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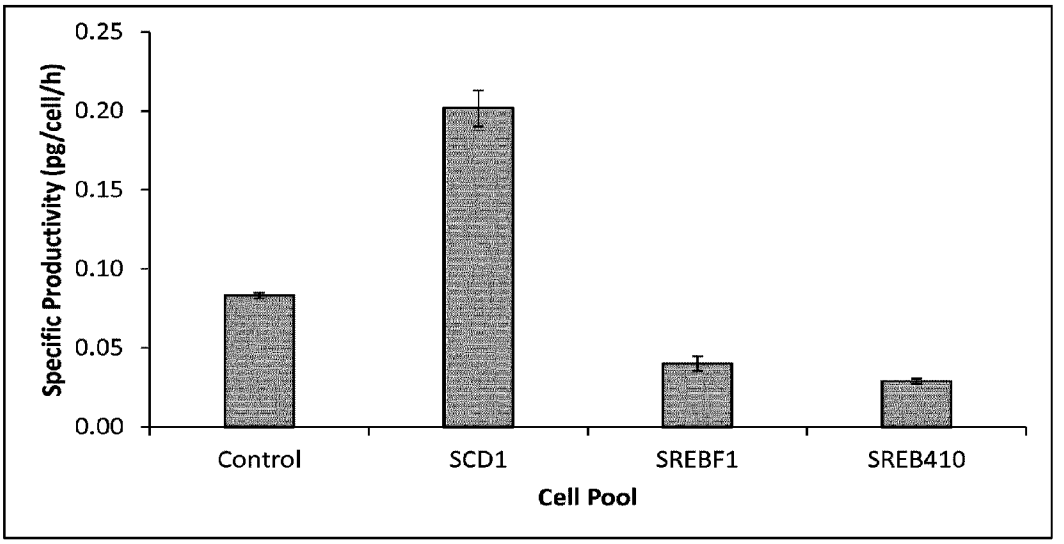
(54) **Titre : MODULATION DU METABOLISME DES LIPIDES POUR LA PRODUCTION DE PROTEINES**
(54) **Title: MODULATION OF LIPID METABOLISM FOR PROTEIN PRODUCTION**



(57) **Abrégé/Abstract:**
The present disclosure features methods and compositions for modulating lipid metabolism to achieve improved production and quality of recombinant products, such as next generation biologics. Modulation of lipid metabolism as described herein includes, for example, introducing a lipid metabolism modulator described herein to a cell or a cell-free system. Also encompassed by the present disclosure are engineered cells with improved production capacity and improved product quality, methods for engineering such cells, and preparations and mixtures comprising the products from such cells.

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(54) **Title:** MODULATION OF LIPID METABOLISM FOR PROTEIN PRODUCTION

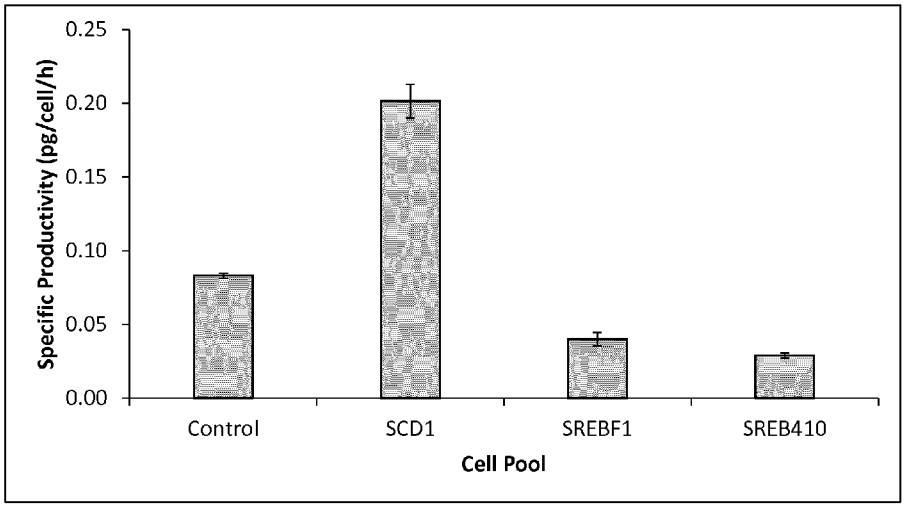

FIG. 16B

(57) **Abstract:** The present disclosure features methods and compositions for modulating lipid metabolism to achieve improved production and quality of recombinant products, such as next generation biologics. Modulation of lipid metabolism as described herein includes, for example, introducing a lipid metabolism modulator described herein to a cell or a cell-free system. Also encompassed by the present disclosure are engineered cells with improved production capacity and improved product quality, methods for engineering such cells, and preparations and mixtures comprising the products from such cells.

WO 2017/191165 A1

MODULATION OF LIPID METABOLISM FOR PROTEIN PRODUCTION

RELATED APPLICATIONS

This application claims priority to U.S. Serial No.: 62/330973, filed May 3, 2016.

FIELD OF THE INVENTION

The present disclosure relates to methods and compositions for modulating the lipid metabolism pathways of a cell and engineering cells and cell lines for production of a product, e.g., a recombinant protein.

BACKGROUND

Recombinant therapeutic proteins are commonly expressed in cell expression systems, e.g., mammalian cell expression systems. In 2014, the total number of market approved biopharmaceuticals was 212, and 56% of the therapeutic products approved for market by the FDA are produced in mammalian cell lines. However, the high cost associated with production contributes to increasing global health costs.

Moreover, next generation protein biologics (NGBs) such as next generation fusion proteins, multimeric glycoproteins, or next generation antibodies often have a complex and/or non-natural structure and are proving more difficult to express than molecules such as monoclonal antibodies. Current host cell lines have not evolved pathways for the efficient synthesis and secretion of NGBs, resulting in significantly reduced growth, low productivity and often resulting in products with poor product quality attributes. Thus, these NGBs are considered difficult to express, in which the productivity and product quality do not meet clinical and market needs.

Accordingly, there is an increasing need to develop and produce recombinant biotherapeutics rapidly, efficiently, and cost-effectively while maintaining final product quality.

SUMMARY

The present disclosure is based, in part, on the discovery that modulation of lipid metabolism pathways by overexpression of a component of one or more lipid metabolism pathways increases the productivity and product quality of a cell that produces a recombinant

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polypeptide product. Here, it is demonstrated that modulation of the lipid metabolism, e.g., by modulating one or more lipid metabolism pathways, can be used to engineer cells and cell-free systems that produce higher yields of products and products with improved quality. Importantly, the present disclosure features global regulation of lipid metabolism by using global regulators that modulate more than one process or pathway associated with lipid metabolism, thereby causing multiple downstream effects to achieve improved product production and quality. The methods and compositions described herein are particularly useful for improved production of recombinant products or next generation biologics (e.g., fusion proteins, bispecific or multi-format antibody molecules, multimeric proteins, and glycosylated proteins), and for development of more efficient systems for production of such products (e.g., cell lines or cell-free systems).

In one aspect, the present disclosure features a method for producing a product described herein in a cell. In an embodiment, the product is a polypeptide, e.g., a recombinant polypeptide. In one embodiment, the method comprises providing a cell comprising a modification that modulates lipid metabolism, and culturing the cell, e.g., under conditions suitable for modulation of lipid metabolism by the modification, thereby producing the product.

In another aspect, the present disclosure features a method for producing product, e.g., a polypeptide, e.g., a recombinant polypeptide, in a cell-free system comprising: providing a cell-free system comprising a modification that modulates lipid metabolism, e.g., a cell-free system derived from a cell or cell line comprising a modification that modulates lipid metabolism, and placing the cell-free system under conditions suitable for production of the product; thereby producing the product, e.g., polypeptide, e.g., recombinant polypeptide. In one embodiment, the cell-free system is derived from a cell or cell line comprising a modification that modulates lipid metabolism. In one embodiment, the cell-free system comprises one or more components, e.g., an organelle or portion of an organelle, from a cell or cell line comprising a modification that modulates lipid metabolism. In some embodiments, the modification comprises an exogenous nucleic acid encoding a lipid metabolism modulator (LMM) and wherein the cell or cell line expresses a LMM, e.g., an LMM selected from the group consisting of SREBF1, SREBF2, SCD1, SCD2, SCD3, SCD4, SCD5, or a functional fragment thereof. In some embodiments, the LMM alters one or more characteristics of a cell-free system selected from the group consisting of: increases the production, e.g., yield and rate of production, of the product, e.g., polypeptide, e.g., recombinant polypeptide (NGB) produced; and increases the quality, e.g., decreases

aggregation, decreases glycosylation heterogeneity, decreases fragmentation, and increases ratio of properly folded to misfolded or unfolded product, of the product.

Examples of products that can be produced using any of the methods or compositions described herein include recombinant products, or products in which at least one portion or moiety is a result of genetic engineering. Recombinant products described herein can be useful for diagnostic or therapeutic purposes. In one embodiment, a product comprises a polypeptide, such as an antibody molecule (e.g., a bispecific or multi-format antibody molecule), a fusion protein, or a protein-conjugate; a nucleic acid molecule (e.g., a DNA or RNA molecule); or a lipid-encapsulated particle (e.g., an exosome or virus-like particle). The methods and compositions described herein may be particularly useful for products that are difficult to produce, e.g., in high quantities or with sufficient quality for commercial or therapeutic use, such as next generation biologics (e.g., fusion proteins, bispecific or multi-format antibody molecules, multimeric proteins, and glycosylated proteins). In one embodiment, a cell as described herein, e.g., for producing the product, expresses the product. In one embodiment, the cell comprises an exogenous nucleic acid that encodes a product described herein, e.g., a polypeptide selected from Table 2 or 3. Additional examples of products are described in the section titled "Products".

The modifications disclosed herein that modulate lipid metabolism include agents or molecules that increase or decrease the expression of a lipid metabolism modulator (LMM) or increase or decrease the expression or activity of a component of a lipid metabolism pathway. In one embodiment, the modification is a nucleic acid, e.g., a nucleic acid encoding a LMM or an inhibitory nucleic acid that inhibits or decreases the expression of a LMM.

In one embodiment, the modification increases expression of a LMM, and comprises an exogenous nucleic acid encoding the LMM. In one embodiment, the method comprises forming, in the cell, an exogenous nucleic acid encoding a LMM or an exogenous LMM. In one embodiment, the forming comprises introducing an exogenous nucleic acid encoding a lipid metabolism modulator. In one embodiment, the forming comprises introducing an exogenous nucleic acid which increases the expression of an endogenous nucleic acid encoding a LMM. Examples of LMMs suitable for use in any of the methods and compositions described herein are further described in the sections titled "Modulation of Lipid Metabolism" and "Lipid Metabolism Modulators".

In one embodiment, the cell comprises one or more modifications. In one embodiment, the cell comprises one, two, three, four, five, six, seven, eight, nine or ten modifications. In some embodiments, the cell comprises more than one modification. In some embodiments, the cell comprises at least two, three, four, five, six, seven, eight, nine, or ten modifications. In one embodiment, the cell comprises a one or more second modification that modulates lipid metabolism. In one embodiment, the second modification comprises a second exogenous nucleic acid encoding a second LMM, e.g., a LMM different from the LMM of the first modification. In one embodiment, the second exogenous nucleic acid and the first exogenous nucleic acid are disposed on the same nucleic acid molecule. In one embodiment, the second exogenous nucleic acid and the first exogenous nucleic acid are disposed on different nucleic acid molecules. In one embodiment, the second modification provides increased the production or improved quality of the product, as compared to a cell not having the second modification. In one embodiment, the method comprises forming, in the cell, a second exogenous nucleic acid encoding a second LMM or a second exogenous LMM. In one embodiment, the forming comprises introducing the second exogenous nucleic acid encoding a second LMM. In one embodiment, the forming comprises introducing the second exogenous nucleic acid which increases the expression of an endogenous nucleic acid encoding a LMM.

Modulating lipid metabolism by any of the methods or compositions described herein can comprise or result in altering, e.g., increasing or decreasing, any one or more of the following:

i) the expression (e.g., transcription and/or translation) of a component involved in a lipid metabolism pathway;

ii) the activity (e.g., enzymatic activity) of a component involved in a lipid metabolism pathway;

iii) the amount of lipids (e.g., phospholipids, or cholesterol) present in a cell;

iv) the amount of lipid rafts or rate of lipid raft formation;

v) the fluidity, permeability, and/or thickness of a cell membrane (e.g., a plasma membrane, a vesicle membrane, or an organelle membrane);

vi) the conversion of saturated lipids to unsaturated lipids or conversion of unsaturated lipids to saturated lipids;

vii) the amount of saturated lipids or unsaturated lipids, e.g., monounsaturated lipids;

viii) the composition of lipids in the cell to attain a favorable composition that increases ER activity;

ix) the expansion of the ER (e.g., size of the ER, the ER membrane surface, or the amounts of the proteins and lipids that constitute and/or reside within the ER);

x) the expansion of the Golgi (e.g., the number and size of the Golgi, the Golgi surface, or the number or amounts of proteins and molecules that reside within the Golgi);

xi) the amount of secretory vesicles or the formation of secretory vesicles;

xii) the amount or rate of secretion of the product;

xiii) the proliferation capacity, e.g., the proliferation rate;

xiv) culture viability or cell survival;

xv) activation of membrane receptors;

xvi) the unfolded protein response (UPR);

xvii) the yield or rate of production of the product;

xviii) the product quality (e.g., aggregation, glycosylation heterogeneity, fragmentation, proper folding or assembly, post-translational modification, or disulfide bond scrambling); and /or

xix) cell growth/proliferation or cell specific growth rate.

In such embodiments, the increase or decrease of any of the aforementioned characteristics of the cell can be determined by comparison with a cell not having a modification.

The methods and compositions described herein result in increased production of the product as compared to a cell not having the modification. An increase in production can be characterized by increased amounts, yields, or quantities of product produced by the cell and/or increased rate of production, where the rate of production is equivalent to the amount of product over time. In one embodiment, production of the product, e.g., a recombinant polypeptide, is increased by 1%, 5%, 10%, 15%,20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 85%, or 100%, or more e.g., as compared to the production of by a cell without modulation of the lipid metabolism; or 1-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, e.g., as compared to the production of by a cell without modulation of the lipid metabolism.

The methods and compositions described herein can also result in improved quality of the product (i.e. product quality) as compared to a cell not having the modification. Improvements in

the quality of the product (i.e. product quality) can be characterized by one or more of: aggregation (e.g., a decrease in aggregates or aggregation); proper folding or assembly (e.g., a decrease in misfolded or unfolded products; or partially assembled or disassembled products); post-translation modification (e.g., increase or decrease in glycosylation heterogeneity, higher percentage of desired or predetermined post-translational modifications); fragmentation (e.g., a decrease in fragmentation); disulfide bond scrambling (e.g., a decrease in undesired isoforms or structures due to disulfide bond scrambling). In one embodiment, the quality of the product, e.g., recombinant polypeptide, is increased, e.g., 1%, 5%, 10%, 15%,20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 85%, or 100%, e.g., as compared to the production of by a cell without modulation of the lipid metabolism; or by 1-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, e.g., as compared to the quality of product produced by a cell without modulation of the lipid metabolism.

In embodiments, the method for producing a product as described herein can comprise one or more additional steps, which include, but are not limited to: introducing a modification to the cell that improves ER processing capacity (ER expansion) or secretion; obtaining the product from the cell, or a descendent of the cell, or from the medium conditioned by the cell, or a descendent of the cell; separating the product from at least one cellular or medium component; and/or analyzing the product, e.g., for activity or for the presence of a structural moiety. In one embodiment, the method further comprises a step for improving ER processing capacity (or ER expansion) by introducing a nucleic acid encoding PDI, BiP, ERO, or XBP1. In one embodiment, the method further comprises an additional step for improving secretory capacity or rate of secretion by modulating SNARE machinery or other machinery involved in the secretory pathway, e.g., by introducing a nucleic acid encoding a SNARE component.

Modulation of Lipid Metabolism

The present disclosure features methods and compositions for modulating lipid metabolism. In one embodiment, the modification results in modulating, e.g., increasing, one or more lipid metabolism pathways, which include, but are not limited to: *de novo* lipogenesis, fatty acid re-esterification, fatty acid saturation or desaturation, fatty acid elongation, and phospholipid biosynthesis.

The modifications described herein suitable for modulating lipid metabolism include introduction of an exogenous nucleic acid that increase or decreases the expression or activity of a component of a lipid metabolism pathway or a LMM, a LMM polypeptide, or other molecule that increases or decreases the expression or activity of a component of the lipid metabolism pathway. The present disclosure features the use of lipid metabolism modulators to modulate lipid metabolism, e.g., by increasing or decreasing expression or activity of a component associated with lipid metabolism. In an embodiment, the LMM is a global regulator described herein

In one embodiment, the modification that modulates lipid metabolism results in the global regulation of lipid metabolism, e.g., by increasing or decreasing the expression or activity of a global regulator. Such global regulators are molecules that are sufficiently upstream in one or more pathways, such that it can influence multiple downstream effects, for example, increasing the expression or activity of more than one, e.g., two, three, four, five, or more, components of different lipid metabolism processes or pathways. A component of a lipid metabolism process or pathway can include, but is not limited to, an enzyme, a cofactor, or other molecule that is involved in the synthesis, degradation, elongation, or structural conformation of lipid molecules.

In one embodiment, the global regulator described herein is a transcription factor that upregulates, e.g., increases the expression, of a component of the lipid metabolism, e.g., a lipid metabolism gene product selected from Table 1. By way of example, a global regulator increases the expression of two or more lipid-associated gene products, e.g., an enzyme involved in lipid biosynthesis and an enzyme involved in the saturation level of a lipid molecule.

In any of the methods or compositions described herein, the LMM comprises any of the following: a global regulator of lipid metabolism, e.g., a transcription factor that upregulates lipid metabolism genes, or a component (e.g., an enzyme, a cofactor, or a molecule) that plays a role in the *de novo* lipogenesis, fatty acid re-esterification, fatty acid saturation or desaturation, fatty acid elongation, or phospholipid biosynthesis pathways.

In one embodiment, the lipid metabolism modulator comprises a transcription regulator, e.g., a transcription factor, that mediates, e.g., upregulates, the expression of a lipid metabolism gene product. Examples of lipid metabolism gene products include, but are not limited to, those

provided in Table 1. a global regulator of lipid metabolism, e.g., a transcription factor that upregulates lipid metabolism genes.

In one embodiment, the LMM comprises SREBF1, or SREBF2, or a functional fragment or analog thereof. In one embodiment, the lipid metabolism modulator comprises at least 60, 70, 80, 90, 95, 98, 99 or 100% identity with the amino acid sequence of SREBF1; e.g., SEQ ID NOs:1 or 34, or a functional fragment thereof, e.g., SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 36; or differs by 1, 2, or 3 or more amino acid residues but no more than 50, 40, 30, 20, 15, or 10 amino acid residues from the amino acid sequence of SREBF1, e.g., SEQ ID NOs: 1 or 34, or a functional fragment thereof, e.g., SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 36. In one embodiment, the nucleic acid encoding the lipid metabolism modulator comprises at least 60, 70, 80, 90, 95, 98, 99 or 100% identity with any of the nucleic acid sequences selected from SEQ ID NOs: 2 or 32, or the nucleic acids encoding SEQ ID NO: 26, SEQ ID NO: 27, or SEQ ID NO: 36.

In one embodiment, the LMM comprises SCD1, SCD2, SCD3, SCD4, or SCD5, or a functional fragment or analog thereof. In one embodiment, the lipid metabolism modulator comprises at least 60, 70, 80, 90, 95, 98, 99 or 100% identity with the amino acid sequence of SCD1; e.g., SEQ ID NO:3, or a functional fragment thereof; or differs by 1, 2, or 3 or more amino acid residues but no more than 50, 40, 30, 20, 15, or 10 amino acid residues from the amino acid sequence of SCD1, e.g., SEQ ID NO: 3, or a functional fragment thereof. In one embodiment, the nucleic acid encoding the lipid metabolism modulator comprises at least 60, 70, 80, 90, 95, 98, 99 or 100% identity with any of the nucleic acid sequences selected from SEQ ID NOs: 4.

In one embodiment, the LMM comprises any of the components provided in Table 1 or a functional fragment thereof. In one embodiment, the LMM comprises at least 60, 70, 80, 90, 95, 98, 99 or 100% identity with the amino acid sequence of any of the components provided in Table 1 or a functional fragment thereof; or differs by 1, 2, or 3 or more amino acid residues but no more than 50, 40, 30, 20, 15, or 10 amino acid residues from the amino acid sequence of any of the components provided in Table 1 or a functional fragment thereof. In one embodiment, the nucleic acid encoding the lipid metabolism modulator comprises at least 60, 70, 80, 90, 95, 98, 99 or 100% identity with a nucleic acid sequence encoding any of the components provided in Table 1 or a functional fragment thereof.

In one embodiment, the modification comprises a *cis* or *trans* regulatory element that increases the expression of a nucleic acid that encodes a lipid metabolism gene product, e.g., a lipid metabolism gene product selected from Table 1.

In one embodiment, the nucleic acid encoding the lipid metabolism modulator comprises a plasmid or a vector.

In one embodiment, the nucleic acid encoding the lipid metabolism modulator is introduced into the cell by transfection (e.g., electroporation), transduction, or any other delivery method described herein.

In one embodiment, the nucleic acid encoding the lipid metabolism modulator is integrated into the chromosomal genome of the cell. In one embodiment, the LMM is stably expressed.

In one embodiment, the nucleic acid encoding the lipid metabolism modulator is not integrated into the chromosomal genome of the cell. In one embodiment, the LMM is transiently expressed.

Products

Products described herein include polypeptides, e.g., recombinant proteins; nucleic acid molecules, e.g., DNA or RNA molecules; multimeric proteins or complexes; lipid-encapsulated particles, e.g., virus-like particles, vesicles, or exosomes; or other molecules, e.g., lipids. In an embodiment, the product is a polypeptide, e.g., a recombinant polypeptide. For example, the recombinant polypeptide can be a difficult to express protein or a protein having complex and/or non-natural structures, such as a next generation biologic, e.g., a bispecific antibody molecule, a fusion protein, or a glycosylated protein.

In any of the methods described herein, the method for producing a product further comprises introducing to the cell an exogenous nucleic acid encoding the product, e.g., polypeptide, e.g., recombinant polypeptide.

In one embodiment, the exogenous nucleic acid encoding the recombinant polypeptide is introduced after providing a cell comprising a modification that modulates lipid metabolism. In another embodiment, the exogenous nucleic acid encoding the recombinant polypeptide is introduced after culturing the cell, e.g., under conditions suitable for modulation of lipid metabolism by the modification.

In one embodiment, the exogenous nucleic acid encoding the product, e.g., recombinant polypeptide, is introduced prior to providing a cell comprising a modification that modulates lipid metabolism. In another embodiment, the exogenous nucleic acid encoding the recombinant polypeptide is introduced prior to culturing the cell, e.g., under conditions suitable for modulation of lipid metabolism by the modification.

In any of the compositions, preparations, or methods described herein, the product, e.g., recombinant polypeptide, is a therapeutic polypeptide or an antibody molecule, e.g., an antibody or an antibody fragment thereof. In one embodiment, the antibody molecule is a monoclonal antibody. In one embodiment, the antibody molecule is a bispecific antibody molecule, e.g., a BiTE (Bispecific T cell Engager), a DART (Dual Affinity Re-Targeting or Redirected T cell).

In one embodiment, the product, e.g., recombinant polypeptide, is selected from Table 2 or 3.

In embodiments, the product is stably expressed by the cell. In one embodiment, the exogenous nucleic acid encoding the product, e.g., recombinant polypeptide, is integrated into the chromosomal genome of the cell. Alternatively, the product is transiently expressed by the cell. In one embodiment, the exogenous nucleic acid encoding the product, e.g., the recombinant polypeptide, is not integrated into the chromosomal genome of the cell.

Host Cells

Provided herein are cells for producing the products described herein and methods of engineering such cells.

In any of the compositions, preparations, or methods described herein, the cell is a eukaryotic cell. In one embodiment, the cell is a mammalian cell, a yeast cell, an insect cell, an algae cell, or a plant cell. In one embodiment, the cell is a rodent cell. In one embodiment, the cell is a Chinese hamster ovary (CHO) cell. Examples of CHO cells include, but are not limited to, CHO-K1, CHOK1SV, Potelligent CHOK1SV (FUT8-KO), CHO GS-KO, Exceed (CHOK1SV GS-KO), CHO-S, CHO DG44, CHO DXB11, CHOZN, or a CHO-derived cell.

In any of the compositions, preparations, or methods described herein, the cell is selected from the group consisting of HeLa, HEK293, H9, HepG2, MCF7, Jurkat, NIH3T3, PC12, PER.C6, BHK, VERO, SP2/0, NS0, YB2/0, EB66, C127, L cell, COS, e.g., COS1 and COS7, QC1-3, CHO-K1, CHOK1SV, Potelligent CHOK1SV (FUT8-KO), CHO GS-KO, Exceed

(CHOK1SV GS-KO), CHO-S, CHO DG44, CHO DXB11, and CHOZN.

In one embodiment, the cell is a eukaryotic cell other than a mammalian cell, e.g., an insect, a plant, a yeast, or an algae cell. In one embodiment, the cell is a prokaryotic cell.

In one aspect, the present disclosure features a method of engineering a cell having increased production capacity and/or improved quality of production (e.g., producing product with one or more improved product quality) comprising introducing to the cell or forming in the cell an exogenous nucleic acid encoding a lipid metabolism modulator, thereby engineering a cell having increased production capacity and/or improved quality of production . In an embodiment, the exogenous nucleic acid encoding a lipid metabolism modulator is introduced to the cell by transfection, transduction, e.g., viral transduction, electroporation, nucleofection, or lipofection. In an embodiment, the exogenous nucleic acid encoding a lipid metabolism modulator is integrated into the chromosomal genome of the cell. In an embodiment, the method further comprises introducing to the cell an exogenous nucleic acid encoding a recombinant polypeptide. In an embodiment, the exogenous nucleic acid encoding a recombinant polypeptide is introduced prior to introducing the exogenous nucleic acid encoding the LMM. In an embodiment, the exogenous nucleic acid encoding a recombinant polypeptide is introduced after introducing the exogenous nucleic acid encoding the LMM.

In one aspect, the present disclosure features a cell produced by providing a cell and introducing to the cell a LMM described herein, e.g., introducing an exogenous nucleic acid encoding a LMM.

In one aspect, the present disclosure features a cell comprising an exogenous nucleic acid encoding a LMM described herein

In one aspect, the present disclosure features a cell engineered to produce a LMM, wherein the LMM modulates the expression of a product, e.g., a next generation biologic (NGB) described herein. In one embodiment, the cell is a CHO cell.

In one aspect, the present disclosure features a CHO cell engineered to produce a LMM, wherein the LMM modulates the expression of a product, e.g., a Next generation biologic (NGB) described herein.

In one aspect, the present disclosure features a CHO cell engineered to express an LMM and a NGB, wherein the population has been selected for high level expression of the NGB.

In one aspect, the present disclosure features a CHO cell engineered to express an LMM, wherein the LMM modulates one or more characteristics of the CHO cell, wherein the engineered CHO cell is selected based on modulation of one or more characteristics selected from the group consisting of

i) the expression (e.g., transcription and/or translation) of a component involved in a lipid metabolism pathway;

ii) the activity (e.g., enzymatic activity) of a component involved in a lipid metabolism pathway;

iii) the amount of lipids (e.g., phospholipids, or cholesterol) present in a cell;

iv) the amount of lipid rafts or rate of lipid raft formation;

v) the fluidity, permeability, and/or thickness of a cell membrane (e.g., a plasma membrane, a vesicle membrane, or an organelle membrane);

vi) the conversion of saturated lipids to unsaturated lipids or conversion of unsaturated lipids to saturated lipids;

vii) the amount of saturated lipids or unsaturated lipids, e.g., monounsaturated lipids;

viii) the composition of lipids in the cell to attain a favorable composition that increases ER activity;

ix) the expansion of the ER (e.g., size of the ER, the ER membrane surface, or the amounts of the proteins and lipids that constitute and/or reside within the ER);

x) the expansion of the Golgi (e.g., the number and size of the Golgi, the Golgi surface, or the number or amounts of proteins and molecules that reside within the Golgi);

xi) the amount of secretory vesicles or the formation of secretory vesicles;

xii) the amount or rate of secretion of the product;

xiii) the proliferation capacity, e.g., the proliferation rate;

xiv) culture viability or cell survival;

xv) activation of membrane receptors;

xvi) the unfolded protein response (UPR);

xvii) the yield or rate of production of the product;

xviii) the product quality (e.g., aggregation, glycosylation heterogeneity, fragmentation, proper folding or assembly, post-translational modification, or disulfide bond scrambling); and /or

xix) cell growth/proliferation or cell specific growth rate.

In any of the methods or cells, e.g., engineered cells, described herein, the cell expresses or comprises the LMM is selected from a group consisting of SREBF1, SREBF2, SCD1, SCD2, SCD3, SCD4, and SCD5, or a functional fragment thereof.

In any of the methods or cells, e.g., engineered cells, described herein, the cell expresses or comprises a product, e.g., a recombinant product, e.g., a next generation biologic selected from a group consisting of a bispecific antibody, a fusion protein, or a glycosylated protein.

In any of the methods or cells, e.g., engineered cells described herein, the cell is a CHO cell selected from the group consisting of CHO-K1, CHOK1SV, Potelligent CHOK1SV (FUT8-KO), CHO GS-KO, Exceed (CHOK1SV GS-KO), CHO-S, CHO DG44, CHO DXB11, CHOZN, or a CHO-derived cell.

Compositions and Preparations

In one aspect, the present disclosure also features a preparation of a product described herein made by a method described herein. In one embodiment, at least 70, 80, 90, 95, 98 or 99 %, by weight or number, of the products in the preparation are properly folded or assembled. In one embodiment, less than 50%, 40%, 30%, 25%, 20%, 15%, 10%, or 5%, by weight or number, of the products in the preparation are aggregated. In one embodiment, less than 50%, 40%, 30%, 25%, 20%, 15%, 10%, or 5%, by weight or number, of the products in the preparation are fragments of the product.

In some embodiments, the present disclosure features a preparation of a polypeptide, e.g., a polypeptide of Table 2 or Table 3, made by a method described herein. In some embodiments, the cell used in the method is a CHO cell selected from the group consisting of CHOK1, CHOK1SV, Potelligent CHOK1SV, CHO GS knockout, CHOK1SV GS-KO, CHOS, CHO DG44, CHO DXB11, CHOZN, or a CHO-derived cell.

In one aspect, the present disclosure features a mixture comprising a cell described herein, e.g., a cell comprising a modification that modulates lipid metabolism, and a product produced by the cell. In one embodiment, the mixture comprises the product at a higher

concentration, e.g., at least, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 20%, or 30% higher concentration, by weight or number, of product than would be seen without the modification. In one embodiment, at least 70%, 80%, 90%, 95%, 98 %or 99%, by weight or number, of the products in the mixture are properly folded or assembled. In one embodiment, less than 50%, 40%, 30%, 25%, 20%, 15%, 10%, or 5%, by weight or number, of the products in the mixture are aggregated. In one embodiment, less than 50%, 40%, 30%, 25%, 20%, 15%, 10%, or 5%, by weight or number, of the products in the mixture are fragments of the product. In some embodiments, the product is a recombinant polypeptide, e.g., a recombinant polypeptide of Table 2 or Table 3.

In one aspect, the present disclosure features a preparation of medium conditioned by culture of a cell described herein, wherein the cell comprises a modification that modulates lipid metabolism. In one embodiment, the product is present in the preparation at a higher concentration, e.g., at least, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 20%, or 30% higher concentration, by weight or number, than would be seen without the modification. In one embodiment, at least 70%, 80%, 90%, 95%, 98% or 99%, by weight or number, of the product in the preparation are properly folded or assembled. In one embodiment, less than 50%, 40%, 30%, 25%, 20%, 15%, 10%, or 5%, by weight or number, of the products in the preparation are aggregated. In one embodiment, less than 50%, 40%, 30%, 25%, 20%, 15%, 10%, or 5%, by weight or number, of the products in the preparation are fragments of the product. In some embodiments, the product is a recombinant polypeptide, e.g., a recombinant polypeptide of Table 2 or Table 3.

In an embodiment, there is provided a method for producing a recombinant polypeptide in a eukaryotic cell, comprising: i) providing the eukaryotic cell comprising: a first exogenous nucleic acid encoding a first lipid metabolism modulator (LMM) comprising stearoyl CoA desaturase-1 (SCD1) or a functional fragment or isoform thereof; and a second exogenous nucleic acid encoding the recombinant polypeptide, wherein the recombinant polypeptide is: a. a therapeutic polypeptide, b. an antibody or fragment thereof, a monoclonal antibody, or a bispecific molecule, or c. selected from a hormone, a blood clotting or coagulation factor, a cytokine or growth factor, a fusion protein and a protein vaccine; and (ii) culturing the cell under conditions where the first LMM and the recombinant polypeptide are expressed, thereby producing the recombinant polypeptide.

Date reçue / Date received 2021-12-13

In another embodiment, there is provided a eukaryotic cell comprising: a first exogenous nucleic acid encoding a first lipid metabolism modulator (LMM), wherein the first LMM comprises stearoyl CoA desaturase-1 (SCD1) or a functional fragment or isoform thereof; and a second exogenous nucleic acid encoding a recombinant polypeptide, wherein the first exogenous nucleic acid is integrated into the chromosomal genome of the cell and wherein the recombinant polypeptide is: i) a therapeutic polypeptide, ii) an antibody or fragment thereof, a monoclonal antibody, or a bispecific molecule, or iii) selected from a hormone, a blood clotting or coagulation factor, a cytokine or growth factor, a fusion protein and a protein vaccine.

In yet another embodiment, there is provided use of the cell as described herein in the production of a therapeutic recombinant polypeptide of interest.

In an embodiment, there is provided a method for producing a recombinant polypeptide in a eukaryotic cell, comprising: i) providing the eukaryotic cell comprising: a first exogenous nucleic acid encoding a first lipid metabolism modulator (LMM) comprising Sterol Regulatory Element-Binding Transcription Factor 1 (SREBF1) or a functional fragment or isoform thereof; and a second exogenous nucleic acid encoding the recombinant polypeptide, wherein the recombinant polypeptide is: a. a therapeutic polypeptide, b. an antibody or fragment thereof, a monoclonal antibody, or a bispecific molecule, or c. selected from a hormone, a blood clotting or coagulation factor, a cytokine or growth factor, a fusion protein and a protein vaccine; and (ii) culturing the cell under conditions where the first LMM and the recombinant polypeptide are expressed, thereby producing the recombinant polypeptide.

In another embodiment, there is provided a eukaryotic cell comprising: a first exogenous nucleic acid encoding a first lipid metabolism modulator (LMM), wherein the first LMM comprises Sterol Regulatory Element-Binding Transcription Factor 1 (SREBF1) or a functional fragment or isoform thereof; and a second exogenous nucleic acid encoding a recombinant polypeptide, wherein the first exogenous nucleic acid is integrated into the chromosomal genome of the cell and wherein the recombinant polypeptide is: i) a therapeutic polypeptide, ii) an antibody or fragment thereof, a monoclonal antibody, or a bispecific molecule, or iii) selected from a hormone, a blood

Date reçue / Date received 2021-12-13

clotting or coagulation factor, a cytokine or growth factor, a fusion protein and a protein vaccine.

In another embodiment, there is provided use of the cell as described herein in the production of a therapeutic recombinant polypeptide of interest.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. In addition, the materials, methods, and examples are illustrative only and are not intended to be limiting. Headings, sub-headings or numbered or lettered elements, e.g., (a), (b), (i) etc., are presented merely for ease of reading.

The use of headings or numbered or lettered elements in this document does not require the steps

Date reçue / Date received 2021-12-13

or elements be performed in alphabetical order or that the steps or elements are necessarily discrete from one another. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

Brief Description of the Drawings

Figure 1 is a series of immunofluorescent images obtained of Flp-In CHO engineered cell pools, separately transfected with either a control expression vector (Ctrl), or ones encoding SCD1 fused at its C-terminus to a V5 epitope tag (SCD1-V5) or SREBF1 fused at its C-terminus to a V5 epitope tag (SREBF1-V5). The pools were imaged with an anti-V5 primary antibody and a secondary anti-mouse FITC antibody (middle images) as well as DAPI (left images) and an overlay of both the left and middle images (right hand column) is shown. Images were generated using a Leica Confocal Microscope.

Figure 2 shows a series of immunofluorescent images obtained of CHOK1SV glutamine synthetase knock-out (GS-KO) cell pools, transfected with either a control expression vector (Ctrl), or ones encoding SCD1-V5 or SREBF1-V5. The pools were imaged with an anti-V5 primary and anti-mouse secondary TRITC antibody (middle images) as well as DAPI (left images) and an overlay of both the left and middle images (right hand column) is also shown. Images were generated using a Leica Confocal Microscope.

Figures 3A, 3B, and 3C show the determination of exogenous SCD1-V5 and SREBF1-V5 expressed in CHO Flp-In™ cell pools following transient transfection with a plasmid encoding a difficult to express recombinant Fc fusion protein (also referred to as Fc fusion protein or FP) (Fig. 3A) or eGFP (Fig. 3B). Fig 3C shows determination of exogenous V5-tagged SCD1 and SREBF1 expressed in untransfected stably expressing CHO Flp-In™ cell pools. Western blot analysis was performed on cell lysates obtained 96 hours following electroporation with the Fc fusion protein, as well as the cell pool solely expressing the indicated V5-tagged lipid metabolism modulator (LMM), SCD1 or SREBF1. Anti-V5 primary antibody and anti-mouse HRP conjugated secondary antibody was used to detect expression of the V5-tagged LMM and anti-β-actin or anti L7a (as indicated) followed by exposure with anti-mouse and anti-rabbit HRP conjugated secondary antibodies respectively were used as loading controls for LMM detection.

Figure 4 shows the viable cell concentration, as determined using a ViCell cell counter, of the CHO Flp-In cell pools engineered to stably overexpress the LMM SCD1-V5 and SREBF1-V5 post transfection with eGFP-containing construct JB3.3 (n=2).

Figures 5A and 5B show the cell culture concentration and culture viability at 24, 48, 72, and 96 hours after transfection of control, SCD1-V5, SREBF1-V5 and SREBF410-V5 over-expressing CHOK1SV GS-KO cell pools with an eGFP containing plasmid. Figure 5A shows cell concentration. The lower columns represent viable cell concentration whilst the whole column represents the total concentration of cells; lower error bars represent the standard deviation of viable cells whilst upper error bars represent that of the total cell concentration. Figure 5B shows culture viability based on the data outlined in Fig. 5A. Error bars represent standard deviation. Statistical significance was calculated using two-tailed T-test compared to the control values of the particular time points: *Viable cell concentration significance using two-tailed T-test [$p<0.05$]. †Total cell concentration significance using two-tailed T-tests [$p<0.05$] (n=3).

Figures 6A, 6B and 6C show flow cytometry generated data using a FACSCalibur instrument (BD Biosciences). Median (Fig. 6A), geometric mean (Fig. 6B) and arithmetic mean (Fig. 6C) values were acquired at 24, 48, 72 and 96 hours post transfection with an eGFP containing plasmid where samples were taken from control, SCD1-V5 or SREBF1-V5 overexpressing Flp-In CHO cell pools (n=2).

Figures 7A, 7B and 7C show flow cytometry generated data using a FACSCalibur instrument (BD Biosciences). Median (Fig. 7A), geometric mean (Fig. 7B) values were acquired at 24, 48, 72 and 96 hours post transfection with an eGFP containing plasmid where samples were taken from control, SCD1-V5, SREBF1-V5 or SREBF410-V5 overexpressing CHOK1SV GS-KO derived cells. Figure 7C shows the total fluorescence per ml of culture as calculated by multiplying the measured arithmetic mean fluorescence by total cell concentration ($x10^6$/ml). Error bars indicate standard deviation. Statistical significance was calculated using a two-tailed T-test compared to the control values of the particular time points (n=3). *Indicates statistically significant values [$p<0.05$]. Data was generated using FACSCalibur (BD Biosciences).

Figures 8A and 8B show antibody A production in CHO Flp-In cells stably overexpressing SCD1-V5 and SREBF1-V5 after transient transfection of a nucleic acid construct encoding antibody A heavy and light chains. Fig. 8A is a western blot showing bands

corresponding to antibody A, as detected by using an anti-heavy chain primary antibody and an anti-rabbit HRP conjugated secondary antibody. Fig. 8B shows the average fold change in antibody production in the LMM engineered cell pools compared to values generated from the control cell pool as determined by Protein A HPLC.

Figures 9A and 9B show the production of an Fc fusion protein in CHO Flp-In cell pools stably overexpressing SCD1-V5 and SREBF1-V5 after transient transfection of a nucleic acid construct encoding the fusion protein. Fig. 9A is a western blot showing the bands representative of the Fc fusion protein as detected by using an anti-heavy chain primary antibody and an anti-rabbit HRP conjugated secondary antibody. Fig. 9B shows the average fold change in the Fc fusion protein production in the LMM engineered cell pools compared to values generated from the control cell pool as determined by Protein A HPLC.

Figures 10A and 10B show the production of a well expressed antibody A in CHO GSKO cell pools stably overexpressing SCD1-V5, SREBF1-V5 and SREBF410-V5 after transient transfection of a nucleic acid construct encoding antibody A heavy and light chains at 48, 72 and 96 h post transfection and in a control, Null CHOK1SV GS-KO cell pool (a control pool of cells generated using an empty plasmid to express selection GS gene only, no LMM agents). Fig. 10A is a western blot showing the bands representative of antibody A as detected by using an anti-heavy chain primary antibody and an anti-rabbit HRP conjugated secondary antibody. Fig. 10B shows the average fold change in antibody production in the LMM engineered cell pools compared to values generated in the control cell pool as determined by Protein A HPLC.

Figures 11A and 11B shows the relative production of a difficult to express Fc fusion protein in CHOK1SV GS-KO cell pools stably overexpressing SCD1-V5 and SREBF1-V5 or in a control cell pool after transient transfection of a nucleic acid construct encoding the Fc fusion protein. Fig. 11A shows a western blot of the transiently produced fusion protein, as detected by using an anti-heavy chain primary antibody followed by exposure with an anti-rabbit HRP conjugated secondary antibody. Fig. 11B shows the average fold change in the Fc fusion protein production in the LMM engineered cell pool compared to the control cell pools as determined by Protein A HPLC.

Figures 12A and 12B show the analysis of antibody A production from supernatant harvested after 48 and 72 hours from a CHO cell line stably expressing antibody A which have

been transiently transfected with plasmid constructs containing either control (empty), SCD1-V5, SREBF1-V5 or SREBF410-V5 genes. Fig. 12A shows a western blot of the supernatants from the cells; antibody A was detected by using an anti-heavy chain primary antibody followed by exposure with an anti-rabbit HRP conjugated secondary antibody. Figure 12B shows Coomassie analysis in which the bands show the relative levels of antibody A present in the supernatant at 168 hours post transfection.

Figure 13 shows analysis of antibody A production from supernatant harvested after 48, 72, 96 and 144 hours from a CHO cell line stably expressing antibody A which had been transiently transfected with plasmid constructs containing either control (empty), SCD1-V5, SREBF1-V5 or SREBF410-V5 genes where protein A Octet analysis was used to determine volumetric antibody concentration (n=2).

Figure 14 shows analysis of an FC fusion protein from supernatant samples harvested after 48, 72, 96 and 144 hours from a CHO cell line stably expressing antibody A which had been transiently transfected with plasmid constructs containing either control (empty), SCD1-V5, SREBF1-V5 or SREBF410-V5 genes where viable cell number and protein A titre measurements were used to determine specific productivity of the FC fusion protein Error bars show standard deviation (n=3).

Figure 15A and 15B shows analysis of antibody A production from supernatant samples harvested after 48, 72, 96 and 144 hours from CHO cell pools stably integrated with control, SCD1-V5 or SREBF1-V5 containing vectors and subsequently stably integrated with an antibody A construct. Figure 15A shows volumetric antibody concentration whilst Figure 15B shows specific productivity of antibody A. Error bars show standard deviation (n=3).

Figure 16A and 16B shows analysis of FC fusion protein production from supernatant samples harvested after 48, 72, 96 and 144 hours from a CHO cell pools stably integrated with control, SCD1-V5, SREBF1-V5 or SREBF410-V5 containing vectors and subsequently stably integrated with an FC fusion protein construct. Figure 16A shows volumetric FC fusion protein concentration whilst Figure 16B shows specific productivity of the FC fusion protein. Error bars show standard deviation (n=3).

Figures 17A shows western analysis of immunocytokine expression from CHO GSKO cells following transient transfection of a nucleic acid construct encoding genes appropriate for expression of the immunocytokine and either no LMM (control), SCD1, SREBF1 or SREB411

genes at 48 and 96 h post transfection. Supernatant samples were reduced and bands present detected using an anti heavy chain primary antibody followed by exposure to an anti-rabbit HRP conjugated secondary antibody. The lower band represents a native heavy chain antibody whilst the upper band is indicative of a heavy chain molecule fused to a cytokine. Figure 17B shows relative immunocytokine abundance of samples obtained at 96 hours post transfection.

DETAILED DESCRIPTION

As both current and next generation biologics continue to gain therapeutic utility in patients, the demand for large quantities of next generation biologic products having a high grade of quality for therapeutic use, as well as efficient means for production and efficient development of production cell line will escalate. Furthermore, many next generation biologics are difficult to express and produce in conventional cell lines using conventional expression techniques known in the art. The current methods are not sufficient to produce these products in the large quantities and at the high grade of quality required for clinical use. As such, the present disclosure features methods and compositions for obtaining higher yields of a product, e.g., a next generation biologics, with improved quality as compared to the yield and quality obtained from current production methods. The methods and compositions described herein are also useful for engineering cells or cell lines with improved productivity, product quality, robustness, and/or culture viability, as compared to the cell expression systems currently used to produce recombinant products.

DEFINITIONS

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the invention pertains. Although any methods and materials similar or equivalent to those described herein can be used in the practice of and/or for the testing of the present invention, the preferred materials and methods are described herein. In describing and claiming the present invention, the following terminology will be used according to how it is defined, where a definition is provided.

It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

The articles "a" and "an" are used herein to refer to one or to more than one (*i.e.*, to at least one) of the grammatical object of the article. By way of example, "a cell" can mean one cell or more than one cell.

"Component of a lipid metabolism pathway", as used herein, refers to a molecule, polypeptide, or enzyme that, directly or indirectly, synthesizes a lipid, degrades a lipid, converts a lipid from one lipid species to another lipid species, or modifies a lipid. In one embodiment, the component can be an enzyme substrate, an enzyme reaction product, or an enzyme cofactor. In one embodiment, the component of a lipid metabolism pathway is a LMM. In one embodiment, the component of a lipid metabolism pathway is provided in Table 1.

"Endogenous", as used herein, refers to any material from or naturally produced inside an organism, cell, tissue or system.

"Exogenous", as used herein, refers to any material introduced to or produced outside of an organism, cell, tissue or system. Accordingly, "exogenous nucleic acid" refers to a nucleic acid that is introduced to or produced outside of an organism, cell, tissue or system. In an embodiment, sequences of the exogenous nucleic acid are not naturally produced, or cannot be naturally found, inside the organism, cell, tissue, or system that the exogenous nucleic acid is introduced into. In embodiments, non-naturally occurring products, or products containing portions that are non-naturally occurring are exogenous materials with respect to the host cells described herein.

"Forming", as used herein, refers to introducing into the cell, synthesizing within the cell, or any other process that results in the nucleic acid encoding a LMM or an exogenous LMM being located within the cell.

"Heterologous", as used herein, refers to any material from one species, when introduced to an organism, cell, tissue or system from a different species. In embodiments, a heterologous material also encompasses a material that includes portions from one or multiple species or portions that are non-naturally occurring. By way of example, in an embodiment, a nucleic acid encoding a fusion protein wherein a portion of the fusion protein is human, a portion of the fusion protein is bacteria, and a portion of the fusion protein is non-naturally occurring, and the nucleic acid is introduced to a human cell, the nucleic acid is a heterologous nucleic acid.

"Lipid metabolism pathway", as used herein, refers to a process associated with the synthesis of a lipid or lipid-associated molecule, the elongation of a lipid or lipid-associated molecule, the degradation of a lipid or lipid-associated molecule, the incorporation of a lipid or lipid-associated molecule into a membrane, the state of saturation of a lipid or lipid-associated molecule (e.g., saturated or unsaturated), or conversion or modification of the chemical structure (e.g., re-esterification) of a lipid or lipid-associated molecule. In one embodiment, the lipid metabolism pathway results in lipid synthesis, lipid elongation, lipid degradation, changes in membrane composition or fluidity, formation or modulation of lipid rafts, or modification or conversion of a lipid (e.g., saturation or de-saturation of a lipid, or re-esterification of a lipid). Examples of lipid metabolism pathways include, but are not limited to: *de novo* lipogenesis, fatty acid re-esterification, fatty acid saturation, fatty acid de-saturation, fatty acid elongation, and phospholipid biosynthesis, and unfolded protein response.

"Lipid metabolism modulator" or "LMM", as used herein, refers to a molecule, gene product, polypeptide, or enzyme that modulates, e.g., increases or decreases, one or more of the following: the expression (e.g., transcription or translation) of a component involved in a lipid metabolism pathway; the activity (e.g., enzymatic activity) of a component, e.g., gene product, involved in a lipid metabolism pathway; the level or amount of lipids present in a cell; the level or amount of lipid rafts or rate of lipid raft formation; the fluidity, permeability, or thickness of a cell membrane, e.g., plasma membrane or an organelle membrane; the conversion of saturated lipids to unsaturated lipids or vice versa; the level or amount of saturated lipids or unsaturated lipids in a cell, e.g., monounsaturated lipids; lipid composition to achieve a favorable lipid composition that has a favorable impact on the activity of the ER; the expansion of the ER; the expansion of the Golgi; the level or amount of secretory vesicles or secretory vesicle formation; the level or rate of secretion; activation or inactivation of membrane receptors (e.g., ATR (see e.g., The increase of cell-membranous phosphatidylcholines containing polyunsaturated fatty acid residues induces phosphorylation of p53 through activation of ATR. Zhang XH, Zhao C, Ma ZA. J Cell Sci. 2007 Dec 1;120(Pt 23):4134-43 PMID: 18032786; ATR (ataxia telangiectasia mutated- and Rad3-related kinase) is activated by mild hypothermia in mammalian cells and subsequently activates p53. Roobol A, Roobol J, Carden MJ, Bastide A, Willis AE, Dunn WB, Goodacre R, Smales CM. Biochem J. 2011 Apr 15;435(2):499-508. doi: 10.1042/BJ20101303. PMID: 21284603) and SREPB (see e.g., Int J Biol Sci. 2016 Mar 21;12(5):569-79. doi:

10.7150/ijbs.14027. eCollection 2016. Dysregulation of the Low-Density Lipoprotein Receptor Pathway Is Involved in Lipid Disorder-Mediated Organ Injury. Zhang Y, Ma KL, Ruan XZ, Liu BC); and additional receptors, see e.g., Biochim Biophys Acta. 2016 Mar 17. pii: S1388-1981(16)30071-3. doi: 10.1016/j.bbalip.2016.03.019; and/or the unfolded protein response (UPR) . In one embodiment, the LMM comprises a polypeptide. In one embodiment, the LMM comprises a transcriptional regulator, e.g., a transcription factor. In one embodiment, the LMM comprises SREBF1 or a functional fragment thereof (e.g., SREBF-410). In one embodiment, the LMM comprises an enzyme. In one embodiment, the LMM comprises SCD1 or a functional fragment thereof.

"Modification" as used herein in the expression "modification that modulates lipid metabolism" refers to an agent that is capable of effecting an increase or decrease in the expression or activity of a component, e.g., gene product, of a lipid metabolism pathway described herein. In embodiments, the modification results in increasing the expression or activity of a component of a lipid metabolism pathway, e.g., a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90% 95%, 99%, 1-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, or 100-fold or more increase in expression or activity of a component of a lipid metabolism pathway, e.g., as compared to the expression or activity of the component in the absence of the modification. In embodiments, the modification results in decreasing the expression or activity of a component of a lipid metabolism pathway, e.g., a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90% 95%, 99%%, 1-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, or 100-fold or more decrease in expression or activity of a component of a lipid metabolism pathway, e.g., as compared to the expression or activity of the component in the absence of the modification. In some embodiments where the expression or activity of a component of the lipid metabolism pathway is decreased, the component is a negative regulator of a lipid metabolism pathway. In one embodiment, the modification comprises a heterologous or exogenous nucleic acid sequence encoding a lipid metabolism modulator. In one embodiment, the modification is an exogenous lipid metabolism modulator, e.g., small molecule or polypeptide, that can be introduced to a cell, e.g., by culturing the cell in the presence of the molecule or polypeptide, to modulate the lipid metabolism of the cell.

The terms "nucleic acid", "polynucleotide", and "nucleic acid molecule", as used interchangeably herein, refer to deoxyribonucleic acid (DNA) or ribonucleic acid (RNA), or a combination of a DNA or RNA thereof, and polymers thereof in either single-, double-, or triple-stranded form. The term "nucleic acid" includes, but is not limited to, a gene, cDNA, or an mRNA. In one embodiment, the nucleic acid molecule is synthetic (*e.g.*, chemically synthesized or artificial) or recombinant. Unless specifically limited, the term encompasses molecules containing analogues or derivatives of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally or non-naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions), alleles, orthologs, SNPs, and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., Nucleic Acid Res. 19:5081 (1991); Ohtsuka et al., J. Biol. Chem. 260:2605-2608 (1985); and Rossolini et al., Mol. Cell. Probes 8:91-98 (1994)).

"Peptide," "polypeptide," and "protein", as used interchangeably herein, refer to a compound comprised of amino acid residues covalently linked by peptide bonds, or by means other than peptide bonds. A protein or peptide must contain at least two amino acids, and no limitation is placed on the maximum number of amino acids that can comprise a protein's or peptide's sequence. In one embodiment, a protein may comprise of more than one, e.g., two, three, four, five, or more, polypeptides, in which each polypeptide is associated to another by either covalent or non-covalent bonds/interactions. Polypeptides include any peptide or protein comprising two or more amino acids joined to each other by peptide bonds or by means other than peptide bonds. As used herein, the term refers to both short chains, which also commonly are referred to in the art as peptides, oligopeptides and oligomers, for example, and to longer chains, which generally are referred to in the art as proteins, of which there are many types. "Polypeptides" include, for example, biologically active fragments, substantially homologous polypeptides, oligopeptides, homodimers, heterodimers, variants of polypeptides, modified polypeptides, derivatives, analogs, fusion proteins, among others.

"Recombinant product" refers to a product that can be produced by a cell or a cell-free system. The product can be a molecule, a nucleic acid, a polypeptide, or any hybrid thereof. A recombinant product is one for at which at least one component of the product or at least one nucleotide of a sequence which controls the production or expression of the product, was formed by genetic engineering. Genetic engineering as used herein to generate a recombinant product or a construct that encodes a recombinant product encompasses recombinant DNA expression techniques known in the art (e.g., as described in Current Protocols in Molecular Biology); site-directed, scanning, or random mutagenesis; genome modification strategies employing CRISPR-based strategies; and zinc finger nuclease (ZFN)-based strategies. By way of example, in embodiments where the recombinant product is a nucleic acid, at least one nucleotide of the recombinant nucleic acid, or at least one nucleotide of a sequence that controls the production, e.g., transcription, of the recombinant nucleic acid was formed by genetic engineering. In one embodiment, the recombinant product is a recombinant polypeptide. In one embodiment, the recombinant product is a naturally occurring product. In one embodiment, the recombinant product is a non-naturally occurring product, e.g., a synthetic product. In one embodiment, a portion of the recombinant product is naturally occurring, while another portion of the recombinant product is non-naturally occurring. In another embodiment, a first portion of the recombinant product is one naturally occurring molecule, while another portion of the recombinant product is another naturally occurring molecule that is different from the first portion.

"Recombinant polypeptide" refers to a polypeptide that can be produced by a cell described herein. A recombinant polypeptide is one for which at least one nucleotide of the sequence encoding the polypeptide, or at least one nucleotide of a sequence which controls the expression of the polypeptide, was formed by genetic engineering or manipulation (of the cell or of a precursor cell). E.g., at least one nucleotide was altered, e.g., it was introduced into the cell or it is the product of a genetically engineered rearrangement. In an embodiment, the sequence of a recombinant polypeptide does not differ from a naturally or non-naturally occurring isoform of the polypeptide or protein. In an embodiment, the amino acid sequence of the recombinant polypeptide differs from the sequence of a naturally occurring or a non-naturally isoform of the polypeptide or protein. In an embodiment, the recombinant polypeptide and the cell are from the same species. In an embodiment, the amino acid sequence of the recombinant polypeptide is

the same as or is substantially the same as, or differs by no more than 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% from, a polypeptide encoded by the endogenous genome of the cell. In an embodiment, the recombinant polypeptide and the cell are from the same species, e.g., the recombinant polypeptide is a human polypeptide and the cell is a human cell. In an embodiment, the recombinant polypeptide and the cell are from different species, e.g., the recombinant polypeptide is a human polypeptide and the cell is a non-human, e.g., a rodent, e.g., a CHO, other mammalian cell, an insect cell, a plant cell, a fungal cell, a viral cell, or a bacterial cell. In an embodiment, the recombinant polypeptide is exogenous to the cell, in other words, the cell is from a first species and the recombinant polypeptide is from a second species. In one embodiment, the polypeptide is a synthetic polypeptide. In one embodiment, the polypeptide is derived from a non-naturally occurring source. In an embodiment, the recombinant polypeptide is a human polypeptide or protein which does not differ in amino acid sequence from a naturally or non-naturally occurring isoform of the human polypeptide or protein. In an embodiment, the recombinant polypeptide differs from a naturally or non-naturally occurring isoform of the human polypeptide or protein at no more than 1, 2, 3, 4, 5, 10, 15 or 20 amino acid residues. In an embodiment, the recombinant polypeptide differs from a naturally occurring isoform of the human polypeptide at no more than 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, or 15% of its amino acid residues. In embodiments where a portion of the recombinant polypeptide comprises a sequence derived from a portion of a naturally or non-naturally occurring isoform of a human polypeptide, the portion of the recombinant polypeptide differs from the corresponding portion of the naturally or non-naturally occurring isoform by no more than 1, 2, 3, 4, 5, 10, 15, or 20 amino acid residues, or 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, or 15% of its amino acid residues.

"Homologous", "identity", or "similarity" as used herein refers to the subunit sequence identity between two polymeric molecules, e.g., between two nucleic acid molecules, such as, two DNA molecules or two RNA molecules, or between two polypeptide molecules. When a subunit position in both of the two molecules is occupied by the same monomeric subunit; e.g., if a position in each of two DNA molecules is occupied by adenine, then they are homologous or identical at that position. The homology between two sequences is a direct function of the number of matching or homologous positions; e.g., if half (e.g., five positions in a polymer ten

subunits in length) of the positions in two sequences are homologous, the two sequences are 50% homologous; if 90% of the positions (e.g., 9 of 10), are matched or homologous, the two sequences are 90% homologous.

The term "next generation biologic" or "NGB" as used herein refers to a biological composition comprising a cell or a composition produced by a cell. The biological composition is selected from the group consisting of a composition with at least one natural component, a composition with at least one natural component and at least one non-natural component, a composition with at least one natural component and at least one natural structure, and a composition with at least one natural component and at least one non-natural structure, or any combinations thereof. Next generation biologics often comprise complex and/or non-natural structures. Examples of next generation biologics include, but are not limited to, fusion proteins, enzymes or recombinant enzymes, proteins or recombinant proteins, recombinant factors with extended half-lives, growth hormones with long acting therapies, multimeric glycoproteins, next generation antibodies, antibody fragments, or antibody-like proteins (ALPs), vesicles, exosomes, liposomes, viruses, and virus-like particles, mucins, nanoparticles, extracts of a cell, and a cell being used as a reagent.

While this invention has been disclosed with reference to specific aspects, it is apparent that other aspects and variations of this invention may be devised by others skilled in the art without departing from the true spirit and scope of the invention. The appended claims are intended to be construed to include all such aspects and equivalent variations.

MODULATION OF LIPID METABOLISM

The present disclosure features methods and compositions for modulating lipid metabolism in a cell or a cell-free system, for example, by introducing a modification to the cell or cell-free system that results in the modulation of lipid metabolism. In embodiments, the present disclosure features the use of global regulators that impact multiple aspects of pathways or processes involved in lipid metabolism, e.g., the *de novo* lipogenesis, fatty acid re-esterification, fatty acid saturation or desaturation, fatty acid elongation, and phospholipid

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biosynthesis pathways. By way of example, the global regulator is upstream in one or more lipid metabolism pathways or processes such that the global regulator impacts several, e.g., two or more, downstream processes or downstream components of lipid metabolism. In one embodiment, the global regulator is a transcription factor that can activate the expression of more than one, e.g., two or more, target genes involved in different lipid metabolism processes or pathways. Accordingly, without wishing to be bound by any theory, the use of a global regulator as described herein can result in a greater increase in production capacity, robustness, and survival of the cell than compared to the use of a downstream effector that modulates only a single target or other component of lipid metabolism. While not wishing to be bound by any theory, it is believed that a global or more widespread modulation of multiple lipid metabolism pathways increases the production capacity of a cell by affecting more processes involved in improving production capacity, product quality, and robustness of the cell.

Lipid metabolism pathways as described herein refer to processes that relate to the synthesis, degradation, conversion, or modification of lipids or lipid-associated molecules. Lipid molecules include, but are not limited to, fatty acids, glycerolipids, glycerophospholipids, phospholipids, saccharolipids, sphingolipids, and sterol lipids, e.g., cholesterol, and polyketides. Examples of lipid metabolism pathways include, but are not limited to: *de novo* lipogenesis, fatty acid re-esterification, fatty acid saturation, fatty acid de-saturation, fatty acid elongation, and phospholipid biosynthesis. In one embodiment, the methods described herein provide a cell comprising a modification that modulates lipid metabolism. The modification that modulates lipid metabolism can be an agent that increases or decreases the expression of a component involved in lipid metabolism. In one embodiment, the modification that modulates lipid metabolism comprises an exogenous nucleic acid encoding a lipid metabolism modulator (LMM). In such embodiments, the exogenous nucleic acid encoding a LMM is introduced to the cell by any of the nucleic acid delivery methods or techniques described herein, e.g., transduction or transfection

In one embodiment, the methods described herein provide a cell comprising one or more, e.g., one, two, three, four, five, six, seven, eight, nine or ten, modifications that modulate lipid metabolism. In embodiments where the cell comprises two or more modifications that modulate lipid metabolism, each modification that modulates lipid metabolism comprises an exogenous nucleic acid that encodes a LMM. In one embodiment, each of the two or more exogenous

nucleic acids that encode a LMM can be located within the same nucleic acid molecule, or are placed on two or more different nucleic acid molecules. In such embodiments where the cell comprises two or more nucleic acid sequences encoding LMMs, the LMMs are different from each other, e.g., encode a different polypeptide sequence or have a different function.

In embodiments, modulation of lipid metabolism in a cell, e.g., by introducing and expressing an exogenous nucleic acid encoding an LMM described herein, alters, e.g., increases or decreases, one or more of the following:

i) the expression (e.g., transcription and/or translation) of a component involved in a lipid metabolism pathway;

ii) the activity (e.g., enzymatic activity) of a component involved in a lipid metabolism pathway;

iii) the amount of lipids (e.g., phospholipids, or cholesterol) present in a cell;

iv) the amount of lipid rafts or rate of lipid raft formation;

v) the fluidity, permeability, and/or thickness of a cell membrane (e.g., a plasma membrane, a vesicle membrane, or an organelle membrane);

vi) the conversion of saturated lipids to unsaturated lipids or conversion of unsaturated lipids to saturated lipids;

vii) the amount of saturated lipids or unsaturated lipids, e.g., monounsaturated lipids;

viii) the composition of lipids in the cell to attain a favorable composition that increases ER activity;

ix) the expansion of the ER (e.g., size of the ER, the ER membrane surface, or the amounts of the proteins and lipids that constitute and/or reside within the ER);

x) the expansion of the Golgi (e.g., the number and size of the Golgi, the Golgi surface, or the number or amounts of proteins and molecules that reside within the Golgi);

xi) the amount of secretory vesicles or the formation of secretory vesicles;

xii) the amount or rate of secretion of the product;

xiii) the proliferation capacity, e.g., the proliferation rate;

xiv) culture viability or cell survival;

xv) activation of membrane receptors;

xvi) the unfolded protein response (UPR);

xvii) the yield or rate of production of the product;

xviii) the product quality (e.g., aggregation, glycosylation heterogeneity, fragmentation, proper folding or assembly, post-translational modification, or disulfide bond scrambling); and /or

xix) cell growth/proliferation or cell specific growth rate.

In an embodiment, modulation of lipid metabolism results in an increase in any of the properties listed above, e.g., a 1%, 2%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 99%, or more, or at least 1-fold, 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 50-fold, or 100-fold or more, increase in any of the properties listed above as compared to a cell without modulation of lipid metabolism. In an embodiment, modulation of lipid metabolism results in a decrease in any of the properties listed above, e.g., a 1%, 2%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 99%, or more, or at least 1-fold, 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 50-fold, or 100-fold or more, decrease in any of the properties listed above as compared to a cell without modulation of lipid metabolism.

In an embodiment, a modification that modulates lipid metabolism increases or decreases the expression or activity of a component involved in one or more lipid metabolism pathways. In embodiments where the modification that modulates lipid metabolism results in an increase in the expression, e.g., transcription or translation, or an increase in the activity of a component of a lipid metabolism pathway, the component is a positive regulator of the lipid metabolism pathway. In embodiments where the modification that modulates lipid metabolism results in a decrease in the expression, e.g., transcription or translation, or a decrease in the activity of a component of a lipid metabolism pathway, the component is a negative regulator of the lipid metabolism pathway. Assays for quantifying the expression, e.g., transcription and/or translation, of a gene of the lipid metabolism pathway, are known in the art, and include quantifying the amount of mRNA encoding the gene; or quantifying the amount of the gene product, or polypeptide; PCR-based assays, e.g., quantitative real-time PCR; Northern blot; or microarray. Assays for quantifying the activity of a component of the lipid metabolism pathway, e.g., an enzyme of the lipid metabolism pathway, will be specific to the particular component of the lipid metabolism pathway.

In embodiments where the modulation of the lipid metabolism of a cell results in an increase in the level or amount of lipids in the cell, the total level or total amount of lipids in the

cell can be increased. In another embodiment, the level or amount of one or more species of lipids, e.g., a phospholipid or cholesterol, in the cell can be increased. An increase in the level or amount of lipids in the cell (e.g., total or a select lipid species) comprises a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more, or a one-fold, two-fold, three-fold, four-fold, or five-fold, 10-fold, 20-fold, 50-fold, or 100-fold, increase in the level or amount of lipids in the cell after modulation of lipid metabolism, e.g., live cells, as compared to cells that do not comprise a modification that modulates lipid metabolism. Assays for quantifying the level or amount of lipids in a cell are known in the art, and include enzymatic assays and oxidation assays and measurement by mass spectrometry of lipid components in a particular compartment (e.g., organelle) or from the total cell.

In one embodiment, a modification that modulates lipid metabolism results in increased cell survival. For example, cell survival can be measured by determining or quantifying cell apoptosis, e.g., the number or amount of cells that have been killed or died. An increase in cell survival comprises a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more, or a one-fold, two-fold, three-fold, four-fold, or five-fold, 10-fold, 20-fold, 50-fold, or 100-fold,, increase in the number of cells after modulation of lipid metabolism, e.g., live cells, as compared to cells that do not comprise a modification that modulates lipid metabolism. Alternatively, an increase in cell survival comprises a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or more decrease in the number of apoptotic cells after modulation of lipid metabolism, e.g., as compared to cells without modulation of lipid metabolism. Methods for detecting cell survival or apoptosis are known in the art, e.g., Annexin V assays, and are described herein in the Examples.

In one embodiment, a modification that modulates lipid metabolism results in increased culture viability. For example, culture viability can be measured by determining or quantifying the number or amount of live cells, e.g., live cells in a culture or population of cells, or cells that have a characteristic related to being viable, e.g., proliferation markers, intact DNA, or do not display apoptotic markers. An increase in culture viability comprises a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more, or a one-fold, two-fold, three-fold, four-fold, or five-fold, 10-fold, 20-fold, 50-fold, or

100-fold, or more increase in the number of cells, e.g., live cells, after modulation of lipid metabolism, e.g., as compared to cells without modulation of lipid metabolism. Methods for determining culture viability are known in the art, and are described herein in Example 3. Other methods for assessing culture viability include, but are not limited to, trypan blue exclusion methods followed by counting using a hemocytometer or Vi-CELL (Beckman-Coulter). Other methods for determining viable biomass include methods using radiofrequency impedance or capacitance (e.g., Carvell and Dowd, 2006, Cytotechnology, 50:35-48), or using Raman spectroscopy (e.g., Moretto et al., 2011, American Pharmaceutical Review, Vol. 14).

In one embodiment, a modification that modulates lipid metabolism results in increased cell proliferation. For example, the ability of a cell to proliferate can be measured by quantifying or counting the number of cells, cell doublings, or growth rate of the cells. Alternatively, proliferating cells can be identified by analysis of the genomic content of the cells (e.g., replicating DNA), e.g., by flow cytometry analysis, or presence of proliferation markers, e.g., Ki67, phosphorylated cyclin-CDK complexes involved in cell cycle. An increase in the ability to proliferate comprises a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or more, or one-fold, two-fold, three-fold, four-fold, five-fold, 10-fold, 20-fold, 50-fold, or 100-fold, or more increase in the number of cells, or number of cells expressing a proliferation marker, after modulation of lipid metabolism. Alternatively, an increase in the ability to proliferate comprises a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or more, or one-fold, two-fold, three-fold, four-fold, five-fold, 10-fold, 20-fold, 50-fold, or 100-fold, or more increase in the doubling or growth rate of the cells after modulation of lipid metabolism. Cell counting can be performed using a cell counting machine, or by use of a hemacytometer.

In one embodiment, a modification that modulates lipid metabolism results in an increase in production capacity, e.g., the amount, quantity, or yield of product produced, or the rate of production. An increase in the amount, quantity, or yield of the product produced comprises 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or more, or by 1-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold or more increase in the amount, quantity, or yield of the product produced after modulation of lipid metabolism, e.g., as compared to the amount, quantity, or yield of the product produced

by a cell without modulation of the lipid metabolism. An increase in the rate of production comprises 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or more, or by1-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, or more increase in the amount, quantity, or yield of the product produced after modulation of lipid metabolism, after modulation of lipid metabolism, e.g., as compared to the rate of production of a cell without modulation of the lipid metabolism. In one embodiment, the rate of production is determined by determining the amount, quantity, or yield of the product produced in a specific unit of time.

In one embodiment, a modification that modulates lipid metabolism results in an increase in the quality of the product, e.g., aggregation, glycosylation status or heterogeneity, fragmentation, proper folding or assembly, post-translational modification, or disulfide bond scrambling. An increase quality of the product comprises a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or more, or by 1-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold or more of: an increase in the amount or quantity of non-aggregated product, an increase in the ratio of non-aggregated product to aggregated product, or decrease in the amount or quantity of aggregated product, after modulation of lipid metabolism e.g., as compared to that observed in a cell without modulation of the lipid metabolism. An increase quality of the product comprises a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or more, or by 1-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold or more of: an increase in the amount or quantity of properly folded or assembled product, an increase in the ratio of properly folded or assembled product to misfolded, unfolded, partially assembled, or non-assembled product, or decrease in the amount or quantity of misfolded, unfolded, partially assembled, or non-assembled product, after modulation of lipid metabolism e.g., as compared to that observed in a cell without modulation of the lipid metabolism. An increase quality of the product comprises a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or more, or by 1-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold or more of: an increase in the amount or quantity of non-fragmented or full-length product, or a decrease in the amount or quantity of fragmented product after modulation of lipid metabolism, e.g., as compared to that observed in a cell without modulation of the lipid metabolism. An increase quality of the product comprises a 1%, 2%, 5%,

10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or more, or by 1-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold or more of: an increase in the amount or quantity of functional product, or a decrease in the amount or quantity of non-functional or dysfunctional product after modulation of lipid metabolism, e.g., as compared to that observed in a cell without modulation of the lipid metabolism. An increase quality of the product comprises a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or more, or by 1-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold or more of: an increase or decrease in the glycan heterogeneity after modulation of lipid metabolism, e.g., as compared to that observed in a cell without modulation of the lipid metabolism. An increase quality of the product comprises a 1%, 2%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98%, 99%, or more, or by 1-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold or more of: an increase in the amount or quantity of functional product, or a decrease in the amount or quantity of non-functional or dysfunctional product after modulation of lipid metabolism, e.g., as compared to that observed in a cell without modulation of the lipid metabolism.

LIPID METABOLISM MODULATORS

As described herein, modulation of the lipid metabolism can be achieved by expressing or introducing a LMM, or by altering the regulation of a LMM. In one embodiment, an LMM is overexpressed in a cell, e.g., by introducing an exogenous nucleic acid encoding a LMM or by increasing expression by introducing promoter elements or other regulatory transcriptional elements. In another embodiment, the expression or activity of an LMM is inhibited or decreased, e.g., by introducing an inhibitor of the LMM or an exogenous inhibitory nucleic acid, e.g., an RNA interfering agent. Examples of inhibitory nucleic acids include short interfering RNAs (siRNAs) and short hairpin RNAs (shRNAs) that target the LMM, e.g, the mRNA encoding the LMM. In one embodiment, the activity or expression of an LMM is increased or decreased by altering the post-translational modifications or other endogenous regulatory mechanisms that regulate LMM activity or expression. Regulation by post-translational modifications include, but are not limited to, phosphorylation, sumoylation, ubiquitination, acetylation, methylation, or glycosylation can increase or decrease LMM expression or activity.

By way of example, regulation of post-translational modifications can be achieved through modulation of the enzyme or molecule that modifies the LMM, or modification of the LMM such that the post-translational modification cannot occur or occurs more frequently or constitutively. Regulation of the LMM can also include modulating endogenous regulatory mechanisms that can increase or decrease LMM expression or activity, e.g., increase or decrease one or more of: miRNA regulation, protein cleavage, expression of specific isoforms, alternative splicing, and degradation.

In one embodiment, the LMM modulates, e.g., increases or decreases, the expression, e.g., transcription, or activity of a component of the lipid metabolism pathway. In another embodiment, the LMM modulates, e.g., increases or decreases, the synthesis, degradation, elongation, or structural conformation (e.g., saturation or desaturation, or esterification) of a lipid or lipid-associated molecule. Exemplary LMMs and/or components of the lipid metabolism pathway are listed, but not limited, to those listed in Table 1.

Table 1. Lipid Metabolism Pathways and Components/Gene Products Thereof

Pathway	Component/Gene Product
Global Lipid Metabolism Regulators	SREBF1 (sterol regulatory element-binding transcription factor 1) SREBF2 (sterol regulatory element-binding transcription factor 2) PRMT5
De Novo Lipogenesis	FAS (fatty acid synthase) ACC (acetyl-coA carboxylase) ACL (ATP citrate lyase)
Fatty Acid Re-esterification	DGAT (diglyceride acyltransferase) GPAT (glycerol 3-phosphate acyltransferase) LPL (lipoprotein lipase)
Phospholipid Biosynthesis	AGPAT (1-actyl-sn-glycerol-3-phosphate O-acyltransferase) AGNPR (acyl/alkylglycerone-phosphate reductase) CCT (phosphocholine cytidyltransferase) CDS (phosphatidate cytidylyltransferase) CEPT (diacylglycerol choline/ehtanolaminephosphotransferase) CERT (ceramide transfer protein) CGT (N-acylsphingosine galactosyltransferase) CPT (diacylglycerol cholinephosphotransferase) CLS (cardiolipin synthase) CRD (ceramidase) GNPAT (glycerone-phosphate O-acyltransferase)

	KDSR (3-ketosphinganine reductase) LCS (polypeptide N-acetylgalactosaminyltransferase) PAP (phosphatidic acid phosphatase) PEMT (phosphatidylethanolamine N-methyltransferase) PGP (phosphatidylglycerophosphatase) PGS (CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase) PIS (CDP-diacylglycerol-inositol 3-phosphatidyltransferase) PSD (phosphatidylserine decarboxylase) PSS1 (phosphatidylserine synthase 1) PSS2 (phosphatidylserine synthase 2) SGMS (ceramide choline phosphotransferase) SNAT (sphingosine N-acyltransferase) SPK (sphinganine kinase) SPP (sphingosine-1-phosphate phosphatase) SPT (serine Co-palmitoyltransferase)
Fatty Acid Desaturation	SCD1 (stearoyl CoA desaturase-1) SCD2 (stearoyl CoA desaturase-2) SCD3 (stearoyl CoA desaturase-3) SCD4 (stearoyl CoA desaturase-4) SCD5 (Steoryl CoA desaturase-5) PED (plasmanylethanolamine desaturase)
Regulation of SREBF1 and other pathways	S1P (site-1 protease) S2P (site-2 protease) SCAP (SREBF cleavage-activating protein) INSIG1 (insulin induced gene 1) INSIG2 (insulin induced gene 2) HMG CoA reductase (2-hydroxy-3-methylgulatryl-CoA reductase) PPAR receptors, e.g., PPARα, PPARγ

In one embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% amino acid sequence identity or homology with a component, e.g., gene product, involved in a lipid metabolism pathway, e.g., provided in Table 1; or differs by 1, 2, or 3 or more amino acid residues but no more than 50, 40, 30, 20, 15, or 10 amino acid residues from the amino acid sequence of a component, e.g., gene product, involved in the lipid metabolism pathway, e.g., provided in Table 1.

In one embodiment, the LMM comprises a functional fragment of a component involved in the lipid metabolism pathway, e.g., provided in Table 1. A functional fragment of an LMM as

described herein may comprise one or more functional domains of the LMM. By way of example, a functional fragment of a LMM that is a transcription factor comprises a DNA binding domain and a transactivation domain. By way of example, a functional fragment of a LMM that is an enzyme comprises a domain with enzymatic activity. A functional fragment of an LMM as described herein retains functional activity, e.g., at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% of the functional activity, of the full-length LMM. Functional fragments of an LMM can be experimentally determined by one skilled in the art, or can be predicted using algorithms based on sequence homology of functional domains. Exemplary LMMs are further described below.

In any of the embodiments of the methods described herein, the LMM is a transcriptional regulator. In one embodiment, the LMM is a transcription factor or transcriptional activator, that binds to the DNA or associates in a complex that binds to DNA, and recruits or associates in a complex that recruits RNA polymerase for transcription of one or more gene products involved in lipid metabolism. In one embodiment, the LMM binds to a sterol binding element and/or E-box promoter sequences. In one embodiment, the LMM comprises sterol regulatory element binding factor 1 (SREBF1) or sterol regulatory element binding factor 2 (SREBF2) or a functional fragment or isoform thereof.

In an embodiment, the LMM comprises a global transcriptional activator or transcription factor. In one embodiment, the LMM is capable of modulating the transcription of two or more, e.g., two, three, four, five, six, or more, components of a lipid metabolism pathway, e.g., as provided in Table 1. In another embodiment, the LMM is capable of modulating the transcription of one or more, e.g., one, two, three, four, or five, or more, components of two or more lipid metabolism pathways, e.g., components and pathways as provided in Table 1.

Sterol regulatory element binding factor 1 (SREBF1) is a global transcriptional activator which upregulates the transcription of genes involved in lipogenesis, fatty acid re-esterification, fatty acid desaturation and elongation, and phospholipid biosynthesis by binding to sterol regulatory element (SRE) and E-box promoter sequences (Hagen, Rodriguez-Cuenca et al. 2010) present in the promoter regions of target genes. Transcription of the SREBF1 gene itself is endogenously regulated by the presence of the sterol regulatory element (SRE) amongst other transcriptional regulating elements in the promoter region of the gene. On top of this, a multitude of posttranslational regulating mechanisms including phosphorylation, ubiquitination,

sumoylation, acetylation, fatty acid-mediated modifications and proteolytic processing make for a tightly controlled but adaptable homeostatic system fixed around SREBF1.

Full-length SREBF1 is synthesized and localizes primarily to the endoplasmic reticulum (ER). Membrane integral SREBF1 forms a complex with SREBF cleavage-activating protein (SCAP) which can facilitate migration of SREBF1 to the Golgi. However, when high sterol levels (particularly cholesterol) are present, a conformational change in SCAP is induced which aids binding to the membrane integral protein insig (insulin induced gene), thus inhibiting migration of this complex. In the absence of sterols, insig does not bind to SCAP, therefore allowing COPII mediated vesicle formation, and subsequent migration of the SREBF:SCAP complex to the Golgi. Sequential proteolytic cleavage occurs in the Golgi mediated by site-1 protease (S1P) and site-2 protease (S2P) proteins liberating the N-terminal basic helix loop helix leucine zipper (bHLHlz) of SREBF1 which is immediately present in the cytoplasm, but migrates to the nucleus. Lysine residues present on the cleaved SREBF1 are ubiquitinated and degraded by the 26S proteasome but this ubiquitination can be inhibited through acetylation of the lysine residues which allows migration to the nucleus. Finally, nuclear SREBF1 can bind to sterol regulatory element (SRE) sequences upstream of a number of genes responsible for *de novo* lipogenesis (fatty acid synthase (FAS) and acetyl coA carboxylase (ACC)), fatty acid re-esterfication (diacylglycerol acyltransferase (DGAT), glycerol-3-phosphate (GPAT) and lipoprotein lipase (LPL)), phospholipid biosynthesis (CTP:phosphocholine cytidylyltransferase (CCT)), fatty acid desaturation (stearoyl-coA desaturase 1 (SCD1)). Nuclear SREBF1 is also capable of activating transcription of the full length SREBF1 gene itself, but this is also dependent on activation of the liver X receptor (LXR) promoter sequence also located upstream of the gene (Brown, Goldstein 1997- BROWN, M.S. and GOLDSTEIN, J.L., 1997. The SREBP Pathway: Regulation of Cholesterol Metabolism by Proteolysis of a Membrane-Bound Transcription Factor. Cell, 89(3), pp. 331-340) (Hagen, Rodriguez-Cuenca- HAGEN, R.M., RODRIGUEZ-CUENCA, S. and VIDAL-PUIG, A., 2010. An allostatic control of membrane lipid composition by SREBP1. FEBS letters, 584(12), pp. 2689-2698).

In one embodiment, the LMM comprises SREBF1, an isoform, or a functional fragment thereof. The amino acid sequence for SREBF1 is provided below:

MDELAFGEAALEQTLAEMCELDTAVLNDIEDMLQLINNQDSDFPGLFDAPYAGGETGDTGPSSPGANSPESFSSASL
ASSLEAFLGGPKVTPAPLSPPPSAPAALKMYPSVSPFSPGPGIKEEPVPLTILQPAAPQPSPGTLLPPSFPAPPVQL

SPAPVLGYSSLPSGFSGTLPGNTQQPPSSLPLAPAPGVLPTPALHTQVQSLASQQPLPASAAPRTNTVTSQVQQVPV
VLQPHFIKADSLLLTAVKTDAGATVKTAGISTLAPGTAVQAGPLQTLVSGGTILATVPLVVDTDKLPIHRLAAGSKA
LGSAQSRGEKRTAHNAIEKRYRSSINDKIVELKDLVVGTEAKLNKSAVLRKAIDYIRFLQHSNQKLKQENLTLRSAH
KSKSLKDLVSACGSGGGTDVSMEGMKPEVVETLTPPPSDAGSPSQSSPLSFGSRASSSGGSDSEPDSPAFEDSQVKA
QRLPSHSRGMLDRSRLALCVLAFLCLTCNPLASLFGWGILTPSDATGTHRSSGRSMLEAESRDGSNWTQWLLPPLVW
LANGLLVLACLALLFVYGEPVTRPHSGPAVHFWRHRKQADLDLARGDFPQAAQQLWLALQALGRPLPTSNLDLACSL
LWNLIRHLLQRLWVGRWLAGQAGGLLRDRGLRKDARASARDAAVVYHKLHQLHAMGKYTGGHLAASNLALSALNLAE
CAGDAISMATLAEIYVAAALRVKTSLPRALHFLTRFFLSSARQACLAQSGSVPLAMQWLCHPVGHRFFVDGDWAVHG
APPESLYSVAGNPVDPLAQVTRLFREHLLERALNCIAQPSPGAADGDREFSDALGYLQLLNSCSDAAGAPACSFSVS
SSMAATTGPDPVAKWWASLTAVVIHWLRRDEEAAERLYPLVEHIPQVLQDTERPLPRAALYSFKAARALLDHRKVES
SPASLAICEKASGYLRDSLASTPTGSSIDKAMQLLLCDLLLVARTSLWQRQQSPASVQVAHGTSNGPQASALELRGF
QHDLSSLRRLAQSFRPAMRRVFLHEATARLMAGASPARTHQLLDRSLRRRAGSSGKGGTTAELEPRPTWREHTEALL
LASCYLPPAFLSAPGQRMSMLAEAARTVEKLGDHRLLLDCQQMLLRLGGGTTVTSS (SEQ ID NO: 1).

The nucleotide sequence for SREBF1 is provided below:

atggacgagctggccttcggtgaggcggctctggaacagacactggccgagatgtgcgaactggacacagcggtttt
gaacgacatcgaagacatgctccagctcatcaacaaccaagacagtgacttcccgggcctgtttgacgccccctatg
ctgggggtgagacaggggacacaggccccagcagcccaggtgccaactctcctgagagcttctcttctgcttctctg
gcctcctctctggaagccttcctgggaggacccaaggtgacacctgcacccttgtcccctccaccatcggcacccgc
tgctttaaagatgtacccgtccgtgtccccctttcccctgggcctgggatcaaagaggagccagtgccactcacca
tcctacagcctgcagcgccacagccgtcaccggggaccctcctgcctccgagcttccccgcaccacccgtacagctc
agccctgcgcccgtgctgggttactcgagcctgccttcaggcttctcagggacccttccaggaaacactcagcagcc
accatctagcctgccgctggcccctgcaccaggagtcttgcccacccctgccctgcacacccaggtccaaagcttgg
cctcccagcagccgctgccagcctcagcagcccctagaacaaacactgtgacctcacaggtccagcaggtcccagtt
gtactgcagccacacttcatcaaggcagactcactgctgctgacagctgtgaagacagatgcaggagccaccgtgaa
gactgcaggcatcagcaccctggctcctggcacagccgtgcaggcaggtcccctgcagaccctggtgagtggaggga
ccatcttggccacagtacctttggttgtggacacagacaaactgcccatccaccgactcgcagctggcagcaaggcc
ctaggctcagctcagagccgtggtgagaagcgcacagcccacaatgccattgagaagcgctaccggtcttctatcaa
tgacaagattgtggagctcaaagacctggtggtgggcactgaagcaaagctgaataaatctgctgtcttgcgcaagg
ccatcgactacatccgcttcttgcagcacagcaaccagaagctcaagcaggagaacctgaccctacgaagtgcacac
aaaagcaaatcactgaaggacctggtgtcagcttgtggcagtggaggaggcacagatgtgtctatggagggcatgaa
acccgaagtggtggagacgcttacccctccaccctcagacgccggctcaccctcccagagtagccccttgtcttttg
gcagcagagctagcagcagtggtggtagtgactctgagcccgacagtccagcctttgaggatagccaggtcaaagcc
cagcggctgccttcacacagccgaggcatgctggaccgctcccgcctggccctgtgtgtactggcctttctgtgtct
gacctgcaatcctttggcctcgcttttcggctggggcattctcactccctctgatgctacgggtacacaccgtagtt
ctgggcgcagcatgctggaggcagagagcagagatggctctaattggacccagtggttgctgccacccctagtctgg
ctggccaatggactactagtgttggcctgcttggctcttctctttgtctatggggaacctgtgactaggccacactc
tggcccggctgtacacttctggagacatcgcaaacaagctgacctggatttggcccggggagatttcccccaggctg
ctcaacagctgtggctggccctgcaagcgctgggccggcccctgcccacctcaaacctggatctggcctgcagtctg
ctttggaacctcatccgccacctgctccagcgtctctgggtgggccgctggctggcaggccaggccgggggcctgct
gagggaccgtgggctgaggaaggatgcccgtgccagtgcccgggatgcggctgttgtctaccataagctgcaccagc
tgcatgccatgggcaagtacacaggaggacatcttgctgcttctaacctggcactaagtgccctcaacctggctgag
tgcgcaggagatgctatctccatggcaacactggcagagatctatgtggcagcggccctgagggtcaaaaccagcct
cccaagagccctgcacttcttgacacgtttcttcctgagcagcgcccgccaggcctgcctagcacagagcggctcgg
tgcctcttgccatgcagtggctctgccaccctgtaggtcaccgtttctttgtggacggggactgggccgtgcacggt
gccccccccggagagcctgtacagcgtggctgggaacccagtggatccgctggcccaggtgacccggctattccgtga
acatctcctagagcgagcgttgaactgtattgctcagcccagcccaggggcagctgacggagacagggagttctcag
atgcccttggatatctgcagttgctaaatagctgttctgatgctgccggggctcctgcttgcagtttctctgtcagc
tccagcatggctgccaccactggcccagacccagtggccaagtggtgggcctcactgacagctgtggtgatccactg
gctgaggcgggatgaagaggcagctgagcgcttgtacccactggtagagcatatcccccaggtgctgcaggacactg
agagacccctgcccagggcagctctgtactccttcaaggctgcccgggctctgctggaccacagaaaggtggaatct
agcccagccagcctggccatctgtgagaaggccagtgggtacctgcgggacagcttagcctctacaccaactggcag
ttccattgacaaggccatgcagctgctcctgtgtgatctacttcttgtggcccgtaccagtctgtggcagcggcagc
agtcaccagcttcagtccaggtagctcacggtaccagcaatggaccccaggcctctgctctggagctgcgtggtttc
caacatgacctgagcagcctgcggcggttggcacagagcttccggcctgctatgaggagggtattcctacatgaggc
cacagctcggctgatggcaggagcaagtcctgcccggacacaccagctcctggatcgcagtctgaggaggagggcag

gttccagtggcaaaggaggcactacagctgagctggagccacggcccacatggcgggagcacaccgaggccctgctg
ttggcatcctgctatctgccccctgccttcctgtcggctcctgggcagcgaatgagcatgctggccgaggcggcacg
caccgtagagaagcttggcgatcaccggctactgctggactgccagcagatgctcctgcgcctgggcggcggaacca
ccgtcacttccagctag (SEQ ID NO: 2).

In one embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity with the amino acid sequence of SREBF1 ; e.g., SEQ ID NO: 1; or differs by 1, 2, or 3 or more amino acid residues but no more than 50, 40, 30, 20, 15, or 10 amino acid residues from the amino acid sequence of SREBF1, e.g., SEQ ID NO: 1.

Isoforms of SREBF1 are known in the art, and include isoform a and isoform b, as well as species or cell specific, e.g., CHO cell specific, isoforms, such as isoform c. The amino acid sequence for SREBF1 isoform a (GenBank Accession No. NP_001005291.2) is provided below.

MDEPPFSEAALEQALGEPCDLDAALLTDIEGEVGAGRGRANGLDAPRAGADRGAMDCTFEDMLQLINNQD
SDFPGLFDPPYAGSGAGGTDPASPDTSSPGSLSPPPATLSSSLEAFLSGPQAAPSPLSPPQPAPTPLKMY
PSMPAFSPGPGIKEESVPLSILQTPTPQPLPGALLPQSFPAPAPPQFSSTPVLGYPSPPGGFSTGSPPGN
TQQPLPGLPLASPPGVPPVSLHTQVQSVVPQQLLTVTAAPTAAPVTTTVTSQIQQVPVLLQPHFIKADSL
LLTAMKTDGATVKAAGLSPLVSGTTVQTGPLPTLVSGGTILATVPLVVDAEKLPINRLAAGSKAPASAQS
RGEKRTAHNAIEKRYRSSINDKIIELKDLVVGTEAKLNKSAVLRKAIDYIRFLQHSNQKLKQENLSLRTA
VHKSKSLKDLVSACGSGGNTDVLMEGVKTEVEDTLTPPPSDAGSPFQSSPLSLGSRGSGSGGSGSDSEPD
SPVFEDSKAKPEQRPSLHSRGMLDRSRLALCTLVFLCLSCNPLASLLGARGLPSPSDTTSVYHSPGRNVL
GTESRDGPGWAQWLLPPVVWLLNGLLVLVSLVLLFVYGEPVTRPHSGPAVYFWRHRKQADLDLARGDFAQ
AAQQLWLALRALGRPLPTSHLDLACSLLWNLIRHLLQRLWVGRWLAGRAGGLQQDCALRVDASASARDAA
LVYHKLHQLHTMGKHTGGHLTATNLALSALNLAECAGDAVSVATLAEIYVAAALRVKTSLPRALHFLTRF
FLSSARQACLAQSGSVPPAMQWLCHPVGHRFFVDGDWSVLSTPWESLYSLAGNPVDPLAQVTQLFREHLL
ERALNCVTQPNPSPGSADGDKEFSDALGYLQLLNSCSDAAGAPAYSFSISSSMATTTGVDPVAKWWASLT
AVVIHWLRRDEEAAERLCPLVEHLPRVLQESERPLPRAALHSFKAARALLGCAKAESGPASLTICEKASG
YLQDSLATTPASSSIDKAVQLFLCDLLLVVRTSLWRQQQPPAPAPAAQGTSSRPQASALELRGFQRDLSS
LRRLAQSFRPAMRRVFLHEATARLMAGASPTRTHQLLDRSLRRRAGPGGKGGAVAELEPRPTRREHAEAL
LLASCYLPPGFLSAPGQRVGMLAEAARTLEKLGDRRLLHDCQQMLMRLGGGTTVTSS (SEQ ID NO: 28)

The nucleic acid sequence, or mRNA sequence, for SREBF1 isoform a (GenBank Accession No. NM_001005291.2) is provided below.

AGCAGAGCTGCGGCCGGGGGAACCCAGTTTCCGAGGAACTTTTCGCCGGCGCCGGGCCGCCTCTGAGGCC
AGGGCAGGACACGAACGCGCGGAGCGGCGGCGGCGACTGAGAGCCGGGGCCGCGGCGGCGCTCCCTAGGA
AGGGCCGTACGAGGCGGCGGGCCCGGCGGGCCTCCCGGAGGAGGCGGCTGCGCCATGGACGAGCCACCCT
TCAGCGAGGCGGCTTTGGAGCAGGCGCTGGGCGAGCCGTGCGATCTGGACGCGGCGCTGCTGACCGACAT
CGAAGGTGAAGTCGGCGCGGGGAGGGGTAGGGCCAACGGCCTGGACGCCCCAAGGGCGGGCGCAGATCGC
GGAGCCATGGATTGCACTTTCGAAGACATGCTTCAGCTTATCAACAACCAAGACAGTGACTTCCCTGGCC
TATTTGACCCACCCTATGCTGGGAGTGGGGCAGGGGGCACAGACCCTGCCAGCCCCGATACCAGCTCCCC
AGGCAGCTTGTCTCCACCTCCTGCCACATTGAGCTCCTCTCTTGAAGCCTTCCTGAGCGGGCCGCAGGCA
GCGCCCTCACCCCTGTCCCCTCCCCAGCCTGCACCCACTCCATTGAAGATGTACCCGTCCATGCCCGCTT
TCTCCCCTGGGCCTGGTATCAAGGAAGAGTCAGTGCCACTGAGCATCCTGCAGACCCCCACCCCACAGCC
CCTGCCAGGGGCCCTCCTGCCACAGAGCTTCCCAGCCCCAGCCCCACCGCAGTTCAGCTCCACCCCTGTG
TTAGGCTACCCCAGCCCTCCGGGAGGCTTCTCTACAGGAAGCCCTCCCGGGAACACCCAGCAGCCGCTGC
CTGGCCTGCCACTGGCTTCCCCGCCAGGGGTCCCGCCCGTCTCCTTGCACACCCAGGTCCAGAGTGTGGT
CCCCCAGCAGCTACTGACAGTCACAGCTGCCCCCACGGCAGCCCCTGTAACGACCACTGTGACCTCGCAG
ATCCAGCAGGTCCCGGTCCTGCTGCAGCCCCACTTCATCAAGGCAGACTCGCTGCTTCTGACAGCCATGA

AGACAGACGGAGCCACTGTGAAGGCGGCAGGTCTCAGTCCCCTGGTCTCTGGCACCACTGTGCAGACAGG
GCCTTTGCCGACCCTGGTGAGTGGCGGAACCATCTTGGCAACAGTCCCACTGGTCGTAGATGCGGAGAAG
CTGCCTATCAACCGGCTCGCAGCTGGCAGCAAGGCCCCGGCCTCTGCCCAGAGCCGTGGAGAGAAGCGCA
CAGCCCACAACGCCATTGAGAAGCGCTACCGCTCCTCCATCAATGACAAAATCATTGAGCTCAAGGATCT
GGTGGTGGGCACTGAGGCAAAGCTGAATAAATCTGCTGTCTTGCGCAAGGCCATCGACTACATTCGCTTT
CTGCAACACAGCAACCAGAAACTCAAGCAGGAGAACCTAAGTCTGCGCACTGCTGTCCACAAAAGCAAAT
CTCTGAAGGATCTGGTGTCGGCCTGTGGCAGTGGAGGGAACACAGACGTGCTCATGGAGGGCGTGAAGAC
TGAGGTGGAGGACACACTGACCCCACCCCCCTCGGATGCTGGCTCACCTTTCCAGAGCAGCCCCTTGTCC
CTTGGCAGCAGGGGCAGTGGCAGCGGTGGCAGTGGCAGTGACTCGGAGCCTGACAGCCCAGTCTTTGAGG
ACAGCAAGGCAAAGCCAGAGCAGCGGCCGTCTCTGCACAGCCGGGGCATGCTGGACCGCTCCCGCCTGGC
CCTGTGCACGCTCGTCTTCCTCTGCCTGTCCTGCAACCCCTTGGCCTCCTTGCTGGGGGCCCGGGGGCTT
CCCAGCCCCTCAGATACCACCAGCGTCTACCATAGCCCTGGGCGCAACGTGCTGGGCACCGAGAGCAGAG
ATGGCCCTGGCTGGGCCCAGTGGCTGCTGCCCCCAGTGGTCTGGCTGCTCAATGGGCTGTTGGTGCTCGT
CTCCTTGGTGCTTCTCTTTGTCTACGGTGAGCCAGTCACACGGCCCCACTCAGGCCCCGCCGTGTACTTC
TGGAGGCATCGCAAGCAGGCTGACCTGGACCTGGCCCGGGGAGACTTTGCCCAGGCTGCCCAGCAGCTGT
GGCTGGCCCTGCGGGCACTGGGCCGGCCCCTGCCCACCTCCCACCTGGACCTGGCTTGTAGCCTCCTCTG
GAACCTCATCCGTCACCTGCTGCAGCGTCTCTGGGTGGGCCGCTGGCTGGCAGGCCGGGCAGGGGGCCTG
CAGCAGGACTGTGCTCTGCGAGTGGATGCTAGCGCCAGCGCCCGAGACGCAGCCCTGGTCTACCATAAGC
TGCACCAGCTGCACACCATGGGGAAGCACACAGGCGGGCACCTCACTGCCACCAACCTGGCGCTGAGTGC
CCTGAACCTGGCAGAGTGTGCAGGGGATGCCGTGTCTGTGGCGACGCTGGCCGAGATCTATGTGGCGGCT
GCATTGAGAGTGAAGACCAGTCTCCCACGGGCCTTGCATTTTCTGACACGCTTCTTCCTGAGCAGTGCCC
GCCAGGCCTGCCTGGCACAGAGTGGCTCAGTGCCTCCTGCCATGCAGTGGCTCTGCCACCCCGTGGGCCA
CCGTTTCTTCGTGGATGGGGACTGGTCCGTGCTCAGTACCCCATGGGAGAGCCTGTACAGCTTGGCCGGG
AACCCAGTGGACCCCCTGGCCCAGGTGACTCAGCTATTCCGGGAACATCTCTTAGAGCGAGCACTGAACT
GTGTGACCCAGCCCAACCCCAGCCCTGGGTCAGCTGATGGGGACAAGGAATTCTCGGATGCCCTCGGGTA
CCTGCAGCTCCTGAACAGCTGTTCTGATGCTGCCGCGCCTCCTGCCTACAGCTTCTCCATCAGTTCCACC
ATGGCCACCACCACCGGCGTAGACCCGGTGGCCAAGTGGTGGGCCTCTCTGACAGCTGTGGTGATCCACT
GGCTGCGGCGGGATGAGGAGGCGGCTGAGCGGCTGTGCCCGCTGGTGGAGCACCTGCCCCGGGTGCTGCA
GGAGTCTGAGAGACCCCTGCCCAGGGCAGCTCTGCACTCCTTCAAGGCTGCCCGGGCCCTGCTGGGCTGT
GCCAAGGCAGAGTCTGGTCCAGCCAGCCTGACCATCTGTGAGAAGGCCAGTGGGTACCTGCAGGACAGCC
TGGCTACCACACCAGCCAGCAGCTCCATTGACAAGGCCGTGCAGCTGTTCCTGTGTGACCTGCTTCTTGT
GGTGCGCACCAGCCTGTGGCGGCAGCAGCAGCCCCCGGCCCCGGCCCCAGCAGCCCAGGGCACCAGCAGC
AGGCCCCAGGCTTCCGCCCTTGAGCTGCGTGGCTTCCAACGGGACCTGAGCAGCCTGAGGCGGCTGGCAC
AGAGCTTCCGGCCCGCCATGCGGAGGGTGTTCCTACATGAGGCCACGGCCCGGCTGATGGCGGGGGCCAG
CCCCACACGGACACACCAGCTCCTCGACCGCAGTCTGAGGCGGCGGGCAGGCCCCGGTGGCAAAGGAGGC
GCGGTGGCGGAGCTGGAGCCGCGGCCCACGCGGCGGGAGCACGCGGAGGCCTTGCTGCTGGCCTCCTGCT
ACCTGCCCCCCGGCTTCCTGTCGGCGCCCGGGCAGCGCGTGGGCATGCTGGCTGAGGCGGCGCGCACACT
CGAGAAGCTTGGCGATCGCCGGCTGCTGCACGACTGTCAGCAGATGCTCATGCGCCTGGGCGGTGGGACC
ACTGTCACTTCCAGCTAGACCCCGTGTCCCCGGCCTCAGCACCCCTGTCTCTAGCCACTTTGGTCCCGTG
CAGCTTCTGTCCTGCGTCGAAGCTTTGAAGGCCGAAGGCAGTGCAAGAGACTCTGGCCTCCACAGTTCGA
CCTGCGGCTGCTGTGTGCCTTCGCGGTGGAAGGCCCGAGGGGCGCGATCTTGACCCTAAGACCGGCGGCC
ATGATGGTGCTGACCTCTGGTGGCCGATCGGGGCACTGCAGGGGCCGAGCCATTTTGGGGGGCCCCCCTC
CTTGCTCTGCAGGCACCTTAGTGGCTTTTTTCCTCCTGTGTACAGGGAAGAGAGGGGTACATTTCCCTGT
GCTGACGGAAGCCAACTTGGCTTTCCCGGACTGCAAGCAGGGCTCTGCCCCAGAGGCCTCTCTCTCCGTC
GTGGGAGAGAGACGTGTACATAGTGTAGGTCAGCGTGCTTAGCCTCCTGACCTGAGGCTCCTGTGCTACT
TTGCCTTTTGCAAACTTTATTTTCATAGATTGAGAAGTTTTGTACAGAGAATTAAAAATGAAATTATTTA
TAATCTGGGTTTTGTGTCTTCAGCTGATGGATGTGCTGACTAGTGAGAGTGCTTGGGCCCTCCCCCAGCA
CCTAGGGAAAGGCTTCCCCTCCCCCTCCGGCCACAAGGTACACAACTTTTAACTTAGCTCTTCCCGATGT
TTGTTTGTTAGTGGGAGGAGTGGGGAGGGCTGGCTGTATGGCCTCCAGCCTACCTGTTCCCCCTGCTCCC
AGGGCACATGGTTGGGCTGTGTCAACCCTTAGGGCCTCCATGGGGTCAGTTGTCCCTTCTCACCTCCCAG
CTCTGTCCCCATCAGGTCCCTGGGTGGCACGGGAGGATGGACTGACTTCCAGGACCTGTTGTGTGACAGG
AGCTACAGCTTGGGTCTCCCTGCAAGAAGTCTGGCACGTCTCACCTCCCCCATCCCGGCCCCTGGTCATC
TCACAGCAAAGAAGCCTCCTCCCTCCCGACCTGCCGCCACACTGGAGAGGGGGCACAGGGGCGGGGGAGG
TTTCCTGTTCTGTGAAAGGCCGACTCCCTGACTCCATTCATGCCCCCCCCCCCAGCCCCTCCCTTCATTC
CCATTCCCCAACCTAAAGCCTGGCCCGGCTCCCAGCTGAATCTGGTCGGAATCCACGGGCTGCAGATTTT
CCAAAACAATCGTTGTATCTTTATTGACTTTTTTTTTTTTTTTTCTGAATGCAATGACTGTTTTTTTAC
TCTTAAGGAAAATAAACATCTTTTAGAAACAAAAAAAAAAAA (SEQ ID NO: 29)

The amino acid sequence for SREBF1 isoform b (GenBank Accession No. NP_004167.3) is provided below.

MDEPPFSEAALEQALGEPCDLDAALLTDIEDMLQLINNQDSDFPGLFDPPYAGSGAGGTDPASPDTSSPG
SLSPPPATLSSSLEAFLSGPQAAPSPLSPPQPAPTPLKMYPSMPAFSPGPGIKEESVPLSILQTPTPQPL
PGALLPQSFPAPAPPQFSSTPVLGYPSPPGGFSTGSPPGNTQQPLPGLPLASPPGVPPVSLHTQVQSVVP
QQLLTVTAAPTAAPVTTTVTSQIQQVPVLLQPHFIKADSLLLTAMKTDGATVKAAGLSPLVSGTTVQTGP
LPTLVSGGTILATVPLVVDAEKLPINRLAAGSKAPASAQSRGEKRTAHNAIEKRYRSSINDKIIELKDLV
VGTEAKLNKSAVLRKAIDYIRFLQHSNQKLKQENLSLRTAVHKSKSLKDLVSACGSGGNTDVLMEGVKTE
VEDTLTPPPSDAGSPFQSSPLSLGSRGSGSGGSGSDSEPDSPVFEDSKAKPEQRPSLHSRGMLDRSRLAL
CTLVFLCLSCNPLASLLGARGLPSPSDTTSVYHSPGRNVLGTESRDGPGWAQWLLPPVVWLLNGLLVLVS
LVLLFVYGEPVTRPHSGPAVYFWRHRKQADLDLARGDFAQAAQQLWLALRALGRPLPTSHLDLACSLLWN
LIRHLLQRLWVGRWLAGRAGGLQQDCALRVDASASARDAALVYHKLHQLHTMGKHTGGHLTATNLALSAL
NLAECAGDAVSVATLAEIYVAAALRVKTSLPRALHFLTRFFLSSARQACLAQSGSVPPAMQWLCHPVGHR
FFVDGDWSVLSTPWESLYSLAGNPVDPLAQVTQLFREHLLERALNCVTQPNPSPGSADGDKEFSDALGYL
QLLNSCSDAAGAPAYSFSISSSMATTTGVDPVAKWWASLTAVVIHWLRRDEEAAERLCPLVEHLPRVLQE
SERPLPRAALHSFKAARALLGCAKAESGPASLTICEKASGYLQDSLATTPASSSIDKAVQLFLCDLLLVV
RTSLWRQQQPPAPAPAAQGTSSRPQASALELRGFQRDLSSLRRLAQSFRPAMRRVFLHEATARLMAGASP
TRTHQLLDRSLRRRAGPGGKGGAVAELEPRPTRREHAEALLLASCYLPPGFLSAPGQRVGMLAEAARTLE
KLGDRRLLHDCQQMLMRLGGGTTVTSS (SEQ ID NO: 30)

The nucleic acid sequence, or mRNA sequence, for SREBF1 isoform b (GenBank Accession No. NM_004176.4) is provided below.

AGCAGAGCTGCGGCCGGGGGAACCCAGTTTCCGAGGAACTTTTCGCCGGCGCCGGGCCGCCTCTGAGGCC
AGGGCAGGACACGAACGCGCGGAGCGGCGGCGGCGACTGAGAGCCGGGGCCGCGGCGGCGCTCCCTAGGA
AGGGCCGTACGAGGCGGCGGGCCCGGCGGGCCTCCCGGAGGAGGCGGCTGCGCCATGGACGAGCCACCCT
TCAGCGAGGCGGCTTTGGAGCAGGCGCTGGGCGAGCCGTGCGATCTGGACGCGGCGCTGCTGACCGACAT
CGAAGACATGCTTCAGCTTATCAACAACCAAGACAGTGACTTCCCTGGCCTATTTGACCCACCCTATGCT
GGGAGTGGGGCAGGGGGCACAGACCCTGCCAGCCCCGATACCAGCTCCCCAGGCAGCTTGTCTCCACCTC
CTGCCACATTGAGCTCCTCTCTTGAAGCCTTCCTGAGCGGGCCGCAGGCAGCGCCCTCACCCCTGTCCCC
TCCCCAGCCTGCACCCACTCCATTGAAGATGTACCCGTCCATGCCCGCTTTCTCCCCTGGGCCTGGTATC
AAGGAAGAGTCAGTGCCACTGAGCATCCTGCAGACCCCCACCCCACAGCCCCTGCCAGGGGCCCTCCTGC
CACAGAGCTTCCCAGCCCCAGCCCCACCGCAGTTCAGCTCCACCCCTGTGTTAGGCTACCCCAGCCCTCC
GGGAGGCTTCTCTACAGGAAGCCCTCCCGGGAACACCCAGCAGCCGCTGCCTGGCCTGCCACTGGCTTCC
CCGCCAGGGGTCCCGCCCGTCTCCTTGCACACCCAGGTCCAGAGTGTGGTCCCCCAGCAGCTACTGACAG
TCACAGCTGCCCCCACGGCAGCCCCTGTAACGACCACTGTGACCTCGCAGATCCAGCAGGTCCCGGTCCT
GCTGCAGCCCCACTTCATCAAGGCAGACTCGCTGCTTCTGACAGCCATGAAGACAGACGGAGCCACTGTG
AAGGCGGCAGGTCTCAGTCCCCTGGTCTCTGGCACCACTGTGCAGACAGGGCCTTTGCCGACCCTGGTGA
GTGGCGGAACCATCTTGGCAACAGTCCCACTGGTCGTAGATGCGGAGAAGCTGCCTATCAACCGGCTCGC
AGCTGGCAGCAAGGCCCCGGCCTCTGCCCAGAGCCGTGGAGAGAAGCGCACAGCCCACAACGCCATTGAG
AAGCGCTACCGCTCCTCCATCAATGACAAAATCATTGAGCTCAAGGATCTGGTGGTGGGCACTGAGGCAA
AGCTGAATAAATCTGCTGTCTTGCGCAAGGCCATCGACTACATTCGCTTTCTGCAACACAGCAACCAGAA
ACTCAAGCAGGAGAACCTAAGTCTGCGCACTGCTGTCCACAAAAGCAAATCTCTGAAGGATCTGGTGTCG
GCCTGTGGCAGTGGAGGGAACACAGACGTGCTCATGGAGGGCGTGAAGACTGAGGTGGAGGACACACTGA
CCCCACCCCCCTCGGATGCTGGCTCACCTTTCCAGAGCAGCCCCTTGTCCCTTGGCAGCAGGGGCAGTGG
CAGCGGTGGCAGTGGCAGTGACTCGGAGCCTGACAGCCCAGTCTTTGAGGACAGCAAGGCAAAGCCAGAG
CAGCGGCCGTCTCTGCACAGCCGGGGCATGCTGGACCGCTCCCGCCTGGCCCTGTGCACGCTCGTCTTCC
TCTGCCTGTCCTGCAACCCCTTGGCCTCCTTGCTGGGGGCCCGGGGGCTTCCCAGCCCCTCAGATACCAC
CAGCGTCTACCATAGCCCTGGGCGCAACGTGCTGGGCACCGAGAGCAGAGATGGCCCTGGCTGGGCCCAG
TGGCTGCTGCCCCCAGTGGTCTGGCTGCTCAATGGGCTGTTGGTGCTCGTCTCCTTGGTGCTTCTCTTTG
TCTACGGTGAGCCAGTCACACGGCCCCACTCAGGCCCCGCCGTGTACTTCTGGAGGCATCGCAAGCAGGC
TGACCTGGACCTGGCCCGGGGAGACTTTGCCCAGGCTGCCCAGCAGCTGTGGCTGGCCCTGCGGGCACTG
GGCCGGCCCCTGCCCACCTCCCACCTGGACCTGGCTTGTAGCCTCCTCTGGAACCTCATCCGTCACCTGC

TGCAGCGTCTCTGGGTGGGCCGCTGGCTGGCAGGCCGGGCAGGGGGCCTGCAGCAGGACTGTGCTCTGCG
AGTGGATGCTAGCGCCAGCGCCCGAGACGCAGCCCTGGTCTACCATAAGCTGCACCAGCTGCACACCATG
GGGAAGCACACAGGCGGGCACCTCACTGCCACCAACCTGGCGCTGAGTGCCCTGAACCTGGCAGAGTGTG
CAGGGGATGCCGTGTCTGTGGCGACGCTGGCCGAGATCTATGTGGCGGCTGCATTGAGAGTGAAGACCAG
TCTCCCACGGGCCTTGCATTTTCTGACACGCTTCTTCCTGAGCAGTGCCCGCCAGGCCTGCCTGGCACAG
AGTGGCTCAGTGCCTCCTGCCATGCAGTGGCTCTGCCACCCCGTGGGCCACCGTTTCTTCGTGGATGGGG
ACTGGTCCGTGCTCAGTACCCCATGGGAGAGCCTGTACAGCTTGGCCGGGAACCCAGTGGACCCCCTGGC
CCAGGTGACTCAGCTATTCCGGGAACATCTCTTAGAGCGAGCACTGAACTGTGTGACCCAGCCCAACCCC
AGCCCTGGGTCAGCTGATGGGGACAAGGAATTCTCGGATGCCCTCGGGTACCTGCAGCTGCTGAACAGCT
GTTCTGATGCTGCGGGGGCTCCTGCCTACAGCTTCTCCATCAGTTCCAGCATGGCCACCACCACCGGCGT
AGACCCGGTGGCCAAGTGGTGGGCCTCTCTGACAGCTGTGGTGATCCACTGGCTGCGGCGGGATGAGGAG
GCGGCTGAGCGGCTGTGCCCGCTGGTGGAGCACCTGCCCCGGGTGCTGCAGGAGTCTGAGAGACCCCTGC
CCAGGGCAGCTCTGCACTCCTTCAAGGCTGCCCGGGCCCTGCTGGGCTGTGCCAAGGCAGAGTCTGGTCC
AGCCAGCCTGACCATCTGTGAGAAGGCCAGTGGGTACCTGCAGGACAGCCTGGCTACCACACCAGCCAGC
AGCTCCATTGACAAGGCCGTGCAGCTGTTCCTGTGTGACCTGCTTCTTGTGGTGCGCACCAGCCTGTGGC
GGCAGCAGCAGCCCCCGGCCCCGGCCCCAGCAGCCCAGGGCACCAGCAGCAGGCCCCAGGCTTCCGCCCT
TGAGCTGCGTGGCTTCCAACGGGACCTGAGCAGCCTGAGGCGGCTGGCACAGAGCTTCCGGCCCGCCATG
CGGAGGGTGTTCCTACATGAGGCCACGGCCCGGCTGATGGCGGGGGCCAGCCCCACACGGACACACCAGC
TCCTCGACCGCAGTCTGAGGCGGCGGGCAGGCCCCGGTGGCAAAGGAGGCGCGGTGGCGGAGCTGGAGCC
GCGGCCCACGCGGCGGGAGCACGCGGAGGCCTTGCTGCTGGCCTCCTGCTACCTGCCCCCCGGCTTCCTG
TCGGCGCCCGGGCAGCGCGTGGGCATGCTGGCTGAGGCGGCGCGCACACTCGAGAAGCTTGGCGATCGCC
GGCTGCTGCACGACTGTCAGCAGATGCTCATGCGCCTGGGCGGTGGGACCACTGTCACTTCCAGCTAGAC
CCCGTGTCCCCGGCCTCAGCACCCCTGTCTCTAGCCACTTTGGTCCCGTGCAGCTTCTGTCCTGCGTCGA
AGCTTTGAAGGCCGAAGGCAGTGCAAGAGACTCTGGCCTCCACAGTTCGACCTGCGGCTGCTGTGTGCCT
TCGCGGTGGAAGGCCCGAGGGGCGCGATCTTGACCCTAAGACCGGCGGCCATGATGGTGCTGACCTCTGG
TGGCCCATCCCCCCACTGCACGCCCCGACCCATTTTGCCGCGCCCCCCCTCCTTGCTCTCCACCCACCTTA
GTGGCTTTTTTCCTCCTGTGTACAGGGAAGAGAGGGGTACATTTCCCTGTGCTGACGGAAGCCAACTTGG
CTTTCCCGGACTGCAAGCAGGGCTCTGCCCCAGAGGCCTCTCTCTCCGTCGTGGGAGAGAGACGTGTACA
TAGTGTAGGTCAGCGTGCTTAGCCTCCTGACCTGAGGCTCCTGTGCTACTTTGCCTTTTGCAAACTTTAT
TTTCATAGATTGAGAAGTTTTGTACAGAGAATTAAAAATGAAATTATTTATAATCTGGGTTTTGTGTCTT
CAGCTGATGGATGTGCTGACTAGTGAGAGTGCTTGGGCCCTCCCCCAGCACCTAGGGAAAGGCTTCCCCT
CCCCCTCCGGCCACAAGGTACACAACTTTTAACTTAGCTCTTCCCGATGTTTGTTTGTTAGTGGGAGGAG
TGGGGAGGGCTGGCTGTATGGCCTCCAGCCTACCTGTTCCCCCTGCTCCCAGGGCACATGGTTGGGCTGT
GTCAACCCTTAGGGCCTCCATGGGGTCAGTTGTCCCTTCTCACCTCCCAGCTCTGTCCCCATCAGGTCCC
TGGGTGGCACGGGAGGATGGACTGACTTCCAGGACCTGTTGTGTGACAGGAGCTACAGCTTGGGTCTCCC
TGCAAGAAGTCTGGCACGTCTCACCTCCCCCATCCCGGCCCCTGGTCATCTCACAGCAAAGAAGCCTCCT
CCCTCCCGACCTGCCGCCACACTGGAGAGGGGGCACAGGGGCGGGGGAGGTTTCCTGTTCTGTGAAAGGC
CGACTCCCTGACTCCATTCATGCCCCCCCCCCCAGCCCCTCCCTTCATTCCCATTCCCCAACCTAAAGCC
TGGCCCGGCTCCCAGCTGAATCTGGTCGGAATCCACGGGCTGCAGATTTTCCAAAACAATCGTTGTATCT
TTATTGACTTTTTTTTTTTTTTTTTTCTGAATGCAATGACTGTTTTTTACTCTTAAGGAAAATAAACATC
TTTTAGAAACAAAAAAAAAAAA (SEQ ID NO: 31)

The nucleic acid sequence, or CDS, for SREBF1 isoform c (GenBank Accession No. NM_001244003) is provided below.

ATGGACGAGCTGCCTTTCGGTGAGGCGGCTGTGGAACAGGCGCTGGACGAGCTGGGCGAACTGGACGCCGCACTGCT
GACCGACATCCAAGACATGCTTCAGCTCATCAACAACCAAGACAGTGACTTCCCTGGCCTGTTTGATTCCCCCTATG
CAGGGGGCGGGGCAGGAGACACAGAGCCCACCAGCCCTGGTGCCAACTCTCCTGAGAGCTTGTCTTCTCCTGCTTCC
CTGGGTTCCTCTCTGGAAGCCTTCCTGGGGGAACCCAAGGCAACACCTGCATCCTTGTCCCCTGTGCCGTCTGCATC
CACTGCTTTAAAGATGTACCCGTCTGTGCCCCCCTTCTCCCCTGGGCCTGGAATCAAAGAAGAGCCAGTGCCACTCA
CCATCCTGCAGCCCCCAGCAGCACAGCCATCACCAGGGACCCTCCTGCCTCCGAGTTTCCCTCCACCACCCCTGCAG
CTCAGCCCGGCTCCTGTGCTGGGGTATTCTAGCCTTCCTTCAGGCTTCTCAGGGACCCTTCCTGGAAATACCCAACA

GCCACCATCTAGCCTGTCACTGGCCTCTGCACCAGGAGTCTCGCCCATCTCTTTACACACCCAGGTCCAGAGCTCAG
CCTCCCAGCAGCCACTGCCAGCCTCAACAGCCCCTAGAACAACCACTGTGACCTCACAGATCCAGCGGGTCCCAGTC
GTACTGCAGCCACATTTCATCAAGGCAGATTCACTGCTACTGACAACTGTAAAAACAGATACAGGAGCCACGATGAA
GACGGCTGGCATCAGTACCTTAGCCCCTGGCACAGCCGTGCAGGCAGGCCCCTTGCAGACCCTGGTGAGTGGTGGGA
CCATCCTGGCCACAGTACCATTGGTTGTGGATACAGACAAACTGCCCATCCATCGACTGGCAGCTGGCAGCAAGGCC
CTGGGCTCAGCTCAGAGCCGTGGTGAGAAGCGCACAGCCCACAATGCCATTGAGAAGCGCTACCGTTCCTCTATCAA
TGACAAGATTGTGGAGCTCAAAGACCTGGTGGTGGGCACTGAGGCAAAGCTGAATAAATCTGCCGTCTTGCGCAAGG
CCATCGACTATATCCGCTTCTTACAGCACAGCAACCAGAAGCTCAAGCAGGAGAACCTGGCCCTGCGAAATGCCGCT
CACAAAAGCAAATCCCTGAAGGACCTGGTGTCGGCCTGTGGCAGTGCAGGAGGCACAGATGTGGCTATGGAGGGTGT
GAAGCCTGAGGTGGTGGATACGCTGACCCCTCCACCCTCAGACGCTGGCTCGCCCTCCCAGAGTAGCCCCTTGTCCC
TCGGCAGCAGAGGTAGCAGCAGTGGTGGCAGTGACTCGGAGCCTGACAGCCCAGTCTTTGAGGATAGCCAGGTGAAA
GCCCAACGGCTGCACAGTCATGGCATGCTGGACCGCTCCCGCCTAGCCCTGTGTGCGCTGGTCTTCCTGTGTCTGAC
CTGCAACCCCTTGGCATCACTGTTTGGCTGGGGCATCCCCGGTCCCTCCAGTGCCTCTGGTGCACACCACAGCTCTG
GGCGTAGCATGCTGGAGGCCGAGAGCAGAGATGGCTCTAATTGGACCCAGTGGTTGCTGCCACCCCTAGTCTGGCTG
GCCAATGGACTACTAGTGTTGGCCTGCCTGGCTCTTCTCTTTGTCTATGGGGAACCTGTGACCCGGCCACACACTAG
CCCAGCTGTACACTTCTGGAGACATCGCAAACAGGCTGACCTGGACTTGGCTCGGGGAGATTTTGCCCAGGCTGCTC
AGCAGCTGTGGCTGGCCCTGCAGGCATTGGGACGGCCCCTGCCCACCTCGAACCTAGACTTGGCCTGCAGCCTGCTT
TGGAACCTCATCCGCCACCTGCTGCAGCGTCTCTGGGTTGGCCGCTGGCTGGCAGGCCGGGCTGGGGGCTTGCGGAG
AGACTGTGGACTGAGAATGGATGCACGTGCCAGTGCTCGAGATGCGGCTCTCGTCTACCATAAGCTGCACCAGCTGC
ATGCCATGGGCAAATACACAGGAGGGCACCTCATTGCTTCTAACCTGGCACTGAGTGCCCTGAACCTGGCCGAGTGC
GCAGGAGATGCTGTATCCATGGCAACGCTGGCAGAGATCTATGTGGCTGCTGCCCTGAGGGTCAAGACCAGTCTCCC
AAGAGCCTTGCACTTTTTGACACGTTTCTTCCTGAGTAGTGCCCGCCAGGCCTGCCTGGCACAGAGTGGCTCAGTGC
CTCTTGCCATGCAGTGGCTCTGCCACCCTGTAGGCCACCGTTTCTTCGTGGATGGGGACTGGGCTGTGCATGGTGCC
CCACAGGAGAGCCTGTACAGCGTGGCTGGGAACCCAGTGGATCCCCTCGCCCAGGTGACTCGACTATTCTGCGAACA
TCTCTTGGAGAGAGCACTGAACTGTATTGCTCAACCCAGCCCGGGGACAGCTGATGGAGACAGGGAGTTCTCTGACG
CACTTGGATACCTGCAGTTGCTAAATCGCTGCTCTGATGCTGTCGGGACTCCTGCCTGCAGCTTCTCTGTCAGCTCC
AGCATGGCTTCCACCACCGGCACAGACCCAGTGGCCAAGTGGTGGGCCTCACTGACGGCTGTGGTGATCCACTGGCT
GCGGCGGGATGAAGAGGCAGCTGAGCGCCTATACCCGCTGGTAGAGCGTATGCCCCACGTGCTGCAGGAGACTGAGA
GACCCCTGCCCAAGGCAGCTCTGTACTCCTTCAAGGCTGCCCGGGCTCTGCTGGACCACAGAAAAGTGGAGTCTGGC
CCAGCCAGCCTGGCCATCTGTGAGAAGGCCAGCGGGTACTTGCGGGACAGCTTAGCCGCTCCACCAACTGGCAGCTC
CATTGACAAGGCCATGCAGCTGCTCCTGTGTGATCTACTTCTTGTGGCCCGCACTAGTATGTGGCAGCGCCAGCAGT
CACCAGCCTCAGCCCAGGTAGCTCACAGTGCCAGCAATGGATCTCAGGCCTCCGCTTTGGAGCTTCGAGGTTTCCAA
CAGGACCTGAGCAGCCTGAGGCGCTTGGCACAGAACTTCCGGCCTGCTATGAGGAGAGTGTTCCTACACGAGGCCAC
AGCTCGGCTGATGGCAGGGGCAAGTCCTGCCCGGACACACCAGCTCCTGGACCGAAGTCTGCGGAGGCGGGCCGGCT
CCAGTGGCAAAGGAGGCACTGTAGCTGAGCTGGAGCCTCGACCCACATGGCGGGAGCACACAGAGGCCTTGCTGCTG
GCCTCCTGCTATCTGCCACCTGCCTTCCTGTCGGCCCCTGGACAGCAAATGAGCATGTTGGCTGAGGCAGCACGCAC
TGTAGAGAAGCTTGGTGATCATCGGCTACTGCTTGACTGCCAGCAGATGCTTCTGCGCCTGGGCGGTGGGACCACTG
TCACTTCCAGCTAA (SEQ ID NO: 32)

The nucleic acid sequence, or mRNA sequence, for SREBF1 isoform c (GenBank Accession No. NM_001244003) is provided below.

CTCCTGCGAAGCCTGGCGGGCGCCGCCGCCATGGACGAGCTGCCTTTCGGTGAGGCGGCTGTGGAACAGGCGCTGGA
CGAGCTGGGCGAACTGGACGCCGCACTGCTGACCGACATCCAAGACATGCTTCAGCTCATCAACAACCAAGACAGTG
ACTTCCCTGGCCTGTTTGATTCCCCCTATGCAGGGGGCGGGGCAGGAGACACAGAGCCCACCAGCCCTGGTGCCAAC
TCTCCTGAGAGCTTGTCTTCTCCTGCTTCCCTGGGTTCCTCTCTGGAAGCCTTCCTGGGGGAACCCAAGGCAACACC
TGCATCCTTGTCCCCTGTGCCGTCTGCATCCACTGCTTTAAAGATGTACCCGTCTGTGCCCCCCTTCTCCCCTGGGC
CTGGAATCAAAGAAGAGCCAGTGCCACTCACCATCCTGCAGCCCCCAGCAGCACAGCCATCACCAGGGACCCTCCTG
CCTCCGAGTTTCCCTCCACCACCCCTGCAGCTCAGCCCGGCTCCTGTGCTGGGGTATTCTAGCCTTCCTTCAGGCTT
CTCAGGGACCCTTCCTGGAAATACCCAACAGCCACCATCTAGCCTGTCACTGGCCTCTGCACCAGGAGTCTCGCCCA
TCTCTTTACACACCCAGGTCCAGAGCTCAGCCTCCCAGCAGCCACTGCCAGCCTCAACAGCCCCTAGAACAACCACT
GTGACCTCACAGATCCAGCGGGTCCCAGTCGTACTGCAGCCACATTTCATCAAGGCAGATTCACTGCTACTGACAAC
TGTAAAAACAGATACAGGAGCCACGATGAAGACGGCTGGCATCAGTACCTTAGCCCCTGGCACAGCCGTGCAGGCAG
GCCCCTTGCAGACCCTGGTGAGTGGTGGGACCATCCTGGCCACAGTACCATTGGTTGTGGATACAGACAAACTGCCC
ATCCATCGACTGGCAGCTGGCAGCAAGGCCCTGGGCTCAGCTCAGAGCCGTGGTGAGAAGCGCACAGCCCACAATGC
CATTGAGAAGCGCTACCGTTCCTCTATCAATGACAAGATTGTGGAGCTCAAAGACCTGGTGGTGGGCACTGAGGCAA
AGCTGAATAAATCTGCCGTCTTGCGCAAGGCCATCGACTATATCCGCTTCTTACAGCACAGCAACCAGAAGCTCAAG
CAGGAGAACCTGGCCCTGCGAAATGCCGCTCACAAAAGCAAATCCCTGAAGGACCTGGTGTCGGCCTGTGGCAGTGC
AGGAGGCACAGATGTGGCTATGGAGGGTGTGAAGCCTGAGGTGGTGGATACGCTGACCCCTCCACCCTCAGACGCTG
GCTCCCCCTCCCACACTAGCCCCTTGTCCCTCGCCAGCAGCAGCTAGCAGCACTGCTGCCAGTCACTCGCAGCCTCAC
AGCCCAGTCTTTGAGGATAGCCAGGTGAAAGCCCAACGGCTGCACAGTCATGGCATGCTGGACCGCTCCCGCCTAGC
CCTGTGTGCGCTGGTCTTCCTGTGTCTGACCTGCAACCCCTTGGCATCACTGTTTGGCTGGGGCATCCCCGGTCCCT
CCAGTGCCTCTGGTGCACACCACAGCTCTGGGCGTAGCATGCTGGAGGCCGAGAGCAGAGATGGCTCTAATTGGACC
CAGTGGTTGCTGCCACCCCTAGTCTGGCTGGCCAATGGACTACTAGTGTTGGCCTGCCTGGCTCTTCTCTTTGTCTA
TGGGGAACCTGTGACCCGGCCACACACTAGCCCAGCTGTACACTTCTGGAGACATCGCAAACAGGCTGACCTGGACT
TGGCTCGGGGAGATTTTGCCCAGGCTGCTCAGCAGCTGTGGCTGGCCCTGCAGGCATTGGGACGGCCCCTGCCCACC
TCGAACCTAGACTTGGCCTGCAGCCTGCTTTGGAACCTCATCCGCCACCTGCTGCAGCGTCTCTGGGTTGGCCGCTG
GCTGGCAGGCCGGGCTGGGGGCTTGCGGAGAGACTGTGGACTGAGAATGGATGCACGTGCCAGTGCTCGAGATGCGG
CTCTCGTCTACCATAAGCTGCACCAGCTGCATGCCATGGGCAAATACACAGGAGGGCACCTCATTGCTTCTAACCTG
GCACTGAGTGCCCTGAACCTGGCCGAGTGCGCAGGAGATGCTGTATCCATGGCAACGCTGGCAGAGATCTATGTGGC
TGCTGCCCTGAGGGTCAAGACCAGTCTCCCAAGAGCCTTGCACTTTTTGACACGTTTCTTCCTGAGTAGTGCCCGCC
AGGCCTGCCTGGCACAGAGTGGCTCAGTGCCTCTTGCCATGCAGTGGCTCTGCCACCCTGTAGGCCACCGTTTCTTC
GTGGATGGGGACTGGGCTGTGCATGGTGCCCCACAGGAGAGCCTGTACAGCGTGGCTGGGAACCCAGTGGATCCCCT
CGCCCAGGTGACTCGACTATTCTGCGAACATCTCTTGGAGAGAGCACTGAACTGTATTGCTCAACCCAGCCCGGGGA
CAGCTGATGGAGACAGGGAGTTCTCTGACGCACTTGGATACCTGCAGTTGCTAAATCGCTGCTCTGATGCTGTCGGG
ACTCCTGCCTGCAGCTTCTCTGTCAGCTCCAGCATGGCTTCCACCACCGGCACAGACCCAGTGGCCAAGTGGTGGGC

CTCACTGACGGCTGTGGTGATCCACTGGCTGCGGCGGGATGAAGAGGCAGCTGAGCGCCTATACCCGCTGGTAGAGC
GTATGCCCCACGTGCTGCAGGAGACTGAGAGACCCCTGCCCAAGGCAGCTCTGTACTCCTTCAAGGCTGCCCGGGCT
CTGCTGGACCACAGAAAAGTGGAGTCTGGCCCAGCCAGCCTGGCCATCTGTGAGAAGGCCAGCGGGTACTTGCGGGA
CAGCTTAGCCGCTCCACCAACTGGCAGCTCCATTGACAAGGCCATGCAGCTGCTCCTGTGTGATCTACTTCTTGTGG
CCCGCACTAGTATGTGGCAGCGCCAGCAGTCACCAGCCTCAGCCCAGGTAGCTCACAGTGCCAGCAATGGATCTCAG
GCCTCCGCTTTGGAGCTTCGAGGTTTCCAACAGGACCTGAGCAGCCTGAGGCGCTTGGCACAGAACTTCCGGCCTGC
TATGAGGAGAGTGTTCCTACACGAGGCCACAGCTCGGCTGATGGCAGGGGCAAGTCCTGCCCGGACACACCAGCTCC
TGGACCGAAGTCTGCGGAGGCGGGCCGGCTCCAGTGGCAAAGGAGGCACTGTAGCTGAGCTGGAGCCTCGACCCACA
TGGCGGGAGCACACAGAGGCCTTGCTGCTGGCCTCCTGCTATCTGCCACCTGCCTTCCTGTCGGCCCCTGGACAGCA
AATGAGCATGTTGGCTGAGGCAGCACGCACTGTAGAGAAGCTTGGTGATCATCGGCTACTGCTTGACTGCCAGCAGA
TGCTTCTGCGCCTGGGCGGTGGGACCACTGTCACTTCCAGCTAAACCTTGGATGGTCTCCCCAGTATTAGAGGCCCT
TAAGGACCTTTGTCACTGGCTGTGGTCGTCCAGAGAGGGTGAGCCTGACAAGCAATCAGGATCATGCCGACCTCTAG
TGACAAATCTAGAAATTGCAGAGGCTGCACTGGCCCAATGCCACCCTCTTGCTCTGTAGGCACCTTTTTCCTGTCCT
ATGGAAAGGAACCTTTCCCCTAGCTGAGGGCCACCCTGTCCTGAGGCTCTCACCCACTCCTGGAAGACTTGTATATA
GTGTAGATCCAGCTGAGCCAGTTTCCTGTGCAGGCTCATGTACTACTTTAACTTTTGCAAACTTTATTTTCATAGGT
TGAGAAATTTTGTACAGAAAATTAAAAAGTGAAATTATTTATA (SEQ ID NO: 33)

The amino acid sequence for SREBF1 isoform c (GenBank Accession No. NM_001244003) is provided below.

MDELPFGEAAVEQALDELGELDAALLTDIQDMLQLINNQDSDFPGLFDSPYAGGGAGDTEPTSPGANSPESLSSPAS
LGSSLEAFLCEPKATPASLSPVPSASTALKMYPSVPPFSPCPCIKEEPVPLTILQPPAAQPSPCTLLPPSFPPPPLQ
LSPAPVLGYSSLPSGFSGTLPGNTQQPPSSLSLASAPGVSPISLHTQVQSSASQQPLPASTAPRTTTVTSQIQRVPV
VLQPHFIKADSLLLTTVKTDTGATMKTAGISTLAPGTAVQAGPLQTLVSGGTILATVPLVVDTDKLPIHRLAAGSKA
LGSAQSRGEKRTAHNAIEKRYRSSINDKIVELKDLVVGTEAKLNKSAVLRKAIDYIRFLQHSNQKLKQENLALRNAA
HKSKSLKDLVSACGSAGGTDVAMEGVKPEVVDTLTPPPSDAGSPSQSSPLSLGSRGSSSGGSDSEPDSPVFEDSQVK
AQRLHSHGMLDRSRLALCALVFLCLTCNPLASLFGWGIPGPSSASGAHHSSGRSMLEAESRDGSNWTQWLLPPLVWL
ANGLLVLACLALLFVYGEPVTRPHTSPAVHFWRHRKQADLDLARGDFAQAAQQLWLALQALGRPLPTSNLDLACSLL
WNLIRHLLQRLWVGRWLAGRAGGLRRDCGLRMDARASARDAALVYHKLHQLHAMGKYTGGHLIASNLALSALNLAEC
AGDAVSMATLAEIYVAAALRVKTSLPRALHFLTRFFLSSARQACLAQSGSVPLAMQWLCHPVGHRFFVDGDWAVHGA
PQESLYSVAGNPVDPLAQVTRLFCEHLLERALNCIAQPSPGTADGDREFSDALGYLQLLNRCSDAVGTPACSFSVSS
SMASTTGTDPVAKWWASLTAVVIHWLRRDEEAAERLYPLVERMPHVLQETERPLPKAALYSFKAARALLDHRKVESG
PASLAICEKASGYLRDSLAAPPTGSSIDKAMQLLLCDLLLVARTSMWQRQQSPASAQVAHSASNGSQASALELRGFQ
QDLSSLRRLAQNFRPAMRRVFLHEATARLMAGASPARTHQLLDRSLRRRAGSSGKGGTVAELEPRPTWREHTEALLL
ASCYLPPAFLSAPGQQMSMLAEAARTVEKLGDHRLLLDCQQMLLRLGGGTTVTSS (SEQ ID NO: 34)

The nucleic acid sequence, or mRNA sequence, for truncated SREBF1 isoform c (GenBank Accession No. NM_001244003), e.g., SREB411, is provided below.

atggacgagctgcctttcggtgaggcggctgtggaacaggcgctggacgagctgggcgaactggacgccgcactgct
gaccgacatccaagacatgcttcagctcatcaacaaccaagacagtgacttccctggcctgtttgattcccctatg
caggggggcggggcaggagacacagagcccaccagccctggtgccaactctcctgagagcttgtcttctcctgcttcc
ctgggttcctctctggaagccttcctgggggaacccaaggcaacacctgcatccttgtcccctgtgccgtctgcatc
cactgctttaaagatgtacccgtctgtgccccccttctcccctgggcctggaatcaaagaagagccagtgccactca
ccatcctgcagcccccagcagcacagccatcaccagggaccctcctgcctccgagtttccctccaccacccctgcag
ctcagcccggctcctgtgctggggtattctagccttccttcaggcttctcagggacccttcctggaaatacccaaca
gccaccatctagcctgtcactggcctctgcaccaggagtctcgcccatctctttacacacccaggtccagagctcag
cctcccagcagccactgccagcctcaacagcccctagaacaaccactgtgacctcacagatccagcgggtcccagtc
gtactgcagccacatttcatcaaggcagattcactgctactgacaactgtaaaaacagatacaggagccacgatgaa
gacggctggcatcagtaccttagcccctggcacagccgtgcaggcaggccccttgcagaccctggtgagtggtggga
ccatcctggccacagtaccattggttgtggatacagacaaactgcccatccatcgactggcagctggcagcaaggcc
ctgggctcagctcagagccgtggtgagaagcgcacagcccacaatgccattgagaagcgctaccgttcctctatcaa
tgacaagattgtggagctcaaagacctggtggtgggcactgaggcaaagctgaataaatctgccgtcttgcgcaagg
ccatcgactatatccgcttcttacagcacagcaaccagaagctcaagcaggagaacctggccctgcgaaatgccgct
cacaaaagcaaatccctgaaggacctggtgtcggcctgtggcagtgcaggaggcacagatgtggctatggagggtgt
g (SEQ ID NO: 35)

The amino acid sequence for truncated SREBF1 isoform c (GenBank Accession No. NM_001244003), e.g., SREB411, is provided below.

MDELPFGEAAVEQALDELGELDAALLTDIQDMLQLINNQDSDFPGLFDSPYAGGGAGDTEPTSPGANSPESLSSPAS
LGSSLEAFLGEPKATPASLSPVPSASTALKMYPSVPPFSPGPGIKEEPVPLTILQPPAAQPSPGTLLPPSFPPPPLQ
LSPAPVLGYSSLPSGFSGTLPGNTQQPPSSLSLASAPGVSPISLHTQVQSSASQQPLPASTAPRTTTVTSQIQRVPV
VLQPHFIKADSLLLTTVKTDTGATMKTAGISTLAPGTAVQAGPLQTLVSGGTILATVPLVVDTDKLPIHRLAAGSKA
LGSAQSRGEKRTAHNAIEKRYRSSINDKIVELKDLVVGTEAKLNKSAVLRKAIDYIRFLQHSNQKLKQENLALRNAA
HKSKSLKDLVSACGSAGGTDVAMEGV (SEQ ID NO: 36)

In one embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity with the amino acid sequence of an isoform of SREBF1 ; e.g., SEQ ID NOs: 28, 30, 34, or 36; or differs by 1, 2, or 3 or more amino acid residues but no more than 50, 40, 30, 20, 15, or 10 amino acid residues from the amino acid sequence of an isoform of SREBF1; e.g., SEQ ID NOs: 28, 30, 34, or 36.

In one embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity with the amino acid sequence of SREBF1 ; e.g., SEQ ID NO: 34; or differs by 1, 2, or 3 or more amino acid residues but no more

than 50, 40, 30, 20, 15, or 10 amino acid residues from the amino acid sequence of SREBF1, e.g., SEQ ID NO: 34.

In another embodiment, the LMM comprises a functional fragment of SREBF1 or an isoform thereof, e.g., a truncated SREBF1. In one embodiment, the LMM comprises a functional fragment of SREBF1, e.g., a functional fragment of SEQ ID NOs: 1 or 34, or a functional fragment of an SREBF1 isoform, e.g., SEQ ID NOs: 28, 30, or 36. In one embodiment, the LMM comprises a functional domain of SREBF1, e.g., the transactivation domain of SREBF1. In one embodiment, the LMM comprises the helix-loop-helix (HLH) domain of SREBF1. In one embodiment, the LMM comprises a functional fragment of SREBF1 that is capable of translocating into the nucleus and/or capable of initiating transcription of SREBF1 target genes.

In one embodiment, the LMM comprises the N-terminal 410 amino acids of SREBF1 (also referred to herein as SREBF410), e.g., amino acids 1-410 of SEQ ID NO: 1. The amino acid sequence of the N-terminal 410 amino acids of SREBF1 is provided below:

MDELAFGEAALEQTLAEMCELDTAVLNDIEDMLQLINNQDSDFPGLFDAPYAGGETGDTGPSSPGANSPESFSSASL
ASSLEAFLGGPKVTPAPLSPPPSAPAALKMYPSVSPFSPGPGIKEEPVPLTILQPAAPQPSPGTLLPPSFPAPPVQL
SPAPVLGYSSLPSGFSGTLPGNTQQPPSSLPLAPAPGVLPTPALHTQVQSLASQQPLPASAAPRTNTVTSQVQQVPV
VLQPHFIKADSLLLTAVKTDAGATVKTAGISTLAPGTAVQAGPLQTLVSGGTILATVPLVVDTDKLPIHRLAAGSKA
LGSAQSRGEKRTAHNAIEKRYRSSINDKIVELKDLVVGTEAKLNKSAVLRKAIDYIRFLQHSNQKLKQENLTLRSAH
KSKSLKDLVSACGSGGGTDVSMEGM (SEQ ID NO:26)

In one embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity with the amino acid sequence of the N-terminal 410 amino acids of SREBF1; e.g., SEQ ID NO: 26; or differs by 1, 2, or 3 or more amino acid residues but no more than 50, 40, 30, 20, 15, or 10 amino acid residues from the amino acid sequence of the N-terminal 410 amino acids of SREBF1; e.g., SEQ ID NO: 26.

In another embodiment, the LMM comprises amino acids 91-410 of SREBF1, e.g., amino acids 91-410 of SEQ ID NO: 1. The amino acid sequence of the amino acids at positions 91-410 of SREBF1 is provided below:

MPAPLSPPPSAPAALKMYPSVSPFSPGPGIKEEPVPLTILQPAAPQPSPGTLLPPSFPAPPVQLSPAPVLGYSSLPS
GFSGTLPGNTQQPPSSLPLAPAPGVLPTPALHTQVQSLASQQPLPASAAPRTNTVTSQVQQVPVVLQPHFIKADSLL
LTAVKTDAGATVKTAGISTLAPGTAVQAGPLQTLVSGGTILATVPLVVDTDKLPIHRLAAGSKALGSAQSRGEKRTA
HNAIEKRYRSSINDKIVELKDLVVGTEAKLNKSAVLRKAIDYIRFLQHSNQKLKQENLTLRSAHKSKSLKDLVSACG
SGGGTDVSMEGM (SEQ ID NO: 27)

In one embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity with the amino acid sequence at positions 91-410 of SREBF1; e.g., SEQ ID NO: 27; or differs by 1, 2, or 3 or more amino acid residues but no more than 50, 40, 30, 20, 15, or 10 amino acid residues from the amino acid sequence at positions 91-410 of SREBF1; e.g., SEQ ID NO: 27. In one embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity with the nucleic acid sequence encoding SREBF1 or a functional fragment thereof; e.g., encoding the amino acid sequence SEQ ID NO: 1 or a functional fragment thereof. In one embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity with the nucleic acid of SEQ ID NO: 2.

In another embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity with SREBF2 or a functional fragment thereof; or differs by 1, 2, or 3 or more amino acid residues but no more than 50, 40, 30, 20, 15, or 10 amino acid residues from SREBF2 or a functional fragment thereof.

In one embodiment, the LMM comprises an enzyme. In one embodiment, the LMM comprises an enzyme that converts saturated fatty acids to unsaturated fatty acids. In one embodiment, the LMM comprises an enzyme that converts saturated fatty acids to monounsaturated fatty acids, e.g., fatty acids with one double bond. In one embodiment, the LMM comprises an enzyme that converts saturated fatty acids to polyunsaturated fatty acids, e.g., fatty acids with more than one, e.g., 2, 3, 4, 5, or more, double bonds. In one embodiment, the LMM comprises stearoyl CoA desaturase 1 (SCD1), stearoyl CoA desaturase 2 (SCD2), stearoyl CoA desaturase 3 (SCD3), stearoyl CoA desaturase 4 (SCD4), stearoyl CoA desaturase 5 (SCD5), an isoform thereof, or a functional fragment thereof.

SCD1 is the rate limiting enzyme responsible for the conversion of saturated fatty acids (SFA) to monounsaturated fatty acids (MUFA). Increased focus has been placed upon SCD1 in recent years due to studies linking expression of this gene to increased cell survival, proliferation and tumorigenesis properties (Angelucci, Maulucci et al. 2015) (Igal 2011). SCD1 has also been shown to play key roles in both cellular metabolic rate control and overall lipogenesis. The latter is controlled through direct interactions with a major biosynthetic pathway regulator acetyl-CoA carboxylase (ACC) as well as conversion of SFA to MUFA

which, since SFA is known to inhibit ACC, facilitates enzyme functionality to increase lipid biosynthesis (Igal 2010). The main regulation of SCD1 is through transcriptional activation whereby transcription factors, such as SREBF1, bind to the SRE sequence in the promoter region of the gene. SCD1 is endogenously located in the ER as a membrane integral protein, where SCD1 carries out its enzymatic function of catalyzing the conversion of SFA to MUFA. Its role in conversion of SFA to MUFA (e.g., upregulation of the ratio of MUFA to SFA) can regulate a decrease in lipid raft domains, which can in turn result in increased membrane fluidity. This change in membrane fluidity and membrane lipid composition may also have implications in vesicle formation and thus cellular communication and ER size or morphology (e.g., ER expansion). Knockdown of the SCD1 gene has also been shown to upregulate the unfolded protein response (Ariyama, Kono et al. 2010). Furthermore, SCD1 negatively regulates cellular palmitic acid which, in turn, is a strong negative regulator of ACC. SCD1 also controls the phosphorylation status of AMP activated protein kinase (AMPK), consequentially reducing its ability to phosphorylate and therefore inhibit ACC; a rate-limiting enzyme in the lipid synthesizing process. Lastly, desaturation of SFA prevents its accumulation which can cause cell death. As such, modulation of SCD1 results in increased lipid biosynthesis, cell survival and proliferation rates. (Hagen, Rodriguez-Cuenca et al.), (Scaglia, Chisholm et al. 2009).

In one embodiment, the LMM comprises SCD1. The amino acid sequence of SCD1 is provided below:

MPAHMLQEISSSYTTTTTITAPPSGNEREKVKTVPLHLEEDIRPEMKEDIHDPTYQDEEGPPPKLEYVWRN
IILMVLLHLGGLYGIILVPSCKLYTCLFGIFYYMTSALGITAGAHRLWSHRTYKARLPLRIFLIIANTMAF
QNDVYEWARDHRAHHKFSETHADPHNSRRGFFFSHVGWLLVRKHPAVKEKGGKLDMSDLKAEKLVMFQRRY
YKPGLLLMCFILPTLVPWYCWGETFVNSLFVSTFLRYTLVLNATWLVNSAAHLYGYRPYDKNIQSRENILV
SLGAVGEGFHNYHHTFPFDYSASEYRWHINFTTFFIDCMAALGLAYDRKKVSKATVLARIKRTGDGSHKSS
(SEQ ID NO: 3)

The nucleotide sequence of SCD1 is provided below:

atgccggcccacatgctccaagagatctccagttcttacacgaccaccaccaccatcactgcacctccctcc
ggaaatgaacgagagaaggtgaagacggtgcccctccacctggaagaagacatccgtcctgaaatgaaagaa
gatattcacgaccccacctatcaggatgaggagggaccccgcccaagctggagtacgtctggaggaacatc
attctcatggtcctgctgcacttgggaggcctgtacgggatcatactggttccctcctgcaagctctacacc
tgcctcttcgggattttctactacatgaccagcgctctgggcatcacagccggggctcatcgcctctggagc
cacagaacttacaaggcacggctgcccctgcggatcttccttatcattgccaacaccatggcgttccagaat
gacgtgtacgaatgggcccgagatcaccgcgcccaccacaagttctcagaaacacacgccgaccctcacaat
tcccgccgtggcttcttcttctctcacgtgggttggctgcttgtgcgcaaacacccggctgtcaaagagaag
ggcggaaaactggacatgtctgacctgaaagccgagaagctggtgatgttccagaggaggtactacaagccc
ggcctcctgctgatgtgcttcatcctgcccacgctggtgccctggtactgctggggcgagacttttgtaaac

agcctgttcgttagcaccttcttgcgatacactctggtgctcaacgccacctggctggtgaacagtgccgcg
catctctatggatatcgcccctacgacaagaacattcaatcccgggagaatatcctggtttccctgggtgcc
gtgggcgagggcttccacaactaccaccacaccttcccctttcgactactctgccagtgagtaccgctggcac
atcaacttcaccacgttcttcatcgactgcatggctgccctgggcctggcttacgaccggaagaaagtttct
aaggctactgtcttagccaggattaagagaactggagacgg gagtcacaagagtagctga
(SEQ ID NO: 4)

In one embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity with the amino acid sequence of SCD1; e.g., SEQ ID NO: 3; or differs by 1, 2, or 3 or more amino acid residues but no more than 50, 40, 30, 20, 15, or 10 amino acid residues from the amino acid sequence of SCD1, e.g., SEQ ID NO: 3. In one embodiment, the LMM comprises a functional fragment of SCD1, e.g., a functional fragment of SEQ ID NO: 3.

In one embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity with the nucleic acid sequence encoding SCD1 or a functional fragment thereof; e.g., encoding the amino acid sequence SEQ ID NO: 3 or a functional fragment thereof. In one embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity with the nucleic acid of SEQ ID NO: 4.

In another embodiment, the LMM comprises at least 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity with the amino acid sequence of SCD2, SCD3, SCD4, SCD5, or a functional fragment thereof; or differs by 1, 2, or 3 or more amino acid residues but no more than 50, 40, 30, 20, 15, or 10 amino acid residues from the amino acid sequence of SCD2, SCD3, SCD4, SCD5, or a functional fragment thereof. In another embodiment, the LMM comprises at least

In another embodiment, the LMM comprises a functional fragment of SCD1, SCD2, SCD3, SCD4, or SCD5, e.g., a truncated SCD1, SCD2, SCD3, SCD4, or SCD5. In one embodiment, the LMM comprises a functional fragment of SCD1, SCD2, SCD3, SCD4, or SCD5, e.g., a functional fragment of SEQ ID NO: 3. In one embodiment, the LMM comprises a functional domain of SCD1, SCD2, SCD3, SCD4, or SCD5, e.g., a domain having enzymatic activity for converting saturated fatty acids to monounsaturated fatty acids.

Percent identity in the context of two or more amino acid or nucleic acid sequences, refers to two or more sequences that are the same. Two sequences are "substantially identical" if two sequences have a specified percentage of amino acid residues or nucleotides that are the

same (e.g., 60% identity, optionally 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identity over a specified region, or, when not specified, over the entire sequence, when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. In some embodiments, alignment may result in gaps or inserted sequences, in which sequence similarity can be determined for specified regions flanking the gaps or inserted sequences, or sequence similarity can be determined across a region that includes the gaps or inserted sequences. Optionally, the identity exists over a region that is at least about 50 amino acids or nucleotides, 100 amino acids or nucleotides, 150 amino acids or nucleotides, in length. More preferably, the identity exists over a region that is about 200 or more amino acids or nucleotides, or about 500 or 1000 or more amino acids or nucleotides, in length.

For sequence comparison, one sequence typically acts as a reference sequence, to which one or more test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith and Waterman, (1970) Adv. Appl. Math. 2:482c, by the homology alignment algorithm of Needleman and Wunsch, (1970) J. Mol. Biol. 48:443, by the search for similarity method of Pearson and Lipman, (1988) Proc. Nat'l. Acad. Sci. USA 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Brent et al., (2003) Current Protocols in Molecular Biology). Multiple sequence alignments can be performed by algorithms such as ClustalW, Clustal Omega, and MAFFT. Other algorithms for comparing relationships between two or more sequences include the Hidden Markov models. A hidden Markov Model is a model that describes the probability of a having a

particular nucleotide (or amino acid) type following another (the probability path being hidden). It is really a probabilistic model not an algorithm. Example of an algorithm (or program implementing the algorithm) might be HMMER (http://hmmer.org/).

Two examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., (1977) Nuc. Acids Res. 25:3389-3402; and Altschul et al., (1990) J. Mol. Biol. 215:403-410, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (NCBI).

PRODUCTS

Provided herein are methods and compositions for engineering or making a cell or a cell-free expression system capable of producing high yields of a product and/or improved product quality. Products described herein include polypeptides, e.g., recombinant proteins; nucleic acid molecules, e.g., DNA or RNA molecules; multimeric proteins or complexes; lipid-encapsulated particles, e.g., virus-like particles, vesicles, or exosomes; or other molecules, e.g., lipids. In an embodiment, the product is a polypeptide, e.g., a recombinant polypeptide. In an embodiment, the product is an exosome. For example, the recombinant polypeptide can be a difficult to express protein or a protein having complex and/or non-natural structures, such as a next generation biologic, e.g., a bispecific antibody molecule, a fusion protein, or a glycosylated protein.

In embodiments, the cell or cell line generated by the methods or compositions described herein produces a product, e.g., a recombinant polypeptide, useful in the treatment of a medical condition, disorder or disease. Examples of medical conditions, disorders or diseases include, but are not limited to, metabolic disease or disorders (e.g., metabolic enzyme deficiencies), endocrine disorders (e.g., hormone deficiencies), dysregulation of hemostasis, thrombosis, hematopoietic disorders, pulmonary disorders, gastro-intestinal disorders, autoimmune diseases, immuno-dysregulation (e.g., immunodeficiency), infertility, transplantation, cancer, and infectious diseases.

In embodiments, the product is an exogenous protein, e.g., a protein that is not naturally expressed by the cell. In one embodiment, the protein is from one species while the cell is from a different species. In another embodiment, the protein is a non-naturally occurring protein.

In other embodiments, the product is a protein that is endogenously expressed by the cell. In one embodiment, the product is a protein that is endogenously expressed by the cell at endogenous or natural levels. The present methods and compositions described herein are used to increase the production and quality of the endogenous product, e.g., a naturally occurring product that is naturally produced by the cell. In another embodiment, an exogenous nucleic acid encoding the product, e.g., protein, is introduced to and expressed by the cell. In another embodiment, an exogenous nucleic acid that increases the expression of a product that is endogenously expressed by the cell is introduced into the cell. By way of example, the exogenous nucleic acid comprises a sequence that activates the promoter (e.g., SRF promoter sequence, see e.g., The transcription factor Ap-1 regulates monkey 20α-hydroxysteroid dehydrogenase promoter activity in CHO cells. Nanjidsuren T, Min KS. BMC Biotechnol. 2014 Jul 30;14:71. doi: 10.1186/1472-6750-14-71.PMID: 25073972) that controls the expression of an endogenous product of the cell.

The recombinant product can be a therapeutic product or a diagnostic product, e.g., useful for drug screening. The therapeutic or diagnostic product can include, but is not limited to, an antibody molecule, e.g., an antibody or an antibody fragment, a fusion protein, a hormone, a cytokine, a growth factor, an enzyme, a glycoprotein, a lipoprotein, a reporter protein, a therapeutic peptide, or a structural and/or functional fragment or hybrid of any of these. In other embodiments, the therapeutic or diagnostic product is a synthetic polypeptide, e.g., wherein the entire polypeptide or portions thereof is not derived from or has any sequence or structural similarity to any naturally occurring polypeptide, e.g., a naturally occurring polypeptide described above.

In one embodiment, the recombinant product is an antibody molecule. In one embodiment, the recombinant product is a therapeutic antibody molecule. In another embodiment, the recombinant product is a diagnostic antibody molecule, e.g., a monoclonal antibody useful for imaging techniques or diagnostic tests.

An antibody molecule, as used herein, is a protein, or polypeptide sequence derived from an immunoglobulin molecule which specifically binds with an antigen. In an embodiment, the antibody molecule is a full-length antibody or an antibody fragment. Antibodies and multiformat proteins can be polyclonal or monoclonal, multiple or single chain, or intact immunoglobulins, and may be derived from natural sources or from recombinant sources. Antibodies can be

tetramers of immunoglobulin molecules. In an embodiment, the antibody is a monoclonal antibody. The antibody may be a human or humanized antibody. In one embodiment, the antibody is an IgA, IgG, IgD, or IgE antibody. In one embodiment, the antibody is an IgG1, IgG2, IgG3, or IgG4 antibody.

"Antibody fragment" refers to at least one portion of an intact antibody, or recombinant variants thereof, and refers to the antigen binding domain, e.g., an antigenic determining variable region of an intact antibody, that is sufficient to confer recognition and specific binding of the antibody fragment to a target, such as an antigen. Examples of antibody fragments include, but are not limited to, Fab, Fab', $F(ab')_2$, and Fv fragments, scFv antibody fragments, linear antibodies, single domain antibodies such as sdAb (either VL or VH), camelid VHH domains, and multi-specific antibodies formed from antibody fragments such as a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region, and an isolated CDR or other epitope binding fragments of an antibody. An antigen binding fragment can also be incorporated into single domain antibodies, maxibodies, minibodies, nanobodies, intrabodies, diabodies, triabodies, tetrabodies, v-NAR and bis-scFv (see, e.g., Hollinger and Hudson, Nature Biotechnology 23:1126-1136, 2005). Antigen binding fragments can also be grafted into scaffolds based on polypeptides such as a fibronectin type III (Fn3)(see U.S. Patent No.: 6,703,199, which describes fibronectin polypeptide minibodies).

Exemplary recombinant products that can be produced using the methods described herein include, but are not limited to, those provided in the tables below.

Table 2. Exemplary Recombinant Products

Therapeutic Protein type	Therapeutic	Trade Name
Hormone	Erythropoietin, Epoein-α Darbepoetin–α Insulin Growth hormone (GH), somatotropin Human follicle-stimulating hormone (FSH) Human chorionic gonadotropin Lutropin-α Glucagon Growth hormone releasing hormone (GHRH) Secretin Thyroid stimulating hormone	Epogen, Procrit Aranesp Humulin, Novolin Genotropin , Humatrope, Norditropin, NovIVitropin, Nutropin, Omnitrope, Protropin, Siazen, Serostim, Valtropin Gonal-F, Follistim Ovidrel Luveris GlcaGen Geref ChiRhoStim (human peptide), SecreFlo (porcine peptide) Thyrogen

	(TSH), thyrotropin	
Blood Clotting/Coagulation Factors	Factor VIIa Factor VIII Factor IX Antithrombin III (AT-III) Protein C concentrate	NovoSeven Bioclate, Helixate, Kogenate, Recombinate, ReFacto Benefix Thrombate III Ceprotin
Cytokine/Growth factor	Type I alpha-interferon Interferon-αn3 (IFNαn3) Interferon-β1a (rIFN- β) Interferon-β1b (rIFN- β) Interferon-γ1b (IFN γ) Aldesleukin (interleukin 2(IL2), epidermal theymocyte activating factor; ETAF Palifermin (keratinocyte growth factor; KGF) Becaplemin (platelet-derived growth factor; PDGF) Anakinra (recombinant IL1 antagonist)	Infergen Alferon N Avonex, Rebif Betaseron Actimmune Proleukin Kepivance RegranexAnril, Kineret
Antibody molecules	Bevacizumab (VEGFA mAb) Cetuximab (EGFR mAb) Panitumumab (EGFR mAb) Alemtuzumab (CD52 mAb) Rituximab (CD20 chimeric Ab) Trastuzumab (HER2/Neu mAb) Abatacept (CTLA Ab/Fc fusion) Adalimumab (TNFα mAb) Infliximab (TNFα chimeric mAb) Alefacept (CD2 fusion protein) Efalizumab (CD11a mAb) Natalizumab (integrin α4 subunit mAb) Eculizumab (C5mAb) Muromonab-CD3	Avastin Erbitux Vectibix Campath Rituxan Herceptin Orencia Humira Remicade Amevive Raptiva Tysabri Soliris Orthoclone, OKT3
Other: Fusion proteins/Protein vaccines/Peptides	Hepatitis B surface antigen (HBsAg) HPV vaccine OspA Anti-Rhesus(Rh) immunoglobulin G Enfuvirtide Spider silk, e.g., fibrion Etanercept (TNF receptor/Fc fusion) Cergutuzumab Amunaleukin	Engerix, Recombivax HB Gardasil LYMErix Rhophylac Fuzeon QMONOS Enbrel

Table 3. Additional Exemplary Recombinant Products: Bispecific Formats

Name (other names, sponsoring organizations)	BsAb format	Targets	Proposed mechanisms of action	Development stages	Diseases (or healthy volunteers)
Catumaxomab (Removab®, Fresenius Biotech, Trion Pharma, Neopharm)	BsIgG: Triomab	CD3, EpCAM	Retargeting of T cells to tumor, Fc mediated effector functions	Approved in EU	Malignant ascites in EpCAM positive tumors
Ertumaxomab (Neovii Biotech, Fresenius Biotech)	BsIgG: Triomab	CD3, HER2	Retargeting of T cells to tumor	Phase I/II	Advanced solid tumors
Blinatumomab (Blincyto®, AMG 103, MT 103, MEDI 538, Amgen)	BiTE	CD3, CD19	Retargeting of T cells to tumor	Approved in USA Phase II and III Phase II Phase I	Precursor B-cell ALL ALL DLBCL NHL
REGN1979 (Regeneron)	BsAb	CD3, CD20			
Solitomab (AMG 110, MT110, Amgen)	BiTE	CD3, EpCAM	Retargeting of T cells to tumor	Phase I	Solid tumors
MEDI 565 (AMG 211, MedImmune, Amgen)	BiTE	CD3, CEA	Retargeting of T cells to tumor	Phase I	Gastrointestinal adenocancinoma
RO6958688 (Roche)	BsAb	CD3, CEA			
BAY2010112 (AMG 212, Bayer; Amgen)	BiTE	CD3, PSMA	Retargeting of T cells to tumor	Phase I	Prostate cancer
MGD006 (Macrogenics)	DART	CD3, CD123	Retargeting of T cells to tumor	Phase I	AML
MGD007 (Macrogenics)	DART	CD3, gpA33	Retargeting of T cells to tumor	Phase I	Colorectal cancer
MGD011 (Macrogenics)	DART	CD19, CD3			
SCORPION (Emergent Biosolutions, Trubion)	BsAb	CD3, CD19	Retargeting of T cells to tumor		
AFM11 (Affimed Therapeutics)	TandAb	CD3, CD19	Retargeting of T cells to tumor	Phase I	NHL and ALL
AFM12 (Affimed Therapeutics)	TandAb	CD19, CD16	Retargeting of NK cells to tumor cells		
AFM13 (Affimed Therapeutics)	TandAb	CD30, CD16A	Retargeting of NK cells to tumor cells	Phase II	Hodgkin's Lymphoma
GD2 (Barbara Ann Karmanos Cancer Institute)	T cells preloaded with BsAb	CD3, GD2	Retargeting of T cells to tumor	Phase I/II	Neuroblastoma and osteosarcoma
pGD2 (Barbara Ann Karmanos Cancer	T cells preloaded	CD3, Her2	Retargeting of T cells to tumor	Phase II	Metastatic breast cancer

Name (other names, sponsoring organizations)	BsAb format	Targets	Proposed mechanisms of action	Development stages	Diseases (or healthy volunteers)
Institute)	with BsAb				
EGFRBi-armed autologous activated T cells (Roger Williams Medical Center)	T cells preloaded with BsAb	CD3, EGFR	Autologous activated T cells to EGFR-positive tumor	Phase I	Lung and other solid tumors
Anti-EGFR-armed activated T-cells (Barbara Ann Karmanos Cancer Institute)	T cells preloaded with BsAb	CD3, EGFR	Autologous activated T cells to EGFR-positive tumor	Phase I	Colon and pancreatic cancers
rM28 (University Hospital Tübingen)	Tandem scFv	CD28, MAPG	Retargeting of T cells to tumor	Phase II	Metastatic melanoma
IMCgp100 (Immunocore)	ImmTAC	CD3, peptide MHC	Retargeting of T cells to tumor	Phase I/II	Metastatic melanoma
DT2219ARL (NCI, University of Minnesota)	2 scFv linked to diphtheria toxin	CD19, CD22	Targeting of protein toxin to tumor	Phase I	B cell leukemia or lymphoma
XmAb5871 (Xencor)	BsAb	CD19, CD32b			
NI-1701 (NovImmune)	BsAb	CD47, CD19			
MM-111 (Merrimack)	BsAb	ErbB2, ErbB3			
MM-141 (Merrimack)	BsAb	IGF-1R, ErbB3			
NA (Merus)	BsAb	HER2, HER3			
NA (Merus)	BsAb	CD3, CLEC12A			
NA (Merus)	BsAb	EGFR, HER3			
NA (Merus)	BsAb	PD1, undisclosed			
NA (Merus)	BsAb	CD3, undisclosed			
Duligotuzumab (MEHD7945A, Genentech, Roche)	DAF	EGFR, HER3	Blockade of 2 receptors, ADCC	Phase I and II Phase II	Head and neck cancer Colorectal cancer
LY3164530 (Eli Lily)	Not disclosed	EGFR, MET	Blockade of 2 receptors	Phase I	Advanced or metastatic cancer
MM-111 (Merrimack Pharmaceuticals)	HSA body	HER2, HER3	Blockade of 2 receptors	Phase II Phase I	Gastric and esophageal cancers Breast cancer
MM-141, (Merrimack Pharmaceuticals)	IgG-scFv	IGF-1R, HER3	Blockade of 2 receptors	Phase I	Advanced solid tumors

Name (other names, sponsoring organizations)	BsAb format	Targets	Proposed mechanisms of action	Development stages	Diseases (or healthy volunteers)
RG7221 (RO5520985, Roche)	CrossMab	Ang2, VEGF A	Blockade of 2 proangiogenics	Phase I	Solid tumors
RG7716 (Roche)	CrossMab	Ang2, VEGF A	Blockade of 2 proangiogenics	Phase I	Wet AMD
OMP-305B83 (OncoMed)	BsAb	DLL4/VEGF			
TF2 (Immunomedics)	Dock and lock	CEA, HSG	Pretargeting tumor for PET or radioimaging	Phase II	Colorectal, breast and lung cancers
ABT-981 (AbbVie)	DVD-Ig	IL-1α, IL-1β	Blockade of 2 proinflammatory cytokines	Phase II	Osteoarthritis
ABT-122 (AbbVie)	DVD-Ig	TNF, IL-17A	Blockade of 2 proinflammatory cytokines	Phase II	Rheumatoid arthritis
COVA322	IgG-fynomer	TNF, IL17A	Blockade of 2 proinflammatory cytokines	Phase I/II	Plaque psoriasis
SAR156597 (Sanofi)	Tetravalent bispecific tandem IgG	IL-13, IL-4	Blockade of 2 proinflammatory cytokines	Phase I	Idiopathic pulmonary fibrosis
GSK2434735 (GSK)	Dual-targeting domain	IL-13, IL-4	Blockade of 2 proinflammatory cytokines	Phase I	(Healthy volunteers)
Ozoralizumab (ATN103, Ablynx)	Nanobody	TNF, HSA	Blockade of proinflammatory cytokine, binds to HSA to increase half-life	Phase II	Rheumatoid arthritis
ALX-0761 (Merck Serono, Ablynx)	Nanobody	IL-17A/F, HSA	Blockade of 2 proinflammatory cytokines, binds to HSA to increase half-life	Phase I	(Healthy volunteers)
ALX-0061 (AbbVie, Ablynx;	Nanobody	IL-6R, HSA	Blockade of proinflammatory cytokine, binds to HSA to increase half-life	Phase I/II	Rheumatoid arthritis
ALX-0141 (Ablynx, Eddingpharm)	Nanobody	RANKL, HSA	Blockade of bone resorption, binds to HSA to increase half-life	Phase I	Postmenopausal bone loss
RG6013/ACE910 (Chugai, Roche)	ART-Ig	Factor IXa, factor X	Plasma coagulation	Phase II	Hemophilia

In one embodiment, the product differs from a polypeptide from Table 2 or 3 at no more than 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 amino acid residues. In another

embodiment, the product differs from a polypeptide from Table 2 or 3 at no more than 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, or 15% of its amino acid residues.

In one embodiment, the product is a nucleic acid molecule, e.g., a DNA or RNA molecule, or hybrid thereof. In one embodiment, the product is an origami nucleic acid molecule, e.g., an origami DNA, in which the nucleic acid molecule has a predetermined secondary, tertiary, or quaternary structure. In one embodiment, the origami nucleic acid molecule has functional activity. In one embodiment, the product comprises an origami nucleic acid molecule encapsulated in a lipid membrane. In one embodiment, the lipid membrane comprises the cell membrane or components of the cell membrane of the host cell from which it was produced. In one embodiment, the lipid-encapsulated DNA is as described in "Cloaked DNA nanodevices survive pilot mission", April 22, 2014, Wyss Institute for Biologically Inspired Engineering at Harvard University website.

Other recombinant products include non-antibody scaffolds or alternative protein scaffolds, such as, but not limited to: DARPins, affibodies and adnectins.

Other exemplary therapeutic or diagnostic proteins include, but are not limited to any protein described in Tables 1-10 of Leader et al., "Protein therapeutics: a summary and pharmacological classification", Nature Reviews Drug Discovery, 2008, 7:21-39 and as described in Walsh, "Biopharmaceutical benchmarks 2014", Nature Biotechnology, 2014, 32:992-1000; or any conjugate, variant, analog, or functional fragment of the recombinant polypeptides described herein.

NUCLEIC ACIDS

Also provided herein are nucleic acids, e.g., exogenous nucleic acids, that encode the lipid metabolism modulators and the recombinant products described herein. The nucleic acid sequences coding for the desired LMM or recombinant product, e.g., recombinant polypeptides, can be obtained using recombinant methods known in the art, such as, for example by screening libraries from cells expressing the desired nucleic acid sequence, e.g., gene, by deriving the nucleic acid sequence from a vector known to include the same, or by isolating directly from cells and tissues containing the same, using standard techniques. Alternatively, the nucleic acid encoding the LMM or recombinant polypeptide can be produced synthetically, rather than cloned. Recombinant DNA techniques and technology are highly advanced and well established

Date reçue / Date received 2021-12-13

in the art. Accordingly, the ordinarily skilled artisan having the knowledge of the amino acid sequence of a recombinant polypeptide described herein can readily envision or generate the nucleic acid sequence that would encode the LMM or the recombinant polypeptide.

Exemplary nucleic acid sequences encoding the LMM SREBF1 and SCD1 are provided as SEQ ID NO: 3 and SEQ ID NO: 4, respectively, herein.

The expression of a desired polypeptide, e.g., a LMM or a recombinant polypeptide, is typically achieved by operably linking a nucleic acid encoding the desired polypeptide or portions thereof to a promoter, and incorporating the construct into an expression vector. The vectors can be suitable for replication and integration into eukaryotic or prokaryotic cells. Typical cloning vectors contain other regulatory elements, such as transcription and translation terminators, initiation sequences, promoters, selection markers, or tags useful for regulation or identification of the expression of the desired nucleic acid sequence.

The nucleic acid sequence encoding the LMM or recombinant polypeptide can be cloned into a number of types of vectors. For example, the nucleic acid can be cloned into a vector including, but not limited to a plasmid, a phagemid, a phage derivative, an animal virus, and a cosmid. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors, and sequencing vectors. In embodiments, the expression vector may be provided to a cell in the form of a viral vector. Viral vector technology is well known in the art and is described, for example, in Sambrook et al., 2012, MOLECULAR CLONING: A LABORATORY MANUAL, volumes 1 -4, Cold Spring Harbor Press, NY), and in other virology and molecular biology manuals. Viruses, which are useful as vectors include, but are not limited to, retroviruses, adenoviruses, adeno- associated viruses, herpes viruses, and lentiviruses. In general, a suitable vector contains an origin of replication functional in at least one organism, a promoter sequence, convenient restriction endonuclease sites, and one or more selectable markers, (e.g., WO 01/96584; WO 01/29058; and U.S. Pat. No. 6,326,193). Vectors derived from viruses are suitable tools to achieve long-term gene transfer since they allow long-term, stable integration of a transgene and its propagation in daughter cells.

A vector may also include, in any of the embodiments described herein, one or more of the following: a signal sequence to facilitate secretion, a polyadenylation signal, a transcription terminator (e.g., from Bovine Growth Hormone (BGH) gene), an element allowing episomal replication and replication in prokaryotes (e.g. SV40 origin and ColE1 or others known in the

art), and/or elements to allow selection, e.g., a selection marker or a reporter gene.

In one embodiment, the vector comprising a nucleic acid sequence encoding a polypeptide, e.g., a LMM or a recombinant polypeptide, further comprises a promoter sequence responsible for the recruitment of polymerase to enable transcription initiation for expression of the polypeptide, e.g., the LMM or recombinant polypeptide. In one embodiment, promoter sequences suitable for the methods described herein are usually associated with enhancers to drive high amounts of transcription and hence deliver large copies of the target exogenous mRNA. In an embodiment, the promoter comprises cytomegalovirus (CMV) major immediate early promoters (Xia, Bringmann et al. 2006) and the SV40 promoter (Chernajovsky, Mory et al. 1984), both derived from their namesake viruses or promoters derived therefrom. Several other less common viral promoters have been successfully employed to drive transcription upon inclusion in an expression vector in mammalian cells including *Rous Sarcoma* virus long terminal repeat (RSV-LTR) and *Moloney murine leukemia* virus (MoMLV) LTR (Papadakis, Nicklin et al. 2004). In another embodiment, specific endogenous mammalian promoters can be utilized to drive constitutive transcription of a gene of interest (Pontiller, Gross et al. 2008). The CHO specific Chinese Hamster elongation factor 1-alpha (CHEF1α) promoter has provided a high yielding alternative to viral based sequences (Deer, Allison 2004).

Other promoters suitable for expression in non-mammalian cells, e.g., fungi, insect, and plant cells, are also known in the art. Examples of suitable promoters for directing transcription in a fungal or yeast host cell include, but are not limited to, promoters obtained from the fungal genes of *Trichoderma Reesei*, methanol-inducible alcohol oxidase (AOX promoter), *Aspergillus nidulans* tryptophan biosynthesis (trpC promoter), *Aspergillus niger var. awamori* flucoamylase (*glaA*), *Saccharomyces cerevisiae* galactokinase (GAL1), *Kluyveromyces lactis* Plac4-PBI promoter, or those described in PCT Publication WO 2005/100573. Examples of suitable promoters for directing transcription in an insect cell include, but are not limited to, T7 lac promoter and polyhedrin promoter. An example of a suitable promoter for directing transcription in a plant cell includes, but is not limited to, the cauliflower mosaic virus promoter CaMV35S. Examples of suitable promoters for directing transcription of the nucleic acid constructs of the present invention in a prokaryotic host cell, e.g., a bacterial cell, are the promoters obtained from the *E. coli* lac operon, *E. coli* tac promoter (hybrid promoter, DeBoer et al, PNAS, 1983, 80:21-25), *E. coli* rec A, *E. coli* araBAD, *E. coli* tetA, and prokaryotic beta-

lactamase. Other examples of suitable promoters include viral promoters, such as promoters from bacteriophages, including a T7 promoter, a T5 promoter, a T3 promoter, an M13 promoter, and a SP6 promoter.

In addition to promoters, the vectors described herein may further comprise an enhancer region as described above; a specific nucleotide motif region, proximal to the core promoter, which can recruit transcription factors to upregulate the rate of transcription (Riethoven 2010). Similar to promoter sequences, these regions are often derived from viruses and are encompassed within the promoter sequence such as hCMV and SV40 enhancer sequences, or may be additionally included such as adenovirus derived sequences (Gaillet, Gilbert et al. 2007).

In one embodiment, the vector comprising a nucleic acid sequence encoding a polypeptide, e.g., a LMM or a recombinant product, described herein further comprises a nucleic acid sequence that encodes a selection marker. In one embodiment, the selectable marker comprises glutamine synthetase (GS); dihydrofolate reductase (DHFR) e.g., an enzyme which confers resistance to methotrexate (MTX); or an antibiotic marker, e.g., an enzyme that confers resistance to an antibiotic such as: hygromycin, neomycin (G418), zeocin, puromycin, or blasticidin.

In one embodiment, the vector comprising a nucleic acid sequence encoding a recombinant product described herein comprises a selection marker that is useful in identifying a cell or cells containing the nucleic acid encoding a recombinant product described herein. In another embodiment, the selection marker is useful in identifying or selecting a cell or cells that containing the integration of the nucleic acid sequence encoding the recombinant product into the genome, as described herein. The identification of a cell or cells that have integrated the nucleic acid sequence encoding the recombinant protein can be useful for the selection and engineering of a cell or cell line that stably expresses the product.

In one embodiment, the vector comprising a nucleic acid sequence encoding a LMM described herein comprises a mechanism for site-specific integration of the nucleic acid sequence encoding the LMM. For example, the vector is compatible with the Flp-In™ system and comprises two FRT sites (comprising a specific nucleotide sequence) that, in the presence of Flp recombinase, directs the recombination and subsequent integration of the desired sequence, e.g., the nucleic acid sequence encoding the LMM, at the desired site, e.g., between the two FRT sites, present in the genome of a Flp-In cell, e.g., a Flp-In CHO cell. Other systems used for site-

specific integration of nucleic acids encoding a desired product are known in art, e.g., the Cre-lox recombinase system, or CRISPR/CAS-mediated strategies.

Suitable vectors for use are commercially available, and include vectors associated with the GS Expression System™, GS Xceed™ Gene Expression System, or Potelligent® CHOK1SV technology available from Lonza Biologics, Inc, e.g., pCon vectors. Additional vectors include, but are not limited to, other commercially available vectors, such as, pcDNA3.1/Zeo, pcDNA3.1/CAT, pcDNA3.3TOPO (Thermo Fisher, previously Invitrogen); pTarget, HaloTag (Promega); pUC57 (GenScript); pFLAG-CMV (Sigma-Aldrich); pCMV6 (Origene); or pBK-CMV/ pCMV-3Tag-7/ pCMV-Tag2B (Stratagene).

CELLS AND CELL CULTURE

In one aspect, the present disclosure relates to methods and compositions for engineering or making a cell or cell line that produces a product, e.g., a recombinant polypeptide as described herein. In another aspect, the present disclosure relates to methods and compositions for engineering or making a cell or cell line with improved, e.g., increased productivity and product quality. Characteristics associated with improved productivity and product quality are described herein, for example, in the section titled "Modulation of Lipid Metabolism".

In embodiments, the cell is a mammalian or non-mammalian cell, e.g., an insect cell, a yeast cell, a fungal cell, a plant cell, an archaeal cell, e.g., a cell from a species of *Archaea*, or a bacterial cell. In an embodiment, the cell is from human, mouse, rat, Chinese hamster, Syrian hamster, monkey, ape, dog, duck, horse, parrot, ferret, fish or cat. In an embodiment, the cell is an animal cell. In embodiments, the cell is a mammalian cell, e.g., a human cell or a rodent cell, e.g., a hamster cell, a mouse cell, or a rat cell. In an embodiment, the cell is a prokaryotic cel, e.g., a bacterial cell. In an embodiment, the cell is a species of Actinobacteria, e.g., *Mycobacterium tuberculosis*).

In one embodiment, the cell is a Chinese hamster ovary (CHO) cell. In one embodiment, the cell is a , CHO-K1, CHOK1SV, Potelligent CHOK1SV (FUT8-KO), CHO GS-KO, Exceed (CHOK1SV GS-KO), CHO-S, CHO DG44, CHO DXB11, CHOZN, or a CHO-derived cell. The CHO FUT8 knockout cell is, for example, the Potelligent® CHOK1 SV (Lonza Biologics, Inc.).

In another embodiment, the cell is a HeLa, HEK293, HT1080, H9, HepG2, MCF7, Jurkat, NIH3T3, PC12, PER.C6, BHK (baby hamster kidney cell), VERO, SP2/0, NS0, YB2/0, Y0, EB66, C127, L cell, COS, e.g., COS1 and COS7, QC1-3, , CHO-K1, CHOK1SV,

Potelligent CHOK1SV (FUT8-KO), CHO GS-KO, Exceed (CHOK1SV GS-KO), CHO-S, CHO DG44, CHO DXB11, CHOZN, or a CHO-derived cell, or any cells derived therefrom. In one embodiment, the cell is a stem cell. In one embodiment, the cell is a differentiated form of any of the cells described herein. In one embodiment, the cell is a cell derived from any primary cell in culture.

In an embodiment, the cell is any one of the cells described herein that produces a product, e.g., a product as described herein. In an embodiment, the cell is any one of the cells described herein that comprises an exogenous nucleic acid encoding a recombinant polypeptide, e.g., expresses a recombinant polypeptide, e.g., a recombinant polypeptide selected from Table 2 or 3.

In an embodiment, the cell culture is carried out as a batch culture, fed-batch culture, draw and fill culture, or a continuous culture. In an embodiment, the cell culture is an adherent culture. In an embodiment, the cell culture is a suspension culture. In one embodiment, the cell or cell culture is placed *in vivo* for expression of the recombinant polypeptide, e.g., placed in a model organism or a human subject.

In one embodiment, the culture medium is free of serum.

Other suitable media and culture methods for mammalian cell lines are well-known in the art, as described in U.S. Pat. No. 5,633,162 for instance. Examples of standard cell culture media for laboratory flask or low density cell culture and being adapted to the needs of particular cell types are for instance: Roswell Park Memorial Institute (RPMI) 1640 medium (Morre, G., The Journal of the American Medical Association, 199, p. 519 f. 1967), L-15 medium (Leibovitz, A. et al., Amer. J. of Hygiene, 78, 1p. 173 ff, 1963), Dulbecco's modified Eagle's medium (DMEM), Eagle's minimal essential medium (MEM), Ham's F12 medium (Ham, R. et al., Proc. Natl. Acad. Sc.53, p288 ff. 1965) or Iscoves' modified DMEM lacking albumin, transferrin and lecithin (Iscoves et al., J. Exp. med. 1, p. 923 ff., 1978). For instance, Ham's F10 or F12 media were specially designed for CHO cell culture. Other media specially adapted to CHO cell culture are described in EP-481 791.Other suitable cultivation methods are known to the skilled artisan and may depend upon the recombinant polypeptide product and the host cell utilized. It is within the skill of an ordinarily skilled artisan to determine or optimize conditions suitable for the expression and production of the product, e.g., the recombinant polypeptide, to be expressed by the cell.

METHODS FOR ENGINEERING A CELL AND PRODUCING A PRODUCT

The methods and compositions described herein are useful for engineering a cell or cell line with improved productivity and improved product quality. In embodiments, a cell is modified such that the lipid metabolism of the cell is modulated. For example, an exogenous nucleic acid encoding an LMM is introduced into the cell. The cell is subsequently cultured under conditions suitable for the expression of the LMM and LMM-mediated modulation of lipid metabolism. The characteristics of a cell having its lipid metabolism modulated are described herein, e.g., in the section titled "Modulation of Lipid Metabolism".

In some embodiments, the cell further comprises an exogenous nucleic acid that encodes a product, e.g., a recombinant polypeptide. In another embodiment, the cell further comprises an exogenous nucleic acid that increases the expression of an endogenous product. In any of such embodiments, the exogenous nucleic acid that encodes a product or increases expression of an endogenous product is introduced prior to the modification of lipid metabolism, e.g., the introduction of an exogenous nucleic acid encoding a LMM described herein. Alternatively, in other embodiments, the exogenous nucleic acid that encodes a product or increases expression of an endogenous product is introduced after the modification of lipid metabolism, e.g., the introduction of an exogenous nucleic acid encoding a LMM described herein. In any of the embodiments, the product is a therapeutic or diagnostic protein. In any of the embodiments, the product is selected from Table 2 or 3.

Methods for genetically modifying or engineering a cell to express a desired polypeptide or protein, e.g., an LMM described herein or a product described herein, are well known in the art, and include, for example, transfection, transduction (e.g., viral transduction), or electroporation.

Physical methods for introducing a nucleic acid, e.g., an exogenous nucleic acid or vector described herein, into a host cell include calcium phosphate precipitation, lipofection, particle bombardment, microinjection, electroporation, and the like. Methods for producing cells comprising vectors and/or exogenous nucleic acids are well-known in the art. See, for example, Sambrook et al., 2012, MOLECULAR CLONING: A LABORATORY MANUAL, volumes 1 - 4, Cold Spring Harbor Press, NY).

Chemical means for introducing a nucleic acid, e.g., an exogenous nucleic acid or vector described herein, into a host cell include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. An exemplary colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (e.g., an artificial membrane vesicle). Other methods of state-of-the-art targeted delivery of nucleic acids are available, such as delivery of polynucleotides with targeted nanoparticles or other suitable sub-micron sized delivery system.

Nucleic acids containing the sequence for a desired polypeptide, e.g., a LMM and/or product described herein, are delivered into a cell and can be integrated into its genome via recombination. The resulting recombinant cells are then capable of stable expression of the desired polypeptide, e.g., a LMM and/or product described herein, thus enabling consistent and efficient protein production over long periods of time. Several advantages accompany stable integration of a gene of interest including the fact that only a single DNA delivery process is required to induce prolonged expression since the gene of interest is simultaneously replicated with host chromosomes; this means that the gene is transferred from one generation to the next without the necessity for additional machinery. This also, in theory, produces a more consistent product and yield across batch-to-batch fermentations. In line with this, stable expression methods are capable of generating high product yields compared to those generated without a modification that modulates lipid metabolism described herein, e.g., introduction of an exogenous nucleic acid encoding a LMM.

Protocols to establish recombinant cell lines that stably overexpress the desired polypeptides, e.g., a LMM and/or product described herein, typically involve integration of linearized DNA (usually plasmid based) at random sites into the host genome facilitated by random recombination. Site specific protocols have also been developed and implemented which promote integration of an expression cassette at specific regions of the host genome (O'Gorman, Fox et al. 1991). These protocols often exploit recombinases capable of site specific recombination, and include, but are not limited to, the Flp-In™ system (e.g., utilizing Flp-In CHO cells), CHOK1SV Flp cell line (Lonza) (as described in Zhang L. et al. (2015). Biotechnol. Prog. 31:1645-5), or the Cre-lox system.

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As described above, in some embodiments, the vector comprising a nucleic acid encoding a product and/or a LMM, further comprises a selection marker to facilitate selection of successfully expressing cells from a transfected pool (Browne, Al-Rubeai 2007). Although numerous selection methods are commercially available, the most commonly used of these are methotrexate (MTX) and Lonza's glutamine synthetase (GS) system (Bebbington, Renner et al. 1992, Lai, Yang et al. 2013). Dihydrofolate reductase (DHFR) is a protein responsible for the conversion of folic acid to tetrahydrofolate and is necessary for essential biosynthetic pathways that produce glycine, purines, and thymidylic acid. MTX can be used to inhibit DHFR activity and inclusion of DHFR in a stably transfected culture can therefore be used to select for stably integrated cells; only those cells successfully expressing sufficient recombinant DHFR will survive selection using MTX (Cacciatore, Chasin et al. 2010). Another selection method commonly employed is the use of GS; an enzyme responsible for the synthesis of glutamine from glutamate and ammonia and, since glutamine is vital for mammalian cell survival, cells lacking sufficient GS will not survive in culture. Initially the addition of methionine sulphoximine (MSX), an inhibitor of GS, ensures that the presence of endogenous GS in CHOK1SV cells is not adequate to maintain cell survival and therefore only cells expressing additional GS brought about through stable integration of a recombinant construct survive the selection process. Lonza and others have now established CHO host cell lines in which the endogenous GS gene has been knocked down/out such that all cells perish that are not successfully integrated with the construct of interest without the presence of exogenous glutamine in the media (Fan, Kadura et al. 2012). Many other selection methods are available which elicit a resistance to a particular selection agent such that only cells harboring the resistance gene will survive the selection process; these include hygromycin, neomycin, blasticidin and zeocin (Browne, Al-Rubeai 2007). In embodiments, the vector comprising an exogenous nucleic acid encoding a LMM and the vector comprising an exogenous nucleic acid encoding a product, e.g., a recombinant polypeptide as described herein, further comprise different selection markers.

Following the successful recovery of stably expressing cell pools, the isolation of individual clones, originating from a single cell, facilitates` the selection of cell lines that are capable of high product yields and quality, or the cell lines with the highest capability of high product yields and high quality product. Differences in cellular properties are likely associated

with heterogeneity observed in cells and both the number and specific integration site(s) of recombinant DNA. Clonal screening properties have therefore been developed to rapidly assess multiple clones and subsequently select high expressing cells. Fluorescence Activated Cell Sorting (FACS) is a method which can rapidly sort cells based on fluorescence intensity and therefore can be employed to select for high expressing clones. Several protocols have been established which involve fluorescent tagging of the protein of interest (Powell, Weaver 1990), fluorescent tagging of cell surface molecules co-expressed with the recombinant gene (Holmes, Al-Rubeai 1999) and detection of fluorescence intensity based on eGFP expression co-expressed with the gene of interest (Meng, Liang et al. 2000). A high fluorescence intensity observed with these methods suggests a high level of recombinant protein production and thus these cells can be preferentially selected from a recombinant cell pool. FACS-based selection methods to isolate high expressing recombinant clones are more suited to recombinant products which remain associated with the cell and, since mammalian expressed biotherapeutic recombinant protein products are secreted, methods have been developed which are more appropriate for the selection of clones for secreted recombinant proteins. For example, ClonePix is an automated colony selection method which picks clones grown on a semi-solid media based on secretion of recombinant products into the media surrounding the colony and associating with Fluorescin Isothiocyanante (FITC) therefore creating a fluorescent halo around the colonies (Lee, Ly et al. 2006). Clones are selected based on the fluorescence intensity of the halo surrounding the colony. Many other clone selection protocols have been established which rapidly isolate recombinant cells based on desired biological properties with particular interest on productivity and are reviewed in Browne and Al-Rubeai (Browne, Al-Rubeai 2007). Expansion of a clone selected as described herein results in the production of a cell line.

In one embodiment, the methods described herein produce a cell with improved productivity. Improved productivity or production capacity of a cell includes a higher yield or amount of product that is produced, and/or an increased rate of production (as determined by the yield or amount of product produced over a unit of time). In one embodiment, improvement of the productivity of a cell, e.g., the capacity to produce a product, results in an increase, e.g., a 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% increase; or a 1-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 50-fold, or 100-fold, or more increase in the amount,

level, or quantity of product produced, e.g., compared to the amount, level, or quantity of product produced by a cell that does not have a lipid metabolism pathway modulated. In one embodiment, improvement of the productivity of a cell, e.g., the rate of production of the product, results in an increase, e.g., a 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99% increase; or a 1-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 50-fold, or 100-fold, or more increase in the rate of production of the product, e.g., compared to the rate of production of the product produced by a cell that does not have a lipid metabolism pathway modulated.

The methods described herein for engineering a cell produce a high production cell or a high production cell line. A high production cell or cell line is capable of producing higher yields of a recombinant polypeptide product than compared to a reference cell or a cell that has not been selected or engineered by the methods described herein. In an embodiment, a high production cell line is capable of producing 100 mg/L, 200 mg/L, 300 mg/L, 400 mg/L, 500 mg/L, 600 mg/L, 700 mg/L, 800 mg/L, 900 mg/L,1 g/L, 2 g/L, 3 g/L, 4 g/L, 5g/L, 10 g/L, 15 g/L, 20 g/L, 25 g/L, 30 g/L, 35 g/L, 40 g/L, 45 g/L, 50 g/L, 55 g/L, 60 g/L, 65 g/L, 70 g/L, 75 g/L, 80 g/L, 85 g/L, 90 g/L, 95 g/L, or 100 g/L or more of a product, e.g., a recombinant polypeptide product. In an embodiment, a high production cell line is produces 100 mg/L, 200 mg/L, 300 mg/L, 400 mg/L, 500 mg/L, 600 mg/L, 700 mg/L, 800 mg/L, 900 mg/L, 1 g/L, 2 g/L, 3 g/L, 4 g/L, 5g/L, 10 g/L, 15 g/L, 20 g/L, 25 g/L, 30 g/L, 35 g/L, 40 g/L, 45 g/L, 50 g/L, 55 g/L, 60 g/L, 65 g/L, 70 g/L, 75 g/L, 80 g/L, 85 g/L, 90 g/L, 95 g/L, or 100 g/L or more of a product, e.g., a recombinant polypeptide product. The quantity of product produced may vary depending on the cell type, e.g., species, and the product, e.g., recombinant polypeptide, to be expressed. By way of example, a high production CHO cell that expresses a monoclonal antibody may be capable of producing at least 1 g/L, 2 g/L, 5g/L, 10 g/L, 15 g/L, 20 g/L, or 25 g/L of a monoclonal antibody.

Described herein are methods and compositions that may be particularly useful for the expression of products that are difficult to express or produce in cells or cell-free systems using the conventional methods presently known in the art. As such, a production cell line producing such difficult to express products, e.g., next generation biologics described herein, may produce at least 1 mg/L, 5 mg/L, 10 mg/L, 15 mg/L, 20 mg/L, 25 mg/L, 30 mg/L, 35 mg/L, 40 mg/L, 45

mg/L, 50 mg/L, 55 mg/L, 60 mg/L, 65 mg/L, 70 mg/L, 75 mg/L, 80 mg/L, 85 mg/L, 90 mg/L, 95 mg/L, or 100 mg/L or more. Production capacity (e.g., yield, amount, or quantity of product or rate of production of product) achieved by the methods and compositions described herein for difficult to express proteins can be increased by 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 99%, or more, or 1-fold, 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 50-fold, or 100-fold or more, in comparison to the production capacity of a cell or system that does not have a modification that modulates lipid metabolism as described herein.

Assays for quantifying the amount, level, or quantity of product produced or secreted, e.g., secreted into the culture media, include protein quantification assays, such as the Bradford protein assay, SDS-PAGE analysis, immunoblotting, e.g., western blot, and automated means, e.g., using a nanodrop device. Other methods for measuring increased protein production are well-known to those skilled in the art. For example, an increase in recombinant protein production might be determined at small-scale by measuring the concentration in tissue culture medium by ELISA (Smales et al. 2004 Biotechnology Bioengineering 88:474-488). It can also be determined quantitatively by the ForteBio Octet, for example for high throughput determination of recombinant monoclonal antibody (mAb) concentration in medium (Mason et al. 2012 Biotechnology Progress 28:846-855) or at a larger-scale by protein A HPLC (Stansfield et al. 2007 Biotechnology Bioengineering 97:410-424). Other methods for determining production of a product, e.g., a recombinant polypeptide described herein, can refer to specific production rate (qP) of the product, in particular the recombinant polypeptide in the cell and/or to a time integral of viable cell concentration (IVC). In an embodiment, the method for determining production includes the combination of determining qP and IVC. Recombinant polypeptide production or productivity, being defined as concentration of the polypeptide in the culture medium, is a function of these two parameters (qP and IVC), calculated according to Porter et al. (Porter et al. 2010 Biotechnology Progress 26:1446-1455). Methods for measuring protein production are also described in further detail in the Examples provided herein.

In one embodiment, the methods described herein produce a cell with improved product quality. In one embodiment, improvement of the quality of the product results in the increase, e.g., a 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 99%, or more, increase in product quality; or a 1-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 50-fold, or 100-

fold, or more increase, in product quality, e.g., as compared to the amount, level, or quantity of product produced by a cell that does not have a lipid metabolism pathway modulated. Such increases in product quality can be exemplified, for example, by one or more of the following:

i) an increase in the amount or quantity of non-aggregated product (or a decrease in the amount or quantity of aggregated product);

ii) an increase in the amount or quantity of properly folded or assembled product (or a decrease in the amount or quantity of misfolded, unfolded, partially assembled, or non-assembled product), or an increase in the ratio of properly folded or assembled product to unfolded, misfolded, partially assembled, or non-assembled product;

iii) an increase in the amount or quantity of full-length product (or a decrease in fragmentation of the product);

iv) an increase in the desired post-translational modifications (or a decrease in unmodified or incorrectly modified product);

v) an increase or decrease in glycan heterogeneity (e.g., for glycosylated products);

vi) an increase in the amount or quantity of functional product (or a decrease in the amount or quantity of a nonfunctional or dysfunctional product), or an increase in the ratio of function to nonfunctional or dysfunctional product; and/or

vii) an increase or decrease in disulfide bond scrambling (e.g., an increase or decrease the desired isoform or structure as a result to increased or decreased disulfide bond scrambling, e.g., for antibody molecule products).

Methods for measuring product quality, e.g., the improvement of the product quality, of a cell or cell line generated as described herein are known in the art. In one embodiment, methods for determining the fidelity of the primary sequence of the expressed recombinant polypeptide product are known in the art, e.g., mass spectrometry. An increase in the amount or concentration of properly folded product, e.g., expressed recombinant polypeptide, can be determined by circular dichroism or assessing the intrinsic fluorescence of the expressed recombinant polypeptide. An increase in the amount or concentration of functional product can be tested using various functional assays depending on the identity of the recombinant product, e.g., recombinant polypeptide. For example, antibodies can be tested by the ELISA or other immunoaffinity assay. Other methods for determining an increase in product quality, e.g.,

determining aggregation, post-translational modifications, disulfide bond scrambling, can be assessed by size exclusion chromatography, high performance liquid chromatography, dynamic light scattering (DLS) approaches, and protein electrophoresis (PAGE) methods.

In an embodiment, the methods for producing a product, e.g., as described herein, comprise providing a cell engineered to comprise a modification that modulates lipid metabolism, as described above. In one embodiment, the cell comprising a modification that modulates lipid metabolism further comprises an exogenous nucleic acid encoding a product, e.g., a recombinant polypeptide as described herein. In one embodiment, the exogenous nucleic acid encoding a product, e.g., a recombinant polypeptide described herein is introduced to the engineered cell comprising a modification that modulates lipid metabolism. In another embodiment, the exogenous nucleic acid encoding a product, e.g., a recombinant polypeptide described herein, is introduced to a cell prior to the introduction of an exogenous nucleic acid encoding a LMM as described herein. The exogenous nucleic acid encoding a product further comprises a selection marker, for efficient selection of cells that stably express, e.g., overexpress, the product as described herein.

In some embodiments, additional steps may be performed to improve the expression of the product, e.g., transcription, translation, and/or secretion of the product, or the quality of the product, e.g., proper folding and/or fidelity of the primary sequence. Such additional steps include introducing an agent that improves product expression or product quality. In an embodiment, an agent that improves product expression or product quality can be a small molecule, a polypeptide, or a nucleic acid that encodes a polypeptide that improves protein folding, e.g., a chaperone protein. In an embodiment, the agent that assists in protein folding comprises a nucleic acid that encodes a chaperone protein, e.g., BiP, PD1, or ERO1 (Chakravarthi & Bulleid 2004; Borth et al. 2005; Davis et al. 2000). Other additional steps to improve yield and quality of the product include overexpression of transcription factors such as XBP1 and ATF6 (Tigges & Fussenegger 2006; Cain et al. 2013; Ku et al. 2008) and of lectin binding chaperone proteins such as calnexin and calreticulin (Chung et al. 2004). Overexpression of the agents that assist or improve protein folding, product quality, and product yield described herein can be achieved by introduction of exogenous nucleic acids encoding the agent. In another embodiment, the agent that improves product expression or product quality is a small molecule that can be added to the cell culture to increase expression of the product or quality of

the product, e.g., DMSO. In one embodiment, culturing the cells at a lower temperature, e.g., 1°C, 2°C, 3°C, 4°C, 5°C, 6°C, 7°C, 8°C, 9°C, or 10°C lower, than the temperature that the cells are normally grown can improve productivity.

Any of the methods described herein can further include additional selection steps for identifying cells that have high productivity or produce high quality products. For example, FACS selection can be utilized to select specific cells with desired characteristics, e.g., higher expression of a protein folding proteins, e.g., chaperones.

In one aspect, the disclosure provides methods that include a step for recovering or retrieving the recombinant polypeptide product. In embodiments where the recombinant polypeptide is secreted from the cell, the methods can include a step for retrieving, collecting, or separating the recombinant polypeptide from the cell, cell population, or the culture medium in which the cells were cultured. In embodiments where the recombinant polypeptide is within the cell, the purification of the recombinant polypeptide product comprises separation of the recombinant polypeptide produced by the cell from one or more of any of the following: host cell proteins, host cell nucleic acids, host cell lipids, and/or other debris from the host cell.

In embodiments, the process described herein provides a substantially pure protein product. As used herein, "substantially pure" is meant substantially free of pyrogenic materials, substantially free of nucleic acids, and/or substantially free of endogenous cellular proteins enzymes and components from the host cell, such as polymerases, ribosomal proteins, and chaperone proteins. A substantially pure protein product contains, for example, less than 25%, 20%, 15%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, or 1% of contaminating endogenous protein, nucleic acid, or other macromolecule from the host cell.

Methods for recovering and purification of a product, e.g., a recombinant polypeptide, are well established in the art. For recovering the recombinant polypeptide product, a physical or chemical or physical-chemical method is used. The physical or chemical or physical-chemical method can be a filtering method, a centrifugation method, an ultracentrifugation method, an extraction method, a lyophilization method, a precipitation method, a chromatography method or a combination of two or more methods thereof. In an embodiment, the chromatography method comprises one or more of size-exclusion chromatography (or gel filtration), ion exchange chromatography, e.g., anion or cation exchange chromatography, affinity chromatography, hydrophobic interaction chromatography, and/or multimodal chromatography.

EXAMPLES

The invention is further described in detail by reference to the following experimental examples. These examples are provided for purposes of illustration only, and are not intended to be limiting unless otherwise specified. Thus, the invention should in no way be construed as being limited to the following examples, but rather, should be construed to encompass any and all variations which become evident as a result of the teaching provided herein.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples specifically point out various aspects of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

Example 1: Generation of Stable Cells Overexpressing a Lipid Metabolism Modulator

In order to investigate the effect of overexpression of two lipid metabolism modulators, SCD1 and SREBF1, in CHO cells, these genes were successfully cloned and stably integrated into adherent CHO Flp-In cells using a site directed approach, and into suspension GS knockout (GSKO) CHO cells using a random integration approach.

Molecular Cloning of SCD1 and SREBF1 containing FRT vectors

Molecular cloning was carried out in order to generate FRT based vectors which facilitate the expression of SCD1 and SREBF1 proteins both with and without a V5/His tag at the C-terminus of each protein. The use of these vectors, in conjunction with Thermo Fisher's commercially available Flp-In host CHO cell pool enabled site specific integration of the genes of interest to generate stable CHO adherent cell pools. The primers described in Table 4 were used in a Phusion® Polymerase based PCR reaction to amplify these genes such that double stranded DNA fragments were produced flanked by the restriction sites also detailed in Table 4. SCD1 and SREBF1 genes were amplified from Mouse P19 derived cDNA and Origene mouse cDNA clone (NCBI accession no. NM_011480), respectively.

Following successful amplification of the target genes, double restriction digests were undertaken on FRT-V5 vectors as well as the previously generated PCR products of the genes of

interest using the appropriate restriction enzymes. Ligations were incubated overnight before subsequent transformations and miniprep purification was carried out on the resulting colonies.

Generation of SCD1 and SREBF1 Overexpressing Adherent Flp-In CHO Cells

The aforementioned FRT-based constructs were used in conjunction with Thermo Fisher's commercially available adherent Flp-In CHO cells to generate stable cell pools. FRT vectors containing the genes of interest and an empty FRT construct (used to generate a control cell pool) were co-transfected with recombinase containing pOG44 vector into Flp-In cells. Recombinase sites present in the FRT vectors and Flp-In CHO genome initiate site specific recombination and successful clones can be isolated using hygromycin as a selection agent. Stably expressing recombinant CHO adherent cell pools in a site specific manner were generated according to the manufacturer's instructions, e.g., as described in the Thermo Fisher's Flp-In manual, e.g., available from the Thermo Fisher's references and protocols website. This method was used to generate and recover control, SCD1-V5, and SREBF1-V5 Flp-In CHO polyclonal cell pools.

Molecular Cloning of SCD1 and SREBF1 into pcDNA3.1 Vectors

Expression vectors were generated to stably integrate, and therefore overexpress, in industrially relevant CHO suspension cells with one of SCD1, SREBF1 or a truncated SREBF1 gene. The pcDNA3.1V5-His/TOPO vector consists of an appropriate CMV promoter and downstream multiple cloning site, facilitating expression of the gene of interest, while also including elements enabling expression of a neomycin gene which can be utilized for selection of successful clones following integration of DNA into the genome.

Initially, the Phusion® PCR protocol was used to amplify SCD1, SREBF1 and a SREBF1 truncation using the primers indicated in Table 4, designed so that restriction sites were simultaneously added to the flanks of the resulting PCR products. The previously generated SCD1-FRT vector was used as a template to amplify the SCD1 genes while Origene mouse cDNA (NCBI accession no. NM_011480) was used to amplify the SREBF1 gene and its truncation. The SREBF1 truncation hereby referred to as SREB410, codes for a 410 amino acid long polypeptide sequence, which includes the helix-loop-helix (HLH) domain of SREBF1. This domain is endogenously cleaved from the full-length protein allowing migration of this fragment to the nucleus and subsequent gene transcription activation as previously outlined. Primers were designed to amplify this region with the aim to express a protein (encoded by this sequence)

which is localized directly in the nucleus and thus to carry out its function as a transcriptional activator without the need for endogenous processing.

Double restriction digests were carried out on purified PCR products as appropriate (see Table 4), and pcDNA3.1/V5-His/TOPO, where primers amplified a gene with no stop codon, in order to allow read through into an in-frame sequence encoding a V5 and His tag. The resulting DNA fragments were ligated to yield vectors containing SCD1, SREBF1 or SREB410 genes with a V5-His tag. These reactions were transformed and mini preps were carried out on a number of the resulting colonies. Restriction digests were carried out and the resulting DNA fragments were run on an agarose gel to ascertain which samples were successful.

Generation of SCD1 and SREBF1 Overexpressing Suspension GSKO CHO Cells

Suspension CHOK1SV GS-KO cell pools grown in chemically-defined, protein and serum-free media, stably transfected with the previously synthesized pcDNA3.1V5-His/TOPO derived constructs were generated in order to investigate the effect of constitutive expression of the inserted genes in an industrially relevant cell line. In order to achieve this, stable integration was carried out using Lonza's CHOK1SV GS-KO host cell line. Initially, SCD1-V5, SREBF1-V5, SREB410-V5 and control (empty pcDNA3.1V5-His/TOPO) constructs were linearized by overnight digestion with PvuI restriction enzyme (NEB). Following linearization, DNA was purified using ethanol precipitation and CHOK1SV GS-KO cells were electroporated using 20 µg DNA and 1 x 10^7 viable cells before immediate transfer to T75 flasks containing CD-CHO medium (Thermo Fisher) at 37°C to make a final volume of 20 mL. Flasks were placed in a humidified static incubator at 37°C with a 5% CO_2 in air atmosphere for 24 hours. A concentrated stock of G418 (Melford) selection agent was diluted in CD-CHO medium and 5 mL of this stock was added to the T75 flasks and gently mixed to yield a final concentration of 750 µg/mL in a 25 mL total volume. Cell counts were performed every 3-4 days to determine growth and culture viability and 750 µg/ml G418 in CD-CHO media was renewed approximately every 6 days by centrifugation and resuspension. Cells were transferred to 125 mL Erlenmeyer flasks and routine suspension cell culture was established once cells had reached a concentration of 2 x 10^5 viable cells/mL.

Table 4: Summary of primer sequences

Primer Name	Primer Sequence (5'–3')	Restriction Sites	SEQ ID NO:

eGFP SV40 For	TAT **GCTAGC** GGTACCATGGTGAGCAAGGGCGAGGA	**NheI**, KpnI*	5
SREBF1 For FRT	TAT GGTACC ATGGACGAGCT	**KpnI**	6
SREBF1 Rev FRT	ATA GGGCCC TTAGCTGGAA	**ApaI**	7
SREBF1 V5 For FRT	TAT GCGGCCGC ATGGACGAG	**NotI**	8
SREBF1 V5 Rev	ATA CTCGAG CGGCTACTCTT	**ApaI**	9
SCD1 For FRT	TAT GGTACC ATGCCGGCC	**KpnI**	10
SCD1 Rev FRT	ATA CTCGAG TCAGCTACTCTTGT	**XhoI**	11
SCD1 V5 For FRT	TAT GGTACC ATGCCGGCC	**KpnI**	12
SCD1 V5 Rev FRT	ATA CTCGAG CGGCTACTCTT	**XhoI**	13
SREBF1 For 3.1	TAT GCGGCCGC ATGGACGAG	**NotI**	14
SREBF1 Rev 3.1	ATA TCTAGA CTAGCTGGAAGTGACGGTGGTTCC	**XbaI**	15
SREBF1 V5 For 3.1	TAT GCGGCCGC ATGGACGAG	**NotI**	16
SREBF1 V5 Rev 3.1	ATA TCTAGA CTGCTGGAAGTGACGGTGGTTC	**XbaI**	17
SREB410 For 3.1	TAT GCGGCCGC ATGGACGAG	**NotI**	18
SREBF410 Rev 3.1	ATA TCTAGA TCACATGCCCTCCATAGACACATCTGTG	**XbaI**	19
SREB410 V5 For	TAT GCGGCCGC ATGGACGAG	**NotI**	20
SREB410 V5 Rev	ATA TCTAGA CTCATGCCCTCCATAGACACATCTGTG	**XbaI**	21
SCD1 For 3.1	TAT GGTACC ATGCCGGCC	**KpnI**	22
SCD1 Rev 3.1	ATA CTCGAG TCAGCTACTCTTGT	**XhoI**	23
SCD1 V5 For 3.1	TAT GGTACC ATGCCGGCC	**KpnI**	24
SCD1 V5 Rev 3.1	ATA CTCGAG CGGCTACTCTT	**XhoI**	25

Example 2: Expression Analysis of LMM in Stable Cells Overexpressing a LMM

Following the establishment of stable Flp-In CHO cell pools stably integrated with either a control (empty pcDNA5 FRT), SCD1-V5 or SREBF1 V5, immunofluorescence was undertaken to confirm both the expression of the stably exogenous integrated genes and additionally the intracellular location of the expressed proteins. Control, SCD1-V5 and SREBF1-V5 cell lines were seeded at 2 x 10^5 viable cells per well in a 24 well plate in Ham Nutrient Mix F12 medium supplemented with 10% FBS. Samples were methanol-fixed and first exposed to anti-V5 antibody (produced in mouse- *Sigma V8012*) and successively anti-mouse FITC secondary conjugate (raised in goat-*Sigma F0257*). Furthermore, the cells were exposed to DAPI stain (10 µg/mL working stock) in order to stain cellular DNA thus highlighting the nuclei. The resulting immunofluorescent images are shown in Figure 1.

The presence of the FITC stains in SCD1-V5 and SREBF1-V5 cell lines shows that the exogenous/recombinant genes were successfully expressed and, moreover, the cellular localization of SCD1-V5 and SREBF1-V5 proteins was clearly evident. Constitutively expressed

SCD1-V5 protein was present and abundant throughout the cell, with the images showing their localization to be in the cytoplasm and in the ER. Conversely, the SREBF1-V5 protein was expressed to a much lower amount, but it was very prominently located at the peri-nucleus forming a ring around the nuclei. It is important to consider that the V5 epitope sequence was added to the 3' end of the gene and, because of the natural regulation of SREBF1, specific domains are cleaved and relocated within the cell. The mature, cleaved bHLH (basic helix loop helix) region is of particular importance as it is responsible for transcriptional activation of many genes with implications on lipid biosynthesis and conformation. Because this region is encoded at the 5' end of the gene, this region would not be detected upon staining of the 3' V5 tag and thus it is impossible to determine whether any of the constitutively expressed, cleaved portion of the translated protein is present in the imaged cells.

Staining of intracellular V5-tagged stable proteins was carried out to determine the presence of SCD1-V5 and SREBF1-V5 in engineered CHOK1SV GS-KO suspension cell lines. In order to adhere these cells to a coverslip in a 24 well plate, coverslips were first treated with poly-L-lysine and cells were seeded at 2 x 10^5 cells per well and left to incubate at 37°C in a 5% CO_2 environment static humidified incubator overnight. Following methanol fixing and permeablisation, anti-V5 (produced in mouse - *Sigma V8012*) was conjugated with anti-mouse TRITC (produced in goat- *T5393)* secondary antibody. The resulting images are shown in Figure 2.

Western blots were performed using an anti-V5 antibody, an anti-mouse HRP conjugated secondary antibody, and the appropriate detection system, was used to further confirm expression of the lipid constructs with the V5 tag. Equivalent amounts of total protein (determined using the Bradford assay) were loaded for SDS-PAGE followed by western blotting onto nitrocellulose. The resulting blots are shown in Figures 3A, 3B, and 3C with the V5 tag only detected in those cells expressing the SCD1 construct. However, the low levels of expression achieved with the SREBF1 construct may explain the lack of detection of V5 in cell lines expressing this construct.

Example 3: Growth Characteristics of Stable Cells Overexpressing a LMM

In this example, the growth characteristics, such as viable cell counts, cell number, and culture viability were assessed in two different cell lines engineered to overexpress LMMs, a

CHO Flp-In™ and the CHOK1SV GS-KO (Lonza Biologics) cell lines. The LMM-engineered cell lines were generated as described in Example 1. Control cell lines were engineered to express an empty V5 tagged expression vector. An eGFP encoding expression vector was transfected into the LMM-engineered cell lines by electroporation. Electroporations were carried out using 1 x 10^7 viable LMM-engineered Flp-In CHO cells or CHOK1SV GS-KO cells and 20 µg of plasmid DNA (eGFP encoding expressing vector) and these cells were diluted to a final volume of about 20 or 32 mL in Ham Nutrient Mix F12 medium. Viable cell concentrations were determined using a ViCell cell counter and recorded at 24, 48, 72, and 96 hours post transfection of the eGFP encoding expression vector.

The results for the Flp-In™ cells engineered to express SCD1 and SREBF1 are shown in Figure 4. Cells overexpressing SCD1 and SREBF1 generally showed some increase in the viable cell concentation compared to control cells across all time points.

The results for the CHOK1SV GS-KO cells engineered to express SCD1, SREBF1, and SREBF410 are shown in Figures 5A and 5B. Viable cell concentration compared to total cell cocentration are shown in Figure 5A, with the viable cell concentration represented by the lower column, and the whole column representing the total number of cells counted. As shown in Figure 5A, expression of LMM (SCD1 and SREBF1) results in a general increase in viable and total cell numbers across all time points. By 48, 72 and 96 hours, viable and total cell concentration were significantly higher in SCD1 and SREBF1-engineered cells. At 96 hours, viable cell counts for SCD1 and SREBF1-engineered cells were more than 1 x 10^6 cells/mL higher than control cells. Culture viability was also calculated and shown in Figure 5B. The LMM-engineered cells generally showed an increase in culture viability as compared to control cells.

Example 4: Increased eGFP Induced Fluorescence in Stable Cells Overexpressing a LMM

In this example, the production capacity for producing a recombinant protein was assessed in the CHO-Flp-In™ and the CHOK1SV GS-KO cell lines that were engineered to stably express LMMs, as described in Example 1. The LMM-engineered cells were transfected with an eGFP encoding expression vector as described in Example 3, and production capacity was assessed by measuring the amount of eGFP produced by flow cytometry at 24, 48, 72, and

96 hours after transfection. A FACSCalibur (BD Biosciences) instrument was used to measure the eGFP-mediated fluorescence of the cells and generate the data shown here.

Production of eGFP was measured in Flp-In cells engineered to express V5-tagged SCD1 and SREBF1. Figures 6A, 6B, and 6C show the median fluorescence, the geometric mean fluorescence, and the arithmetic mean fluorescence, respectively, of the LMM-engineered Flp-In cells recorded using flow cytometry at the specified time points. These values are increased in SCD1 overexpressing cells for median fluorescence, geometric mean fluorescence, and arithmetic mean fluorescence, thereby demonstrating that cells stably expressing SCD1 are capable of producing more eGFP compared to the control cells.

Production of eGFP was measured in CHOK1SV GS-KO cells engineered to express V5-tagged SCD1, SREBF1, and SREBF410. Median fluorescence is shown in Figure 7A and geometric mean fluorescence is shown in Figure 7B. Increased median fluorescence and geometric mean fluorescence was observed for cells engineered to overexpress SREBF1.

In order to account for differences in cell concentration and proliferation properties observed in CHOK1SV GS-KO derived cell lines. Total fluorescence per mL of culture was calculated by multiplying the measured arithmetic mean fluorescence by the total cell concentration ($x10^6$ per mL), and the calculated values are shown in Figure 7C. As shown in Figure 7C, SCD1 overexpressing cells produced a significantly increased amount of recombinant protein (eGFP) at 24 hours after transfection as compared to control cells. SREBF1 overexpressing cells generally produced an increased amount of eGFP at all time points tested as compared to control cells, and significantly increased amounts at 72 and 96 hours after transfection.

Collectively, these data show that engineering cells to express an LMM, such as SCD1 and SREBF1, increases production capacity of a transiently expressed recombinant protein such as eGFP. Furthermore, as demonstrated by the fluorescence measured, the cells produced increased correctly folded and functional eGFP as compared to cells that did not have a modification that modulates lipid metabolism, thereby demonstrating that modulation of lipid metabolism increases both production yields and quality.

Example 5: Improved Productivity in Stable Cells Overexpressing an LMM

Similar to the experiments described in Example 4, cell lines that stably express LMMs were assessed for production capacity of different products, such as a model IgG4 antibody molecule (referred to herein as antibody A) and a fusion protein (referred to herein as Fc fusion protein or FP).

Flp-In cells stably expressing V5-tagged SCD1 and SREBF1 (engineered as described in Example 1) were electroporated with expression vectors encoding antibody A or a Fc fusion protein. Following electroporation, the quantity of recombinant antibody A and FP in culture supernatant was determined at 24, 48, 72, and 96 hours after electroporation by western blotting. An anti-heavy chain primary antibody, an anti-rabbit-HRP conjugated secondary antibody, and the appropriate detection reagent were used to detect antibody A (Figure 8A) and the Fc fusion protein (Figure 9A). Average fold change in production of the antibody A and Fc fusion protein was determined by Protein A HPLC, and shown in Figures 8B and 9B, respectively. Cell lines expressing exogenous SCD1 demonstrated increased productivity compared to the control cell lines with both recombinant proteins. Furthermore, this effect was consistent across the 24, 48, 72, and 96 hour time points analyzed.

Lonza's CHOK1SV GS-KO (Xceed™) cells stably expressing the SCD1, SREBF1, and SREBF410 constructs (engineered as described in Example 1) were transiently transfected with two recombinant proteins; a model IgG4 (antibody A) and an Fc fusion protein. Following electroporation, the quantity of recombinant antibody A and FP in culture supernatant was determined every 24 hours up to 96 hours by western blotting using an anti-heavy chain primary antibody, an anti-rabbit-HRP conjugated secondary antibody, and the appropriate detection reagent (Figures 10A and 11A). Average fold change in production of the antibody A and Fc fusion protein was determined by Protein A HPLC, and shown in Figures 10B and 11B, respectively. CHOK1SV GS-KO cells lines expressing exogenous SCD1, SREBF1, and SREBF410 demonstrated increased productivity compared to the control cell lines with both recombinant proteins (Figures 10B and 11B). Furthermore, this effect was consistent across the 48, 72, and 96 hour time points analyzed.

Lonza's CHOK1SV GS-KO (Xceed™) cells stably expressing the SCD1, SREBF1, and SREBF410 constructs (engineered as described in Example 1) were stably transfected with two recombinant proteins; a model IgG4 (antibody A) and an Fc fusion protein. Figure 15A and 16A show volumetric productivity of antibody A and FC fusion protein respectively at 48, 96, 144

and 192 hours after initial seeding at 0.2 x 10^6 viable cells/ml. Results show that the SCD1 overexpressing cell pools improve the absolute yield of both recombinant molecules. Furthermore, upon calculations to include cell numbers, the specific productivity of both recombinant molecules was also greatly increased in SCD1 overexpressing cell pools (Figure 15B and 16B).

These results collectively show that engineering cells to express an LMM, such as SCD1, SREBF1, and a functional fragment of SREBF1 (SREBF410) increases production capacity of transiently expressed recombinant proteins, such as antibody molecules and fusion proteins.

Example 6: Improving Established Production Cell Lines

Examples 4 and 5 demonstrate that cell lines stably expressing LMMs have improved production when transiently expressing a recombinant product, such as a GFP, an antibody molecule, or a fusion protein. In this example, analysis was performed to determine the effect of LMMs on the enhancing existing stable yields of a recombinant product in established cell lines.

CHO121 cells that have been previously engineered to stably express a model IgG4 antibody molecule (antibody A) were used. Constructs encoding V5-tagged SCD1, SREBF1 and a truncated SREBF1 (SREBF410) were transiently expressed in the antibody A-stably expressing cells. Control cells were transfected with an empty V5 tag vector. Supernatants from the cells were harvested at 48, 72, and 168 hours. Western blot analysis was performed to determine the amount of antibody A produced by using an anti-heavy chain primary antibody (Sigma 19764), followed by anti-rabbit HRP conjugated secondary antibody (Sigma A6154), and the results are shown in Figure 12A. As shown, expression of LMMs SCD1 and SREBF410 resulted in an increase in the amount of antibody A produced by the cells as compared to control at both 48 and 72 hours after introduction of the LMMs. Supernatants from cells were subjected to Coomassie analysis to show the amount of antibody A produced after 168 hours after introduction of the LMMs, and demonstrate that LMM transient expression (SCD1 and SREBF410) resulted in improved production of the recombinant protein (Figure 12B). Figure 13 shows quantitative analysis of antibody A using protein A HPLC highlighting a marked increase in the average product titre following transient transfections with SCD1 and SREB410 containing plasmids at 48, 72, 96 and 144 hours post transfection. Figure 14 shows quantitative analysis of the FC fusion protein using protein A analysis to determine product titres and viable

cell numbers to determine specific productivity. This data shows an increase in the average specific productivity of cells transiently transfected with vectors containing LMM elements and the SREBF1 containing construct yields the highest average value.

These results show that modulation of the lipid metabolism in established cell lines can further improve production capacity compared to established yields.

Example 7: Improved Productivity by Simultaneous Introduction of Recombinant Genes and LMMs

Plasmids/constructs were generated which comprise of genes for appropriate expression of both an exemplary immunocytokine and either a control (no LMM), SCD1, SREBF1 or SREB411 (SREBF1 derived sequences were CHO specific; NM_001244003, SEQ ID NOs: 34 and 36). These constructs were then used to transiently transfect Lonza's CHOK1SV GS-KO cells. Figure 17A shows western analysis of supernatants harvested at 48 and 96 hours post transfection. The supernatant samples used were reduced and the transient product was detected by probing with an anti-heavy chain primary antibody and HRP conjugated anti-rabbit secondary to highlight a native heavy chain (lower band) and cytokine fused heavy chain (upper band). Inclusion of SCD1, SREBF1 and SREB411 genes in the transfected construct resulted in an increase in both band intensities at both 48 and 96 hours post transfection. Furthermore, figure 17B shows quantitative analysis of samples obtained at 96 hours post transfection using protein A analysis. Relative abundances of the immunocytokine support the data presented in western analysis (Figure 17A).

These data show that the simultaneous inclusion of an LMM, such as SCD1, SREBF1, and a functional fragment of SREBF1 (SREBF411), with recombinant product genes can improve production capacity.

SEQUENCE LISTING IN ELECTRONIC FORM

In accordance with Section 111(1) of the Patent Rules, this description contains a sequence listing in electronic form in ASCII text format (file: 84902958 Seq 29-JAN-19 v1.txt).

A copy of the sequence listing in electronic form is available from the Canadian Intellectual Property Office.

CLAIMS:

1. A method for producing a recombinant polypeptide in a eukaryotic cell, comprising:

i) providing the eukaryotic cell comprising:

a first exogenous nucleic acid encoding a first lipid metabolism modulator (LMM) comprising stearoyl CoA desaturase-1 (SCD1) or a functional fragment or isoform thereof; and

a second exogenous nucleic acid encoding the recombinant polypeptide, wherein the recombinant polypeptide is:

a. a therapeutic polypeptide,

b. an antibody or fragment thereof, a monoclonal antibody, or a bispecific molecule, or

c. selected from a hormone, a blood clotting or coagulation factor, a cytokine or growth factor, a fusion protein and a protein vaccine;

and

(ii) culturing the cell under conditions where the first LMM and the recombinant polypeptide are expressed,

thereby producing the recombinant polypeptide.

2. The method of claim 1, wherein the first LMM provides increased yield or rate of production of the recombinant polypeptide as compared to a cell not having the first LMM.

3. The method of claim 1, wherein the first LMM provides an increased ratio of properly folded product to misfolded or unfolded recombinant polypeptide as compared to a cell not having the first LMM.

4. The method of any one of claims 1 to 3 wherein the first LMM has at least 80% identity with the amino acid sequence of SEQ ID NO: 3, or a functional fragment

Date reçue / Date received 2021-12-13

thereof; or differs by 1 or more amino acid residues but no more than 50 amino acid residues from the amino acid sequence of SEQ ID NO: 3, or a functional fragment thereof.

5. The method of any one of claims 1 to 4, wherein the cell further comprises a second exogenous nucleic acid encoding a second LMM comprising Sterol Regulatory Element-Binding Transcription Factor 1 (SREBF1) or a functional fragment or isoform thereof, and in step (ii) the cell is cultured under conditions where the second LMM is expressed.

6. The method of claim 5 wherein the second LMM comprises an amino acid sequence with at least 80% identity with the amino acid sequence of SREBF1 corresponding to SEQ ID NOs: 1 or 34, or a functional fragment thereof, corresponding to SEQ ID NOs: 26, 27, or 36; or differs by 1 or more amino acid residues but no more than 50 amino acid residues from the amino acid sequence of SREBF1, corresponding to SEQ ID NOs: 1 or 34, or a functional fragment thereof corresponding to SEQ ID NOs: 26, 27, or 36.

7. The method of claim 5 or claim 6 wherein the second LMM provides increased yield of rate of production of the recombinant polypeptide as compared to a cell not having the second LMM.

8. The method of any one of claims 1 to 7, wherein production of the recombinant polypeptide is increased by 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, or 100-fold as compared to the level or quantity of recombinant polypeptide produced by a cell without the first LMM.

9. The method of any one of claims 1 to 8, wherein the first exogenous nucleic acid encoding the first LMM is integrated into the chromosomal genome of the cell and the LMM is stably expressed.

10. The method of any one of claims 1 to 9, wherein the cell is a mammalian cell.

11. The method of any one of claims 1 to 10, further comprising separating the recombinant polypeptide from at least one cellular or medium component.

Date reçue / Date received 2021-12-13

12. The method of any one of claims 1 to 11 wherein the second exogenous nucleic acid encoding a recombinant polypeptide has been introduced after introducing the first exogenous nucleic acid encoding the first LMM.

13. A eukaryotic cell comprising:

a first exogenous nucleic acid encoding a first lipid metabolism modulator (LMM), wherein the first LMM comprises stearoyl CoA desaturase-1 (SCD1) or a functional fragment or isoform thereof; and

a second exogenous nucleic acid encoding a recombinant polypeptide,

wherein the first exogenous nucleic acid is integrated into the chromosomal genome of the cell and wherein the recombinant polypeptide is:

i) a therapeutic polypeptide,

ii) an antibody or fragment thereof, a monoclonal antibody, or a bispecific molecule, or

iii) selected from a hormone, a blood clotting or coagulation factor, a cytokine or growth factor, a fusion protein and a protein vaccine.

14. The cell of claim 13, wherein the cell is a mammalian cell.

15. The cell of claim 14, which is a CHO cell.

16. The cell of any one of claims 13 to 15 wherein the first LMM provides increased yield of rate of production of the recombinant polypeptide as compared to a cell not having the first LMM.

17. The cell of any one of claims 13 to 15, wherein the first LMM provides an increased ratio of properly folded product to misfolded or unfolded recombinant polypeptide as compared to a cell not having the first LMM.

18. The cell of any one of claims 13 to 17, wherein the cell further comprises a third exogenous nucleic acid encoding a second LMM comprising Sterol Regulatory Element-Binding Transcription Factor 1 (SREBF1) or a functional fragment or isoform

Date reçue / Date received 2021-12-13

thereof, and in step (ii) the cell is cultured under conditions where the second LMM is expressed.

19. The cell of claim 18 wherein the second LMM comprises an amino acid sequence with at least 80% identity with the amino acid sequence of SREBF1 corresponding to SEQ ID NOs: 1 or 34, or a functional fragment thereof, corresponding to SEQ ID NOs: 26, 27, or 36; or differs by 1 or more amino acid residues but no more than 50 amino acid residues from the amino acid sequence of SREBF1, corresponding to SEQ ID NOs: 1 or 34, or a functional fragment thereof corresponding to SEQ ID NOs: 26, 27, or 36.

20. Use of the cell of any one of claims 13 to 19 in the production of a therapeutic recombinant polypeptide of interest.

21. A method for producing a recombinant polypeptide in a eukaryotic cell, comprising:

i) providing the eukaryotic cell comprising:

a first exogenous nucleic acid encoding a first lipid metabolism modulator (LMM) comprising Sterol Regulatory Element-Binding Transcription Factor 1 (SREBF1) or a functional fragment or isoform thereof; and

a second exogenous nucleic acid encoding the recombinant polypeptide, wherein the recombinant polypeptide is:

a. a therapeutic polypeptide,

b. an antibody or fragment thereof, a monoclonal antibody, or a bispecific molecule, or

c. selected from a hormone, a blood clotting or coagulation factor, a cytokine or growth factor, a fusion protein and a protein vaccine;

and

(ii) culturing the cell under conditions where the first LMM and the recombinant polypeptide are expressed,

Date reçue / Date received 2021-12-13

thereby producing the recombinant polypeptide.

22. The method of claim 21, wherein the first LMM provides increased yield or rate of production of the recombinant polypeptide as compared to a cell not having the first LMM.

23. The method of claim 21, wherein the first LMM provides an increased ratio of properly folded product to misfolded or unfolded recombinant polypeptide as compared to a cell not having the first LMM.

24. The method of any one of claims 21 to 23 wherein the first LMM comprises an amino acid sequence with at least 80% identity with the amino acid sequence of SEQ ID NOs: 1 or 34, or a functional fragment thereof, corresponding to SEQ ID NOs: 26, 27, or 36; or differs by 1 or more amino acid residues but no more than 50 amino acid residues from the amino acid sequence of SEQ ID NOs: 1 or 34, or a functional fragment thereof corresponding to SEQ ID NOs: 26, 27, or 36.

25. The method of any one of claims 21 to 24, wherein the cell further comprises a third exogenous nucleic acid encoding a second LMM comprising stearoyl CoA desaturase (SCD1) or a functional fragment or isoform thereof, and in step (ii) the cell is cultured under conditions where the second LMM is expressed.

26. The method of claim 25 wherein the second LMM has at least 80% identity with the amino acid sequence of SEQ ID NO: 3, or a functional fragment thereof; or differs by 1 or more amino acid residues but no more than 50 amino acid residues from the amino acid sequence of SEQ ID NO: 3, or a functional fragment thereof.

27. The method of claim 25 or 26 wherein the second LMM provides increased yield of rate of production of the recombinant polypeptide as compared to a cell not having the second LMM.

28. The method of any one of claims 21 to 27, wherein production of the recombinant polypeptide is increased by 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, or 100-fold as compared to the level or quantity of recombinant polypeptide produced by a cell without the first LMM.

Date reçue / Date received 2021-12-13

29. The method of any one of claims 21 to 28, wherein the first exogenous nucleic acid encoding the first LMM is integrated into the chromosomal genome of the cell and the LMM is stably expressed.

30. The method of any one of claims 21 to 29, wherein the cell is a mammalian cell.

31. The method of any one of claims 21 to 30, further comprising separating the recombinant polypeptide from at least one cellular or medium component.

32. The method of any one of claims 21 to 31 wherein the second exogenous nucleic acid encoding a recombinant polypeptide has been introduced after introducing the first exogenous nucleic acid encoding the first LMM.

33. A eukaryotic cell comprising:

a first exogenous nucleic acid encoding a first lipid metabolism modulator (LMM), wherein the first LMM comprises Sterol Regulatory Element-Binding Transcription Factor 1 (SREBF1) or a functional fragment or isoform thereof; and

a second exogenous nucleic acid encoding a recombinant polypeptide,

wherein the first exogenous nucleic acid is integrated into the chromosomal genome of the cell and wherein the recombinant polypeptide is:

i) a therapeutic polypeptide,

ii) an antibody or fragment thereof, a monoclonal antibody, or a bispecific molecule, or

iii) selected from a hormone, a blood clotting or coagulation factor, a cytokine or growth factor, a fusion protein and a protein vaccine.

34. The cell of claim 33, wherein the cell is a mammalian cell.

35. The cell of claim 34, which is a CHO cell.

Date reçue / Date received 2021-12-13

36. The cell of any one of claims 33 to 35 wherein the first LMM provides increased yield of rate of production of the recombinant polypeptide as compared to a cell not having the first LMM.

37. The cell of any one of claims 33 to 35, wherein the first LMM provides an increased ratio of properly folded product to misfolded or unfolded recombinant polypeptide as compared to a cell not having the first LMM.

38. The cell of any one of claims 33 to 37, wherein the cell further comprises a third exogenous nucleic acid encoding a second LMM comprising stearoyl CoA desaturase-1 (SCD1) or a functional fragment or isoform thereof, and in step (ii) the cell is cultured under conditions where the second LMM is expressed.

39. The cell of claim 38 wherein the second LMM has at least 80% identity with the amino acid sequence of SEQ ID NO: 3, or a functional fragment thereof; or differs by 1 or more amino acid residues but no more than 50 amino acid residues from the amino acid sequence of SEQ ID NO: 3, or a functional fragment thereof.

40. Use of the cell of any one of claims 33 to 39 in the production of a therapeutic recombinant polypeptide of interest.

Date reçue / Date received 2021-12-13

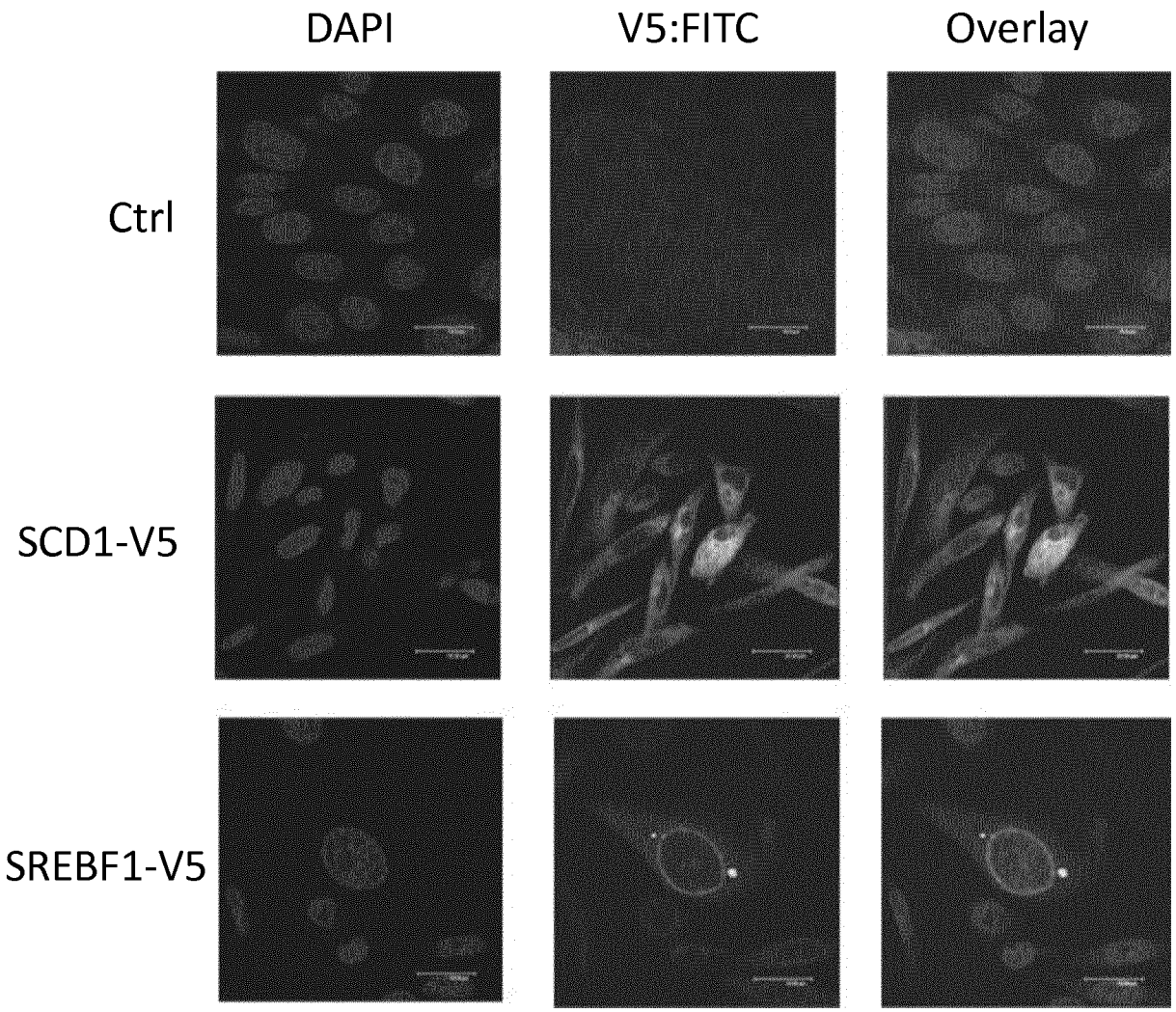


FIG. 1

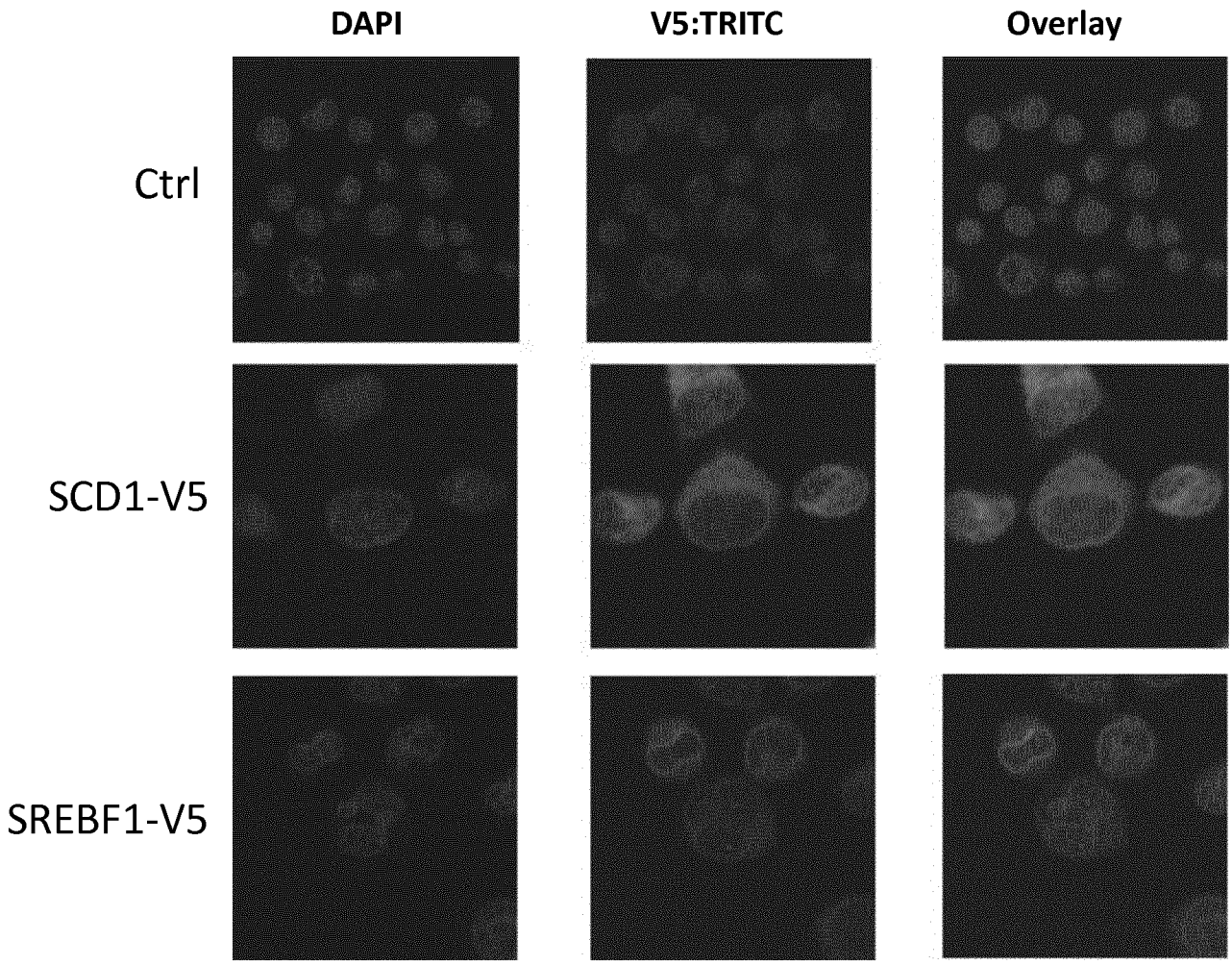


FIG. 2

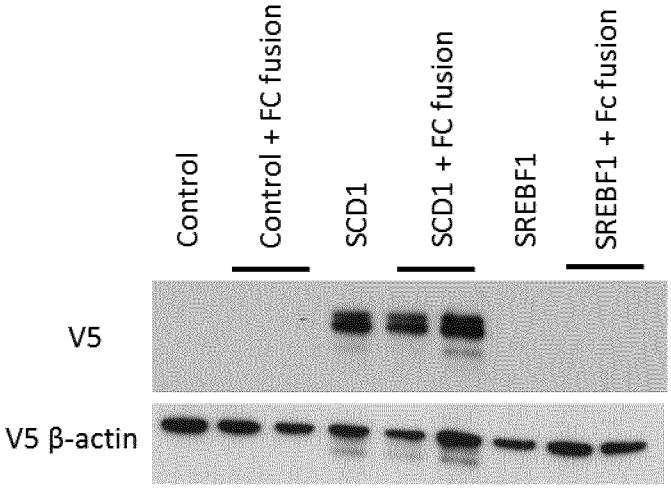


FIG. 3A

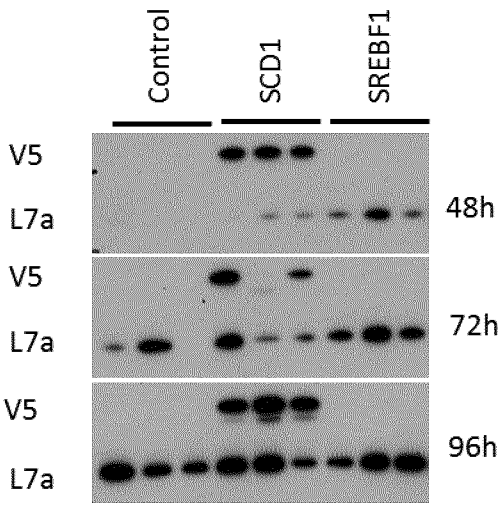


FIG. 3B

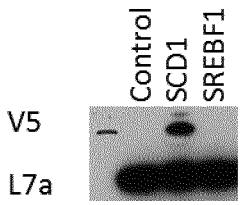


FIG. 3C

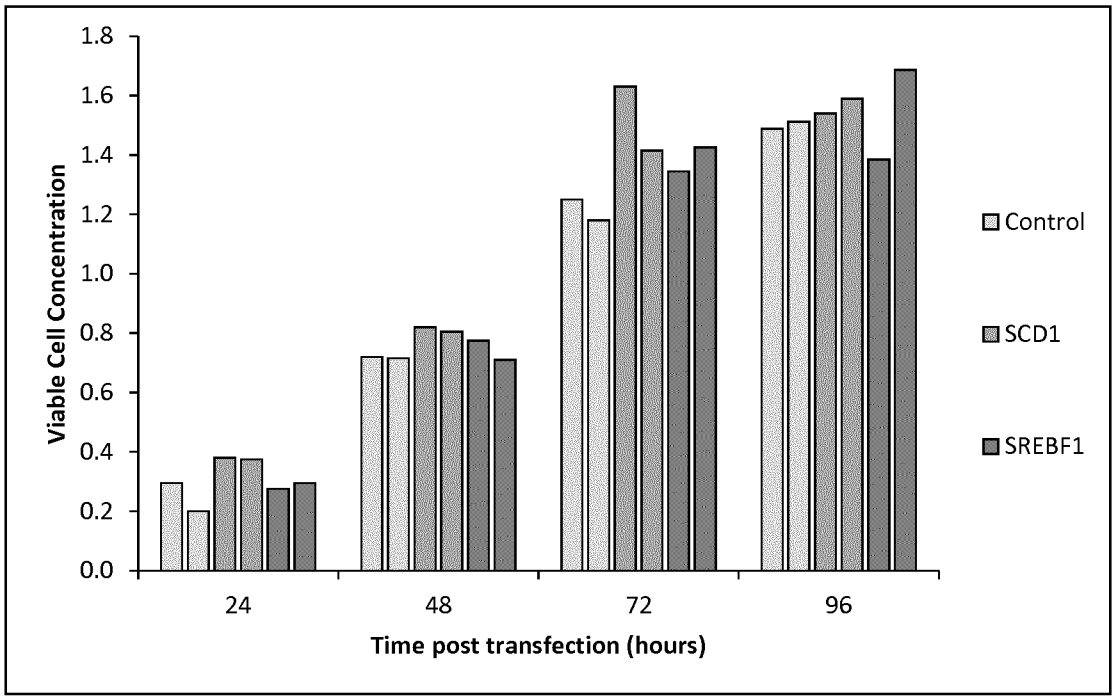

1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Viable Cell Concentration
24
48
72
96
Time post transfection (hours)
Control
SCD1
SREBF1

FIG. 4

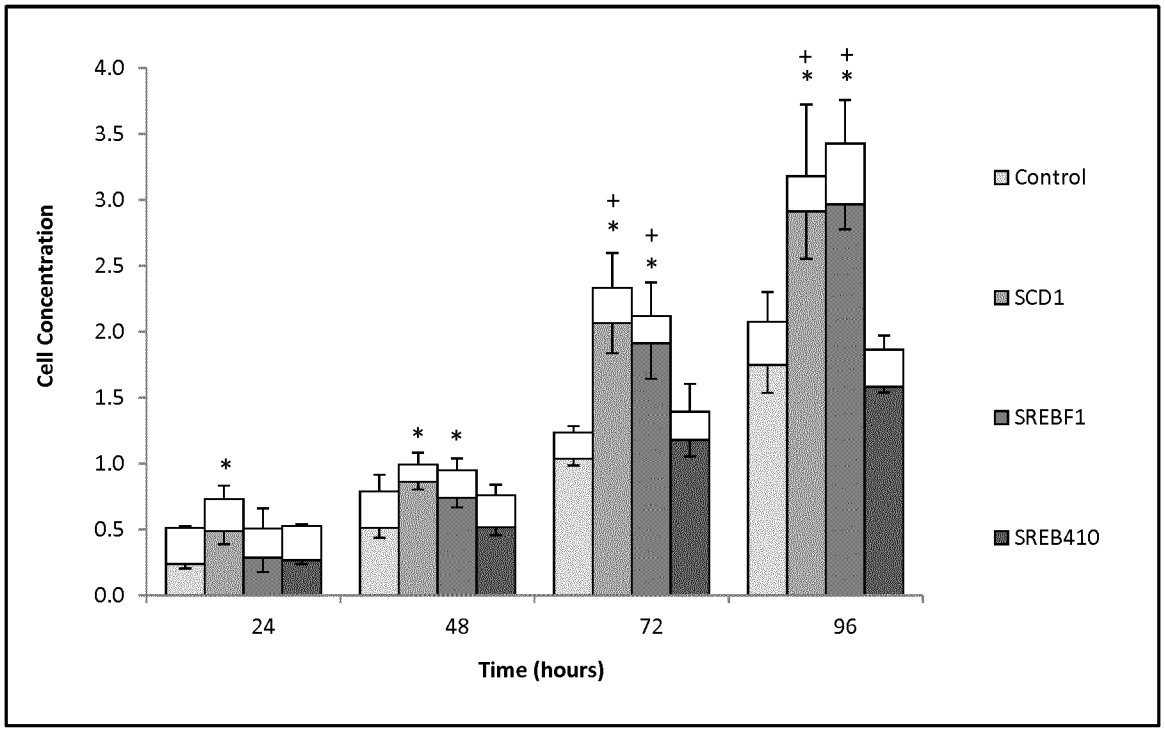

Cell Concentration
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
24
48
72
96
Time (hours)
Control
SCD1
SREBF1
SREB410

FIG. 5A

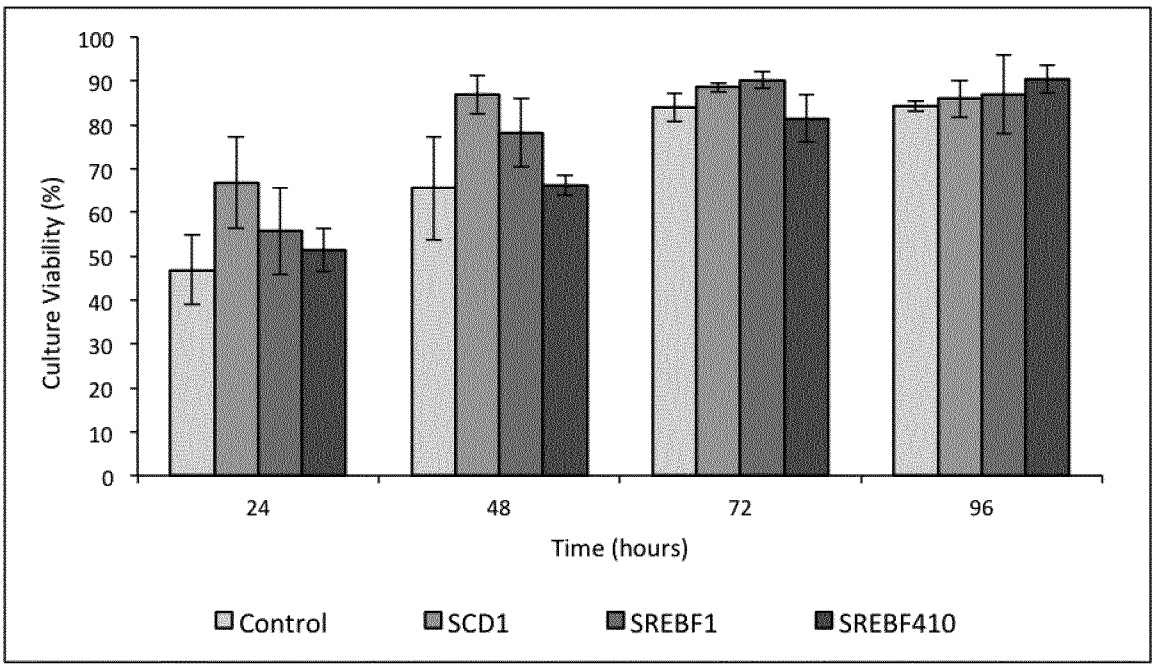

Culture Viability (%)
100
90
80
70
60
50
40
30
20
10
0
24
48
72
96
Time (hours)
Control
SCD1
SREBF1
SREBF410

FIG. 5B

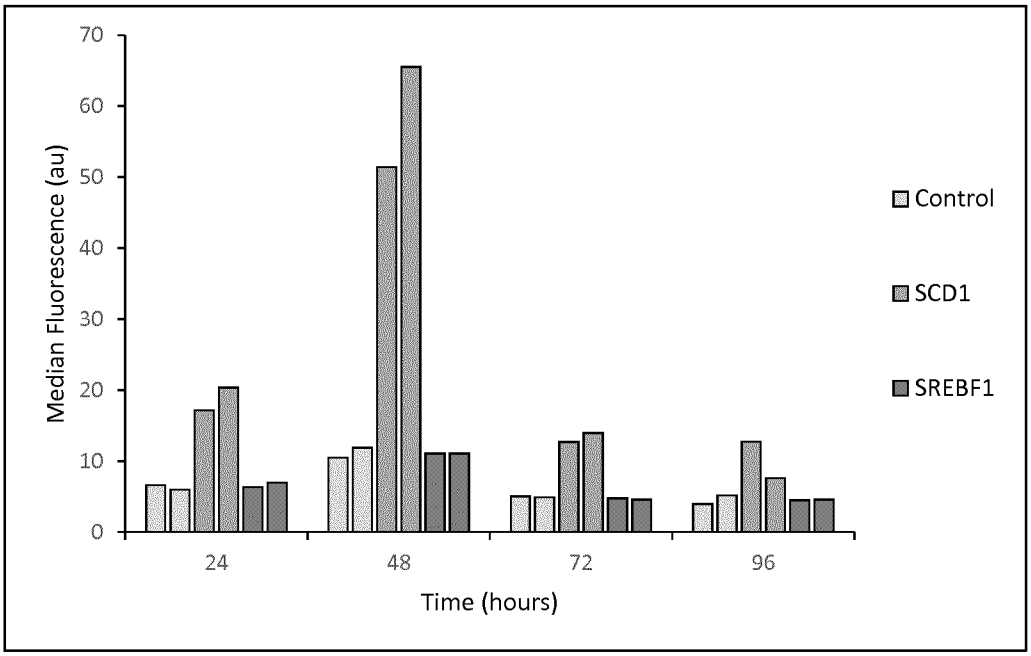

70
60
50
40
30
20
10
0
Median Fluorescence (au)
24
48
72
96
Time (hours)
Control
SCD1
SREBF1

FIG. 6A

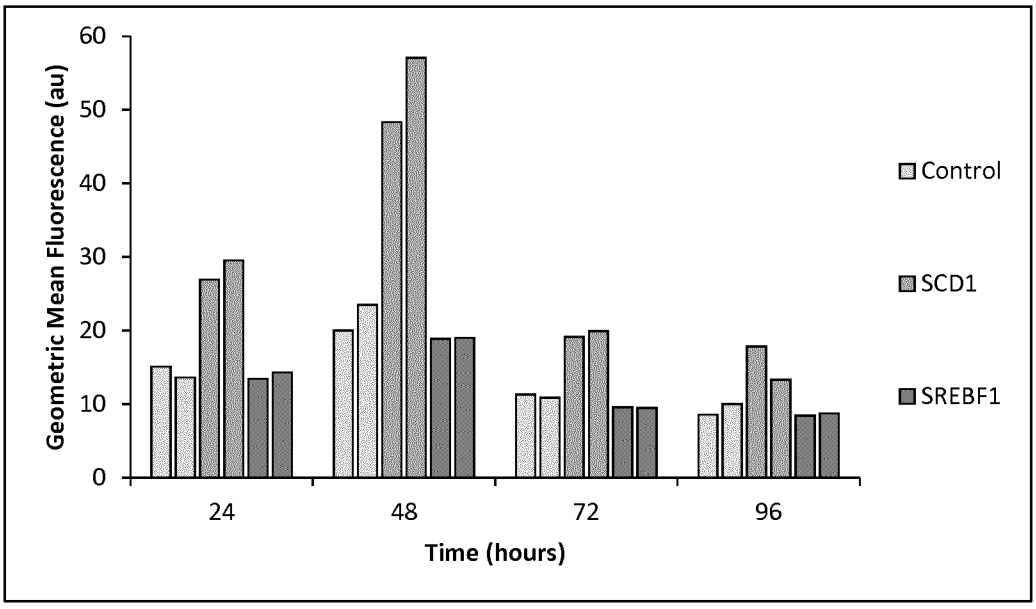

60
50
40
30
20
10
0
Geometric Mean Fluorescence (au)
24
48
72
96
Time (hours)
Control
SCD1
SREBF1

FIG. 6B

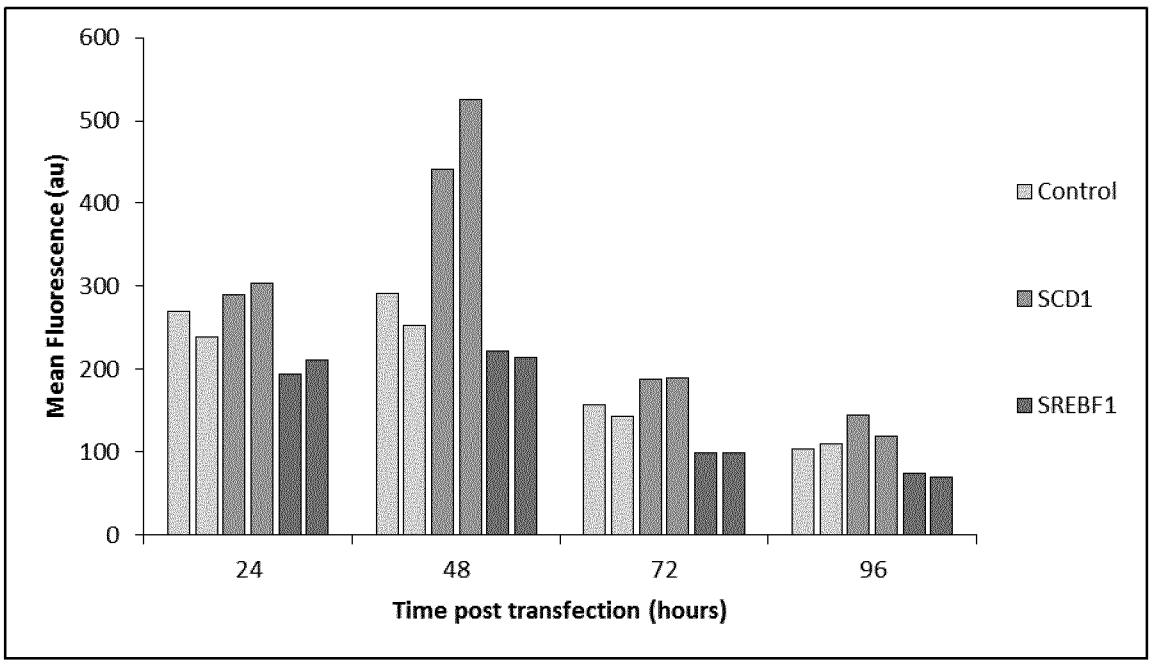

600
500
400
300
200
100
0
Mean Fluorescence (au)
24
48
72
96
Time post transfection (hours)
Control
SCD1
SREBF1

FIG. 6C

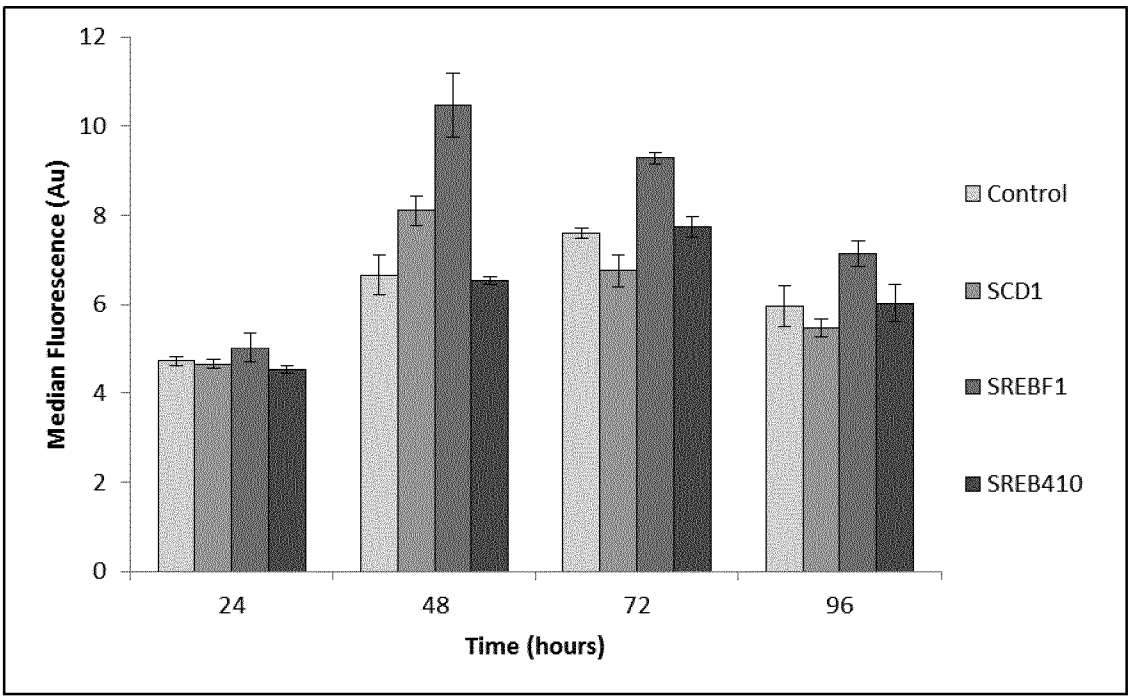

12
10
8
6
4
2
0
Median Fluorescence (Au)
24
48
72
96
Time (hours)
Control
SCD1
SREBF1
SREB410

FIG. 7A

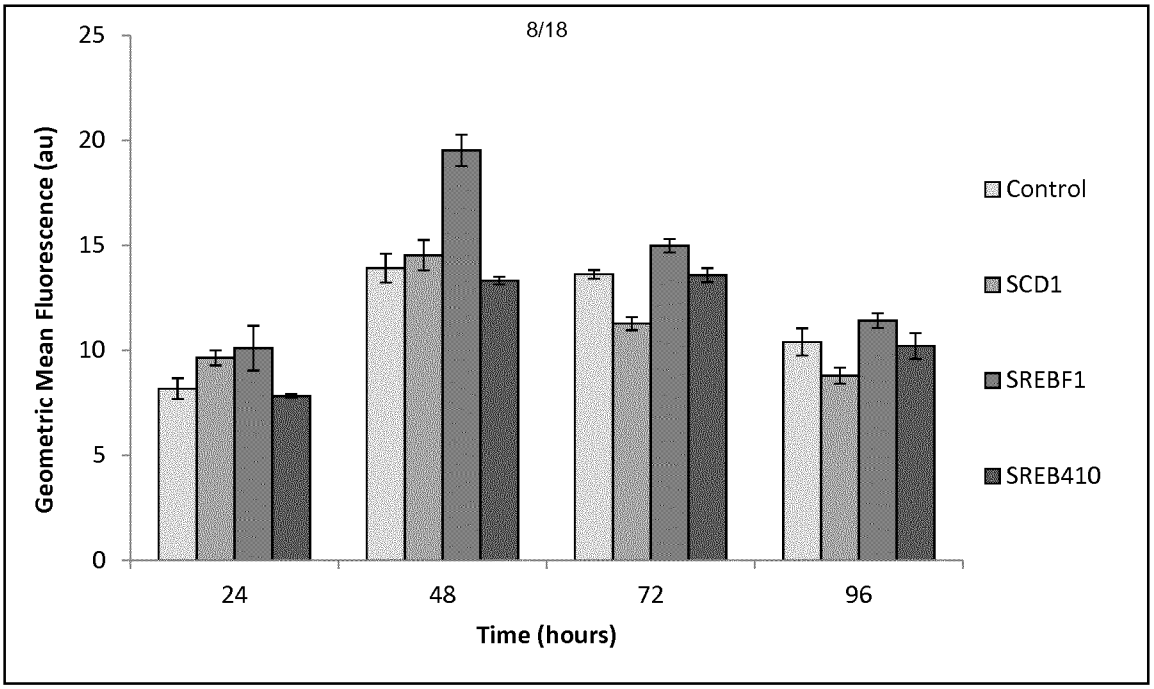

Geometric Mean Fluorescence (au)
25
20
15
10
5
0
24
48
72
96
Time (hours)
Control
SCD1
SREBF1
SREB410

FIG. 7B

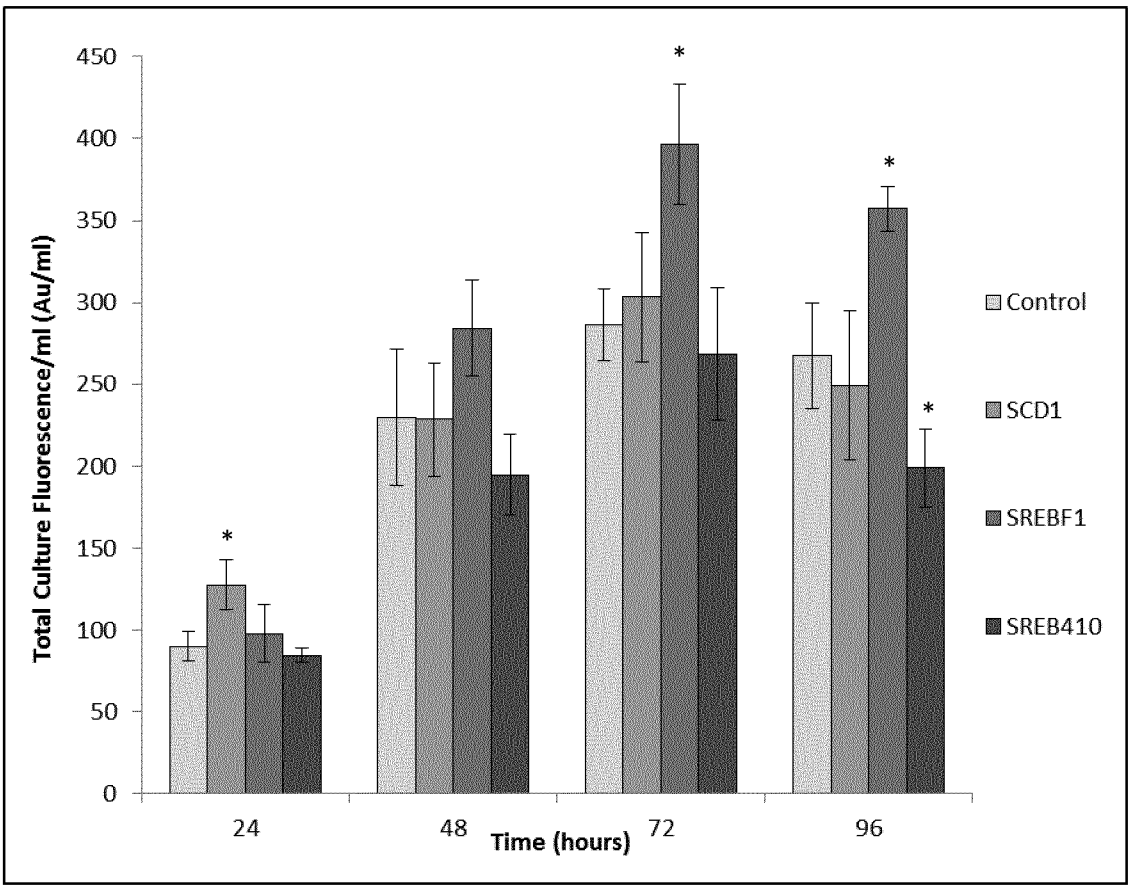

Total Culture Fluorescence/ml (Au/ml)
450
400
350
300
250
200
150
100
50
0
*
*
*
*
24
48
72
96
Time (hours)
Control
SCD1
SREBF1
SREB410

FIG. 7C

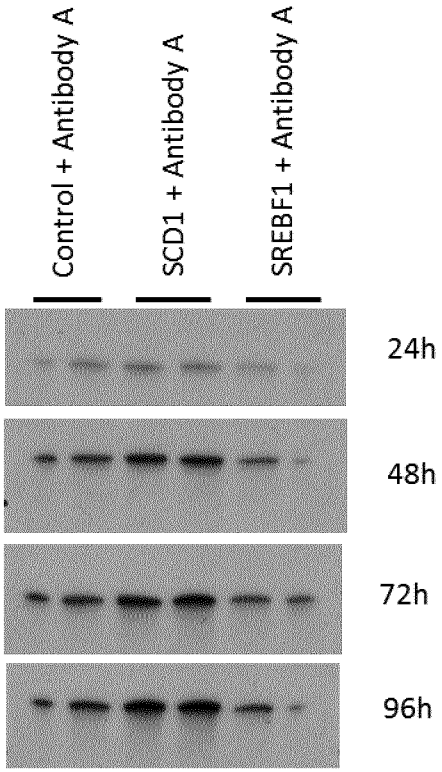

Control + Antibody A
SCD1 + Antibody A
SREBF1 + Antibody A
24h
48h
72h
96h

FIG. 8A

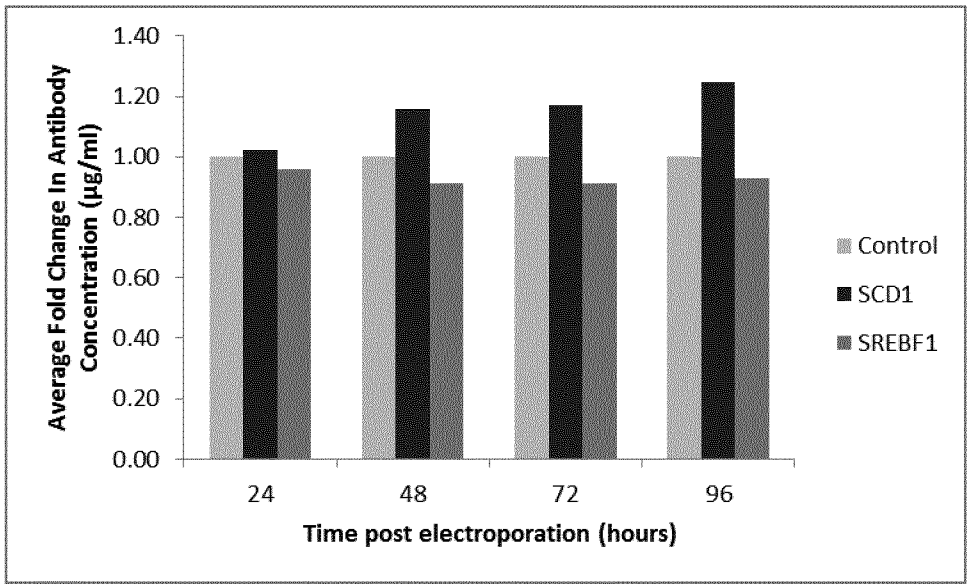

Average Fold Change In Antibody Concentration (µg/ml)
1.40
1.20
1.00
0.80
0.60
0.40
0.20
0.00
24
48
72
96
Time post electroporation (hours)
Control
SCD1
SREBF1

FIG. 8B

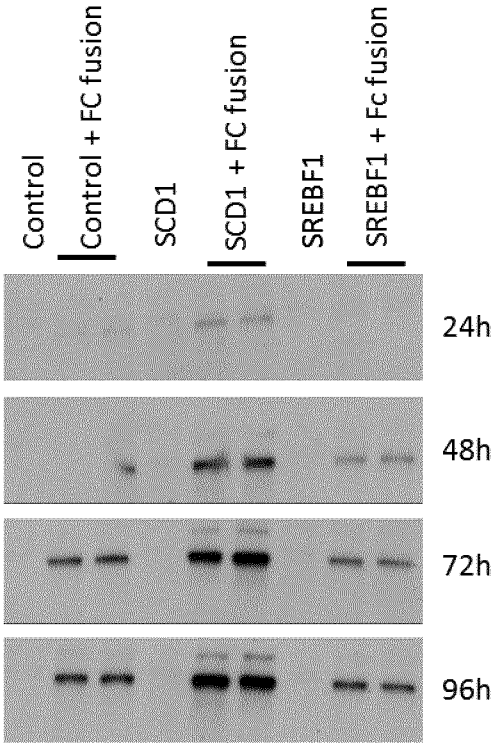

Control
Control + FC fusion
SCD1
SCD1 + FC fusion
SREBF1
SREBF1 + Fc fusion
24h
48h
72h
96h

FIG. 9A

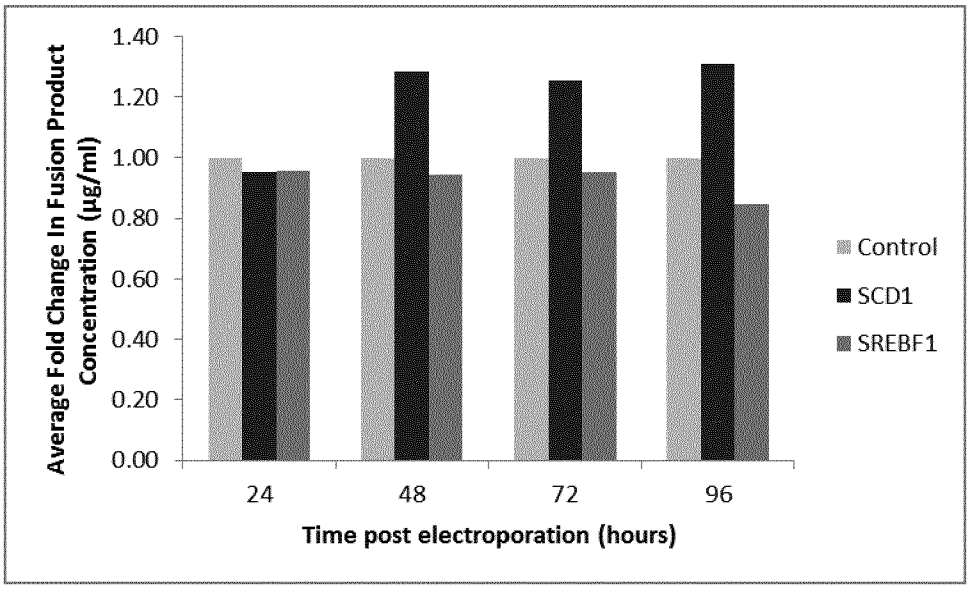

Average Fold Change In Fusion Product Concentration (µg/ml)
1.40
1.20
1.00
0.80
0.60
0.40
0.20
0.00
24
48
72
96
Time post electroporation (hours)
Control
SCD1
SREBF1

FIG. 9B

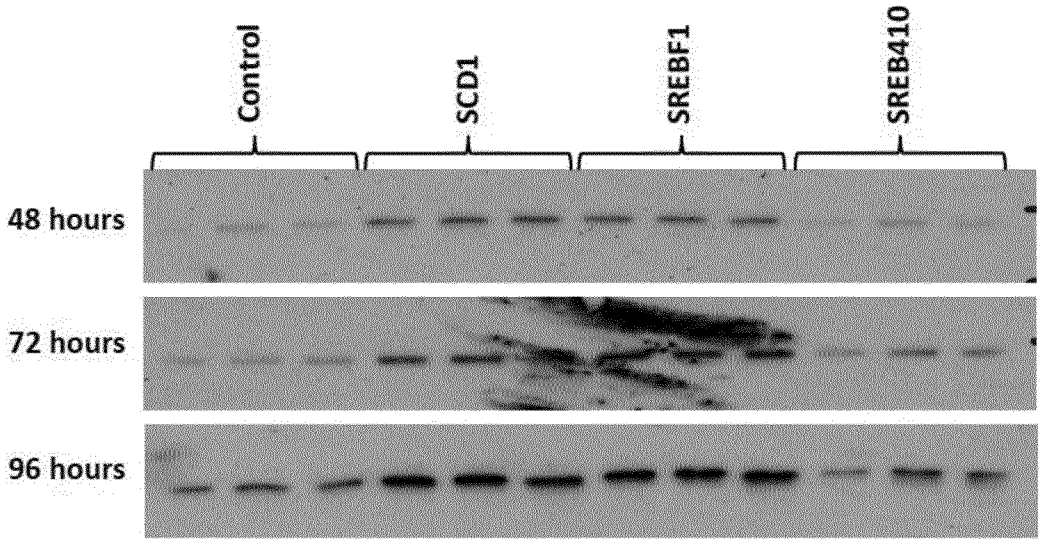


FIG. 10A

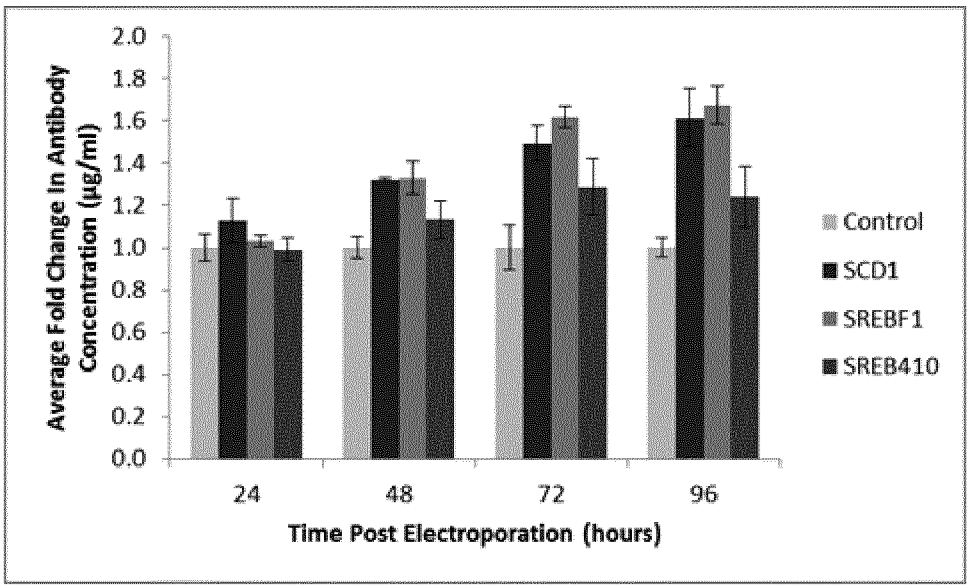


FIG. 10B

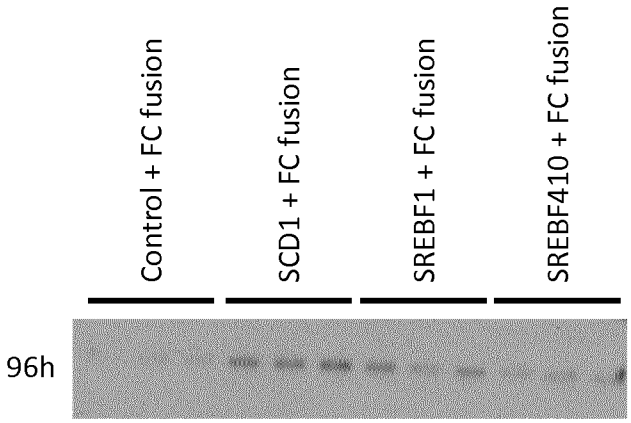


FIG. 11A

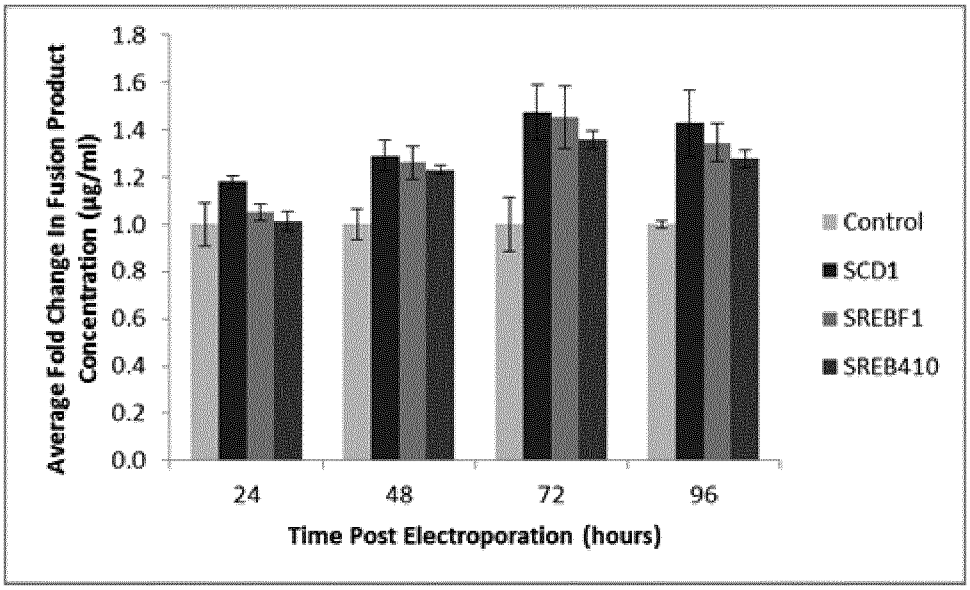


FIG. 11B

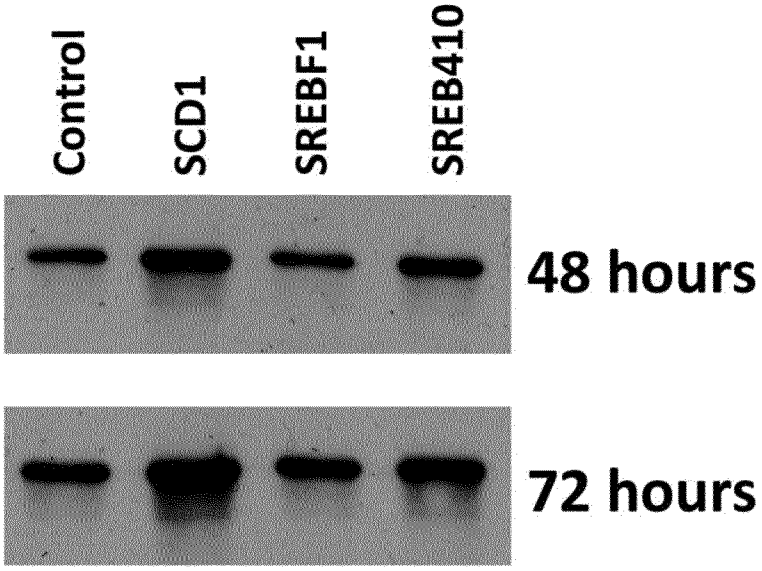


FIG. 12A

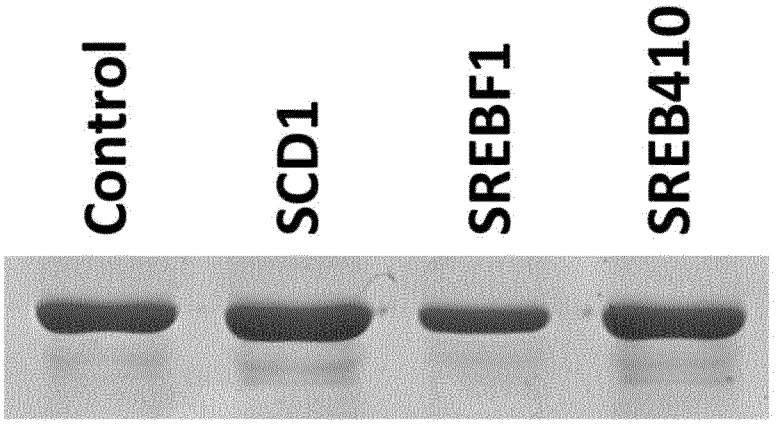


FIG. 12B

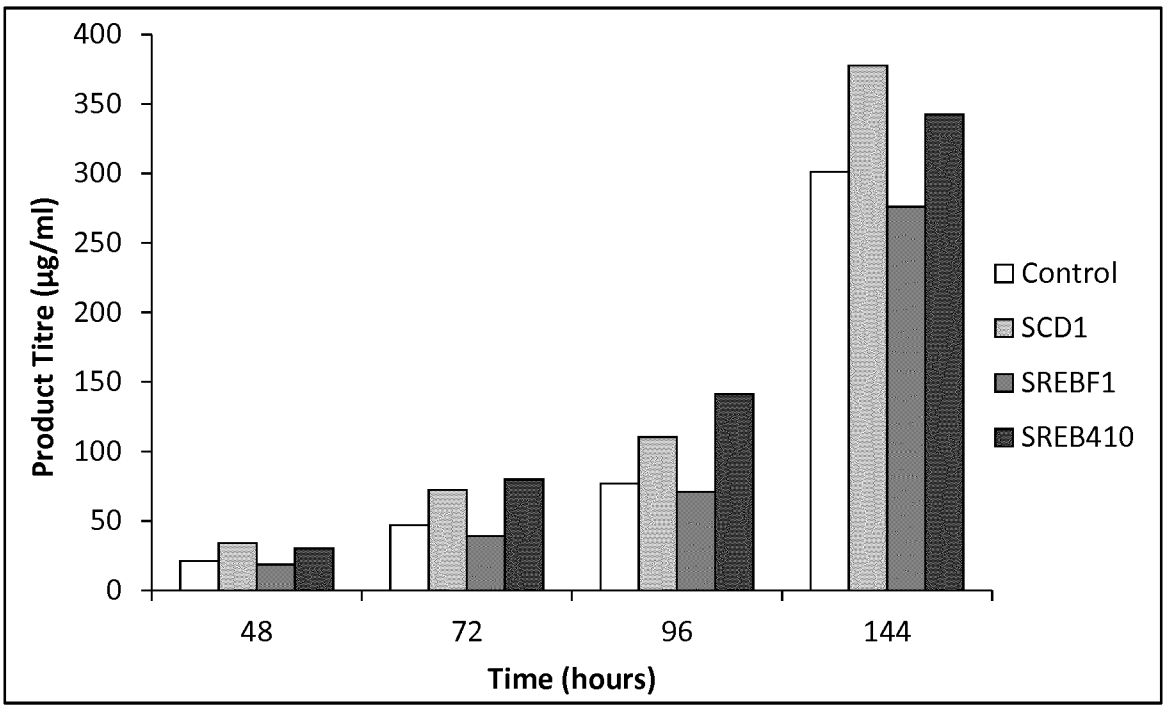

400
350
300
250
200
150
100
50
0
Product Titre (µg/ml)
48
72
96
144
Time (hours)
Control
SCD1
SREBF1
SREB410

FIG. 13

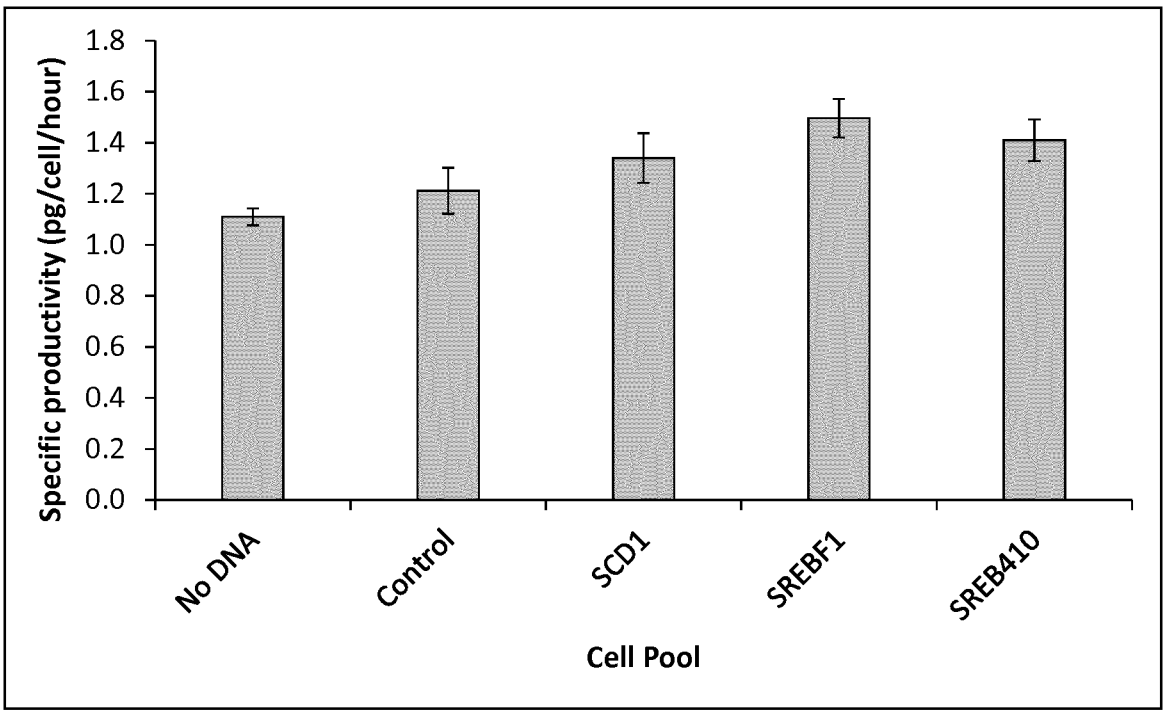

Specific productivity (pg/cell/hour)
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
No DNA
Control
SCD1
SREBF1
SREB410
Cell Pool

FIG. 14

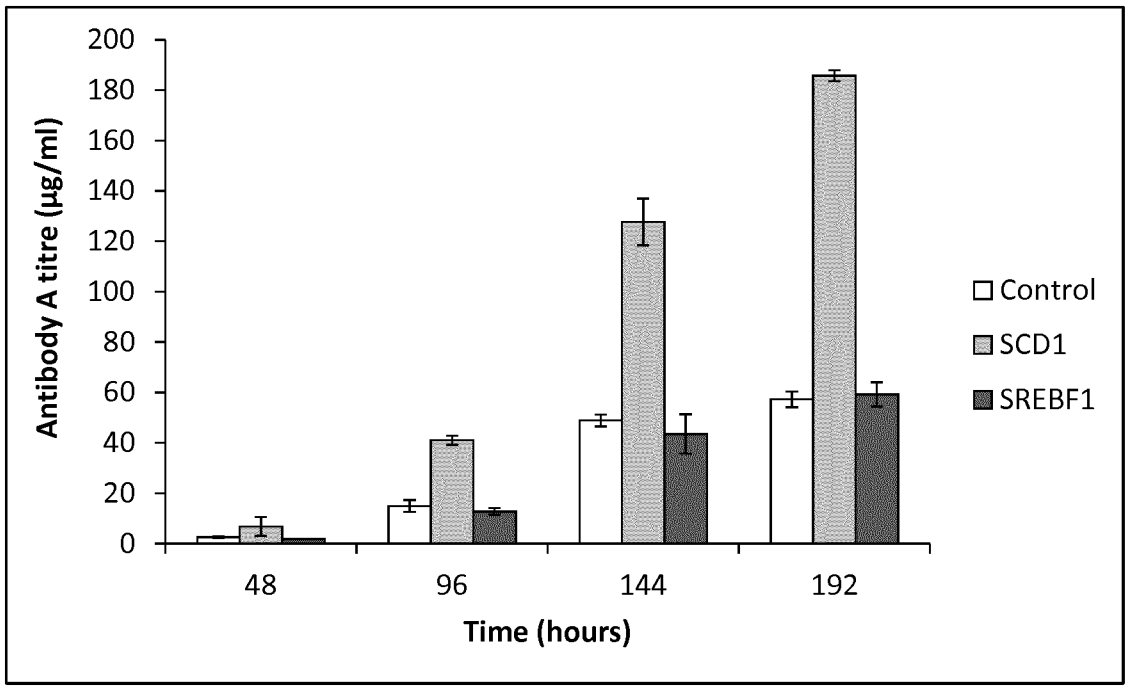


FIG. 15A

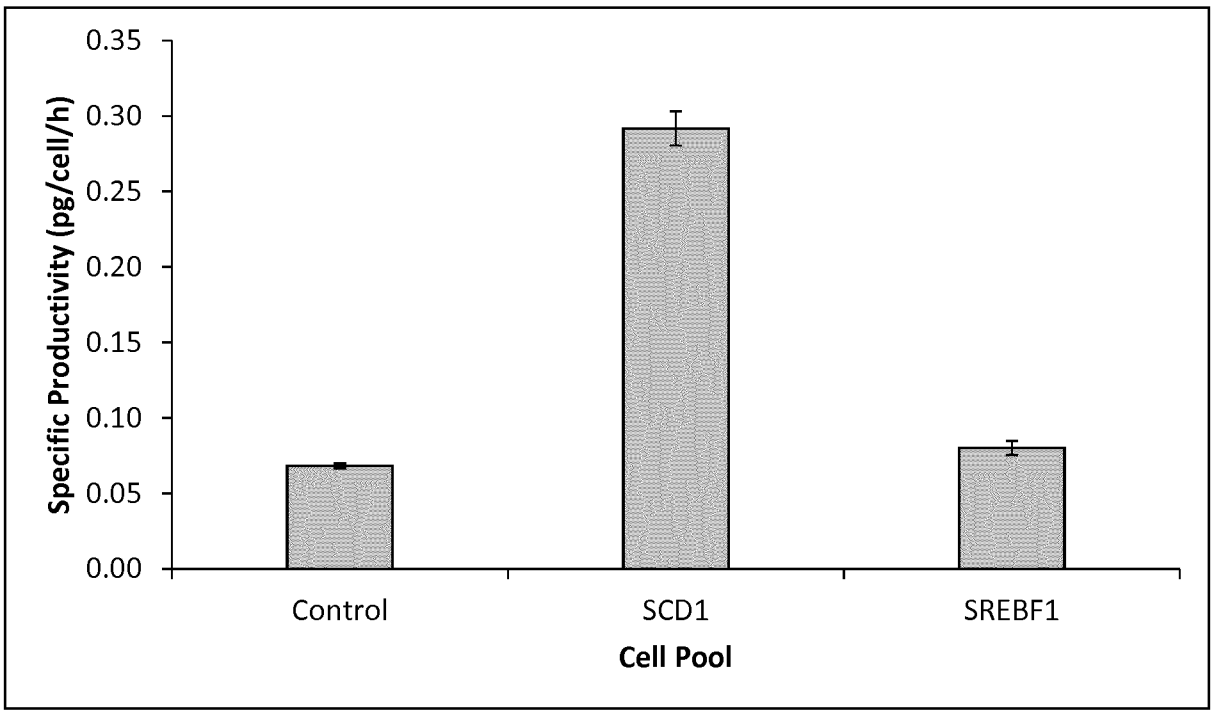


FIG. 15B

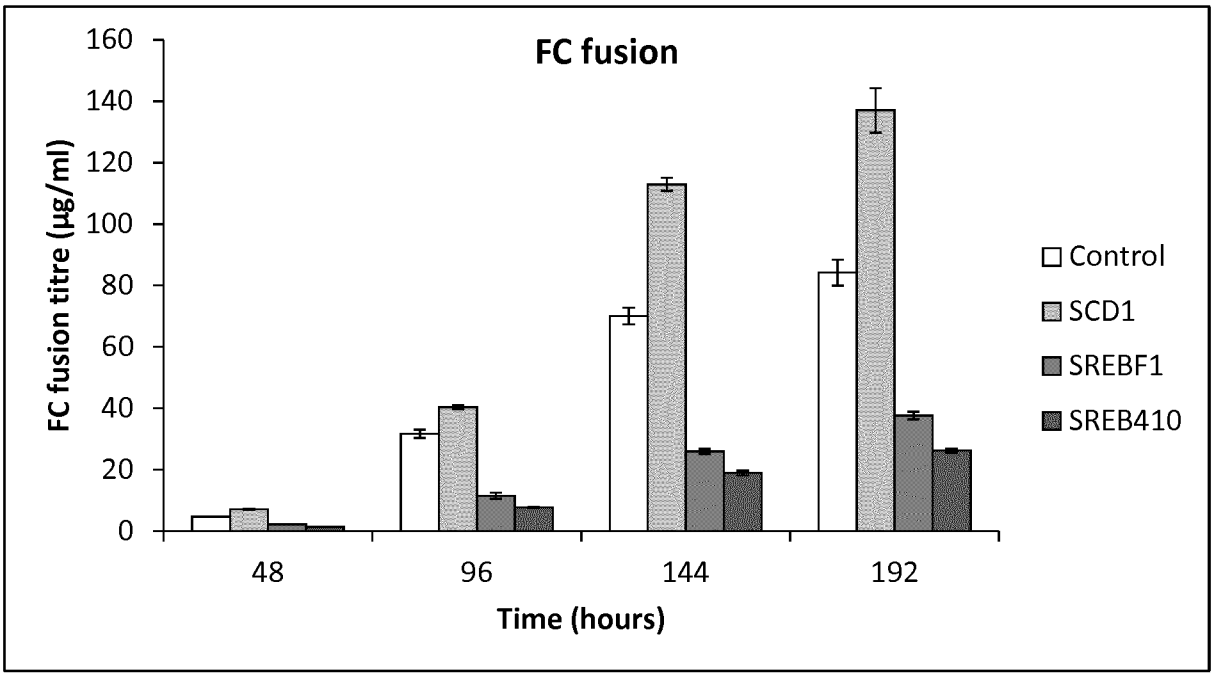


FIG. 16A

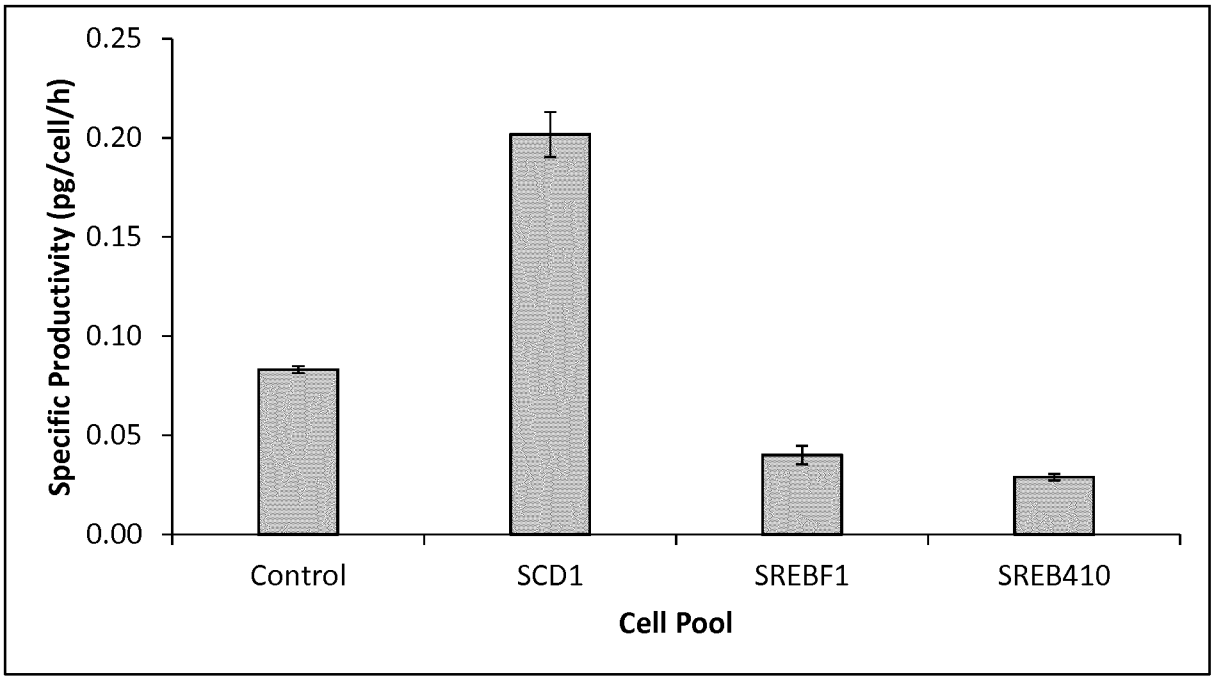


FIG. 16B

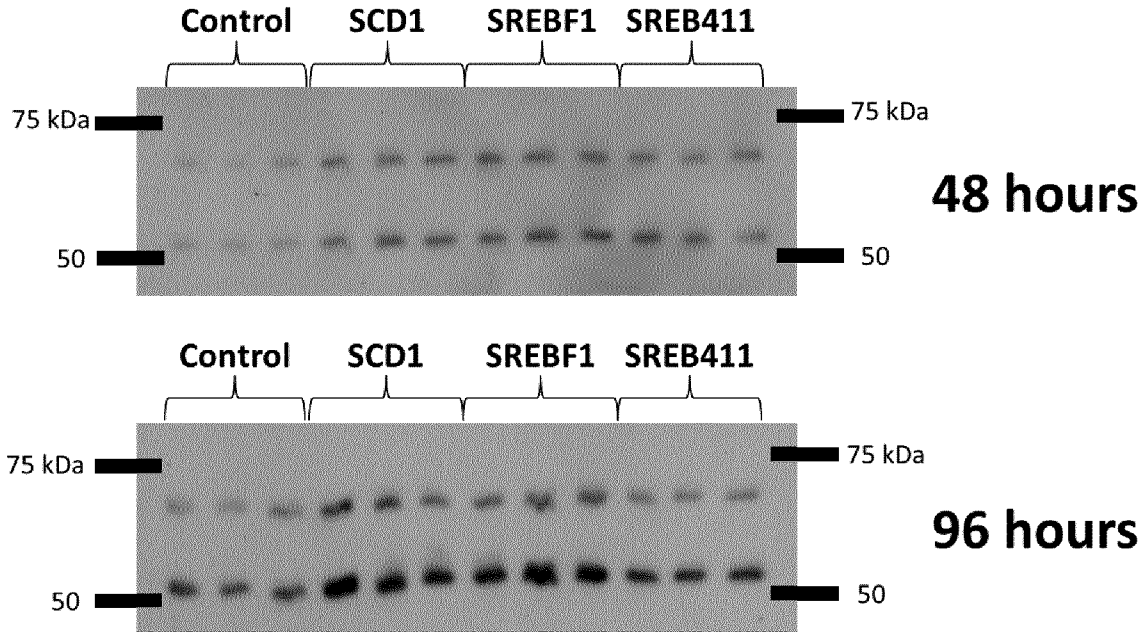


FIG. 17A

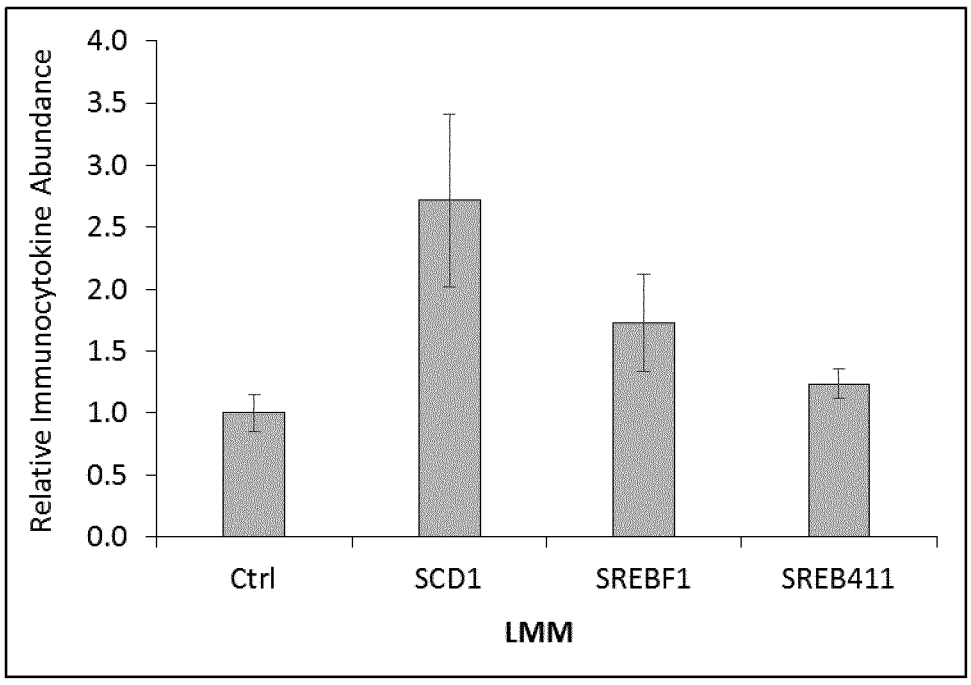
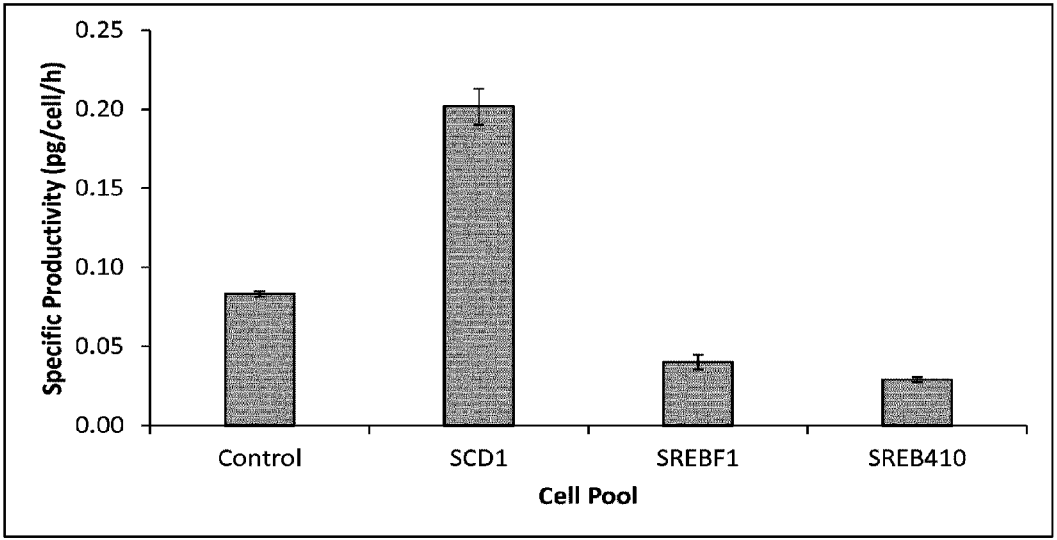


FIG. 17B


0.25
0.20
0.15
0.10
0.05
0.00
Specific Productivity (pg/cell/h)
Control
SCD1
SREBF1
SREB410
Cell Pool