

-continued

- (ix) FEATURE:
  - (A) NAME/KEY: Other
  - (B) LOCATION: 1...16
  - (D) OTHER INFORMATION: N-terminal acetylated and C-terminal amidated

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256 :

Pro Val Leu Asp Leu Phe Arg Glu Leu Leu Glu Ala Leu Lys Gln Lys  
 1                    5                                    10                                    15

(2) INFORMATION FOR SEQ ID NO:257:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

- (ix) FEATURE:
  - (A) NAME/KEY: Other
  - (B) LOCATION: 1...16
  - (D) OTHER INFORMATION: N-terminal acetylated and C-terminal amidated

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257 :

Pro Val Leu Asp Leu Phe Glu Asn Leu Leu Glu Arg Leu Lys Gln Lys  
 1                    5                                    10                                    15

(2) INFORMATION FOR SEQ ID NO:258:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

- (ix) FEATURE:
  - (A) NAME/KEY: Other
  - (B) LOCATION: 1...16
  - (D) OTHER INFORMATION: N-terminal acetylated and C-terminal amidated

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258 :

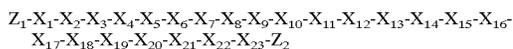
Pro Val Leu Asp Leu Phe Arg Glu Leu Leu Asn Glu Leu Lys Gln Lys  
 1                    5                                    10                                    15

What is claimed is:

1. An ApoA-I agonist-lipid complex comprising an ApoA-I agonist compound and a lipid.

2. The complex of claim 1 in which the ApoA-I agonist compound comprises:

- (i) a 15 to 29-residue peptide or peptide analogue which forms an amphipathic  $\alpha$ -helix in the presence of lipids and which comprises formula (I):



or a pharmaceutically acceptable salt thereof, wherein:

- X<sub>1</sub> is Pro (P), Ala (A), Gly (G), Gln (Q), Asn (N), Asp (D) or D-Pro (p);
- X<sub>2</sub> is an aliphatic residue;
- X<sub>3</sub> is Leu (L) or Phe (F);
- X<sub>4</sub> is an acidic residue;
- X<sub>5</sub> is Leu (L) or Phe (F);

- X<sub>6</sub> is Leu (L) or Phe (F);
- X<sub>7</sub> is a hydrophilic residue;
- X<sub>8</sub> is an acidic or a basic residue;
- X<sub>9</sub> is Leu (L) or Gly (G);
- X<sub>10</sub> is Leu (L), Trp (W) or Gly (G);
- X<sub>11</sub> is a hydrophilic residue;
- X<sub>12</sub> is a hydrophilic residue;
- X<sub>13</sub> is Gly (G) or an aliphatic residue;
- X<sub>14</sub> is Leu (L), Trp (W), Gly (G) or Nal;
- X<sub>15</sub> is a hydrophilic residue;
- X<sub>16</sub> is a hydrophobic residue;
- X<sub>17</sub> is a hydrophobic residue;
- X<sub>18</sub> is Gln (Q), Asn (N) or a basic residue;
- X<sub>19</sub> is Gln (Q), Asn (N) or a basic residue;
- X<sub>20</sub> is a basic residue;
- X<sub>21</sub> is an aliphatic residue;