agents, buffering agents, isotonicity agents, antioxidants or antimicrobial preservatives. When used, the excipients of the compositions will not adversely affect the stability, bioavailability, safety, and/or efficacy of the active ingredients, i.e. the MCIM compound and/or the TNF inhibitor compound used in the composition. Thus, the skilled person will appreciate that compositions are provided wherein there is no incompatibility between any of the components of

the dosage form. Excipients may be selected from the group consisting of buffering agents, solubilizing agents, tonicity agents, chelating agents, antioxidants, antimicrobial agents, and preservatives. Suitable carriers, diluents, excipients, etc. can be found in standard pharmaceutical texts, for example, Handbook of Pharmaceutical Excipients, 9th edition, Pharmaceutical Press,

5 American Pharmacists Association, 2020.

It may be convenient or desirable to prepare, purify, and/or handle a corresponding solvate of the active compound(s). The term "solvate" is used herein in the conventional sense to refer to a complex of solute (e.g., active compound, salt of active compound) and solvent. If the solvent is water, the solvate may be conveniently referred to as a hydrate, for example, a mono-hydrate, a di-

10 hydrate, a tri-hydrate, etc.

Unless otherwise specified, a reference to a particular compound also includes the solvate forms thereof.

It may be convenient or desirable to prepare, purify, and/or handle a corresponding salt of the active compound(s), for example, a pharmaceutically-acceptable salt of an MCIM compound, for example

15 HMC-C-01-A, or a DMARD. Examples of pharmaceutically acceptable salts are discussed in Berge et al., 1977, "Pharmaceutically Acceptable Salts," J. Pharm. Sci., Vol. 66, pp. 1-19.

For example, if the compound is anionic, or has a functional group which may be anionic (e.g., COOH may be COO), then a salt may be formed with a suitable cation. If the compound is cationic or has a functional group which may be cationic (e.g., NH₂ may be NH₃⁺), then a salt may be formed with a

20 suitable anion.

Unless otherwise specified, a reference to a particular compound also include salt forms thereof.

SPECIFIC COFORMULATIONS

The pharmaceutical compositions according to this invention include, but are not limited to, dosage forms wherein the active compounds are co-formulated uniformly in a common excipient base, such

25 as a conventional single-layer tablet or conventional powder-in-capsule for oral administration; a solution, suspension or dispersed system for parenteral administration; a lotion, cream, ointment for topical administration; a transdermal patch, microneedle or autoinjector system for transdermal administration; a dry powder, solution or suspension for inhalation administration; and a solution or suspension for intranasal administration.

Alternative pharmaceutical compositions, particularly useful for solid dosage forms for oral administration, are provided according to this invention wherein the active compounds are physically separated within a single pharmaceutical composition to avoid the potential for physical and chemical interactions and incompatibilities. Such pharmaceutical compositions include, but are not limited to, a bi-/multi-layer tablet, wherein the formulation of each layer is optimised for each active compound,

35 which can be combined in a single pharmaceutical composition by conventional tablet compression.

Such pharmaceutical compositions may also include a single-layer or bi-/multi-layer tablet wherein one of the active compounds is contained within a layer that is coated on the outside of the single-layer or bi-/multi-layer compressed tablet core, thus, providing a physical separation of the active compounds and their associated excipient systems. A further alternative pharmaceutical composition according to this invention is a multi-particulate capsule, wherein the formulation of each active compound in a particulate/granular form can be optimised, then combined and encapsulated into a conventional capsule as a single pharmaceutical composition.

The methods for the preparation of the pharmaceutical compositions accordingly to this invention are well known to the skilled person in the art and are well described in standard pharmaceutical formulation textbooks, such as Remington, The Science and Practice of Pharmacy, Editor: Adeboye Adejare, 23rd edition, 2020, publisher: Elsevier, Aulton's Pharmaceutics, The Design and Manufacture of Medicines, editors: Kevin Taylor and Michael Aulton, 6th edition, 2021 publisher: Elsevier, and Lachman/Liebermans: The Theory and Practice of Industrial Pharmacy, Editors: Roop Khar, SP Vyas, Farnham Ahmad, Gaurav Jain, 4th edition, 2014, publisher: CBS.

Sequence Listing

Human NDUF52 amino acid sequence SEQ ID NO: 1:

MAALRALCGFRGVAAQVLRPGAGVRLPIQPSRGVRQWQPDVEWAQQFGGAVMYPKETAHWKPP
PWNDVDPPKDTIVKNITLNFPGQHPAAHGVLRLVMEISGEMVRKCDPHIGLLHRGTEKLIYEKTYLQA
LPYFDRLDYVSMCMNEQAYSLAVEKLLNIRPPRAQWIRVLFGEITRLLNHIMAVTTHALDLGAMTPFF
WLFEEREKMFIFYERVSGARMHAAYIRPGGVHQDLPLGLMDDIYQFSKNFSRLDELEELLTNNRIW
RNRTIDIGVVTAEALNYGFSGVMLRSGSIQWDLRKTQPYDVYDQVEFDVPVGSRGDCYDRYLRCRV
EEMRQSLRIIAQCLNKMPPEIKVDDAKVSPPKRAEMKTSMESLIHHFKLYTEGYQVPPGATYTAIEA
PKGEGFVYLVSDGSSRPYRCKIKAPGFAHLAAGLDKMSKGHMLADVVAIIGTQDIVFGEVDR

Human NDUF57 amino acid sequence SEQ ID NO:2:

MAVLSAPGLRGFRILGLRSSVGPAVQARGVHQSVATDGPSSSTQPALPKARAVAPKSSRGEYVAK
LDDLNVWARRSSLWPMTFGLACCAVEMMHMAAPRYDMDRFGVVFRASPRQSDVMIVAGTLTNKMA
PALRKVYDQMPEPRYVSMGSCANGGGYYHYSYSVVRGCDRIVPVDIYIPGCPPTAEALLYGILQLQ
RKIKRERRRLQIWYRR

The features disclosed in the foregoing description, or in the following claims, or in the accompanying drawings, expressed in their specific forms or in terms of a means for performing the disclosed function, or a method or process for obtaining the disclosed results, as appropriate, may, separately, or in any combination of such features, be utilised for realising the invention in diverse forms thereof.

While the invention has been described in conjunction with the exemplary embodiments described above, many equivalent modifications and variations will be apparent to those skilled in the art when given this disclosure. Accordingly, the exemplary embodiments of the invention set forth above are considered to be illustrative and not limiting. Various changes to the described embodiments may be made without departing from the spirit and scope of the invention.

For the avoidance of any doubt, any theoretical explanations provided herein are provided for the purposes of improving the understanding of a reader. The inventors do not wish to be bound by any of these theoretical explanations.

Any section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

Throughout this specification, including the claims which follow, unless the context requires otherwise, the word “comprise” and “include”, and variations such as “comprises”, “comprising”, and “including” will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

It must be noted that, as used in the specification and the appended claims, the singular forms “a,” “an,” and “the” include plural referents unless the context clearly dictates otherwise. Ranges may be expressed herein as from “about” one particular value, and/or to “about” another particular value. When such a range is expressed, another embodiment includes from the one particular value and/or to the other particular value. Similarly, when values are expressed as approximations, by the use of the antecedent “about,” it will be understood that the particular value forms another embodiment. The term “about” in relation to a numerical value is optional and means for example +/- 10%.

Examples

EXAMPLE 1 – BioMAP profiling

A high-throughput integrative biology platform (BioMAP ®) was used to profile the effect of MCIM compounds on multiple disease-associated regulatory pathways. BioMAP® has been developed as a method to assess efficacy, safety and the mechanism of action of drugs in multiple human cell types stimulated with inflammatory challenges as described in US6656695, which is incorporated herein in its entirety. The BioMAP system reflects human disease pathology and has the ability to detect and distinguish the effects of approved drugs and investigational human therapeutic compounds. BioMAP technology enables rapid determination of efficacy, side effects and mechanism of action of drug candidates.

BioMAP® provides an unbiased, target-agnostic and data-driven approach to understanding compound or combination therapy impact on human disease models and translational biomarkers. The system is validated with clinically approved drugs and known test agents. The principle of the assay is to test compounds in human primary cell-based disease systems, and compare the data with a Reference Database of over 4,500 compounds. The profile of a compound can be compared against a reference compound to see if the biological activity of the test item is differentiated from the reference.

The activity of MCIM compounds was determined in three BioMAP systems; Fibrosis panel, Autoimmune panel HDFSAg and Diversity Plus.

- 10 Thirteen primary human cell and co-culture assays were used to assess the effects of MCIM compounds on clinically relevant protein biomarkers of inflammation, cell growth, and fibrosis as part of the quality controlled BioMAP® Diversity PLUS, commercially available service (Eurofins DiscoverX Corporation, Fremont, CA, USA; for full details <https://www.discoverx.com>). Briefly, the BioMAP® panels consist of human primary cell-based systems designed to model different aspects of the human body in an in vitro format. The 12 cell assays utilised in the Diversity PLUS panel allow characterisation of test agent responses in an unbiased way across a broad set of systems modelling various human disease states compared to historical controls. BioMAP® panels are constructed with primary cell types from healthy human donors, with stimuli (such as cytokines or growth factors) added to capture relevant signalling networks that naturally occur in human tissue or pathological conditions.

- MCIM Compounds were tested in these assays at four concentrations: 4000 nM, 1300 nM, 400 nM & 150 nM. Human primary cells employed in the BioMAP® systems were used at passage 4 or earlier, derived from multiple donors (n = 2–6), commercially purchased and handled according to the recommendations of the manufacturers. Human blood derived CD14 + monocytes were differentiated into macrophages in vitro before being added to the LPS system (Eurofins DiscoverX Corporation).

- The human cell types and stimuli used in each assay system were as follows: 3 C system [human umbilical vein endothelial cells (HUVEC) + (IL-1 β , TNF α and IFN γ)], 4H system [HUVEC + (IL-4 and histamine)], lipopolysaccharide (LPS) system [peripheral blood monocyte cells (PBMC) and HUVEC + LPS (TLR4 ligand)], Sag system [peripheral blood mononuclear cells, PBMC and HUVEC + TCR ligands], HDFSAg system [peripheral blood mononuclear cells, PBMC and human neonatal dermal fibroblasts + TCR ligands], BT system [CD19 + B cells and PBMC + (α -IgM and TCR ligands)], BF4T system [bronchial epithelial cells and human neonatal dermal fibroblasts, HDFn, + (TNF α and IL-4)], BE3C system [bronchial epithelial cells + (IL-1 β , TNF α and IFN γ)], CASM3C system [coronary artery smooth muscle cells + (IL-1 β , TNF α and IFN γ)], HDF3CGF system [HDFn + (IL-1 β , TNF α , IFN γ , EGF, bFGF and PDGF-BB)], KF3CT system [keratinocytes and HDFn + (IL-1 β , TNF α , IFN γ and TGF β)], MyoF system [differentiated lung myofibroblasts + (TNF α and TGF β)], SAEMyoF

system [small airway epithelial cells and differentiated lung myofibroblasts + (TNF α and TGF β)], ReMyoF system [renal epithelial cells and differentiated lung myofibroblasts + (TNF α and TGF β)] and IMphg system [HUVEC and M1 macrophages + Zymosan (TLR2 ligand)].

Assays were derived from either single cell types or co-culture systems. Adherent cell types were
5 cultured in 96 or 384-well plates until confluence, followed by the addition of PBMC (Sag and LPS systems). The BT system consisted of CD19 + B cells co-cultured with PBMC and stimulated with a BCR activator and low levels of TCR stimulation. Test agents prepared in either DMSO (small molecules; final concentration $\leq$ 0.1%) or PBS (biologics) were added at the indicated concentrations 1 h before stimulation, and cells remained in culture for 24 h or as otherwise indicated [48 h, MyoF
10 system; 72 h, BT system (soluble readouts); 168 h, BT system (secreted IgG)]. Each assay plate contained negative controls (e.g., non-stimulated conditions) and vehicle controls (e.g., 0.1% DMSO) appropriate for each system. Direct ELISA was used to measure biomarker levels of cell-associated and cell membrane targets. Soluble factors from supernatants were quantified using either HTRF $\text{\textcircled{R}}$ detection, bead-based multiplex immunoassay, or capture ELISA. Overt adverse effects of
15 (compounds) on cell proliferation and viability (cytotoxicity) were detected by sulforhodamine B (SRB) staining for adherent cells, and alamarBlue $\text{\textcircled{R}}$ reduction for cells in suspension. For proliferation assays, individual cell types were cultured at subconfluence and measured at time points optimised for each system (48 h: 3 C and CASM3C systems; 72 h: BT and HDF3CGF systems; 96 h: HDFSAg and Sag system). Cytotoxicity for adherent cells was measured by SRB (24 h: 3 C, 4H, LPS, Sag, HDFSAg, BF4T, BE3C, CASM3C, HDF3CGF, KF3CT, and IMphg systems; 48 h: MyoF system), and
20 by alamarBlue $\text{\textcircled{R}}$ staining for cells in suspension (24 h: HDFSAg and Sag system; 42 h: BT system) at the time points indicated.

Biomarker measurements in treated samples were divided by the average of the control samples (at least 6 vehicle controls from the same plate) to generate a ratio that was then log₁₀ transformed.
25 Significance prediction envelopes were calculated using proprietary historical vehicle control data at a 95% confidence interval. Biomarker activities were annotated when two or more consecutive concentrations change in the same direction relative to vehicle controls were outside of the significance envelope and had at least one concentration with an effect size > 20% (log₁₀ ratio > 0.1). Biomarker key activities were described as modulated if these activities increase in some systems but
30 decrease in others. Cytotoxic conditions were noted when total protein levels decreased by more than 50% (log₁₀ ratio of SRB or alamarBlue $\text{\textcircled{R}}$ levels < -0.3) and were indicated by a thin black arrow above the X-axis. A compound was considered to have broad cytotoxicity when cytotoxicity was detected in 3 or more systems. Concentrations of test agents with detectable broad cytotoxicity were excluded from biomarker activity annotation and downstream benchmarking, similarity search and
35 cluster analysis. Antiproliferative effects were defined by an SRB or alamar Blue $\text{\textcircled{R}}$ log₁₀ ratio value < -0.1 from cells plated at a lower density and were indicated by grey arrows above the X-axis.

Cytotoxicity and antiproliferative arrows only require one concentration to meet the indicated threshold for profile annotation.

Figure 2 shows the BioMAP profile of several MCIM compounds. (A) ABD599 tested in the full BioMAP profile shows decreased inflammation and immune modulation, and tissue remodelling with increased collagen IV levels. (B) HMC-C-01-A shows anti-inflammatory and immune modulation activity in the BT and Sag systems and (C) HMC-C-01-A in the fibrosis panels increases Collagen type IV.

Figure 3 shows the BioMAP profile of several DMARD drugs in the HDFSag system, modelling inflammation, fibrosis and wound healing biology using fibroblasts and peripheral blood mononuclear cells. (A) methotrexate shows decreased inflammation and immune modulation, and decreased tissue remodelling with reduced VEGF and matrix Type I collagen. Sulfasalazine shows decreased inflammation with reduced sIL-8 and sIL-6, with no effect on Type 1 collagen. (B) tocilizumab shows reduced inflammation and mixed immune modulation activities and reduces tissue remodelling with reduced VEGF. Prednisilone shows decreased inflammation and immune modulation, and decreased tissue remodelling with pronounced reduction in VEGF. (C) abatacept shows decreased inflammation and decreased tissue remodelling with reduced Type I collagen. (D) HMC-C-01-A shows more pronounced effects on inflammation and immune modulation, and tissue remodelling with decreased MMP-1 and sVEGF but increases in the matrix Type I collagen. Apremilast shows limited effects on inflammation and no impact on immune modulation or tissue remodelling. (E) etanercept and adalimumab, both of which act by blocking the action of TNF α , show decreased inflammation and immune modulation. (F) tofacitinib and baricitinib, which both inhibit JAK/STAT signalling, show decreased inflammation and mixes effects on immune modulation and tissue remodelling. (G) ustekinumab shows limited immune modulation, and inflammation activities, but a decrease in tissue remodelling via VEGF.

The data demonstrate that MCIM compounds have a distinct phenotypic profile compared approved DMARDs. MCIM compounds demonstrate multi-modal actions, having specific effects in different cell types following stimulation with different inflammatory mediators. In particular, the MCIM compounds modulate immune activities by reducing the levels of inflammatory mediators such as TNF α , e-selectin, CD38, CD40, CD69, sIgG, sIL-17A, sIL-17F, sIL-2 and sIL-6. In addition, the MCIM compounds show potential for tissue remodelling as indicated by the decrease in Col I and MMP1. Particularly of note, the MCIM compounds increase production of Coll IV, a critical basement membrane collagen which is involved in tissue repair and remodelling activities.

Table 2 shows the key differences between the activities regulated by the MCIM compound HMC-C-01-A and the DMARD drugs methotrexate, leflunomide, and azathioprine, and the corticosteroid prednisolone (O'Mahony et al, 2014 and O'Mahony and Choy, E, 2017). HMC-C-01-A modulates immune activities, with reduced levels of inflammatory mediators such as such as TNF α , eSEL,

CD38, CD40, CD69, sIgG, sIL-17A, sIL-17F, sIL-2 and sIL-6. Particularly of note, the compounds also modulated genes involved in tissue repair and remodelling activities. In particular, HMC-C-01-A caused an increase in Coll IV, a critical basement membrane collagen which is involved in tissue repair and remodelling activities, as well as decreasing Coll I and MMP1.

5

Table 2					
Key activities in bioMAP					
	HMC-C-01-A	Methotrexate	Leflunomide	Azathioprine	Prednisilone
System	Sag, BT, MyoF, SAEMyoF, ReMyoF	All	All	All	All
Inflammation	decreased Esel and sTNF α , M-CSF, ITAC, MCP-1, sIL6	decreased IgG production, T-cell proliferation, VCAM-1, IL-8 IL-2	decreased IgG production, T-cell proliferation	decreased IgG production, T-cell proliferation	Decreased sTNF α , sIL2, MCP-1, SAA, sIL8
Immune modulation	decreased CD38, CD40, CD69, sIgG, sIL-17A, sIL-17F, sIL-2 and sIL-6				
Tissue remodelling	Decreased VEGF, MMP1, MMP9 Increased Coll IV, αSMA	Decreased Coll I, VEGF			

Example 2

The ability of mitochondria to undergo fusion and fission processes is essential to mitochondrial function and cellular health. Qualitative and/or quantitative changes in the mitochondrial reticulum are also observed under pathological conditions that are caused by inherited mutations in mitochondrial DNA or in nuclear OXPHOS genes and suggest a tight relationship between mitochondrial structure and function. In addition, several lines of evidence suggest that the damage response of injured cells can be ameliorated by the presence of healthy mitochondria (Jin,*et al*, 2019, which is hereby incorporated by reference in its entirety). Studying mitochondrial form and function may therefore yield important insights into the potential of cells and tissues to recover from damage. Osteoclasts are a highly energetic cell type sensitive to changes in mitochondrial metabolism that are suitable for evaluating such relationships.

Peripheral blood mononuclear cells were isolated from human whole blood by differential centrifugation over Ficoll-Paque PLUS (GE Healthcare Biosciences). CD14+ monocytes were purified

from the freshly isolated PBMCs using the CD14⁺ selection kit (StemCells. UK) by positive magnetic selection according to manufacturer's instructions. Cells were differentiated to osteoclasts by adding 1x10⁶ ml⁻¹ cells in complete minimum essential medium- α supplemented with 10% heat inactivated fetal bovine serum (FBS, Invitrogen,UK), 2mM glutamine (Invitrogen,UK) 20U ml⁻¹ penicillin, 100ug/ml streptomycin (Sigma ALdrich, UK) along with 25ng ml⁻¹ recombinant human M-CSF (Peprotech, UK) and 25 ng ml⁻¹ RANKL for 6 days. On the 6th day, the cells were treated with test compound (final concentration 0.03–1 μ M, 0,05 % DMSO) or a control, rotenone (100 nM).

Adherent cells were fixed in 2.5% glutaraldehyde in 0.1 M cacodylate buffer, pH 7.4, for 1 h, post fixed with 1% osmium tetroxide (Electron Microscopy Science), dehydrated in a graded series of ethanol, and embedded in Epon (Electron Microscopy Science). The embedded samples were sectioned by an ultramicrotome (Ultracut E, Richert-Jung, Leica Microsystem). Thin sections (90 nm thick) were collected on 300 mesh nickel grids and stained with uranyl acetate (Electron Microscopy Science) and lead citrate. Samples were observed by using a Zeiss EM 109 apparatus (Zeiss). Images were captured using a Nikon digital camera Dmx 170 1200F and ACT-1 software.

Representative images are shown in Figure 4. Top left panel; control cells show a heterogenous and dynamic population of mitochondria with a good balance of fusion and fission (mitochondria (M) and endoplasmic reticulum (ER)). Top right panel; cells treated with the archetypal Complex I inhibitor, rotenone show increased numbers of abnormal mitochondria which were more rounded and had condensed cristae with evidence of fragmentation, and evidence of lysosomes (L) close by. Middle left panel; 0.03 μ M ABD900 showed increased tubular mitochondrial with evidence of extrusion budding, consistent with an adaptive change in mitochondrial structure to increase mitochondrial area without an overt increase in organelle biomass. Dumbbell morphology, consistent with the formation of electron transport chain (ETC) super-complexes, were also observed. Middle right panel; 0.1 μ M ABD900 showed a similar profile with evidence of cristae refraction. Bottom left panel; 0.3 μ M ABD900 shows filamentous extensions in many mitochondria consistent with an attempt to enlarge cristae volume. Bottom right panel; 1 μ M ABD900 shows a heterogenous mitochondrial population with rounded morphology and condensed cristae.

The results demonstrate that, in contrast to the classical Complex I blocker, rotenone, the MCIM compounds elicit a mitochondrial phenotype consistent with differentiation based on maturity. For example, older mitochondria, which are usually cleared by mitophagy, are retained as part of an integrated stress response. To increase ETC efficiency, without an overt increase in biomass, structural adaptation occurs to maintain cellular free energy.

EXAMPLE 3 – Cellular metabolism and viability

The *in vitro* effects of test compounds on cellular metabolism and viability were determined by incubation with human primary lung fibroblasts followed by measurement of cellular ATP concentrations and cell counts.

ATP is an organic compound which can be produced by several cellular processes such as glycolysis and oxidative phosphorylation. However, if levels of oxygen, or substrates to fuel oxidative phosphorylation are insufficient, cells can reprogramme their metabolism towards glycolysis or other pathways to maintain their availability of ATP. Depending on the environment of the cell, such changes in metabolism may be accompanied by adaptive changes in gene expression. For example, under certain culture conditions, cells may upregulate an 'adaptive response' gene known as vascular endothelial growth factor (VEGF); VEGF encodes a proangiogenic protein (VEGF), whose function to induce new blood vessel formation to seek out new sources of oxygen and nutrients. This is critical to eliciting a functional repair response. By modulating the activity of Complex I, the MCIM compounds disclosed herein modulate ATP production, and thereby induce a cellular adaptation response.

The effects of the MCIM compounds on cellular adaptation was assessed in vitro in human primary lung fibroblasts (HLF). Cells were cultured with different metabolic substrates- glucose, L-glutamine, and pyruvate- to explore potential changes according to the microenvironment of the cell. Cells cultured in these conditions were treated with compound at various concentrations, and intracellular ATP concentrations, nucleus counts, and VEGF secretion were measured to quantify cell viability, metabolism, and indications of adaptive response.

Human primary lung fibroblasts were plated at a concentration of 2×10^3 cells/well in 96-well plates in 100 μ L DMEM complete media (5.5 mM glucose, 2 mM L-glutamine, and 1 mM pyruvate) containing 1% penicillin-streptomycin and 10% heat inactivated foetal bovine serum. Cells were incubated at 37°C / 5% CO₂ overnight to allow cell attachment. On the day of the treatment, cell culture medium was removed, and the cells were washed three times with Gibco™ DMEM, no glucose, no L-glutamine, no pyruvate, no phenol red + 1% penicillin-streptomycin and 10% heat inactivated foetal bovine serum (termed 'basal' culture medium). Fresh cell culture supplemented with 5.5 mM glucose alone, 5.5 mM glucose and 2 mM L-glutamine, or 5.5 mM glucose, 2 mM L-glutamine, and 1 mM pyruvate was added to the wells. Test compounds were prepared as 10x final concentration solutions in each appropriate culture medium. Compounds were added to the cultures at 1x final concentration and incubated at 37°C / 5% CO₂ for 1 or 3 days. On day 1, VEGF secretion was measured from cell culture supernatants; 72 hours post treatment, cells were assayed for nucleus counts and ATP generation.

To assess nucleus counts, formaldehyde was added to a final concentration of 4%. Following a further 20-minute incubation at room temperature, the medium was aspirated, the cells were washed twice with 200 μ L TBS-T (1x TBS + 0.1% Tween 20) and the nuclei were stained with 50 μ L of PBS containing 10% heat inactivated foetal bovine serum, 0.1% Triton-X-100 and 2 μ M Hoechst dye. Following a 30-minute incubation at room temperature, protected from light, the cells were washed twice with TBS-T, and cells were counted in 100 μ L PBS solution using an ImageXpress Pico system with stitched plate acquisition (4x magnification), DAPI channel (50ms exposure, -3 digital confocal setting).

To assess ATP concentration, 50 μ L of reconstituted ATPlite substrate solution (ATPlite 1step Luminescence Assay System, Perkin Elmer) was added to the cells. After a 5-minute incubation at room temperature on a plate shaker, luminescence was measured on a BMG Plate reader (PHERAstar) using LUM plus module, gain 3000, CR 96/384 aperture spoon (type A3).

- 5 The average values across the concentrations tested were then plotted and the half-maximal inhibitory concentration (IC_{50}) for the effect on ATP or nuclei counts was calculated by fitting the data to a four-parameter IC_{50} equation using GraphPad Prism software (v9). ATP readout per nuclei count was calculated by dividing ATPlite luminescence readout values by the Hoechst-stained nuclei count number per test concentration.
- 10 To assess VEGF secretion, cell supernatants of three replicate wells were combined and VEGF secretion was measured following the Quantikine® ELISA Human VEGF kit manufacturer instructions. Absorbance at 450 nm was measured on a BMG Plate reader (CLARIOstar plus) using pathlength correction. Background absorbance was measured at 540 nm.

Data were normalised to a VEGF standard curve and expressed as the average of the control wells in pg/mL. Data were plotted and the IC_{50} for the effect on VEGF secretion was calculated by fitting the data to a four-parameter IC_{50} equation using GraphPad Prism software (v9).

The results are shown in Figure 5.

- Figure 5A consists of 3 panels showing intracellular ATP (left panel), nucleus counts (middle panel) and ATP readout per cell (right panel) after 72 hrs incubation with MCIM compound. In cells cultured
- 20 in glucose-supplemented media (squares), there was no effect of the MCIM compound on intracellular ATP levels, nuclei count or ATP readout per cell. In cells cultured in media supplemented with glucose and glutamine (open circles), there was an increase in intracellular ATP levels and nucleus counts given vehicle compared to cells cultured with glucose alone. Treatment of cells cultured in medium supplemented with glucose and glutamine with the MCIM compound reduced intracellular
- 25 ATP levels and nucleus counts, in a concentration-dependent manner, with no effect on ATP levels per cell. When the basal culture media supplemented with glucose, L-glutamine was enriched with pyruvate (filled circles), the effect of the MCIM compound on intracellular ATP and nucleus counts seen in the medium supplemented with glucose and L-glutamine alone was eliminated.

- The results show that in cells cultured in basal medium containing glucose, the MCIM compound had
- 30 showed no cytotoxicity and had no effect on cell viability. When the cells were cultured in medium supplemented with glucose and L-glutamine, there was an increase in intracellular ATP levels and nucleus counts reflecting that L-glutamine is a precursor amino acid essential for cellular proliferation. The reduction in intracellular ATP and nucleus counts seen in the cells cultured with glucose and L-glutamine, and lack of effect on ATP levels per cells shows that the cells were adapting to the
- 35 metabolic effects of Complex I modulation by the MCIM compound by limiting highly energy-demanding processes, such as cellular proliferation, in order to maintain their intracellular levels of

ATP. In addition, the reversal of this effect with the medium was supplemented further with pyruvate (glucose + L-glutamine + pyruvate condition) shows that the adaptive response observed (reduction of cell proliferation) is dependent on nutrient availability to the cell.

Figure 5B shows that in complete medium, there is no effect of the MCIM compound on VEGF secretion (filled circles (●)), but in the absence of pyruvate in the media (open circles (○)), the MCIM compound elicited a concentration-dependent increase in VEGF secretion (half-maximal inhibitory concentration (IC_{50}) = 112 nM).

The results show that by modulating Complex I, in the absence of an excess of substrate, cells trigger an adaptive response to cause growth and repair by upregulating VEGF. The absence of an effect when pyruvate was present in the medium, shows that the adaptive repair response is also dependent on nutrient availability.

In summary, the results show that treatment with MCIM compounds disclosed herein induces an adaptive response to enable cells to maintain their supply of ATP. When cells are treated with MCIM compound, they attempt to restore tissue homeostasis by reducing energy-intensive activities such as proliferation and increasing production of growth factors such as VEGF. This occurs without any effect on cell viability.

EXAMPLE 4

Classical Complex I inhibitors often cause cytotoxicity and cell death and despite reports of anti-tumour effects for compounds such as IACS-010579 the known inhibitors have not found use as approved therapeutics, largely due to mechanism-based toxicity (Yap, T *et al*, 2023). As such, identifying a suitable approach for complex I inhibition that provides a benefit without toxicity has proved to be a challenge. An alternative approach which does not elicit adverse effects may have potential benefits for the treatment of a variety of progressive diseases. In this study, the inventors evaluated whether the MCIM compounds disclosed herein showed differences in their cellular behaviour compared with known Complex I inhibitors, IACS-010579 and rotenone.

Human primary lung fibroblasts were plated at a concentration of 5×10^3 cells/well in 96 well plates in 100 μ L DMEM complete media (5.5 mM glucose, 2 mM L-glutamine, and 1 mM pyruvate) containing 1% penicillin-streptomycin and 10% heat-inactivated foetal bovine serum. Cells were incubated overnight at 37°C / 5% CO₂ to allow cell attachment. On the day of the treatment, cell culture medium was removed, and the cells were washed three times with Gibco™ DMEM, no glucose, no L-glutamine, no pyruvate, no phenol red + 1% penicillin-streptomycin and 10% heat inactivated foetal bovine serum (termed 'basal' culture medium). Fresh cell culture media (without pyruvate) was added to the wells. Test compounds were prepared as 10x final concentration solutions in pyruvate-free medium. Following 24-hours compound treatment (in 5% CO₂, 37°C cell incubator), spent medium was removed from all wells and were thoroughly washed thrice with basal cell culture medium. For

washout assay condition, 100 μ L of pyruvate-free media was added per well. For No Washout, 90 μ L of pyruvate-free media and 10 μ L of 10x final assay concentration prepared test agents (or assay media) were added per well. Recovery of cell proliferation was measured after 24-hours incubation at 37°C / 5% CO₂ with either pyruvate-free media (without re-addition of the compound) or re-addition of compounds in pyruvate-free media.

To assess nucleus counts, formaldehyde was added to a final concentration of 4%. Following a further 20-minute incubation at room temperature, the medium was aspirated, the cells were washed twice with 200 μ L TBS-T (1x TBS + 0.1% Tween 20) and the nuclei were stained with 50 μ L of PBS containing 10% heat inactivated foetal bovine serum, 0.1% Triton-X-100 and 2 μ M Hoechst dye.

- 10 Following a 30-minute incubation at room temperature, protected from light, the cells were washed twice with TBS-T, and cells were counted in 100 μ L PBS solution using an ImageXpress Pico system with stitched plate acquisition (4x magnification), DAPI channel (50 ms exposure, -3 digital confocal setting).

- 15 When cells grow and divide (termed proliferation), cells progress through the cell cycle, a tightly regulated process that consists of two main activities: DNA replication and mitosis/cell division. As a method of accurately quantifying cellular proliferation rate, the pyrimidine analogue, BrdU can be utilised to measure DNA replication. BrdU can be incorporated into the newly synthesized DNA in place of thymidine. Following incubation of proliferating cells with BrdU for 20 hours, labelling solution was removed thoroughly, and cells were fixed with 70 μ L of fix solution for 30 min at room
20 temperature. Fix solution was aspirated, and anti-BrdU-Eu antibodies were added for 2 hours at room temperature in the dark. Wells were washed thrice with wash solution and 70 μ L of DELFIA inducer per well was added and incubated for 30 min, in the dark. Eu-fluorescence was measured in a time-resolved manner using the PHERAstar FSX (Ex337/ Em620 nm). Data were plotted and a curve was fitted using a 4-parameter equation with GraphPad Prism software.

- 25 The results are shown in Figure 6. The figure shows 4 panels: cell proliferation inhibition measured by BrdU incorporation (A) and nucleus counts (B), and effects of compound washout on cell proliferation by BrdU incorporation (C) and nucleus counts (D) at the highest tested concentration. In panels A and B, ABD900 is shown in filled circles (●), rotenone is shown in grey squares (■) and IACS-010759 in open circles (○). In panel C-D, cells without washout are shown in solid black (IACS-010759) and grey (Rotenone) fill, and washout in open black (IACS-010759) and grey (rotenone) bars. For
30 ABD900, washout cells are shown with an open fill pattern and cells not washed out are shown in a checkerboard fill. Data are mean $\pm$ s.e.m..

- The results show that typical Complex I inhibitors such as IACS-010759 and rotenone reduce cell proliferation (BrdU incorporation and nucleus counts) when cells are cultured in pyruvate-restricted
35 conditions. For known Complex 1 inhibitors such as IACS-010759 and rotenone, there is no recovery from these effects when the compounds are washed out. However, for the MCIM compound, there is

a recovery in the proliferative capacity (BrdU incorporation and nucleus counts) of the cells after the compound is washed out. Overall, the data together show that the MCIM compounds disclosed herein display different cellular effects to the known, archetypal, inhibitors of Complex I.

5 EXAMPLE 5 – Single agent and combination treatment of mice with collagen-induced arthritis

Seven- to eight-week-old male DBA/1j mice were used for all procedures. Animals were housed in groups of 10 and were maintained at 21°C ± 2°C on a 12-hour light/dark cycle with food and water ad libitum. Complete Freund's adjuvant (CFA) was prepared by emulsifying bovine type II collagen at 4 mg/mL with a 4 mg/mL suspension of Mycobacterium tuberculosis H37Ra in Incomplete Freund's adjuvant (IFA) (0.85 mL paraffin oil and 0.15 mL mannide monooleate) in a 1:1 (v/v) ratio. All mice were immunised subcutaneously with 200 µg of bovine type II collagen in CFA. 21 days later, all mice were immunised subcutaneously with 100 µg of bovine type II collagen in IFA. The mice started to develop signs and symptoms of arthritis following the 'booster' immunisation.

For macroscopic assessment of arthritis, the following signs were monitored in each paw of each mouse three times per week and summed to generate the Arthritic Index (AI) (the maximum AI for one animal is 16):

- 0 = no visible effects of arthritis.
- 1 = oedema and/or erythema of 1 digit.
- 2 = oedema and/or erythema of 2 digits.
- 20 3 = oedema and/or erythema of more than 2 digits.
- 4 = severe arthritis of entire paw and digits.

Figure 7 shows seven graphs, each of average arthritic index as a function of time (dosing day) for test compound dosed at 10 mg/kg/day by oral gavage (open circles (O)) and control (solid circles (●)), for each of: (A) HMC-C-02-A, (B) HMC-C-01-A, (C) HMC-N-02-A, (D) HMC-N-01-A, (E) NASMP-01-A, (F) CHMSA-01-A, (G) CHMSA-03-A. These data indicate that the MCIM compounds described herein show excellent oral *in vivo* activity in preventing the progression of established, severe arthritis.

Animals were sorted into treatment groups with a mean arthritic index of 2.5 and then dosed once daily for 14 days with compound by oral gavage. On Day 14, animals were sacrificed, and limbs were fixed in 10% neutral buffered formalin.

30 The fixed limbs were processed into paraffin blocks and sectioned, and then stained using Toluidine Blue.

For histopathological assessment of the biological effects of MCIM compounds in arthritis, bone resorption was assessed by a direct count per bone of areas showing evident Howship's lacunae or

active osteolytic foci. To assess the frequency of new bone formation, a total count of cancellous bone osteoid zones was performed.

The data were analysed by generating an aggregate score for each parameter in each treatment group. Test groups were compared to vehicle group by ANOVA using the Kruskal Wallis test statistic with exact P value comparisons. The data are summarised in the Table 3. Data shown as sum from all limbs per animal per group. * p<0.05, ** p<0.01, *** p<0.005 vs vehicle. §§§ p<0.005 vs etanercept.

Table 3 Histological assessment of bone resorption and formation.					
Compound	Dose (mg / kg / day)	Bone resorption (sum)		Bone formation (sum)	
		Vehicle value	Treatment value	Vehicle value	Treatment value
Etanercept	3	150	78**	21	78
Tofacitinib	10	117	48**	0	0
HMC-C-01-A	3	150	30***	21	387***, §§§
ABD900	10	124	24***	19	87***
NASMP-01	10	124	20***	19	77***
CHMSA-03-A	10	124	34***	19	61***
HMC-C-01-B	10	150	60***	21	139
HMC-N-01-B	10	150	30***	21	188*
CHMSA-01-A	10	124	39***	19	64***

10 The data for several of the compounds are also illustrated in Figure 8 and Figure 9.

Figure 8 shows a decrease in bone resorption with approved drugs, etanercept (Figure 8A) and tofacitinib (Figure 8C) and various MCIM compounds (Figure 8A and B). Figure 9A shows a modest increase in bone formation in mice treated with etanercept compared to vehicle control, while no increase in bone formation is seen in mice treated with tofacitinib (Figure 9C). In contrast, mice treated with HMC-C-01-A, HMC-C-01-B, and HMC-N-01-B have significantly increased bone formation compared to vehicle control and etanercept (Figure 9A). Figure 10 shows the appearance of the osteoid/new bone formed in response to treatment with vehicle (top panel), an approved disease modifying anti-rheumatic drug (etanercept; bottom panel) and compound HMC-C-01-A (middle panel). Figure 10, middle panel, demonstrates the new bone formed in response to treatment with HMC-C-01-A has a regular appearance with conservation of the tide-mark (arrows). This indicates that the bone formed is responsive to pressure and has structural integrity in contrast to the reactive and sporadic deposits generated with etanercept (bottom panel) or tofacitinib (data not shown).

Figure 11 shows that improvements in osteoid are achieved in mice treated with HMC-C-01-A without control of inflammation. This indicates a direct remodelling effect that is not dependant on control of inflammation.

- Figures 7-11 show the effects of the MCIM compounds in a model of joint inflammation and bone loss. The results show that the MCIM compounds alone reduce total bone resorption, and local focal areas of bone resorption as well as, or better than, the bDMARD etanercept or the tsDMARD tofacitinib. In addition, the MCIM compounds trigger an adaptive repair response resulting in an increase in new bone deposition (osteoid), both in terms of osteoid counts and the areas of osteoid formation.
- The new bone formed in response to treatment with the MCIM compounds has a regular appearance with conservation of the tide-mark. This indicates that the bone formed is responsive to pressure and has structural integrity in contrast to the reactive and sporadic deposits generated with etanercept.
- Together, the above data indicate that the MCIM compounds show excellent oral *in vivo* activity in preventing the progression of bone loss in established, severe arthritis, but importantly that they increase bone formation, indicating repair, in established arthritis.

EXAMPLE 6 – DMARD and MCIM combination therapy for treatment of mice with collagen-induced arthritis

- Given the improved response of mice to treatment with the MCIM compounds compared to DMARDs, it was next investigated whether combining MCIM compounds with the DMARDs etanercept and tofacitinib could be used to further improve arthritic pathology in the mouse model. The data are summarised in Table 4 (etanercept) and Table 5 (tofacitinib) and illustrated in Figure 12-14.

Table 4				
Comparison of inhibition of arthritis with MCIM, etanercept, or a combination thereof				
Compound	Vehicle	Etanercept	HMC-C-01-A	Combination
Dose (mg / kg / day)	-	1	0.03	1 + 0.03
Arthritic index	13.5 ± 0.5	-0.4	+0.1	-1.5
Synovitis	12.6 ± 1.3	-2.5	-3.4	-6.1*
Bone resorption	535 ± 50	-63	-156*	-229***
Bone pathology	10.2 ± 1.2	-2.2	-2.5	-6.1**
Cartilage	12.8 ± 1.2	-2.3	-4.1	-6.2**

Table 5				
Comparison of inhibition of arthritis with MCIM, tofacitinib, or a combination thereof				
Compound	Vehicle	Tofacitinib	HMC-C-01-A	Combination
Dose (mg / kg / day)	-	0.3	0.03	0.03
Arthritic index	13.0 ± 0.7	+0.5	+0.1	-3.2*§§a
Synovitis	13.4 ± 1.3	-0.8	-0.6	-6.2*§a
Bone resorption score	11.7 ± 1.4	0.9	-0.9	-4.9**§§a
Osteoid	0 ± -	0	1.5*§	2.9***§§§

*vs V, § vs tofa, a vs compound, one-way ANOVA`

Figure 12 shows 4 graphs demonstrating the anti-arthritic effects of the DMARD compound etanercept, the MCIM compound HMC-C-01-A, and the combination of etanercept and HMC-C-01-A on (A) synovitis, (B) cartilage damage, (C) bone resorption, and (D) overall mean change in bone pathology. Figure 13 shows 1 graph demonstrating the effects of the DMARD compound etanercept, the MCIM compound HMC-C-01-A, and the combination of etanercept and HMC-C-01-A on osteoid, or new bone formation.

These data show that etanercept and HMC-C-01-A have an additive effect on synovitis, bone resorption and cartilage damage. Importantly, however, the combination of HMC-C-01-A and etanercept reduces overall bone pathology to a greater extent than either agent alone, with a synergistic effect observed when used in combination compared to either compound alone (Figure 12D). Furthermore, HMC-C-01-A shows a strong effect on osteoid formation when given alone, an indicator of its pro-repair phenotype. The DMARD TNF inhibitor compound etanercept shows limited effects on osteoid formation. Importantly, however, the combination of HMC-C-01-A and etanercept improves overall bone osteoid formation to a greater extent than either agent alone.

Figure 14 shows 4 graphs demonstrating the anti-arthritic effects of the DMARD JAK inhibitor, tofacitinib, the MCIM compound HMC-C-01-A, and the combination of tofacitinib and HMC-C-01-A on (A) arthritic index, (B) synovitis, (C) bone resorption, and (D) osteoid score. These data show that tofacitinib and HMC-C-01-A together have a positive synergistic effect on reducing overall arthritic index, synovitis, bone resorption and repair, as indicated by a significantly increased osteoid score.

The effects demonstrated in Figures 12-14 in reducing bone pathology is thought to be due to the remodelling and repair activities of the MCIM compound, thus augmenting control of pathology over what can be achieved simply through control of synovitis. Thus, unlike standard treatments for arthritis, for example the DMARDs etanercept and tofacitinib, the combination of an MCIM compound with a DMARD leads to not only control of disease symptoms but also promotes tissue repair and reversal of arthritis pathology.

EXAMPLE 7 – Rat Pristane-Induced Arthritis

Seven- to eight-week-old female Lewis rats were used for all procedures. Animals were housed in groups of 5 and were maintained at $21^{\circ}\text{C} \pm 2^{\circ}\text{C}$ on a 12-hour light/dark cycle with food and water ad libitum. Animals were dosed with compound by oral gavage or with methotrexate by intraperitoneal injection. One hour later, arthritis was induced by administration of 0.3 ml pristane by intradermal injection at the base of the tail. Compound administration continued once daily for 28 days.

For macroscopic assessment of arthritis, the following signs were monitored in each paw of each mouse three times per week and summed to generate the Arthritic Index (AI) (the maximum AI for one animal is 16):

0 = no visible effects of arthritis.

1 = oedema and/or erythema of 1 digit.

2 = oedema and/or erythema of 2 joints.

3 = oedema and/or erythema of more than 2 joints.

4 = severe arthritis of the entire paw and digits including limb deformation and ankylosis of the joint.

The data were analysed by generating an average score for each parameter in each treatment group. Test groups were compared to vehicle group by ANOVA using the Kruskal Wallis test statistic with exact P value comparisons.

The data are summarised in the following table.

Table 6			
Inhibition of Arthritis			
Compound	Dose (mg / kg / day)	Body weight, D28	Arthritic index, D28
		grams	Units
Vehicle	-	190 ± 6	8.9 ± 1
Methotrexate	0.05	190 ± 6	$1.5 \pm 0.2^{***}$
HMC-C-01-A	10	202 ± 2	$1.9 \pm 0.2^{***}$
	20	202 ± 3	$3.2 \pm 0.9^{***}$
HMC-N-01	10	196 ± 2	$3.2 \pm 0.6^{***}$
	20	201 ± 2	$2.6 \pm 0.3^{***}$

Mean +/- SEM

These data show that there was no effect of the compounds on body weight of the animals. Both compounds reduced clinical signs of arthritis to the same extent as the existing agent, methotrexate. The data indicate that the compounds reduce clinical signs of disease in rats to the same extent as methotrexate.

Example 8 - Effects in patients with rheumatoid arthritis

Patients with rheumatoid arthritis diagnosed according to the ACR/EULAR 2010 guidelines were enrolled into a clinical trial to assess the impact of adding an MCIM compound to the standard methotrexate treatment regimens. Patients were enrolled if they had previously received a stable
5 dose of methotrexate for a minimum of 3 months and had achieved a treatment target, according to (EULAR) guidelines.

On commencing the combination treatment regimen, patients received methotrexate at their usual dose, and then received HMC-C-01-A 75 mg once daily for two weeks. Plasma samples were collected at baseline and on Day 16 to assess of changes in inflammation, bone degradation and
10 bone formation.

C-reactive protein (CRP) is an acute phase reactant which is increased during systemic inflammation. It is a well-recognised biomarker of inflammation and forms a key component of clinical assessments of arthritis such as the ACR score and the Disease Activity Score. Reductions in CRP are indicative of reduced inflammation.

15 Bone turnover is a function of two opposing and complimentary activities, bone degradation and bone formation. Changes in the ratio between bone formation and bone degradation can indicate either bone loss, as is seen in diseases such as osteoporosis, or bone formation.

Bone degradation was measured using the biomarker Tartrate-resistant acid phosphatase (TRAP5). TRAP5 levels are associated with the activity of osteoclasts, cells which degrade bone. TRAP5 is one
20 of the most abundant enzymes expressed in osteoclasts. It is also expressed in certain differentiated cells of the mononuclear phagocyte system, particularly osteoclasts and alveolar macrophages, and plays an active role in bone resorption processes. High blood levels of TRAP5 are usually associated with active bone remodelling/loss.

Bone formation was measured using the biomarkers osteocalcin and Procollagen 1 intact N-terminal (P1NP). Osteocalcin is secreted by bone-forming cells, osteoblasts, and is a well-established
25 biomarker of the bone formation process. Increasing level of osteocalcin reflect improved bone mineral density and are used as a preliminary marker of the effectiveness of a drug on bone formation. P1NP is produced during bone formation by osteoblasts. P1NP is a propeptide extension of procollagen which is removed during the synthesis of collagen. P1NP levels are reported to be the
30 most specific and sensitive marker of bone formation.

Analyte CRP was measured in patient serum samples by immunoassay. Analytes (TRAP5, osteocalcin and P1NP) were measured in patient serum samples by automated chemiluminescence immunoassays (CLIA) using Immunodiagnosics Systems-iSYS Multi-Discipline Automated System (IDS) with a software version v3R34 and the following assay kits: Serum CrossLaps (CTX-I; Cat# IS-
35 3000, and corresponding control), Intact PINP (Cat# IS-4000 and corresponding control), IDS-iSYS

TRACP 5b (BoneTRAP; Cat# IS-4100 and corresponding control) and IDS-iSYS N-MID® Osteocalcin (Cat# IS-2900 and corresponding control) according to the manufacturer's instructions. These assays enable the quantitative determination of each respective analyte. The data were analysed by subtracting the baseline value from the day 14 value to generate a change from baseline. Individual results were then potted to evaluate the profile of anti-inflammatory and bone remodelling changes in patients.

Figure 15 shows individual changes in biomarkers (A) C-reactive protein, (B) TRAP5, (C) P1NP, (D) osteocalcin after 16 days dosing with MCIM compound. Figure 16 shows median changes in CRP, P1NP and osteocalcin (A) and TRAP5 (B) across the patient group.

- 10 The results show that an MCIM compound is able to further reduce inflammation (as indicated by reduced CRP levels) in patients whose symptoms are already controlled with methotrexate, a csDMARD. In addition, adding an MCIM compound to the treatment regimen shows beneficial effects on bone remodelling, with reduced bone loss (reduced serum TRAP5) and increased bone formation (increased serum osteocalcin and P1NP). The difference in the direction of these two effects (on loss and formation) indicates that there is a pro-remodelling effect in patients despite the presence of methotrexate, which has been reported to accelerate bone loss. The profile of bone marker changes supports the existence of a pro-repair phenotype with increased bone formation and reduced bone loss.

20 EXAMPLE 9 – Enhanced therapy in IBD model

- DSS-induced colitis is a widely used model of IBD (Chassaing *et al*, 2015, which is hereby incorporated by reference in its entirety). Eight- to nine-week-old female C57Bl/6 mice were used for all procedures. Animals were housed in groups of 10 and were maintained at $21^{\circ}\text{C} \pm 2^{\circ}\text{C}$ on a 12-hour light/dark cycle with food and water ad libitum. Dextran sulphate (DSS) was prepared by dissolving DSS in water to a final concentration of 1.5%. All mice were given ad libitum access to the DSS-containing water for 6 hours prior to dosing with vehicle control, 300 mg/kg sulfadiazine (csDMARD), 3 mg/kg etanercept (bDMARD) or 10 mg/kg MCIM test compound by oral gavage, once daily for 8 days. The mice started to develop signs and symptoms of colitis within 1 day.

- For assessment of colitis, mouse body weight, stool consistency and presence/absence of blood in stool were monitored. Depending on the severity of the change in each of these observed parameters, the mice were assigned a score based on the criteria in Table 7. The disease scores were summed to generate the Disease Activity Index (DAI) (the maximum DAI for one animal is 9). The data are presented as mean s.e.m. across the group, and statistical analysis was performed using a two-way ANOVA with multiple comparisons (GraphPad Prism v 9.2.0). * $p < 0.05$, *** $p < 0.005$ vs vehicle, \$\$\$ $p < 0.005$ vs sulfasalazine, aaa $p < 0.005$ vs etanercept.

Table 7 Disease scores associated with observed phenotypes in mice with DSS-induced colitis.					
Parameter	Score				
	0	1	2	3	4
Stool consistency	Separate hard lumps	Sausage like with cracks	soft blobs	watery, no solid pieces	N/A
Fecal blood	No blood in stool	Blood in stool	N/A	N/A	N/A
Body Weight loss	≤ 1%	1≤5%	5≤10%	10≤15%	> 15%

For histopathological assessment of the biological effects of MCIM compounds in colitis, on Day 9, the colon from the rectum to the ileo-caecal junction was removed and the length recorded. The faeces were then removed and the weight of the colon recorded. The colon was preserved in 10% neutral buffered formalin and processed to paraffin blocks.

Tissue sections were then stained with Haematoxylin and Eosin (H&E) and parameters of inflammation, mucosal erosion, epithelial hyperplasia, epithelial metaplasia, mucus cell metaplasia, and fibroplasia were assessed on a scale of 0-5 as follows:

- 0: normal
- 1: minimal, focal
- 2: moderate, focal
- 3: moderate, multi-focal or diffuse
- 4: marked, focal
- 5: marked, multi-focal or diffuse

The data were analysed by generating an average histopathology score across each treatment group. Test groups were compared to the vehicle and positive control groups using two-way ANOVA with correction for multiple comparisons (Prism 9.2.0). Data shown as mean ± s.e.m.. * p<0.05, ** p<0.01, *** p<0.005 vs vehicle. ^{aaa} p<0.005 vs sulfasalazine. § p<0.05, §§ p<0.01, §§§ p<0.005 vs etanercept.

The data are summarised in Figures 17-21.

Figure 17 shows the mean disease activity index for mice with DSS-induced colitis following treatment with vehicle, 300 mg/kg/d sulfasalazine, 3 mg/kg/d etanercept or 10 mg/kg/d MCIM compound, HMC-

C-01-A. These data indicate that the MCI compounds described herein show excellent *in vivo* activity in preventing the progression of established DSS-induced colitis. Furthermore, the data shows that the MCIM compound has greater efficacy than both prior art DMARD treatments, sulfasalazine and etanercept.

- 5 Figure 18 shows two graphs, each of average mucosal erosion score for (A) vehicle control, 300 mg/kg/day sulfasalazine and 10 mg/kg/day ABD900 and (B) vehicle control, 3 mg/kg/day etanercept and 10 mg/kg/day HMC-C-01-A. Mice treated with either sulfasalazine or etanercept did not reduce mucosal erosion appreciably compared to mice treated with vehicle control. In contrast, mice treated with MCIM compound ABD900 (Figure 18A) or HMC-C-01-A (Figure 18B) reduced the mucosal
10 erosion score from between 3-3.5 to approximately 1 and 2, respectively.

- Figure 19 shows two graphs, each of average glandular loss score for each of: (A) vehicle control, 300 mg/kg/day sulfasalazine and 10 mg/kg/day ABD900 and (B) vehicle control, 3 mg/kg/day etanercept and 10 mg/kg/day HMC-C-01-A. Mice treated with either sulfasalazine did not reduce glandular loss appreciably compared to mice treated with vehicle control. Moreover, mice treated with
15 etanercept led to an increase in glandular loss compared to vehicle control treated mice. In contrast, mice treated with MCIM compound ABD900 (Figure 19A) or HMC-C-01-A (Figure 19B) reduced the glandular loss score from between 3-4 to approximately 2.

- Figure 20 shows 2 graphs, each of average epithelial hyperplasia score for each of: (A) vehicle control, 300 mg/kg/day sulfasalazine and 10 mg/kg/day ABD900 and (B) vehicle control, 3 mg/kg/day
20 etanercept and 10 mg/kg/day HMC-C-01-A. Mice treated with sulfasalazine and the MCIM compounds ABD900 and HMC-C-01-A increased epithelial hyperplasia compared to mice treated with vehicle control.

- Figure 21 shows 2 graphs, each of average fibroplasia score for each of: (A) vehicle control, 300 mg/kg/day sulfasalazine and 10 mg/kg/day ABD900, (B) vehicle control, 3 mg/kg/day etanercept and
25 10 mg/kg/day HMC-C-01-A. No appreciable hyperplasia was observed in mice treated with any of vehicle control, sulfasalazine (Figure 21A), or etanercept (Figure 21B). In contrast, significant fibroplasia was observed in mice treated with both ABD900 (Figure 21A) and HMC-C-01-A (Figure 21B), indicating that MCIM compounds are able to promote tissue repair in gastrointestinal tissues.

- Figure 22 shows representative histological cross sections of colon taken from mice with DSS-induced colitis treated with vehicle, 3 mg/kg/day etanercept or 10 mg/kg/day HMC-C-01-A. In vehicle
30 treated mice, there is clear ulceration (top right panel, arrow) and a general loss of tissue architecture of the colon as demonstrated by visible oedema/inflammation and erosion (top left panel, arrow). Mice treated with etanercept display a general conservation of tissue architecture but still display a moderate degree of inflammation and oedema (middle panels, arrows). In contrast, the colon of mice
35 treated with HMC-C-01-A have conserved tissue architecture and no visible signs of inflammation or oedema. Surprisingly, treatment with HMC-C-01-A stimulates an adaptive repair of the colon which is

not seen with Etanercept treatment (bottom panel, arrows). The histological section from mice treated with HMC-C-01-A demonstrates that this reaction is organised and localised within the lamina propria and aligned along the basal layer, with expansion/maintenance of basement membrane and maintenance of crypt architecture.

- 5 Together, these data indicate that HMC-C-01-A and ABD900 compounds have excellent activity in preventing the progression of established colitis and can stimulate repair of damaged tissues. Administration of MCIM compounds inhibited the key histological outcome of mucosal erosion/ulceration, as shown in Figure 18. Importantly, administration also increased hyperplasia of epithelium, suggesting induction of a repair response (Figure 20A and 20B). This is supported by the
10 unique finding of fibroplasia in the MCIM compound treated groups (Figure 21A and 21B).

Overall, Figures 16 to 22 show the effects of the MCIM compounds in a model of gastrointestinal disease. The results show that the MCIM compounds reduce disease signs and symptoms and protect the underlying tissue damage to a greater extent than approved DMARD drugs, sulfasalazine and etanercept, and that the MCIM compounds promote repair responses of epithelial hyperplasia,
15 mucus cell metaplasia and fibroplasia to a greater extent than sulfasalazine and etanercept.

Example 6 and 7 demonstrates that combining DMARDs with MCIM compounds can lead to a synergistic improvement of arthritic symptoms in mice and rats with collagen or pristane-induced arthritis. In addition, Example 8 demonstrates that this effect is recapitulated in human patients with RA receiving the csDMARD methotrexate. These improvements are thought to be due to the unique
20 properties of MCIM compounds promoting tissue repair. Given these results, it is also predicted that, because of these unique reparative properties, combining MCIM compounds (which alone improve clinical symptoms of IBD) with approved DMARDs for the treatment of IBD (e.g. methotrexate, etanercept and sulfasalazine) this combination will also lead to an improved response in subjects suffering from IBD.

25 EXAMPLE 10 – Cellular thermal shift assay (CETSA) and multiplexes quantitative mass spectrometry

Following the observation that MCIM compounds can affect mitochondrial morphology and modulate cellular metabolism it was next investigated whether the reparative properties of the MCIM compounds could be attributed to binding to/modulation of mitochondrial proteins and/or complexes. To this end, MCIM compounds were assessed using a cellular thermal shift assay (CETSA) coupled
30 with quantitative mass spectroscopy (MS) to determine what pathways are modulated by the MCIM compounds.

Thp-1 cells were incubated in the presence of 2 μ M MCIM compound (ABD900) or DMSO (vehicle control) for 4 hours. Following the incubation period, samples were heated to one of the following temperatures: 40.0, 42.9, 46.0, 49.6, 53.2, 56.8, 60.8, 64.0, 67.1, 70.0°C. Each test condition was
35 performed in duplicate.

Following heating, cells were lysed, and the samples digested with trypsin. The digested soluble peptide fractions corresponding to individual temperatures were then labelled with a different isobaric tag, using the TMT10plex system as described in Bantscheff, M., et al (2007), Bantscheff, M., et al (2012) and Franken, H., et al (2015), each of which are incorporated by reference in their entirety.

- 5 Labelling of fractions from individual temperatures with an individual TMT10Plex tag allows the samples to be pooled and analysed by mass spectroscopy in a single run.

- Following TMT10Plex labelling and pooling, the samples were fractionated using hydrophilic strong anion exchange (hSAX) (24 fractions per sample) and Liquid Chromatography with tandem mass spectrometry (LC-MS/MS) performed. The LC-MS/MS data was analysed to identify proteins whose
- 10 thermal stability was shifted in the presence of the MCIM compound using the TPP R Package (Franken, H., et al (2015)) with a procedure described in Savitski., MM et al (2014). Generally, upon compound binding, proteins become more stable and thus more resistant to thermal denaturation. Therefore, a shift in thermal stability of a protein in the described CETSA assay can indicate direct binding of a compound to the protein with shifted thermal stability. Alternatively, a shift on thermal
- 15 stability may indicate the protein is involved in a downstream event from the bound protein, for example, a post-translation modification as a result of an altered metabolic or signalling pathway.

Briefly, criteria for target candidate selection were as follows:

- Min p-value <0.4 (Benjamini-Hochberg corrected)
- DTm of Run 1 (R1) and Run 2 (R2) have same sign
- 20 • DTm (drug vs DMSO) > DTm (DMSO R1 vs DMSO R2)
- Minimum slope less than -0.06

Using the above criteria, 105 proteins were identified as showing a thermal shift when incubated with the MCIM compound indicating that they were either stabilised or destabilised. Of these 105 proteins, 73 were classified as high confidence and 32 as medium confidence hits.

- 25 Functional protein interactions and/or associations of the 105 identified candidate proteins were retrieved using the freely available STRING software (<https://string-db.org>). STRING analysis identified candidates involved in oxidative phosphorylation (e.g. NDUFA6 and SDHB), mitochondrial function and the ER to Golgi apparatus interface.

- In addition, thermal shifts were observed in proteins involved in adaptive stress responses (e.g. YME1L1, OXSR1, MKNK1) and other proteins which play a role in NF- κ B signalling (e.g. OXSR1, RASA1 and BIRC2).
- 30

- It was therefore concluded, in line with the data in Example 3, that incubation with MCIM compounds alters the metabolic activity of cells specifically through modulation of oxidative phosphorylation, as indicated by the thermal shift of NDUFA6 (a Respiratory Complex 1 component). It was hypothesised
- 35 that such modulation of Complex 1 and the oxidative phosphorylation pathway would alter NF κ B and

adaptive response pathways in cells, as indicated by the thermal shift observed for proteins such as YMEL1L1, OXSR1, MKNK1, RASA1 and BIRC2.

EXAMPLE 11 - Photoaffinity labelling (PAL) and quantitative stable isotope labelling by amino acids in cell culture (SILAC)

5 To investigate the binding partner(s) of the MCIM compounds, and the cellular activities modulated by them, Photoaffinity labelling (PAL) and quantitative stable isotope labelling by amino acids in cell culture (SILAC) was performed. A clickable linker probe MCIM compound was generated to do this.

This identified NDUFS2, a subunit of Mitochondrial Complex I, as a binder of the clickable linker probe MCIM compound. Together, the CETSA and PAL/SILAC-MS results strongly indicate that MCIM

10 compounds can modulate oxidative phosphorylation and stress response pathways by binding and modulating the activity of the Mitochondrial Complex I.

EXAMPLE 12 - Computational modelling to identify binding sites in NDUFS2

Given that both CETSA and PAL/SILAC-MS methods identified Complex I subunits as targets of MCIM compounds, an *in silico* computer modelling approach was used to determine the binding site

15 of MCIM compounds with the Complex I subunits.

Initially, homology models were built from publicly available structures of mitochondrial Complex I from five organisms, including human (Table 8). The putative targets were fully resolve in 5 structures. Mitochondrial Complex 1 used for the following modelling approaches is show in Figure 23.

Table 8							
Publicly available Complex I structures. FMN = Flavin mononucleotide.							
Protein	Size	Type	Method	Liganded?		Ref	Protein database ID
				Y/N	Site		
Y. Lipolytica	466 KD	Fungal	X-Ray	N		Zickerman et al Science, 2015, 247, 44-49	4WZ7
T. Thermophilus		Bacterial	X-Ray	FMN	NADH-FMN	Efremov et al Nature, 2010, 465, 441-445	3M9S

T. Thermophilus	536 KD	Bacterial	X-Ray	FMN, Y	NADH-FMN, Quinone	Sazanov et al Nature, 2013, 494, 443-450	4HEA
T. Thermophilus	570 KD	Bacterial	X-Ray	NADH, FMN	NAD-FMN	Sazanov et al JBC, 2009, 284, 29773	3IAM
Bos Taurus	517 KD	Mammalian	Cryo-EM	N		Hirst et al Nature, 2014, 515, 80-84	4UQ8
Bos Taurus	891 KD	Mammalian	Cryo-EM	NADH, FMN	NADH-FMN	Hirst et al Nature, 2016, 536, 354	5LDW, 5LDX, 5LC5
Ovis Aries	978 KD	Mammalian	Cryo-EM	N		Sazanov et al Nature, 2016, 538, 406	5LNK
Ovis Aries	1.28 MD	Mammalian	Cryo-EM	N		Sazanov et al Nature, 2016, 537, 644	5J4Z, 5J7Y, 5J8K
Homo Sapiens		Mammalian	Cryo-EM	NADP, FMN	NADH-FMN	Guo et al Cell, 2017, 170, 1247-1257	5XTD, 5XTH, 5XTI

The homology modelling revealed a lid pocket in the NDUFS2 subunit of Complex I which is in contact with the Q-tunnel. In four of the models the lid pocket was seen to be in an “open” conformation while in the remaining model it was in a “closed” conformation.

- A homology model of the “open” confirmation was constructed and then SiteFinder was used to map
- 5 NDUFS2 in the open and closed conformations. In particular, SiteFinder (Halgren T. A., 2009) was used to build a model of the “drugability” of NDUFS2, as measured by the volume of buried non-polar

available surface area (ASA; Figure 24). This model identified two binding sites on NDUFS2. The first binding site ("Pocket A") is located on the lid pocket in the open conformation and is represented on Figure 24 by a cluster of spheres. Pocket A has a percentage buried non-polar available surface area of 72%. The second binding site ("Pocket B") is located at the "back" of the mitochondrial Complex I, relative to the position of the mitochondrial Complex I subunits NDUFS7 and ND1 and is represented by a second cluster of spheres. Pocket B has a percentage buried non-polar available surface area of 71%.

Further modelling of Q10, the natural ligand of the Q-tunnel, within the Q-site of Complex 1 using SiteFinder indicated that the space for binding in this pocket is limited (Figure 25). The spheres in Figure 25 illustrate the space and channels around NDUFS2 when NDUFS2 is associated with Complex 1. This modelling approach also revealed a further ligand binding site at the junction between NDUFS2 and NDUFS7 (Figure 26). In particular, the MCIM compound is predicted to interact with His38 and Tyr141 of NDUFS2.

Using these protein models it was determined that the optimal binding site of each of ABD900, HMC-C-01-A and HMC-N-01-A was the NDUFS2 lid pocket (as illustrated in Figure 24, "Pocket A"), specifically the lid pocket in the open conformation (Glide score ~6), which is close to the Q-site. Even more particularly, the inventors were able to predict which amino acid residues in NDUFS2 contributed to the binding of the compounds:

- H-bonding with backbone carbonyl of Gly85, backbone amine of Leu95 and carboxylic acid of Asp193
- H-bonding to Tyr141 and His38
- π - π stacking with Phe458 and His88

In conclusion, analysis of the Q-site of NDUFS2 indicates that this site needs to be in the open confirmation to accommodate Q10 or small drug-like compounds.

Example 13 - Virtual Screening to assess structure-activity relationship against the NDUFS2 pocket

As discussed in Example 12, it has been determined that the optimal binding site for MCIM compounds is in the lid pocket of NDUFS2 which is in close proximity to the Q-tunnel. From the data in Example 12, a ligand-protein pharmacophore model was built which identified 9 pharmacophoric features (Figure 27 and Tables 9A to 9C). Table 9-A describes the relationship between the type of pharmacophoric feature and the permissible variation in 3D space for the location of the given pharmacophoric feature. Table 9-B shows a distance matrix describing the 3D relationship between the centre of each pharmacophoric feature. Table 9-C describes the angle between each triplet combination of pharmacophoric features, wherein column "Y" describes the vertex of each angle. Using the parameters described in Tables 9-A to 9-C a visual representation of the pharmacophore model has been produced using the unified annotation scheme in *Molecular Operating Environment*

(MOE) software tool (Figure 27). Using *Molecular Operating Environment (MOE)*, the parameters can also be used to determine if a molecule conforms to the pharmacophore model – i.e. if 4 or more of the annotation points of the pharmacophore model are occupied by a corresponding annotation point located on a test molecule.

Table 9-A		
Pharmacophore feature annotations, and radii		
<i>Feature Number</i>	<i>Feature Annotation</i>	<i>Radius (Å)</i>
F1	Acc	1.2
F2	Acc	1.2
F3	Acc	1.2
F4	Acc2	1.4
F5	Aro	1.4
F6	Hyd	1.4
F7	Hyd	1.4
F8	Hyd	1.4
F9	Don2	1.4

Table 9-B										
Pharmacophore feature distances (Å)										
Dist. (Å)	Feature Number	F1	F2	F3	F4	F5	F6	F7	F8	F9
Feature Number	Feature Ann	Acc	Acc	Acc	Acc2	Aro	Hyd	Hyd	Hyd	Don2
F1	Acc	0.00	2.64	8.50	8.16	8.11	4.07	4.77	3.13	4.82
F2	Acc	2.64	0.00	7.21	9.80	8.48	4.60	3.85	3.85	3.46
F3	Acc	8.50	7.21	0.00	16.55	14.19	10.57	4.37	10.95	9.58
F4	Acc2	8.16	9.80	16.55	0.00	6.76	6.87	12.41	6.05	8.88
F5	Aro	8.11	8.48	14.19	6.76	0.00	4.12	9.96	6.41	5.82
F6	Hyd	4.07	4.60	10.57	6.87	4.12	0.00	6.26	3.31	3.22
F7	Hyd	4.77	3.85	4.37	12.41	9.96	6.26	0.00	7.12	5.90
F8	Hyd	3.13	3.85	10.95	6.05	6.41	3.31	7.12	0.00	3.77
F9	Don2	4.82	3.46	9.58	8.88	5.82	3.22	5.90	3.77	0.00

Table 9-C			
Pharmacophore feature angles between features X-Y-Z (°),			
X	Y	Z	Angle (°)
F1	F2	F3	110.39
F1	F2	F4	45.38
F1	F2	F5	72.94
F1	F2	F6	61.46
F1	F2	F7	92.58
F1	F2	F8	53.87
F1	F2	F9	103.51
F1	F3	F4	6.61
F1	F3	F5	30.48
F1	F3	F6	21.30
F1	F3	F7	22.60
F1	F3	F8	11.59
F1	F3	F9	30.18
F1	F4	F5	65.03
F1	F4	F6	29.85
F1	F4	F7	12.32
F1	F4	F8	18.96
F1	F4	F9	32.52
F1	F5	F6	7.99
F1	F5	F7	28.34
F1	F5	F8	21.01
F1	F5	F9	35.98
F1	F6	F7	49.67
F1	F6	F8	48.90
F1	F6	F9	81.99
F1	F7	F8	20.48
F1	F7	F9	52.40
F1	F8	F9	88.17

Table 9-C			
Pharmacophore feature angles between features X-Y-Z (°),			
X	Y	Z	Angle (°)
F2	F3	F4	15.65
F2	F3	F5	27.53
F2	F3	F6	20.78
F2	F3	F7	26.84
F2	F3	F8	5.82
F2	F3	F9	17.47
F2	F4	F5	58.21
F2	F4	F6	24.99
F2	F4	F7	14.75
F2	F4	F8	6.62
F2	F4	F9	20.61
F2	F5	F6	14.35
F2	F5	F7	22.35
F2	F5	F8	25.41
F2	F5	F9	18.14
F2	F6	F7	37.84
F2	F6	F8	55.34
F2	F6	F9	48.68
F2	F7	F8	22.45
F2	F7	F9	34.01
F2	F8	F9	54.05
F3	F4	F5	58.15
F3	F4	F6	22.97
F3	F4	F7	5.71
F3	F4	F8	18.05
F3	F4	F9	27.40
F3	F5	F6	24.17
F3	F5	F7	5.20

Table 9-C Pharmacophore feature angles between features X-Y-Z (°),			
X	Y	Z	Angle (°)
F3	F5	F8	47.65
F3	F5	F9	29.69
F3	F6	F7	5.20
F3	F6	F8	87.80
F3	F6	F9	63.56
F3	F7	F8	143.73
F3	F7	F9	137.11
F3	F8	F9	59.09
F4	F5	F6	73.80
F4	F5	F7	93.94
F4	F5	F8	54.64
F4	F5	F9	89.42
F4	F6	F7	142.01
F4	F6	F8	61.79
F4	F6	F9	118.85
F4	F7	F8	17.94
F4	F7	F9	41.28
F4	F8	F9	127.89
F5	F6	F7	146.38
F5	F6	F8	118.68
F5	F6	F9	104.33
F5	F7	F8	39.90
F5	F7	F9	31.63
F5	F8	F9	63.74
F6	F7	F8	27.72
F6	F7	F9	30.48
F6	F8	F9	53.57
F7	F8	F9	55.96

Using the *Molecular Operating Environment (MOE)*, 2022.02 Chemical Computing Group ULC, 1010 Sherbooke St. West, Suite #910, Montreal, QC, Canada, H3A 2R7, 2022 MOE docking using the pharmacophore algorithm for ligand placement and the GBVI/WSA dG scoring function, 117 compounds were assessed for their ability to dock in the predicted binding site using the pharmacophore model

5 described above. To be treated as a successful docking in the predicted binding site, it is required that a molecule hits at least 4 features of the pharmacophore model shown in Figure 27 and has a half-maximal inhibitory concentration (IC_{50}) $\leq 1 \mu M$.

Figure 28 shows a MCIM compound that conforms to the pharmacophore model and satisfies 7 out of the 9 annotation points determined to be important for binding to Complex I. Surprisingly, it was also found

10 that out of the 117 compounds assessed for their ability to bind in the pharmacophore model, only 13 compounds had an $IC_{50} > 1 \mu M$, which indicates that these compounds would fail to dock in the predicted binding sites. The remaining 104 compounds hit at least 4 of the pharmacophore features and are predicted to have an $IC_{50} \leq 1 \mu M$. Figure 29 shows representative compound CHMSA-02-A, which fulfils the pharmacophore model and is predicted to have a $pAct (-\log(IC_{50}))$ of ~ 7 .

15 EXAMPLE 14 – Ultra-high throughput virtual screening (uHTVS)

Following building of the pharmacophore model, the inventors next wanted to identify additional NDUFS2 binders using this model.

The 3D model of the entire Complex 1 described in Example 11 (Figure 28) was validated by docking Q10 and active MCIM compounds. This allowed establishment of the bioactive conformation of the MCIM

20 compounds when docked in the Q-tunnel of Complex I. This further allowed a structure-based hypothesis to be generated and to rationalise the structure-activity relationship (SAR) of the compounds and to build the pharmacophore model described in Example 12 and a QSAR model (Figure 30) for activity prediction. The QSAR model is a linear regression model which includes docking scores and parameters related to ligand energies and electrostatics.

25 For uHTVS, a library of compounds was screened against the pharmacophore model described in Example 13. The model identified 37.6 million compounds from the library of compounds which generally hit 3-6 of the pharmacophore features. Of these 37.6 million compounds, those up to a molecular weight of ~ 350 Da were then virtually docked in the 3D Complex I model without imposing pharmacophore constraints. 67,000 compounds were predicted to dock in Complex I and were retained for further

30 screening.

The retained compounds were then filtered through a more theoretically rigorous docking method and evaluated with a QSAR model to predict biological activity of each compound (Figure 30). The GBVI/WSA ΔG forcefield-based scoring function (Naim *et al.* 2007) on the MOE dock (*Molecular Operating Environment (MOE)*, 2022.02 Chemical Computing Group ULC, 1010 Sherbooke St. West,

35 Suite #910, Montreal, QC, Canada, H3A 2R7) was used. Using the screening process described, 756 compounds were identified as potential drug candidates for targeting NDUFS2/NDUFS7 of Complex 1.

References

A number of publications are cited above in order to more fully describe and disclose the invention and the state of the art to which the invention pertains. Full citations for these references are provided below.

5 The entirety of each of these references is incorporated herein.

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Claims

1. A pharmaceutical combination comprising a mitochondrial complex I modulator (MCIM) compound and a disease modifying antirheumatic drug (DMARD), wherein the DMARD is not methotrexate.
2. A pharmaceutical composition comprising a mitochondrial complex I modulator (MCIM) compound and a disease modifying antirheumatic drug (DMARD), optionally wherein the DMARD is methotrexate.
3. A pharmaceutical combination or composition according to claim 1 or claim 2 for use in medicine.
4. A pharmaceutical composition comprising a mitochondrial complex I modulator (MCIM) compound for use in a method of treating an inflammatory and/or progressive disease in a subject, comprising the separate, sequential or simultaneous administration of the pharmaceutical composition and a disease modifying antirheumatic drug (DMARD), wherein the DMARD is not methotrexate.
5. A pharmaceutical composition comprising a disease modifying antirheumatic drug (DMARD) for use in a method of treating an inflammatory and/or progressive disease in a subject comprising the separate, sequential or simultaneous administration of the pharmaceutical composition and a mitochondrial complex I modulator (MCIM) compound, wherein the DMARD is not methotrexate.
6. A pharmaceutical composition comprising a mitochondrial complex I modulator (MCIM) compound and a disease modifying antirheumatic drug (DMARD) for use in a method of treating an inflammatory and/or progressive disease in a subject.
7. The pharmaceutical composition according to any one of claims 4 to 6, wherein the treatment achieves disease control, regression, or tissue repair, or any combination thereof, in a subject in need thereof.
8. The composition for the use according to claim 7, wherein disease control comprises inhibiting disease progression.
9. The composition for the use according to any one of claims 7 or 8, wherein disease control comprises supporting tissue repair.
10. The composition for the use according to any one of claims 7 to 9, wherein disease control comprises the prevention of a loss of anatomically normal tissue architecture, or a reduction in the speed of the loss of anatomically normal tissue architecture.
11. The composition for the use according to any one of claims 7 to 10, wherein the disease control, regression or tissue repair, or any combination thereof, comprises an increased repair score and/or increased wound healing.

12. The composition for the use according to any one of claims 7 to 11, wherein the disease control or regression, and/or tissue repair comprises an increased cell count of reparative cells and/or a decreased cell count of pathology driving cells.

13. The composition for the use according to any one of claims 7 to 12, wherein the disease control, regression, or tissue repair, or any combination thereof, induces a restoration of anatomically normal tissue architecture.

14. The composition for the use according to any one of claims 7 to 13, wherein the inflammatory and/or progressive disease is an autoimmune or autoinflammatory disease.

15. The composition for the use according to any one of claims 7 to 14, wherein the inflammatory and/or progressive disease is an arthritis, inflammatory bowel disease (IBD), atopic dermatitis, psoriasis, or plaque psoriasis.

16. The composition for the use according to claim 15, wherein the arthritis is rheumatoid arthritis (RA), psoriatic arthritis, inflammatory arthritis, ankylosing spondylitis, juvenile idiopathic arthritis, reactive arthritis, gout, septic arthritis, enteropathic arthritis or osteoarthritis.

17. The composition for the use according to any one of claims 7 to 16, wherein the inflammatory and/or progressive disease is an arthritis and wherein the tissue repair and/or disease control or regression comprises increased bone formation and/or decreased bone resorption.

18. The composition for the use according to any one of claims 12 to 17, wherein the inflammatory and/or progressive disease is an arthritis and wherein the reparative cells comprise osteoblasts (OBs) and/or non-transformed fibroblasts and/or the pathology driving cells comprise osteoclasts (OCs) and/or transformed fibroblasts.

19. The composition for the use according to claim 15, wherein the IBD is Crohn's disease or Ulcerative colitis.

20. The composition for the use according to claim 15 or 19, wherein the inflammatory and/or progressive disease is an inflammatory bowel disease (IBD) and wherein the reparative cells comprise epithelial cells and/or mucus cells.

21. The composition for the use according to any one of claims 7 to 20, wherein the disease control, regression, or tissue repair, or any combination thereof, comprises a reduction in cytokine production from pro-inflammatory myeloid cells.

22. The combination according to any one of claims 1 to 3 or the composition for the use according to any one of claims 4 to 21, wherein the binding of the MCIM compound to complex I modulates complex I activity, wherein complex I modulation is determined by detecting a reduction in cellular O₂ consumption without a reduction of cell viability.

23. The combination according to any one of claims 1 to 3 or 22 or the composition for the use according to any one of claims 4 to 22, wherein the binding of the MCIM compound to complex I modulates complex I activity, leading to a reversible reduction in cell proliferation.

24. The combination according to any one of claims 1 to 3 or 22 to 23 or the composition for the use according to any one of claims 4 to 23, wherein the MCIM compound interacts with complex I at a binding site outside the Q tunnel.

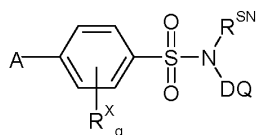
25. The combination according to any one of claims 1 to 3 or 22 to 24 or the composition for the use according to any one of claims 4 to 24, wherein the MCIM binding site comprises one or more amino acid residues from NDUSF2 and/or NDUSF7.

26. The combination or composition for use according claim 25, wherein the MCIM compound interacts with one or more amino acid residues in NDUSF2 selected from His92, Gly85, Tyr141, His88, Leu95, Asp193 and Phe458.

27. The combination or composition for use according to claim 26, wherein the MCIM compound interacts with at least one amino acid residues in NDUSF2 selected from Tyr141, His92 and Asp139.

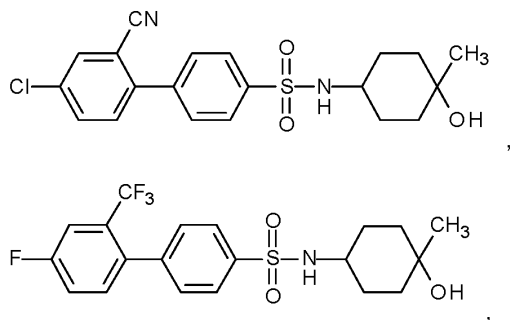
28. The combination according to any one of claims 1 to 3 or 22 to 27 or the composition for use according to any one of claims 4 to 27, wherein a 3D conformation of the MCIM compound as annotated by *Molecular Operating Environment (MOE)* 2022 unified annotation scheme comprises 4 or more pharmacophore features which conform to the pharmacophore model represented in Figure 27, and Tables 9-A, 9-B and 9-C.

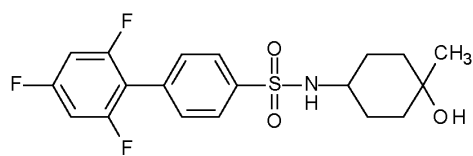
29. The combination according to any one of claims 1 to 3 or 22 to 28 or the composition for use according to any of claims 4 to 28, wherein the MCIM compound is an MCIM compound, or a pharmaceutically acceptable salt, hydrate, or solvate thereof, of the following formula:



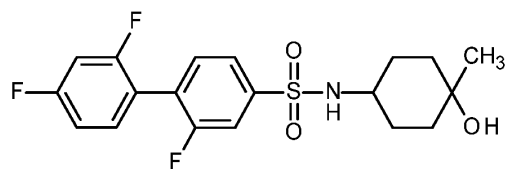
as defined in claim 1 of WO2010/032009.

30. The combination or composition for use according to claim 29, wherein the MCIM compound is an MCIM compound selected from compounds of the following formulae, or a pharmaceutically acceptable salt, hydrate, or solvate thereof:

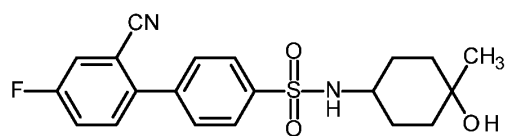




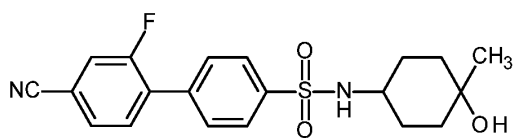
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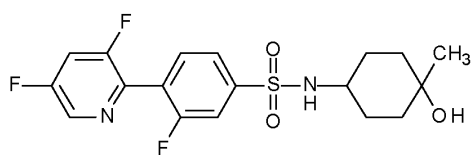
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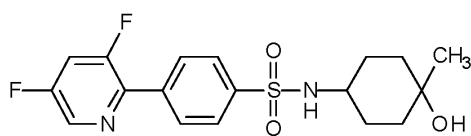
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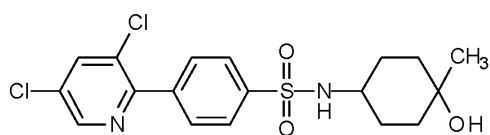
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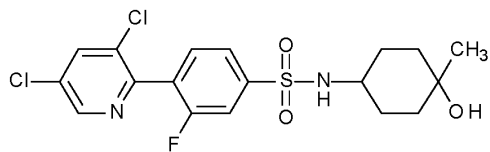
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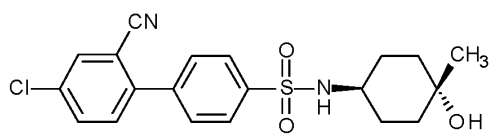
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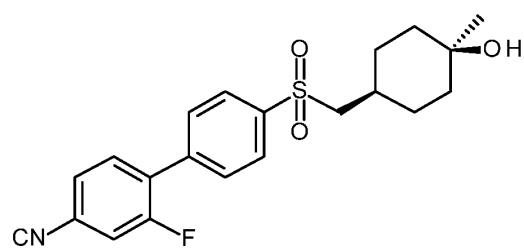
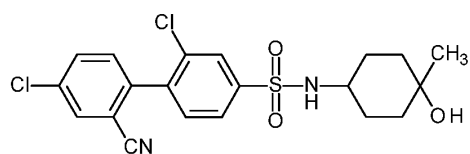
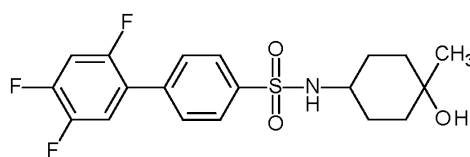
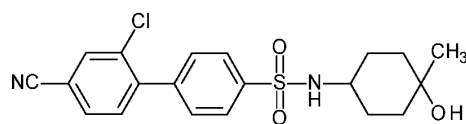
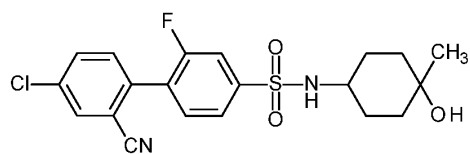
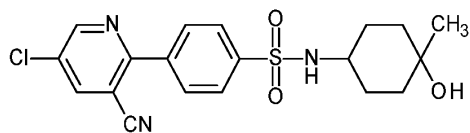
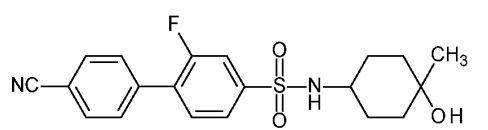
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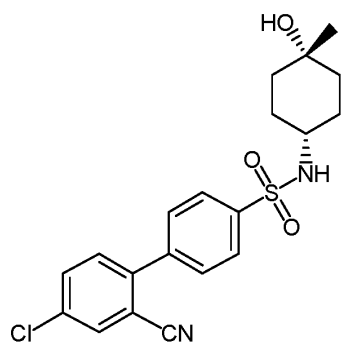
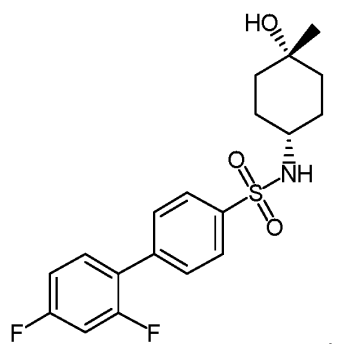
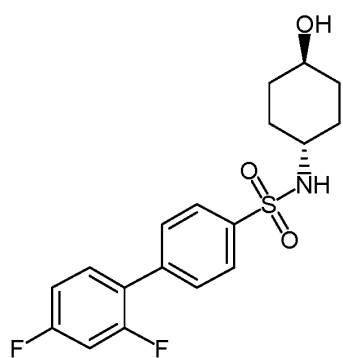
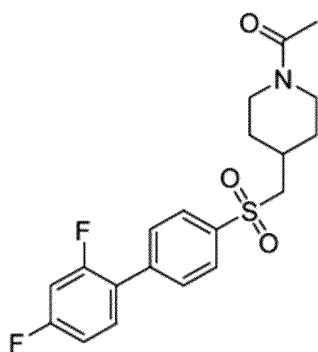


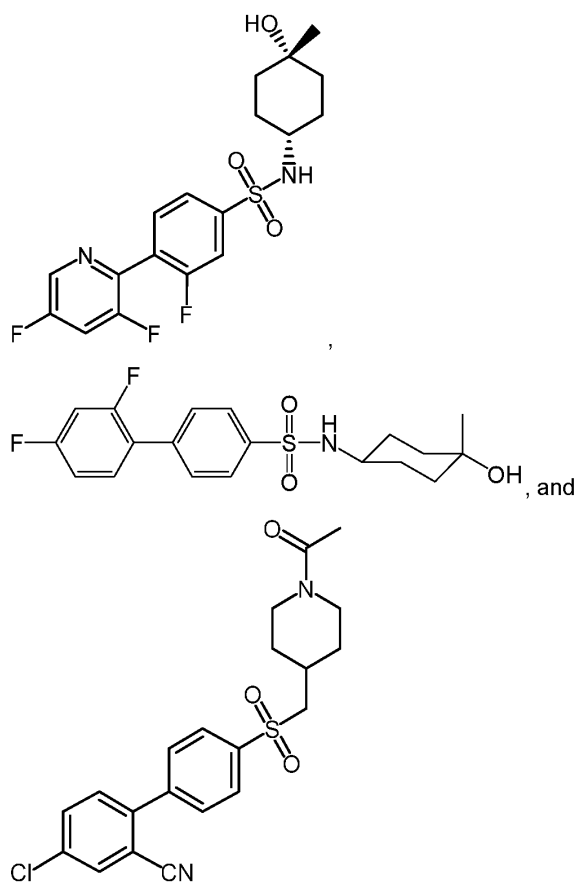
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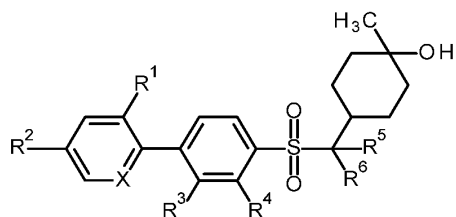
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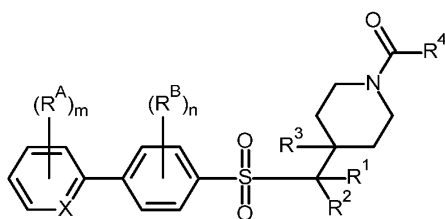


31. The combination according to any one of claims 1 to 3 or 22 to 30 or the composition for use according to any of claims 4 to 30, wherein the MCIM compound is an MCIM compound, or a pharmaceutically acceptable salt, hydrate, or solvate thereof, of the following formula:



as defined in claim 1 of WO2020/035560 A1.

32. The combination according to any one of claims 1 to 3 or 22 to 31 or the composition for use according to any of claims 4 to 31, wherein the MCIM compound is an MCIM compound, or a pharmaceutically acceptable salt, hydrate, or solvate thereof, of the following formula:



as defined in claim 1 of WO2020/212581 A1.

33. The combination according to any one of claims 1 to 3 or 22 to 32 or the composition for use according to any one of claims 4 to 32, wherein the DMARD comprises a conventional synthetic DMARD (csDMARD).

34. The combination or composition for use according to claim 33, wherein the csDMARD comprises azathioprine, chloroquine, hydroxychloroquine, ciclosporin, D-penicillamine, gold salt, sodium aurothiomalate, auranofin, leflunomide, or sulfasalazine, minocycline, or any combination of the foregoing.

35. The combination or composition for use according to claim 33 or 34, wherein the csDMARD comprises sulfasalazine, hydroxychloroquine, leflunomide, azathioprine, or a combination thereof.

36. The combination according to any one of claims 1 to 3 or 22 to 35 or the composition for use according to any one of claims 4 to 35, wherein the DMARD comprises a biological DMARD (bDMARD).

37. The combination or composition for use according to claim 36, wherein the bDMARD comprises rituximab or abatacept.

38. The combination or composition for use according to any one of claims 35 to 38, wherein the combination or composition further comprises methotrexate.