

## CLAIMS

1. A method for identifying a target protein of a drug molecule, comprising the steps of:
  - (a) preparing mixture A comprising cell lysates or human-derived cells;
  - (b) preparing mixture B comprising the mixture of cell lysates or human-derived cells, and a drug molecule;
  - (c) modifying the temperature of mixture A and mixture B to a specific and same temperature in the range from 37 to 70°C;
  - (d) mixing each of mixture A and mixture B at a specific temperature as obtained in step (c) with fluorescent materials having a different wavelength from each other, respectively, so that the proteins existed in a soluble fraction of each of mixture A and mixture B are labelled with the fluorescent materials having a different wavelength from each other, respectively;
  - (e) mixing mixture A and mixture B as obtained in step (d) to prepare mixture C;
  - (f) performing two-dimensional electrophoresis of mixture C; and
  - (g) analyzing a fluorescence wavelength of a protein spot shown in a gel by the electrophoresis of step (f) to confirm a protein showing thermal stability shift resulting from step (c).
2. The method according to Claim 1, characterized in further comprising the step of plotting a melting curve graph for each protein spot in step (g).
3. The method according to Claim 1, characterized in that the drug molecule of step (b) is a bioactive molecule.
4. The method according to Claim 1, characterized in that the protein obtained in step (g) is a membrane-anchored protein.
5. The method according to Claim 1, characterized in that in the thermal stability shift of step (g), the protein existed in mixture B is thermally stabilized by engagement with the drug molecule.

6. The method according to Claim 5, characterized in that the protein is nucleophosmin (NPM) and the drug molecule is hordenine as a bioactive molecule.

7. The method according to Claim 1, characterized in that in the thermal stability shift of step (g), the protein existed in mixture B is thermally destabilized by engagement with the drug molecule.

8. The method according to Claim 7, characterized in that the protein is protein kinase C $\alpha$  (PKC $\alpha$ ) and the drug molecule is bryostatin 1 as a bioactive molecule.

9. The method according to Claim 1, characterized in that the fluorescent material of step (d) is at least one selected from the group consisting of Cy2, Cy3, Cy5, fluorescein, Alexafluor488, R6G, HEX, AlexaFluor32, TAMRA, AlexaFluor546, EtBr, SYPRO Ruby, and Blue FAM.

10. The method according to Claim 9, characterized in that in step (d), the fluorescent material mixed with mixture A is Cy3 and the fluorescent material mixed with mixture B is Cy5.

11. The method according to Claim 10, characterized in that an amine-reactive functional group is further bonded to Cy3 and Cy5.

12. The method according to Claim 1, characterized in that the analysis of the fluorescence wavelength of step (g) consists of the analysis of the ratio between the fluorescence wavelength generated from the fluorescent material labelled on the protein existed in the soluble fraction of mixture A and the fluorescence wavelength generated from the fluorescent material labelled on the protein existed in the soluble fraction of mixture B.