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(54) **INTEGRATION DYSFUNCTION SYNDROME MARKER SET AND UTILIZATION THEREOF**

(57) The object is to provide a combination of biomarkers which allow highly accurate discrimination of schizophrenia, and a utilization thereof. A combination of schizophrenia marker set including a combination of two or more protein molecules selected from the group consisting of trifunctional purine biosynthetic protein adenosine-3, uroporphyrinogen decarboxylase, interferon-in-

duced GTP-binding protein Mx1, glutaredoxin-3, microtubule-associated protein RP/EB family member 1, tubulin folding cofactor B, immunoglobulin mu chain C region, and heat shock 70 kDa protein 4L is provided. In addition, a method for examining schizophrenia using the level of the marker set in a specimen as an index is provided.

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Description

[TECHNICAL FIELD]

5 **[0001]** The present invention relates to a schizophrenia marker useful for the examination of schizophrenia, and more specifically to a combination of biomarkers (biomarker set) usable for the determination of onset possibility (prevalence rate) of schizophrenia, and a method for examining schizophrenia using the same. The present application claims priority based on Japanese Patent Application No. 2012-228417 filed on October 15, 2012, and the content of the patent application is hereby incorporated by reference in its entirety.

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[BACKGROUND ART]

15 **[0002]** Schizophrenia is a chronic and progressive mental disorder developed during puberty and adolescence, and its main symptoms are positive symptoms (hallucinations and delusion, disorganized speech/behavior), negative symptoms (for example, flat affect, poverty of thought content, and loss of motivation) and cognition disorder (attentional dysfunction, poor working memory, and executive function deficits). Schizophrenia is regarded as a multifactorial disorder involved with genetic and environmental factors, and there are still many unknown points regarding the molecular biological mechanism of the disease state of schizophrenia, and thus no biochemical test method has been found.

20 **[0003]** Diagnosis of schizophrenia is carried out by diagnosis (symptomatology) based on medical health questionnaire and patient's complaint, and there is no established diagnosis method by more empirical methods such as biochemical examination or similar. Schizophrenia progresses in several years after development, irreversible damage is caused, which likely causes permanent disturbance in social function. However, therapeutic intervention is delayed because there is no examination method useful for diagnosis, so that considerable cases are advancing in severity. Development of an examination method useful for the diagnosis of schizophrenia is desired. However, this disease is regarded as developed by disorders of cerebral molecules, while it is very difficult to detect the molecular pathogenesis in the brain, so that the development of the examination method is not proceeding.

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30 **[0004]** From the result of studies such as twin studies, it was proved that hereditary factors are markedly involved with the development of schizophrenia. Some candidate genes which are suggested to be involved with the development of schizophrenia have been identified by gene analysis using the patients with schizophrenia and healthy subjects (for example, Non-Patent Literatures 1 to 3), but there are few clues for clarifying the association between these genes and the disease state of schizophrenia, so that the molecular mechanism developing the disease has not been elucidated. As a result of this, pathophysiology of the disease is still unknown, so that there is no established diagnosis method based on biochemical examination.

35 [CITATION LIST]

[PATENT DOCUMENT]

40 **[0005]** Patent Literature 1: Japanese Unexamined Patent Application Publication No. 2012-013415

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[NON-PATENT DOCUMENT]

[0006]

45 Non-Patent Literature 1: Arcos-Burgos M. et al., Am J Hum Genet 77,6 p937-44, 2005
 Non-Patent Literature 2: Lewis CM. et al., Am J Hum Genet 73, 34-48, 2003
 Non-Patent Literature 3: Badner JA. And Gershon ES., Mol Psychiatry 7, 405-11, 2002

50 [SUMMARY OF THE INVENTION]

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[PROBLEM OF BE SOLVED BY INVENTION]

55 **[0007]** The present invention is intended to provide a combination of biomarkers and utilization thereof (for example, an examination method, an examination reagent, and an examination kit) which allow highly accurate discrimination of schizophrenia.

[MEANS FOR SOLVING PROBLEM]

[0008] In order to find biomarkers specific to schizophrenia, the inventors carried out researches with focus on the lymphocytes contained in the peripheral blood. As a result of this, 22 proteins which showed a significant difference between the patient and healthy subject groups in the expression level were reported (Patent Literature 1). Most of the identified proteins were found to be expressed in the brain. Therefore, the possibility of their deep involvement with pathogenesis of schizophrenia was strongly suggested.

[0009] Each of the 22 identified proteins is highly useful. However, high discrimination accuracy as possible is demanded in clinical fields, and such demand is hard to be satisfied by a single biomarker. In addition, in order to achieve further higher accuracy in the discrimination of schizophrenia or other disease developed by various factors, combination of a plurality of biomarkers is considered advantageous. From this viewpoint, the identification of the combinations of biomarkers which allow highly accurate discrimination was aimed using a statistical method. As a result of this, markedly effective biomarkers were found, and the combinations of biomarkers that bring about very high discrimination accuracy were successfully identified. The examination using the combination of the specified biomarkers is markedly practical, and is expected to contribute to dramatic improvement in diagnosis techniques of schizophrenia. The present invention described below is mainly based on the above results.

[1] A schizophrenia marker set including a combination of two or more protein molecules selected from the group consisting of trifunctional purine biosynthetic protein adenosine-3, uroporphyrinogen decarboxylase, interferon-induced GTP-binding protein Mx1, glutaredoxin-3, microtubule-associated protein RP/EB family member 1, tubulin folding cofactor B, immunoglobulin mu chain C region, and heat shock 70 kDa protein 4L.

[2] The schizophrenia marker set of [1], which includes at least trifunctional purine biosynthetic protein adenosine-3, uroporphyrinogen decarboxylase, interferon-induced GTP-binding protein Mx1, and glutaredoxin-3.

[3] The schizophrenia marker set of [2], which further includes microtubule-associated protein RP/EB family member 1 and/or tubulin folding cofactor B.

[4] The schizophrenia marker set of [1], which is a combination of trifunctional purine biosynthetic protein adenosine-3, uroporphyrinogen decarboxylase, interferon-induced GTP-binding protein Mx1, glutaredoxin-3, microtubule-associated protein RP/EB family member 1, and tubulin folding cofactor B.

[5] The schizophrenia marker set of [1], which is a combination of trifunctional purine biosynthetic protein adenosine-3, uroporphyrinogen decarboxylase, interferon-induced GTP-binding protein Mx1, and glutaredoxin-3.

[6] The schizophrenia marker set of [1], which includes at least trifunctional purine biosynthetic protein adenosine-3 and interferon-induced GTP-binding protein Mx1.

[7] The schizophrenia marker set of [1], which is a combination of trifunctional purine biosynthetic protein adenosine-3 and interferon-induced GTP-binding protein Mx1.

[8] The schizophrenia marker set of [1], which includes one or more protein molecules selected from the group consisting of trifunctional purine biosynthetic protein adenosine-3, interferon-induced GTP-binding protein Mx1, and heat shock 70 kDa protein 4L.

[9] An examination method for schizophrenia using the level of the schizophrenia marker set of any one of [1] to [8] in the specimen as an indication.

[10] The examination method for schizophrenia of [9], which includes the following steps (1) to (3):

- (1) a step of preparing a specimen derived from the subject;
- (2) a step of detecting the protein molecules composing the marker set in the specimen; and
- (3) a step of determining the present or future development possibility of schizophrenia based on the detection result.

[11] The examination method for schizophrenia of [10], wherein a lower detected value shows a higher development possibility of schizophrenia for trifunctional purine biosynthetic protein adenosine-3, uroporphyrinogen decarboxylase, glutaredoxin-3, microtubule-associated protein RP/EB family member 1, tubulin folding cofactor B, and heat shock 70 kDa protein 4L, and a higher detected value shows a higher development possibility of schizophrenia for interferon-induced GTP-binding protein Mx1 and immunoglobulin mu chain C region.

[12] The examination method for schizophrenia of [10] or [11], wherein the determination of step (3) is carried out using a logistic model.

[13] The examination method for schizophrenia of any one of [9] to [12], wherein the specimen is blood, blood plasma, blood serum, oral mucosa, nasal mucosa, skin, blood cells, or lymphoblastoid cells prepared by immortalizing the blood lymphocytes collected from the subject.

[14] A kit for examining schizophrenia including a reagent for detecting the protein molecules composing the schizophrenia marker set of [1], and an instruction manual.

[15] The kit for examining schizophrenia of [14], wherein each of the reagents is an antibody to the target protein molecule.

[BRIEF DESCRIPTION OF THE DRAWINGS]

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[0010]

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Fig. 1 shows the result of expression analysis (Western blot test and 2D-DIGE method). The S/C (the ratio between the schizophrenia patient group and the healthy subject group) and the p value (Student's t-test) of each analysis are shown.

Fig. 2 shows the characteristics of the top 30 models with a higher corrected AUC.

Fig. 3 shows the odds ratio of protein contained in the candidate model 1.

Fig. 4 shows the odds ratio of protein contained in the candidate model 2.

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Fig. 5 shows the validation of effectiveness of the selected biomarkers. The 30 specimens used for screening the biomarkers (screening data) and other 30 specimens (validation data) were used for the validation.

Fig. 6 shows the validation of the effectiveness of the selected biomarkers. The validation results are summarized together with the explanation of the functions of the biomarkers.

Fig. 7 shows the validation of the four biomarkers (MX1, GART, UROD, and GLRX3) using a validation data set. The evaluation used a four-variable model.

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Fig. 8 shows the validation of the four biomarkers (MX1, GART, UROD, and GLRX3) using a validation data set. The predicting performance of the four-variable model for the validation data was evaluated. The AUC was 0.724. In consideration of the number of data (N = 30), reproducibility is high.

Fig. 9 shows the validation of the six biomarkers (MX1, GART, UROD, GLRX3, MAPRE1, and TBCB) using the validation data set. The evaluation used a six-variable model.

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Fig. 10 shows the validation of the six biomarkers (MX1, GART, UROD, GLRX3, MAPRE1, and TBCB) using a validation data set. Prediction performance of the six-variable model for the validation data was evaluated. The AUC was 0.664.

Fig. 11 shows the correlation between MX1, GART, and HSPA4L (correlation coefficient for the validation data, and the correlation coefficient integrating the both data).

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Fig. 12 shows various predicting models and their discrimination accuracies. The upper four predicting models constructed the predicting models based on screening data sets, and evaluated them based on a validation data set. The middle four predicting models constructed the predicting models based on validation data sets, and evaluated them based on screening data sets. The lower four predicting models constructed the predicting models based on screening and validation data sets. S: screening data set, V: validation data set, I: integration of screening and validation data sets.

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[DESCRIPTION OF EMBODIMENTS]

1. Schizophrenia marker set

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[0011] A first aspect of the present invention relates to a schizophrenia marker set including a combination of protein molecules (biomarkers) specific to schizophrenia (hereinafter may be referred to as "the biomarker set of the present invention"). The biomarker set of the present invention is useful for the determination and evaluation of present or future development possibility of schizophrenia. The "present development possibility" represents whether the patient is affected by or has developed schizophrenia (whether the patient has schizophrenia or not) at the time of inspection, or the probability of onset or development. On the other hand, the "future development possibility" represents future possibility (risk) of development of schizophrenia. "Schizophrenia" is a generic name of psychiatric disorders based on fragmentation of mental functions. According to the International Statistical Classification of Diseases and Related Health Problems (ICD) by the World Health Organization (WHO), the schizophrenia is classified into Paranoid schizophrenia, Hebephenic schizophrenia, Catatonic schizophrenia, Undifferentiated schizophrenia, Post-schizophrenic depression, Residual schizophrenia, and Simple schizophrenia.

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[0012] The biomarker set of the present invention is a combination of protein molecules that were found to be correlated with schizophrenia. More specifically, the biomarker set of the present invention is composed of two or more protein molecules selected from the eight proteins listed below. The biomarker set of the present invention is composed of preferably three or more, more preferably four or more protein molecules:

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trifunctional purine biosynthetic protein adenosine-3 (hereinafter referred to as "GART", SEQ ID NO. 1);
uroporphyrinogen decarboxylase (hereinafter referred to as "UROD", SEQ ID NO. 2);

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interferon-induced GTP-binding protein Mx1 (hereinafter referred to as "MX1", SEQ ID NO. 3);
glutaredoxin-3 (hereinafter referred to as "GLRX3", SEQ ID NO. 4);
microtubule-associated protein RP/EB family member 1 (hereinafter referred to as "MAPRE1", SEQ ID NO. 5);
tubulin folding cofactor B (hereinafter referred to as "TBCB", SEQ ID NO. 6);
5 immunoglobulin mu chain C region (hereinafter referred to as "IGHM", SEQ ID NO. 7); and
heat shock 70 kDa protein 4L (hereinafter referred to as "HSPA4L", SEQ ID NO. 8).

[0013] The biomarker set of the present invention may include various combinations of the above-described proteins. As shown in the below-described examples (in particular, the table of Fig. 2), GART, UROD, MX1, and GLRX3 are particularly useful and important for allowing highly accurate discrimination. Therefore, according to a preferred embodiment of the present invention, a schizophrenia marker set including at least the four protein molecules is provided. It was also shown that MAPRE1 and TBCB are useful secondary to the above-described four protein molecules. Therefore, it is also preferred that the above-described four protein molecules be combined with one or both of them to make a schizophrenia marker set.

[0014] Specific examples of the biomarker set of the present invention are listed below. They were specified as the combinations achieving high discrimination accuracy, as a result of the analysis by a statistical method:

a combination of GART, UROD, MX1, GLRX3, MAPRE1, and TBCB;
a combination of GART, UROD, MX1, GLRX3, MAPRE1, TBCB, and IGHM;
20 a combination of GART, UROD, MX1, GLRX3, MAPRE1, TBCB, and HSPA4L;
a combination of GART, UROD, GLRX3, MAPRE1, and TBCB;
a combination of GART, UROD, MX1, GLRX3, MAPRE1, TBCB, IGHM, and HSPA4L;
a combination of GART, UROD, MX1, MAPRE1, and TBCB;
a combination of GART, UROD, MX1, GLRX3, TBCB, and IGHM;
25 a combination of GART, UROD, MX1, GLRX3, MAPRE1, and HSPA4L;
a combination of GART, UROD, MX1, MAPRE1, TBCB, and HSPA4L;
a combination of GART, UROD, GLRX3, MAPRE1, TBCB, and HSPA4L;
a combination of GART, UROD, MX1, GLRX3, MAPRE1, IGHM, and HSPA4L;
a combination of GART, MX1, GLRX3, MAPRE1, TBCB, IGHM, and HSPA4L;
30 a combination of GART, UROD, MX1, GLRX3, TBCB, and HSPA4L;
a combination of GART, UROD, GLRX3, MAPRE1, and TBCB;
a combination of GART, UROD, MX1, and GLRX3;
a combination of GART, UROD, MX1, GLRX3, TBCB, IGHM, HSPA4L;
a combination of GART, UROD, MX1, MAPRE1, and IGHM ;
35 a combination of GART, UROD, MX1, MAPRE1, TBCB, and IGHM;
a combination of GART, UROD, MX1, GLRX3, MAPRE1, and IGHM;
a combination of GART, UROD, GLRX3, MAPRE1, TBCB, IGHM, and HSPA4L;
a combination of GART, UROD, MX1, GLRX3, TBCB, and HSPA4L;
a combination of GART, UROD, MX1, MAPRE1, TBCB, and IGHM;
40 a combination of GART, UROD, MX1, GLRX3, and HSPA4L;
a combination of GART, MX1, GLRX3, MAPRE1, IGHM, and HSPA4L;
a combination of GART, UROD, MX1, GLRX3, IGHM, and HSPA4L;
a combination of GART, UROD, MX1, GLRX3, and IGHM;
a combination of GART, MX1, GLRX3, MAPRE1, TBCB, IGHM, and HSPA4L;
45 a combination of GART, UROD, MX1, GLRX3, MAPRE1, and IGHM;
a combination of GART, UROD, MX1, TBCB, and IGHM; and
a combination of GART, UROD, MX1, TBCB, IGHM, and HSPA4L.

[0015] Among the above combinations, the combinations of GART, UROD, MX1, GLRX3, MAPRE1, and TBCB showed the highest discrimination accuracy. In consideration of this fact, this combination is regarded as one of the optimum biomarker sets. In addition, according to the Occam's razor, which is a principle in statistics, the number of proteins used for discrimination is preferably smaller when the discrimination accuracy is at the same level (details will be described later). The combination of GART, UROD, MX1, and GLRX3 most conforms to this principle.

[0016] As shown in the below-described examples, as a result of validation of reproducibility, it was found that GART and MX1 have good reproducibility. In view of this finding, it is preferred that the biomarker set includes GART and MX1. In particular, it is preferred that the biomarker set be composed of GART and MX1. On the other hand, in consideration of the finding that GART and MX1 have good reproducibility and the finding that HSPA4L also has relatively good reproducibility, according to a preferred embodiment of the present invention, the biomarker set includes one or more

protein molecules selected from the group consisting of GART, MX1, and HSPA4L.

2. Method for examining schizophrenia

5 **[0017]** A second aspect of the present invention relates to the utilization of the biomarker set of the present invention, and provides a method for examining the present or future development possibility of schizophrenia (hereinafter may be referred to as "the examination method of the present invention"). The examination method of the present invention is useful as a means for determining whether the patient is affected by or has developed schizophrenia, or a means for determining the possibility of future development of schizophrenia. The examination method of the present invention provides information useful for diagnosing schizophrenia. The examination method of the present invention allows simple and objective determination of development possibility of schizophrenia.

10 **[0018]** The delay of time from the development of a mental disease such as schizophrenia to the initiation of drug therapy is referred to as duration of untreated psychosis (DUP). It is known that the longer the DUP, the worse the clinical outcome. On the other hand, several years from the development are the important period, which influences the prognosis, and is referred to as critical period. According to a finding of cerebral nerve image analysis, it is reported that the longer the DUP, the smaller the volume of the planum temporale, which is a part of left gyrus temporalis superior (Takahashi et al.: Psychiatry Res 154: 209-219, 2007). This finding suggests that the changes in brain morphology proceeds during the untreated duration in the early stage (critical period) of the disease, and that it is very important to shorten the DUP, as well as to early intervene to improve the neurobiological changes in the critical period. The examination method of the present invention can be used also for screening of schizophrenia, and is useful for early detection and early treatment of schizophrenia.

15 **[0019]** The examination method of the present invention uses the level of the biomarker set of the present invention in the specimen derived from the subject as an indication. The "level" herein typically means the "amount" or "concentration". However, according to the convention and technical common knowledge, the term "level" is used also for expressing whether the molecules to be detected can be detected or not (more specifically, the presence or absence of apparent presence). The biomarker set to be used may be selected in consideration of the demanded accuracy and convenience of the examination.

20 **[0020]** The examination method of the present invention carries out the following steps:

- 30 (1) a step of preparing a specimen derived from the subject;
- (2) a step of detecting the protein molecules composing the marker set (more specifically, a combination of two or more (preferably three or more, more preferably four or more) protein molecules selected from the group consisting of GART, UROD, MX1, GLRX3, MAPRE1, TBCB, IGHM, and HSPA4L) in the specimen; and
- 35 (3) a step of determining the present or future development possibility of schizophrenia based on the detection result.

[0021] In the step (1), a specimen derived from a subject is prepared. Examples of the specimen include the blood, blood plasma, blood serum, oral mucosa, nasal mucosa, and skin of the subject. Alternatively, the blood cells derived from the subject may be used as the specimen. Alternatively, the lymphocytes, B-cells, or T-cells separated from the blood cells may be used as the specimen. Alternatively, the cells after subcultivation may be used. On the other hand, lymphoblastoid cells prepared by immortalizing the blood lymphocytes collected from the subject may be used as the specimen. The "lymphoblastoid cells" are the cells similar to the cells before differentiation into mature lymphocytes, and can be prepared by immortalizing the lymphocytes separated from the blood by Epstein-Barr virus. The established lymphoblastoid cells show a protein expression profile, which more highly reflects the features and characteristics of the disease in comparison with fresh blood cells. Accordingly, the use of the lymphoblastoid cells as the specimen prevents masking of the intrinsic expression profile (more specifically, the expression profile to be detected by the method of the present invention) by the conditions of the subject (condition-dependent factors) at the time of collection of the cells, which are the elements other than the disease. As a result of this, an examination result with higher reliability which more highly reflects the features and characteristics of the disease can be obtained. The examination using, for example, the blood, blood plasma, or blood serum as the specimen is easy in operation, and thus is particularly useful as a screening examination. On the other hand, the examination using the lymphoblastoid cells as the specimen gives a result with higher reliability, and thus is particularly useful as a means for secondary examination or definite diagnosis. Accordingly, highly efficient and reliable diagnosis is achieved by targeting the high-risk group (the subjects with high development possibility) by the examination using, for example, the blood, blood plasma, or blood serum as the specimen, followed by carrying out the examination using the lymphoblastoid cells as the specimen.

50 **[0022]** The subject is not particularly limited. More specifically, the present invention is widely applicable to the subjects requiring the determination of the present or future development possibility of schizophrenia (more specifically, the presence or absence of onset or development of schizophrenia, the degree of possibility of development of schizophrenia, and the degree of possibility of future development of schizophrenia). For example, when the present invention is applied

to a patient who has been diagnosed to have schizophrenia by medical health questionnaire, propriety of the diagnosis can be reviewed based on an objective index, or the level of protein expression. More specifically, the examination method of the present invention provides information, which helps or supports prior art diagnosis. This information is useful for the decision of more appropriate treatment policy, and promotes the improvements in therapeutic effect and patient's QOL (Quality of Life). On the other hand, the present invention can be used to monitor the disease condition, thereby preventing the increase in obstinacy and seriousness, and recurrence.

[0023] Those presumed to have a high risk of onset of schizophrenia based on the family background and other factors (high risk subjects) are also preferred subjects. The application of the present invention to the subject before development of the symptoms of schizophrenia allows inhibition or delay of the development, or therapeutic intervention in the early stage of the disease. The present invention is also useful for identification of those having a high risk of onset of schizophrenia. This identification allows, for example, the decrease in the development possibility (possibility of acquiring disease) owing to precautions and improvements in the lifestyle habit. Those who cannot or are difficult to be determined whether they have schizophrenia or not by prior art diagnosis, such as those having no subjective symptom, are also preferred subjects in the present invention. The present invention may be carried out as a term of health examination.

[0024] In the step (2), the biomarkers in the specimen are detected. It is not essential to strictly determine the level of each biomarker. More specifically, the level of the biomarkers is detected to a degree that allows the determination of development possibility of schizophrenia in the subsequent step (3). For example, the detection may be carried out so as to allow the discrimination whether the level of the biomarkers in the specimen exceeds the predetermined criterion value or not.

[0025] The method for detecting each biomarker is not particularly limited, but preferably an immunological method is used. An immunological method allows prompt and highly sensitive detection. In addition, operation is easy. Measurement by an immunological method uses a substance having specific binding property to the biomarker to be used. The substance is usually an antibody, but may be not an antibody as long as the substance has specific binding property to the biomarker, and the amount of binding is measurable. The antibody may be not a commercially available antibody, and may be newly prepared by, for example, an immunological method, a phage display method, or a ribosome display method.

[0026] Examples of the measurement method include latex agglutination assay, fluoroimmunoassay (FIA method), enzyme immunoassay (EIA method), radioimmunoassay (RIA method), and Western blot test method. Examples of the preferred measurement method include the FIA method and EIA method (including ELISA method). These methods allow high-sensitivity, prompt, and convenient detection. The FIA method uses a fluorescent-labeled antibody, and detects an antigen-antibody complex (immune complex) using fluorescence as a signal. On the other hand, the EIA method uses an enzymatically labeled antibody, and detects an immune complex using color development or luminescence based on enzyme reaction as a signal.

[0027] The ELISA method has many advantages such as high detection sensitivity, high specificity, marked quantitative determination performance, easy operation, and suitability for simultaneous processing of multiple specimens. An example of the specific operation method using the ELISA method is described below. Firstly, an anti-biomarker antibody is immobilized on an insoluble support. Specifically, for example, the surface of a microplate is immunized (coated) with an anti-biomarker monoclonal antibody. The specimen is brought into contact with the immobilized antibody. As a result of this operation, an immune complex is formed if the antigen (protein molecule as the biomarker) to the immobilized anti-biomarker antibody is present in the specimen. After the non-specific binding component is removed by washing operation, the immune complex is labeled by adding an enzyme-bound antibody, and then color development by reaction with the enzymatic substrate is carried out. Subsequently, the immune complex is detected using the amount of color development as the index. Details about the ELISA method are described in many publications and literatures, and establishment of the experimental procedure and conditions of the methods may refer to them. A competition method (a method including addition of an antigen and a specimen for competition) may be used in place of non-competition method. Alternatively, a method directly detecting the biomarker in the specimen with a labeling antibody, or a method for sandwich method may be used. The sandwich method uses two antibodies having different epitopes (trapping antibody and detecting antibody).

[0028] A means that allows simultaneous detection of multiple specimens, such as a protein array or protein chip, may be used. As the probe, for example, an antibody specific to the target biomarker is used.

[0029] In the step (3), present or future development possibility of schizophrenia is determined based on the detection result. In order to allow highly accurate determination, the determination is preferably carried out after comparing the detected value obtained in the step (2) with the detected value of the control specimen. The determination of the development possibility may be qualitative or quantitative. As is evident from the criteria for determination, the determination herein may be carried out automatically or mechanically without depending on diagnosis by specialists such as physicians or laboratory technician.

[0030] In the present invention, in principle, the following criteria are applied to each biomarker. More specifically, for GART, UROD, GLRX3, MAPRE1, TBCB, and HSPA4L, the development possibility of schizophrenia is high when the

detected value is low (the detected value and development possibility are in negative correlation with each other), and for MX1 and IGHM, the development possibility of schizophrenia is high when the detected value is high (the detected value and development possibility are in positive correlation with each other).

[0031] The determination in the step (3) may be carried out using a logistic model (statistical model) corresponding to the biomarker set to be used. A specific example (the case using the biomarker set composed of GART, UROD, MX1, GLRX3, MAPRE1, and TBCB) is described below.

<Determination using logistic model>

[0032] In the following logistic model, the p is calculated. Specifically, the level (detected value) of each protein molecule is assigned to the following formula to obtain the development possibility of schizophrenia (prevalence rate of schizophrenia).

[Formula 1]

$$p = \frac{\exp(11.54 - 4.64GART - 2.67UROD + 2.04MX1 - 3.14GLRX3 - 1.65MAPRE1 - 2.01TBCB)}{1 + \exp(11.54 - 4.64GART - 2.67UROD + 2.04MX1 - 3.14GLRX3 - 1.65MAPRE1 - 2.01TBCB)}$$

[0033] Alternatively, a criterion value or cutoff value is established, and qualitative determination such as the following (a) or (b) may be made. The criterion value or cutoff value used for determination may be decided in consideration of the type and condition of the specimen used, and demanded accuracy (confidence level).

(a) The case where all the biomarkers contained in the biomarker set are positive (cutoff value or more) is determined as positive (for example, development possibility is 50% or more), and the other case is determined as negative (for example, development possibility is less than 50%).

(b) The case where at least one of the biomarkers contained in the biomarker set is positive (cutoff value or more) is determined as positive (for example, development possibility is 50% or more), and the other case is determined as negative (for example, development possibility is less than 50%).

[0034] Alternatively, a plurality of determination categories may be provided, and subjected to quantitative or semi-quantitative determination. When quantitative determination is made, for example, a plurality of determination categories related to the ranges of the level of the biomarkers (development possibility of schizophrenia is defined for each determination category) are established in advance, and the determination category of the specimen is specified from the level of the biomarkers. The number of the determination categories, and the level of the biomarkers and determination result related to the determination categories are not particularly limited, and may be freely established based on, for example, a preliminary experiment. For example, the "threshold" determining the level of the development possibility using the predetermined threshold as the border, and "the range of biomarker level" relating to the category concerning with the level of development possibility can be decided by statistical analysis using many specimens. When the analysis is carried out using statistical processing, it is commonly effective to establish high risk and low risk groups. Examples of the high-risk group include the group of patients with schizophrenia and the group of those having many family members with schizophrenia, and examples of the low risk group include the group of healthy subjects and the group without family member with schizophrenia.

[0035] According to one embodiment of the present invention, in one subject, the biomarker level measured at one point is compared with the biomarker level measured past, and the presence or absence and/or the degree of increase and decrease of each biomarker level. The data thus obtained related to the level change of the biomarker set is useful information for monitoring the change of the development possibility of schizophrenia. More specifically, based on the level variation of the biomarker set, determination whether the development possibility is increased, decreased, or not changed during the period from the former examination to the present examination can be made. If this evaluation is carried out in parallel with the treatment of schizophrenia, therapeutic effect can be confirmed, and a foreboding sign of recurrence of schizophrenia can be grasped. As a result of this, more suitable treatment policy can be decided. Accordingly, the present invention can make marked contribution to the maximization of therapeutic effect and the improvement of the QOL (quality of life) of the patient.

3. Schizophrenia examination kit

[0036] The present invention further provides a kit for examining development possibility of schizophrenia. The kit of the present invention includes reagents for detecting the protein molecules composing the schizophrenia marker set. A

reagent is provided for each biomarker (protein molecule). The reagents are composed of substances showing specific binding properties to the corresponding biomarkers (hereinafter referred to as "binding molecule"). For example, a reagent for GART is the substance having specific binding properties to GART. Examples of the binding molecule include antibodies that specifically recognize biomarkers, nucleic acid aptamers, and peptide aptamers. The binding molecules are not particularly limited as to their kind and origin, as long as they have specific binding properties to the biomarkers to be used. In addition, when an antibody is used, it may be a polyclonal antibody, an oligoclonal antibody (a mixture of various antibodies), or a monoclonal antibody. The polyclonal antibody or oligoclonal antibody may be an IgG fraction derived from antiserum obtained by animal immunization, or an affinity-purified antibody by an antigen. The anti-biomarker antibody may be a fragment of an antibody such as Fab, Fab', F(ab')₂, scFv, or dsFv antibody.

[0037] The binding molecule may be prepared in a common procedure. If a commercial product is available, the commercial product may be used. For example, an antibody may be prepared by an immunological method, a phage display method, or a ribosome display method. The preparation of a polyclonal antibody by an immunological method may be carried out by the following procedure. An antigen (biomarker or its portion) is prepared, and an animal such as a rabbit is immunized using the antigen. An antigen is obtained by purification of a living body sample. Alternatively, a recombinant antigen may be used. The recombinant antigen can be prepared by, for example, a gene (or a portion of the gene) coding a biomarker is introduced into an appropriate host using a vector, and expressed in the recombinant cell thus obtained.

[0038] In order to enhance the immunological induction action, an antigen bound with a carrier protein may be used. Examples of the carrier protein include KLH (Keyhole Limpet Hemocyanin), BSA (Bovine Serum Albumin), and OVA (Ovalbumin). Binding between the antigen and the carrier protein can use, for example a carbodiimide method, a glutaraldehyde method, a diazo condensation method, or an MBS (maleimide benzoyloxy succinimide) method. On the other hand, an antigen prepared by expressing a biomarker molecule (or its portion) as a fused protein with GST, β -galactosidase, maltose-bound protein, or histidine (His) tag can be used. The fused protein can be purified simply by a general-purpose method.

[0039] As necessary, immunization is repeated, the blood is collected after the antibody titer is thoroughly increased, and the blood serum is obtained by, for example, centrifugation treatment. The antiserum thus obtained is subjected to affinity purification, and thus obtaining a polyclonal antibody.

[0040] On the other hand, the monoclonal antibody may be prepared by the following procedure. Firstly, immunization operation is carried out by the above-described procedure. As necessary, immunization is repeated, and antibody-producing cells are extracted from the immunized animal after the antibody titer is thoroughly increased. Secondly, the antibody-producing cells thus obtained and myeloma cells are fused to obtain hybridoma. Subsequently, the hybridoma is cloned from a single cell, and then a clone producing an antibody having high specificity to the target protein is selected. The culture solution of the selected clone is purified to obtain the desired antibody. Alternatively, the hybridoma is proliferated to the desired number or more, and then the cells are transplanted into the abdominal cavity of an animal (for example, mouse), and proliferated in the ascites fluid, and the ascites fluid is purified to obtain the desired antibody. Affinity chromatography using, for example, protein G, protein A is suitable for the purification of the above-described culture solution or ascites fluid. Alternatively, affinity chromatography including an immobilized antigen may be used. Other method such as ion exchange chromatography, gel filtration chromatography, ammonium sulfate fractionation, or centrifugation may be used. These methods may be used alone or in combination.

[0041] Providing that the specific binding properties to a biomarker are maintained, the antibody thus obtained may be subjected to various modifications. The modified antibody may be used as the reagent in the present invention.

[0042] When the specific binding molecule is a labeling antibody, the amount of bound antibody can be directly detected using the amount of labeling as the index. Accordingly, the test method is more simplified. On the other hand, there are problems that an antibody bound with a labeling agent must be prepared, and that the detection sensitivity is commonly low. Therefore, an indirect detection method such as a method using a secondary antibody bound to a labeling agent, or a method using a polymer bound to a secondary antibody and a labeling agent is preferred. The secondary antibody herein is an antibody having specific binding properties to the antibody specific to the biomarker to be used. For example, when an antibody specific to the biomarker is prepared as a rabbit antibody, an anti-rabbit IgG antibody may be used as a secondary antibody. Labeled secondary antibodies usable for various types of antibodies such as rabbit, goat, and mouse antibodies are commercially available (for example, Funakoshi Co., Ltd. and Cosmo Bio Co., Ltd.), and suitable one may be appropriately selected according to the reagent in the present invention.

[0043] Examples of the labeling agent include enzymes such as peroxidase, microperoxidase, horseradish peroxidase (HRP), alkaline phosphatase, β -D-galactosidase, glucose oxidase, and glucose-6-phosphate dehydrogenase; fluorescent substances such as fluorescein isothiocyanate (FITC), tetramethyl rhodamine isothiocyanate (TRITC), and europium; chemiluminescence substances such as luminol, isoluminol, and acridinium derivatives; coenzymes such as NAD; biotin; and radioactive materials such as ¹³¹I and ¹²⁵I.

[0044] In one embodiment, the reagent in the present invention is solid-phased according to the intended use. The insoluble support used for solidification is not particularly limited. For example, an insoluble support made of water-

insoluble substance such as a resin including a polystyrene resin, a polycarbonate resin, a silicon resin, and a nylon resin, or glass. The insoluble support carries an antibody by physical adsorption or chemical adsorption.

[0045] The kit of the present invention usually includes an instruction manual. The kit may include other reagents (for example, a buffer, a blocking reagent, an enzymatic substrate, and a color-producing reagent) used when carrying out the examination method and/or an apparatus or instrument (for example, a container, a reaction apparatus, an absorbance meter, and a fluorescence reader). In addition, the kit preferably includes, as the standard samples, the protein molecules or their fragments composing the biomarker set.

[Examples]

[0046] The preceding investigation identified 22 proteins that were found to be related with schizophrenia (Patent Literature 1). With the aim of specifying the combination of biomarkers, which allow highly accurate discrimination, the following study was carried out.

1. Expression analysis by Western blot test

(1) Method

[0047] For the subjects composed of thirty patients with schizophrenia (15 men: 43.7 ± 12.6 years of age, 15 women: 43.1 ± 8.9 years of age) and thirty healthy subjects (15 men: 44.4 ± 12.9 years of age, 15 women: 43.2 ± 9.6 years of age), the amount of expression of 22 identified proteins was reconfirmed by the Western blot test method.

(2) Result

[0048] Of the 22 proteins, eight proteins showed a significant difference in the expression amount (Student's t-test, $p < 0.05$). Two proteins (MX1 and IGHM) showed increased expression, and six proteins (MAPRE1, TBCB, GLRX3, UROD, HSPA4L, and GART) showed decreased expression in the patient group with schizophrenia (Fig. 1).

2. Making of disease discriminant model using statistical method

[0049] The difference in the average of the amount of protein expression in the patient group with schizophrenia and the healthy subject group was compared using statistical hypothesis testing. As a result of this, eight proteins showed a significant difference (Student's t-test, $p < 0.05$) (same as the above-described result). Of the eight proteins, the protein useful for the discrimination of the patient group with schizophrenia and the healthy subject group were identified, and the statistical model that can highly accurately discriminate the disease (logistic model) was made. The logistic model is a statistical model for discriminating the binary response represented by the following formula (formula (1)) (herein, the patient with schizophrenia and healthy subject).

[Formula 2]

$$p = \frac{\exp(\beta_0 + \beta_1 \text{Protein 1} + \dots + \beta_k \text{Protein k})}{1 + \exp(\beta_0 + \beta_1 \text{Protein 1} + \dots + \beta_k \text{Protein k})} \quad (1)$$

[0050] Wherein, p represents the probability of schizophrenia, and protein 1 to protein k represent the expression amount of the proteins used in discrimination. β_0 is the intercept and β_1 to β_k are the parameters expressing the level of influence of the amounts of protein expression on the probability of schizophrenia and are presumed from the protein expression data. When β is positive (negative), the higher the amount of protein expression, the higher (lower) the probability of schizophrenia. In order to make a highly accurate model for discriminating the disease, the optimum combination must be selected from all the 255 combinations of proteins ($= {}_8C_1 + {}_8C_2 + {}_8C_3 + {}_8C_4 + {}_8C_5 + {}_8C_6 + {}_8C_7 + {}_8C_8$). Using the statistical method below, two combinations of proteins (discriminant models) suitable for discrimination of the disease were identified.

<Discriminant model 1>

[0051] For the 255 protein combinations, the predicting errors based on the bias corrected area under the curve (AUC), and leave one out cross validation (LOOCV) were calculated. The closer the corrected AUC to 1.0, the smaller the predicting error based on LOOCV, the higher the discrimination accuracy of the combination. These indices are evaluation

indices recommended in statistical textbooks and literatures. Fig. 2 shows the top 30 combinations of proteins having a high corrected AUC. The table in Fig. 2 indicates that the model using GART, UROD, MX1, GLRX3, MAPRE1, and TBCB (hereinafter referred to as discriminant model 1) achieved the highest discrimination accuracy (corrected AUC: 0.877, predicting error: 0.164). The logistic model of the discriminant model 1 is as follows (formula (2)).

[Formula 3]

$$p = \frac{\exp(11.54 - 4.64GART - 2.67UROD + 2.04MX1 - 3.14GLRX3 - 1.65MAPRE1 - 2.01TBCB)}{1 + \exp(11.54 - 4.64GART - 2.67UROD + 2.04MX1 - 3.14GLRX3 - 1.65MAPRE1 - 2.01TBCB)} \quad (2)$$

[0052] The formula (2) indicates that, the higher the MX1, the higher the probability of schizophrenia. For other proteins, the higher the value, the lower the probability of schizophrenia.

<Discriminant model 2>

[0053] Occam's razor is a statistical concept: "when an event is explained, the number of assumptions is preferably fewer". Specifically, when a dependent variant (presence or absence of schizophrenia) is explained using a statistical model based on the measurement data of a plurality of explanation variables (proteins), conformity to the "measurement data" is improved as the number of explaining variables included in the statistical model is increased to complicate the model. However, this statistical model excessively conforms to "the measurement data (past data)", and conformity to the new measured data decreases. More specifically, the statistical model overfits to the existing data. In order to avoid this problem, the number of explaining variables included in the statistical model is preferably fewer. Based on this concept, when the discrimination accuracy is on a similar level, the number of proteins used for the discrimination is preferably fewer. From the table in Fig. 2, the model using GART, UROD, MX1, and GLRX3 (hereinafter referred to as discriminant model 2) is suitable for the idea (corrected AUC: 0.860, predicting error: 0.178). The logistic model of the discriminant model 2 (formula (3)) is as follows.

[Formula 4]

$$p = \frac{\exp(6.44 - 3.82GART - 2.18UROD + 2.48MX1 - 2.84GLRX3)}{1 + \exp(6.44 - 3.82GART - 2.18UROD + 2.48MX1 - 2.84GLRX3)} \quad (3)$$

[0054] The positive and negative of the parameter are the same as those in the discriminant model 1, and the influences of the proteins on the probability of schizophrenia are the same as those in the discriminant models 1 and 2.

<Comparison between discriminant models 1 and 2>

[0055] The odds ratios of the proteins contained in the discriminant models 1 and 2 are shown in Figs. 3 and 4, respectively. The influence of the protein contained in these models on the prevalence rate of schizophrenia is statistically significant ($p < 0.05$) or limitedly significant ($p < 0.10$), and is suggested to be a protein suitable for discrimination. In addition, the combination of proteins suitable for discrimination was selected using stepwise forward selection method, which is a statistical method. As a result of this, GART, UROD, MX1, and GLRX3 were selected, so that usefulness of the discriminant model 2 was supported by the different statistical method. Furthermore, the table in Fig. 2 shows that the number contained in the model is higher in the order of GART, UROD, MX1, GLRX3, MAPRE1, TBCB, IGHM, and HSPA4L.

[0056] The above results suggest the followings.

- The accuracy of discrimination of schizophrenia by the discriminant models 1 and 2 are almost equal statistically.
- GART, UROD, MX1, and GLRX3 contained in almost all the models in Fig. 2 are particularly important for the discrimination of schizophrenia.
- MAPRE1 and TBCB contained in the discriminant model 1 are also highly useful for discrimination.

<Determination of schizophrenia using discriminant models>

[0057] When determining whether the patient has schizophrenia or not using the discriminant model 1 or 2, the prevalence rate of schizophrenia (p in the formula (2) or (3)) is calculated. For example, when the discriminant model 1 is used, GART, UROD, MX1, GLRX3, MAPRE1, and TBCB in the patient are measured, and the values are assigned to

the formula (2), thereby determining the prevalence rate of schizophrenia.

3. Validation of effectiveness of biomarker

5 **[0058]** Effectiveness of the selected eight biomarkers was validated using other clinical specimens. The results of validation by Western blot test are shown in Figs. 5 and 6. For MX1, GART, and HSPA4L, the screening data (the data of 30 specimens used in the above-described 1.) and the validation data (the data of other 30 specimens) changed in the same direction (statistically significant), and showed reproducibility.

10 **[0059]** Effectiveness of the four biomarkers (MX1, GART, UROD, and GLRX3) was validated using the validation data set; significance was reproduced for MX1 and GART (Figs. 7 and 8). In addition, also when effectiveness of the six biomarkers (MX1, GART, UROD, GLRX3, MAPRE1, and TBCB) was validated using the validation data set, significance was reproduced for MX1 and GART (Figs. 9 and 10). The four-variable model showed a higher predicting accuracy.

15 **[0060]** In consideration that MX1, GART, and HSPA4L showed reproducibility, the correlation between these three molecules was studied by multivariate analysis. The result is shown in Fig. 11. The values in parentheses are, from left to right, correlation coefficient in screening data, correlation coefficient in validation data, and correlation coefficient in the integration of both data. There is no correlation between the three molecules. The cause that HSPA4L showed no significance in the multivariate analysis is not likely due to the influence of multi-collinearity.

20 **[0061]** On the other hand, a plurality of predicting models including different types and numbers of biomarkers were constructed using eight biomarkers (MX1, GART, UROD, GLRX3, MAPRE1, TBCB, HSPA4L, IGHM), with focusing attention on MX1 and GART which reproduced significance, and further validation was carried out. The validation results are shown in Fig. 12. Except for some predicting models, high reproducibility is shown. From the viewpoints of predicting accuracy and reproducibility, the two variable models, MX1 and GART are the most advantageous. The predicting models are represented in the same manner as the above-described formula (1). For example, the discriminant model in the top row in Fig. 12 is represented by: $p = \exp(-0.234 + 3.012MX1 - 2.852GART) / \{1 + \exp(-0.234 + 3.012MX1 - 2.852GART)\}$.

25 **[0062]** The above results suggest the followings.

- MX1 and GART have good reproducibility, and thus are advantageous biomarkers.
- HSPA4L also has relatively good reproducibility, and is highly useful.
- 30 • Discrimination using MX1 and GART gives the most accurate result.

[INDUSTRIAL APPLICABILITY]

35 **[0063]** The examination method of the present invention allows highly accurate discrimination of schizophrenia. The examination method of the present invention is useful as a means for determining whether schizophrenia is developed or not. It is also useful as a means for grasping the future development possibility. Early detection and treatment using the examination method of the present invention are considered effective for the prevention of increase in obstinacy and seriousness (progress of disease), and recurrence of schizophrenia.

40 **[0064]** The present invention will not be limited to the description of the embodiments and examples of the present invention. Various modifications readily made by those skilled in the art are also included in the present invention, without departing from the scope of claims. The entire contents of the articles, unexamined patent publications, patent applications, and the like specified herein are hereby incorporated herein by reference.

[SEQUENCE LIST]

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[0065]

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35 Tyr Glu Ile Glu Ile Ser Asp Ala Ser Glu Val Glu Lys Glu Ile Asn
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40 Lys Ala Gln Asn Ala Ile Ala Gly Glu Gly Met Gly Ile Ser His Glu
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Leu Ile Thr Leu Glu Ile Ser Ser Arg Asp Val Pro Asp Leu Thr Leu
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45 Ile Asp Leu Pro Gly Ile Thr Arg Val Ala Val Gly Asn Gln Pro Ala
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50 Asp Ile Gly Tyr Lys Ile Lys Thr Leu Ile Lys Lys Tyr Ile Gln Arg
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Gln Glu Thr Ile Ser Leu Val Val Val Pro Ser Asn Val Asp Ile Ala
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55 Thr Thr Glu Ala Leu Ser Met Ala Gln Glu Val Asp Pro Glu Gly Asp

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Arg Leu Ala Phe Thr Asp Val Ser Ile Lys Asn Phe Glu Glu Phe Phe
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 5 Asn Leu His Arg Thr Ala Lys Ser Lys Ile Glu Asp Ile Arg Ala Glu
 500 505 510
 10 Gln Glu Arg Glu Gly Glu Lys Leu Ile Arg Leu His Phe Gln Met Glu
 515 520 525
 15 Gln Ile Val Tyr Cys Gln Asp Gln Val Tyr Arg Gly Ala Leu Gln Lys
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 Val Arg Glu Lys Glu Leu Glu Glu Glu Lys Lys Lys Lys Ser Trp Asp
 545 550 555 560
 20 Phe Gly Ala Phe Gln Ser Ser Ser Ala Thr Asp Ser Ser Met Glu Glu
 565 570 575
 25 Ile Phe Gln His Leu Met Ala Tyr His Gln Glu Ala Ser Lys Arg Ile
 580 585 590
 Ser Ser His Ile Pro Leu Ile Ile Gln Phe Phe Met Leu Gln Thr Tyr
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 30 Gly Gln Gln Leu Gln Lys Ala Met Leu Gln Leu Leu Gln Asp Lys Asp
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 35 Thr Tyr Ser Trp Leu Leu Lys Glu Arg Ser Asp Thr Ser Asp Lys Arg
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Leu Leu Val Val His Phe Trp Ala Pro Trp Ala Pro Gln Cys Ala Gln
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 5 Met Asn Glu Val Met Ala Glu Leu Ala Lys Glu Leu Pro Gln Val Ser
 50 55 60
 10 Phe Val Lys Leu Glu Ala Glu Gly Val Pro Glu Val Ser Glu Lys Tyr
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 15 Glu Ile Ser Ser Val Pro Thr Phe Leu Phe Phe Lys Asn Ser Gln Lys
 85 90 95
 20 Ile Asp Arg Leu Asp Gly Ala His Ala Pro Glu Leu Thr Lys Lys Val
 100 105 110
 25 Gln Arg His Ala Ser Ser Gly Ser Phe Leu Pro Ser Ala Asn Glu His
 115 120 125
 30 Leu Lys Glu Asp Leu Asn Leu Arg Leu Lys Lys Leu Thr His Ala Ala
 130 135 140
 35 Pro Cys Met Leu Phe Met Lys Gly Thr Pro Gln Glu Pro Arg Cys Gly
 145 150 155 160
 40 Phe Ser Lys Gln Met Val Glu Ile Leu His Lys His Asn Ile Gln Phe
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 45 Ser Ser Phe Asp Ile Phe Ser Asp Glu Glu Val Arg Gln Gly Leu Lys
 180 185 190
 50 Ala Tyr Ser Ser Trp Pro Thr Tyr Pro Gln Leu Tyr Val Ser Gly Glu
 195 200 205
 55 Leu Ile Gly Gly Leu Asp Ile Ile Lys Glu Leu Glu Ala Ser Glu Glu
 210 215 220
 60 Leu Asp Thr Ile Cys Pro Lys Ala Pro Lys Leu Glu Glu Arg Leu Lys
 225 230 235 240
 65 Val Leu Thr Asn Lys Ala Ser Val Met Leu Phe Met Lys Gly Asn Lys
 245 250 255
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 260 265 270
 75 Ser Thr Gly Val Glu Tyr Glu Thr Phe Asp Ile Leu Glu Asp Glu Glu
 275 280 285

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Val Arg Gln Gly Leu Lys Ala Tyr Ser Asn Trp Pro Thr Tyr Pro Gln
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30 Asp Met Leu Phe Pro Gly Cys Val His Leu Arg Lys Val Lys Phe Gln
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35 Ala Lys Leu Glu His Glu Tyr Ile His Asn Phe Lys Val Leu Gln Ala
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Ala Phe Lys Lys Met Gly Val Asp Lys Ile Ile Pro Val Glu Lys Leu
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40 Val Lys Gly Lys Phe Gln Asp Asn Phe Glu Phe Ile Gln Trp Phe Lys
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45 Lys Phe Phe Asp Ala Asn Tyr Asp Gly Lys Asp Tyr Asn Pro Leu Leu
 115 120 125

Ala Arg Gln Gly Gln Asp Val Ala Pro Pro Pro Asn Pro Gly Asp Gln
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50 Ile Phe Asn Lys Ser Lys Lys Leu Ile Gly Thr Ala Val Pro Gln Arg
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55 Thr Ser Pro Thr Gly Pro Lys Asn Met Gln Thr Ser Gly Arg Leu Ser
 165 170 175

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Asn Val Ala Pro Pro Cys Ile Leu Arg Lys Asn Pro Pro Ser Ala Arg
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 5 Asn Gly Gly His Glu Thr Asp Ala Gln Ile Leu Glu Leu Asn Gln Gln
 195 200 205
 10 Leu Val Asp Leu Lys Leu Thr Val Asp Gly Leu Glu Lys Glu Arg Asp
 210 215 220
 Phe Tyr Phe Ser Lys Leu Arg Asp Ile Glu Leu Ile Cys Gln Glu His
 225 230 235 240
 15 Glu Ser Glu Asn Ser Pro Val Ile Ser Gly Ile Ile Gly Ile Leu Tyr
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 50 Asp Gly Cys Arg Ile His Val Ile Asp His Ser Gly Ala Arg Leu Gly
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 55 Glu Tyr Glu Asp Val Ser Arg Val Glu Lys Tyr Thr Ile Ser Gln Glu
 100 105 110

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Ala Tyr Asp Gln Arg Gln Asp Thr Val Arg Ser Phe Leu Lys Arg Ser
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5 Lys Leu Gly Arg Tyr Asn Glu Glu Glu Arg Ala Gln Gln Glu Ala Glu
 130 135 140

10 Ala Ala Gln Arg Leu Ala Glu Glu Lys Ala Gln Ala Ser Ser Ile Pro
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15 Val Gly Ser Arg Cys Glu Val Arg Ala Ala Gly Gln Ser Pro Arg Arg
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Gly Thr Val Met Tyr Val Gly Leu Thr Asp Phe Lys Pro Gly Tyr Trp
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20 Ile Gly Val Arg Tyr Asp Glu Pro Leu Gly Lys Asn Asp Gly Ser Val
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25 Asn Gly Lys Arg Tyr Phe Glu Cys Gln Ala Lys Tyr Gly Ala Phe Val
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50 Asp Ile Ser Ser Thr Arg Gly Phe Pro Ser Val Leu Arg Gly Gly Lys
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55 Tyr Ala Ala Thr Ser Gln Val Leu Leu Pro Ser Lys Asp Val Met Gln
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Gly Thr Asp Glu His Val Val Cys Lys Val Gln His Pro Asn Gly Asn
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 5 Lys Glu Lys Asn Val Pro Leu Pro Val Ile Ala Glu Leu Pro Pro Lys
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 Val Ser Val Phe Val Pro Pro Arg Asp Gly Phe Phe Gly Asn Pro Arg
 10 115 120 125
 Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly Phe Ser Pro Arg Gln Ile
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 15 Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val Gly Ser Gly Val Thr
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 20 165 170 175
 Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser Asp Trp Leu Ser Gln
 180 185 190
 25 Ser Met Phe Thr Cys Arg Val Asp His Arg Gly Leu Thr Phe Gln Gln
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 30 Asn Ala Ser Ser Met Cys Val Pro Asp Gln Asp Thr Ala Ile Arg Val
 210 215 220
 Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe Leu Thr Lys Ser Thr
 225 230 235 240
 35 Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr Tyr Asp Ser Val Thr
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 40 Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val Lys Thr His Thr Asn
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 45 Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser Ala Val Gly Glu Ala
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 Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu Arg Phe Thr Cys Thr
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 50 Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys Gln Thr Ile Ser Arg
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 55 Pro Lys Gly Val Ala Leu His Arg Pro Asp Val Tyr Leu Leu Pro Pro
 325 330 335

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Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala Thr Ile Thr Cys Leu
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5 Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val Gln Trp Met Gln Arg
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10 Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr Ser Ala Pro Met Pro
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15 Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His Ser Ile Leu Thr Val
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20 Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr Thr Cys Val Val Ala
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25 His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg Thr Val Asp Lys Ser
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45 Arg Cys Thr Pro Ala Cys Ile Ser Leu Gly Ser Arg Thr Arg Ala Ile
35 40 45

Gly Asn Ala Ala Lys Ser Gln Ile Val Thr Asn Val Arg Asn Thr Ile
50 55 60

His Gly Phe Lys Lys Leu His Gly Arg Ser Phe Asp Asp Pro Ile Val
65 70 75 80

55 Gln Thr Glu Arg Ile Arg Leu Pro Tyr Glu Leu Gln Lys Met Pro Asn
85 90 95

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Gly Ser Ala Gly Val Lys Val Arg Tyr Leu Glu Glu Glu Arg Pro Phe
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 5 Ala Ile Glu Gln Val Thr Gly Met Leu Leu Ala Lys Leu Lys Glu Thr
 115 120 125
 10 Ser Glu Asn Ala Leu Lys Lys Pro Val Ala Asp Cys Val Ile Ser Ile
 130 135 140
 15 Pro Ser Phe Phe Thr Asp Ala Glu Arg Arg Ser Val Met Ala Ala Ala
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 20 Gln Val Ala Gly Leu Asn Cys Leu Arg Leu Met Asn Glu Thr Thr Ala
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 25 Val Ala Leu Ala Tyr Gly Ile Tyr Lys Gln Asp Leu Pro Pro Leu Asp
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 195 200 205
 35 Gln Val Leu Val Cys Ala Phe Asn Lys Gly Lys Leu Lys Val Leu Ala
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 40 Thr Thr Phe Asp Pro Tyr Leu Gly Gly Arg Asn Phe Asp Glu Ala Leu
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 45 Val Asp Tyr Phe Cys Asp Glu Phe Lys Thr Lys Tyr Lys Ile Asn Val
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 50 Lys Glu Asn Ser Arg Ala Leu Leu Arg Leu Tyr Gln Glu Cys Glu Lys
 260 265 270
 55 Leu Lys Lys Leu Met Ser Ala Asn Ala Ser Asp Leu Pro Leu Asn Ile
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 60 Glu Cys Phe Met Asn Asp Leu Asp Val Ser Ser Lys Met Asn Arg Ala
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 65 Gln Phe Glu Gln Leu Cys Ala Ser Leu Leu Ala Arg Val Glu Pro Pro
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 70 Leu Lys Ala Val Met Glu Gln Ala Asn Leu Gln Arg Glu Asp Ile Ser
 325 330 335
 75 Ser Ile Glu Ile Val Gly Gly Ala Thr Arg Ile Pro Ala Val Lys Glu

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	340					345					350					
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10	Asp	Glu	Ala	Val	Ala	Arg	Gly	Cys	Ala	Leu	Gln	Cys	Ala	Ile	Leu	Ser
		370					375					380				
15	Pro	Ala	Phe	Lys	Val	Arg	Glu	Phe	Ser	Ile	Thr	Asp	Leu	Val	Pro	Tyr
		385					390					395				400
20	Ser	Ile	Thr	Leu	Arg	Trp	Lys	Thr	Ser	Phe	Glu	Asp	Gly	Ser	Gly	Glu
					405					410					415	
25	Cys	Glu	Val	Phe	Cys	Lys	Asn	His	Pro	Ala	Pro	Phe	Ser	Lys	Val	Ile
				420						425					430	
30	Thr	Phe	His	Lys	Lys	Glu	Pro	Phe	Glu	Leu	Glu	Ala	Phe	Tyr	Thr	Asn
				435				440					445			
35	Leu	His	Glu	Val	Pro	Tyr	Pro	Asp	Ala	Arg	Ile	Gly	Ser	Phe	Thr	Ile
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		465					470					475				480
45	Lys	Val	Arg	Val	Asn	Ile	His	Gly	Ile	Phe	Ser	Val	Ala	Ser	Ala	Ser
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50	Val	Ile	Glu	Lys	Gln	Asn	Leu	Glu	Gly	Asp	His	Ser	Asp	Ala	Pro	Met
				500					505					510		
55	Glu	Thr	Glu	Thr	Ser	Phe	Lys	Asn	Glu	Asn	Lys	Asp	Asn	Met	Asp	Lys
				515				520					525			
60	Met	Gln	Val	Asp	Gln	Glu	Glu	Gly	His	Gln	Lys	Cys	His	Ala	Glu	His
		530					535					540				
65	Thr	Pro	Glu	Glu	Glu	Ile	Asp	His	Thr	Gly	Ala	Lys	Thr	Lys	Ser	Ala
		545					550					555				560
70	Val	Ser	Asp	Lys	Gln	Asp	Arg	Leu	Asn	Gln	Thr	Leu	Lys	Lys	Gly	Lys
					565					570					575	
75	Val	Lys	Ser	Ile	Asp	Leu	Pro	Ile	Gln	Ser	Ser	Leu	Cys	Arg	Gln	Leu
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Gly Gln Asp Leu Leu Asn Ser Tyr Ile Glu Asn Glu Gly Lys Met Ile
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5 Met Gln Asp Lys Leu Glu Lys Glu Arg Asn Asp Ala Lys Asn Ala Val
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10 Glu Glu Tyr Val Tyr Asp Phe Arg Asp Arg Leu Gly Thr Val Tyr Glu
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Lys Phe Ile Thr Pro Glu Asp Leu Ser Lys Leu Ser Ala Val Leu Glu
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15 Asp Thr Glu Asn Trp Leu Tyr Glu Asp Gly Glu Asp Gln Pro Lys Gln
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20 Val Tyr Val Asp Lys Leu Gln Glu Leu Lys Lys Tyr Gly Gln Pro Ile
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Gln Met Lys Tyr Met Glu His Glu Glu Arg Pro Lys Ala Leu Asn Asp
 690 695 700

25 Leu Gly Lys Lys Ile Gln Leu Val Met Lys Val Ile Glu Ala Tyr Arg
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30 Asn Lys Asp Glu Arg Tyr Asp His Leu Asp Pro Thr Glu Met Glu Lys
 725 730 735

Val Glu Lys Cys Ile Ser Asp Ala Met Ser Trp Leu Asn Ser Lys Met
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35 Asn Ala Gln Asn Lys Leu Ser Leu Thr Gln Asp Pro Val Val Lys Val
 755 760 765

40 Ser Glu Ile Val Ala Lys Ser Lys Glu Leu Asp Asn Phe Cys Asn Pro
 770 775 780

45 Ile Ile Tyr Lys Pro Lys Pro Lys Ala Glu Val Pro Glu Asp Lys Pro
 785 790 795 800

Lys Ala Asn Ser Glu His Asn Gly Pro Met Asp Gly Gln Ser Gly Thr
 805 810 815

50 Glu Thr Lys Ser Asp Ser Thr Lys Asp Ser Ser Gln His Thr Lys Ser
 820 825 830

55 Ser Gly Glu Met Glu Val Asp
 835

Claims

- 5 1. A schizophrenia marker set comprising a combination of two or more protein molecules selected from the group consisting of trifunctional purine biosynthetic protein adenosine-3, uroporphyrinogen decarboxylase, interferon-induced GTP-binding protein Mx1, glutaredoxin-3, microtubule-associated protein RP/EB family member 1, tubulin folding cofactor B, immunoglobulin mu chain C region, and heat shock 70 kDa protein 4L.
- 10 2. The schizophrenia marker set of claim 1, which comprises at least trifunctional purine biosynthetic protein adenosine-3, uroporphyrinogen decarboxylase, interferon-induced GTP-binding protein Mx1, and glutaredoxin-3.
- 15 3. The schizophrenia marker set of claim 2, which further comprises microtubule-associated protein RP/EB family member 1 and/or tubulin folding cofactor B.
- 20 4. The schizophrenia marker set of claim 1, which is a combination of trifunctional purine biosynthetic protein adenosine-3, uroporphyrinogen decarboxylase, interferon-induced GTP-binding protein Mx1, glutaredoxin-3, microtubule-associated protein RP/EB family member 1, and tubulin folding cofactor B.
- 25 5. The schizophrenia marker set of claim 1, which is a combination of trifunctional purine biosynthetic protein adenosine-3, uroporphyrinogen decarboxylase, interferon-induced GTP-binding protein Mx1, and glutaredoxin-3.
- 30 6. The schizophrenia marker set of claim 1, which comprises at least trifunctional purine biosynthetic protein adenosine-3 and interferon-induced GTP-binding protein Mx1.
- 35 7. The schizophrenia marker set of claim 1, which is a combination of trifunctional purine biosynthetic protein adenosine-3 and interferon-induced GTP-binding protein Mx1.
- 40 8. The schizophrenia marker set of claim 1, which comprises one or more protein molecules selected from the group consisting of trifunctional purine biosynthetic protein adenosine-3, interferon-induced GTP-binding protein Mx1, and heat shock 70 kDa protein 4L.
- 45 9. An examination method for schizophrenia using the level of the schizophrenia marker set of any one of claims 1 to 8 in a specimen as an indication.
- 50 10. The examination method for schizophrenia of claim 9, comprising the following steps (1) to (3):
 - (1) a step of preparing a specimen derived from the subject;
 - (2) a step of detecting the protein molecules composing the marker set in the specimen; and
 - (3) a step of determining the present or future development possibility of schizophrenia based on the detection result.
- 55 11. The examination method for schizophrenia of claim 10, wherein a lower detected value shows a higher development possibility of schizophrenia for trifunctional purine biosynthetic protein adenosine-3, uroporphyrinogen decarboxylase, glutaredoxin-3, microtubule-associated protein RP/EB family member 1, tubulin folding cofactor B, and heat shock 70 kDa protein 4L, and a higher detected value shows a higher development possibility of schizophrenia for interferon-induced GTP-binding protein Mx1 and immunoglobulin mu chain C region.
12. The examination method for schizophrenia of claim 10 or 11, wherein the determination of step (3) is carried out using a logistic model.
13. The examination method for schizophrenia of any one of claims 9 to 12, wherein the specimen is blood, blood plasma, blood serum, oral mucosa, nasal mucosa, skin, blood cells, or lymphoblastoid cells prepared by immortalizing the blood lymphocytes collected from the subject.
14. A kit for examining schizophrenia comprising a reagent for detecting each of the protein molecules composing the schizophrenia marker set of claim 1, and an instruction manual.
15. The kit for examining schizophrenia of claim 14, wherein each of the reagents is an antibody to the target protein molecule.

[Fig. 1]

SSP No.	Gene Symbol	Protein	Western blotting		2D-DIGE		Confirmation analysis
			S/C	p value	S/C	p value	
SSP 3602	MX1	Interferon-induced GTP-binding protein Mx1	1.35	0.01	1.14	0.01	**
SSP 6617	IGHM	Ig mu chain C region	1.30	0.04	1.48	0.03	*
SSP 0110	MAPRE1	Microtubule-associated protein RP/EB family member 1	0.76	0.01	0.87	0.00	**
SSP 5303	GART	Trifunctional purine biosynthetic protein adenosa-3	0.75	0.02	0.93	0.04	*
SSP 3229	TRCB	Tubulin folding cofactor B	0.68	0.02	0.87	0.00	*
SSP 1208	UROD	Uroporphyrinogen decarboxylase	0.77	0.01	0.94	0.05	**
SSP 3714	GLRX3	Glutathione S-transferase gamma 3	0.74	0.00	0.82	0.04	**
SSP 2409	HSPA4L	Heat shock 70 kDa protein 4L	0.82	0.02	0.70	0.04	*
	HARS	Histidyl-tRNA synthetase, cytoplasmic	1.09	0.59	0.94	0.05	NS
	EFHD2	EF-hand domain-containing protein D2	0.99	0.91	0.87	0.00	NS
SSP 3822	KIF11	Kinesin-like protein KIF11	1.31	0.28	1.2	0.00	NS
SSP 6320	EEF1G	Elongation factor 1-gamma	1.16	0.15	1.16	0.05	NS
SSP 2001	UCHL1	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.97	0.92	0.53	0.01	NS
SSP 0106	ANXA5	Annexin A5	0.88	0.11	0.91	0.02	NS
SSP 2002	APRT	Adenine phosphoribosyltransferase	0.59	0.24	0.92	0.02	NS
SSP 1109	PPA1	Inorganic pyrophosphatase	0.98	0.95	0.83	0.03	NS
SSP 2626	VPS35	Vascular protein sorting-associated protein 35	0.88	0.30	1.73	0.03	NS
SSP 1716	HSP90AB1	Heat shock protein HSP 90-beta	1.12	0.39	0.91	0.04	NS
SSP 1519	LCP1	Plastin-2	1.04	0.79	0.86	0.05	NS
	PDXDC1	Pyridoxal-dependent decarboxylase domain-containing protein 1	1.10	0.60	0.91	0.04	NS
SSP 6131	LACTB2	Beta-lactamase-like protein 2	1.10	0.36	0.88	0.04	NS
	TATDN1	Putative deoxyribonuclease TATDN1	1.14	0.19	0.88	0.04	NS

Fig. 1

[Fig. 2]

Number of proteins	Corrected AUC	Prediction error	Proteins included in Model							
6 (Candidate Model 1)	0.877	0.164	GART	UROD	MX1	GLRX3	MAPRE1	TBCB		
7	0.872	0.181	GART	UROD	MX1	GLRX3	MAPRE1	TBCB	IGHM	
7	0.871	0.171	GART	UROD	MX1	GLRX3	MAPRE1	TBCB		HSPL4L
5	0.871	0.169	GART	UROD		GLRX3	MAPRE1	TBCB		
8	0.870	0.182	GART	UROD	MX1	GLRX3	MAPRE1	TBCB	IGHM	HSPL4L
5	0.868	0.167	GART	UROD	MX1		MAPRE1	TBCB		
6	0.866	0.175	GART	UROD	MX1	GLRX3		TBCB	IGHM	
6	0.865	0.174	GART	UROD	MX1	GLRX3	MAPRE1			HSPL4L
6	0.863	0.174	GART	UROD	MX1		MAPRE1	TBCB		HSPL4L
6	0.863	0.173	GART	UROD		GLRX3	MAPRE1	TBCB		HSPL4L
7	0.863	0.180	GART	UROD	MX1	GLRX3	MAPRE1		IGHM	HSPL4L
6	0.862	0.178	GART		MX1	GLRX3	MAPRE1	TBCB	IGHM	HSPL4L
5	0.862	0.172	GART	UROD	MX1	GLRX3		TBCB		HSPL4L
6	0.860	0.177	GART	UROD		GLRX3	MAPRE1	TBCB		
4 (Candidate Model 2)	0.860	0.178	GART	UROD	MX1	GLRX3				
7	0.859	0.188	GART	UROD	MX1	GLRX3		TBCB	IGHM	HSPL4L
6	0.857	0.177	GART	UROD	MX1		MAPRE1		IGHM	
7	0.856	0.185	GART	UROD	MX1		MAPRE1	TBCB	IGHM	
5	0.856	0.186	GART	UROD	MX1	GLRX3	MAPRE1		IGHM	
7	0.855	0.180	GART	UROD		GLRX3	MAPRE1	TBCB	IGHM	HSPL4L
6	0.855	0.183	GART	UROD	MX1	GLRX3		TBCB		HSPL4L
6	0.854	0.176	GART	UROD	MX1		MAPRE1	TBCB	IGHM	
5	0.853	0.179	GART	UROD	MX1	GLRX3				HSPL4L
6	0.853	0.184	GART		MX1	GLRX3	MAPRE1		IGHM	HSPL4L
6	0.853	0.182	GART	UROD	MX1	GLRX3			IGHM	HSPL4L
5	0.852	0.180	GART	UROD	MX1	GLRX3			IGHM	
7	0.850	0.192	GART		MX1	GLRX3	MAPRE1	TBCB	IGHM	HSPL4L
6	0.848	0.180	GART	UROD	MX1	GLRX3	MAPRE1		IGHM	
5	0.826	0.189	GART	UROD	MX1			TBCB	IGHM	
6	0.824	0.200	GART	UROD	MX1			TBCB	IGHM	HSPL4L

Fig. 2

[Fig. 3]

Protein	OR	95% CI		P-value
GART	0.01	<0.01	0.34	0.011
UROD	0.07	0.01	0.56	0.012
MX1	7.68	0.79	74.81	0.079
GLRX3	0.04	<0.01	0.74	0.030
MAPRE1	0.19	0.03	1.34	0.095
TBCB	0.13	0.02	1.00	0.050

Fig. 3

[Fig. 4]

Protein	OR	95% CI		P-value
GART	0.02	<0.01	0.34	0.006
UROD	0.11	0.02	0.60	0.011
MX1	11.91	1.56	90.91	0.017
GLRX3	0.06	<0.01	0.84	0.036

Fig. 4

[Fig. 5]

SSP No.	Gene Symbol	Protein	2D-DIGE		Screening set		Validation set		Integrated	
			S/C	p value	S/C	p value	S/C	p value	S/C	p value
SSP 3602	MX1	Interferon-induced GTP-binding protein Mx1	1.14	0.009 **	1.39	0.008 **	1.32	0.005 **	1.36	0.001 > **
SSP 5308	GART	Trifunctional purine biosynthetic protein adenosine-3	0.93	0.042 *	0.75	0.022 *	0.73	0.002 **	0.74	0.001 > **
SSP 3228	UROD	Uroporphyrinogen decarboxylase	0.84	0.049 *	0.77	0.01 *	1.03	0.831	0.85	0.118
SSP 1208	GLRX3	Glutaredoxin-3	0.92	0.040 *	0.74	0.002 **	1.12	0.103	0.88	0.073
SSP 0110	MAPRE1	Microtubule-associated protein RP/EB family member 1	0.87	0.003 **	0.76	0.009 **	1.18	0.010 *	0.89	0.182
SSP 0110	TBCB	Tubulin folding cofactor B	0.87	0.003 **	0.68	0.022 *	0.95	0.628	0.82	0.035 *
SSP 6617	IGHM	Ig mu chain C region	1.48	0.031 *	1.8	0.036 *	0.78	0.338	0.8	0.466
SSP 3714	HSPA4L	Heat shock 70 kDa protein 4L	0.78	0.039 *	0.62	0.016 *	0.73	0.014 *	0.65	0.017 *

	Control		Schizophrenia	
	N	Age ± SD	N	Age ± SD
Screening set				
Male	15	44.4 ± 12.9	15	43.7 ± 12.6
Female	15	43.2 ± 9.6	15	43.1 ± 8.9
Total	30	43.8 ± 11.2	30	43.4 ± 10.8
Validation set				
Male	15	34.9 ± 9.5	15	37.0 ± 11.0
Female	15	41.3 ± 12.9	15	45.1 ± 10.0
Total	30	38.1 ± 11.6	30	41.1 ± 11.1

Fig.5

[Fig. 6]

Gene Symbol	Result of expression analysis		Expression change (SCZ)	Result of reconfirmation		Function of protein
	Western Blotting	2D-DIGE		Western Blotting	Reproducibility	
MX1	↑	↑	Increase	↑	+	Regulates calcium channel activity
GART	↓	↓	Decrease	↓	+	Regulates enzymatic activity necessary for de novo purine biosynthesis [highly stored in craniate, involved with formylglycineamide ribonucleotide (FGAR) production]
UROD	↓	↓	Decrease			Catalyzes decarboxylation (involved with coproporphyrinogen production), UROD deficit induces familial porphyria cutanea tarda (FPCT)
GLRX3	↓	↓	Decrease			Catalyzes glutathione-disulfide oxidation-reduction enzyme reaction (reduces low-molecular disulfide and protein)
MAPRE1	↓	↓	Decrease	↑		Involved with microtubule polymerization, spindle function (stabilizes microtubule, and fixes on centrosome)
TBCB	↓	↓	Decrease			Negative regulator of axonal elongation (cofactor of tubulin heterodimer dissociation reaction)
IGHM	↑	↑	Increase			Important in primary defense mechanism Induces cell death through apoptosis
HSPA4L	↓	↓	Decrease	↓	+	Inhibits agglutination of citrate synthetase, has chaperone activity (in vitro)

↑ :Increase ↓ :Decrease + :Reproducible

Fig. 6

[Fig. 7]

Variable	Screening data				Validation data			
	OR	95% CI		P-value	OR	95% CI		P-value
MX1	11.91	1.56	90.91	0.017	26.57	1.84	383.55	0.016
GART	0.02	<0.01	0.34	0.006	0.01	<0.001	0.24	0.006
UROD	0.11	0.02	0.6	0.011	0.55	0.05	5.54	0.609
GLRX3	0.06	<0.01	0.84	0.036	4.99	0.04	570.62	0.507

Fig. 7

[Fig. 8]

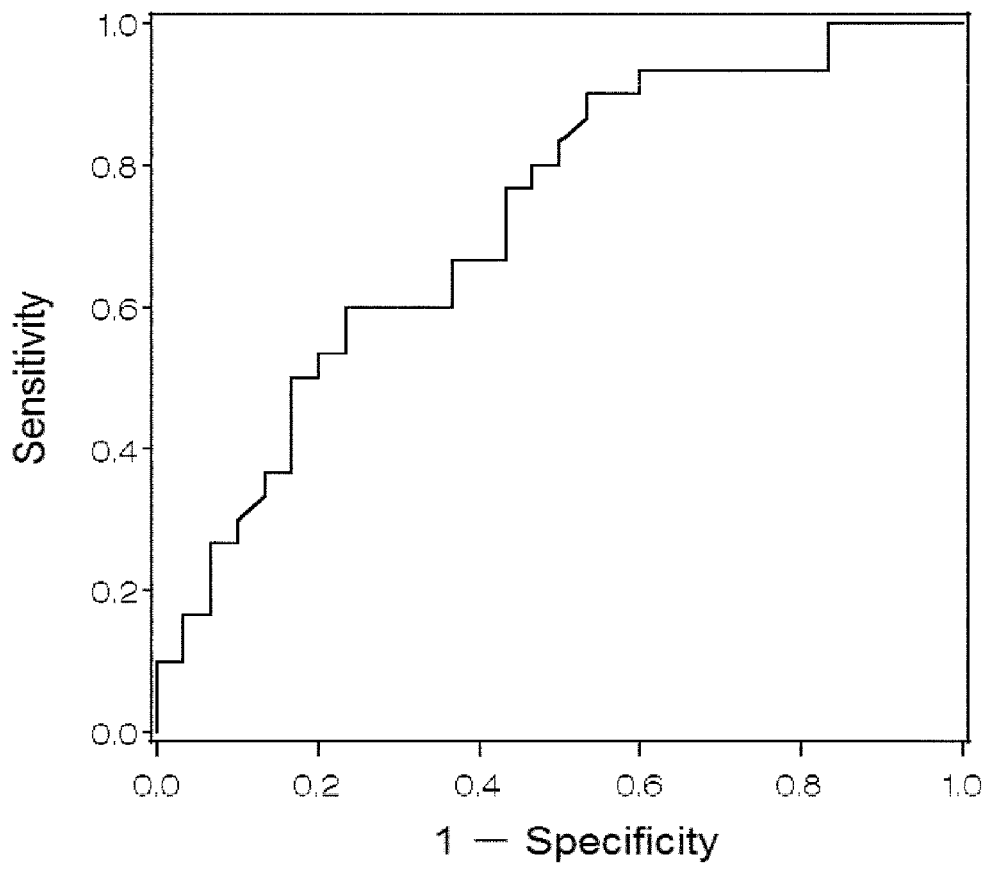


Fig. 8

[Fig. 9]

Variable	Screening data				Validation data			
	OR	95% CI		P-value	OR	95% CI		P-value
MX1	7.68	0.79	74.81	0.079	16.72	1.02	275.33	0.049
GART	0.01	<0.01	0.34	0.011	0.003	<0.001	0.22	0.008
UROD	0.07	0.01	0.56	0.012	0.79	0.04	14.57	0.875
GLRX3	0.04	<0.01	0.74	0.03	2.37	0.01	391.90	0.741
MAPRE1	0.19	0.03	1.34	0.095	103.76	0.97	>999.99	0.052
TBCB	0.13	0.02	1	0.05	1.93	0.15	24.91	0.616

Fig. 9

[Fig. 10]

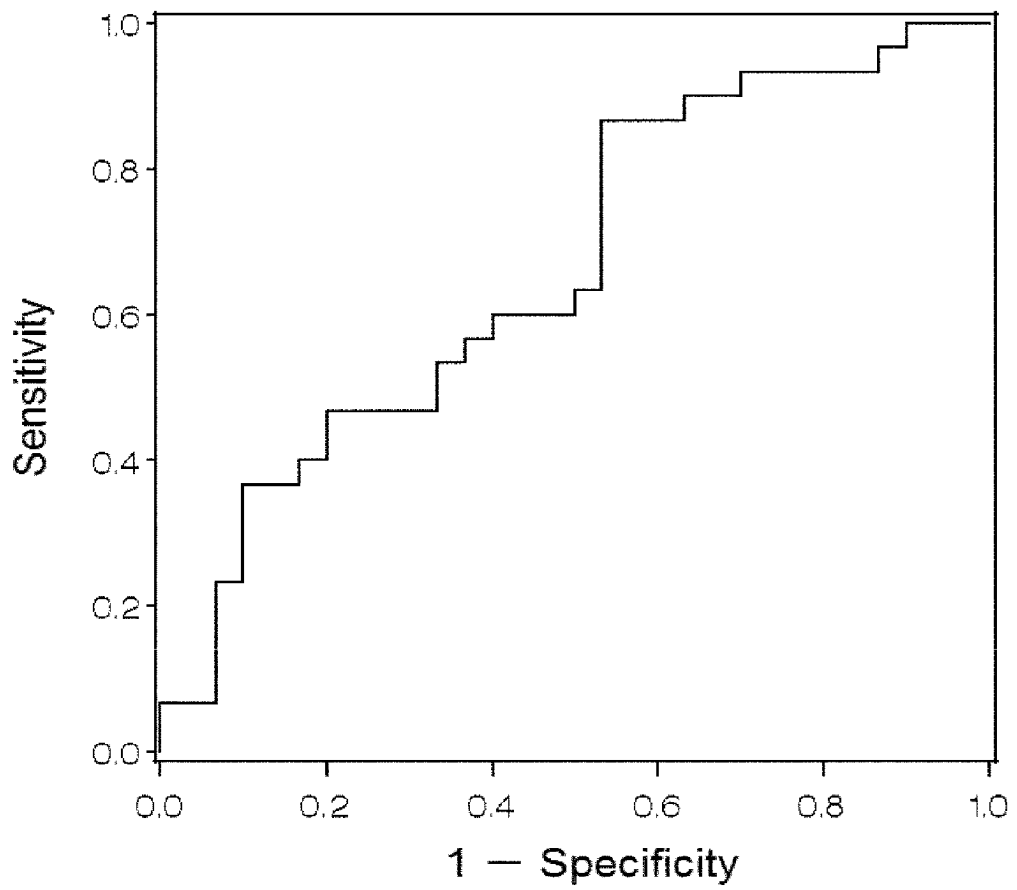


Fig. 10

[Fig. 11]

	MX1	GART	HSPA4L
MX1	(1, 1, 1)	(0.14, 0.02, 0.10)	(-0.17, 0.03, -0.15)
GART		(1, 1, 1)	(-0.10, 0.13, -0.13)
HSPA4L			(1, 1, 1)

Fig. 11

[Fig. 12]

Modeling	Validation	Intercept	MX1 (b1)	GART (b2)	UROD (b3)	GLRX3 (b4)	MAPRE1 (b5)	TBCB (b6)	HSPA4L (b7)	IGHM (b8)	AUC	Corrected AUC	AUC for validation	
S	V	-0.234	3.012	-2.852	0.000	0.000	0.000	0.000	0.000	0.000	0.80	0.78	0.82	
		6.440	2.477	-3.823	-2.178	-2.841	0.000	0.000	0.000	0.000	0.000	0.89	0.86	0.72
		11.537	2.038	-4.641	-2.674	-3.139	-1.651	-2.012	0.000	0.000	0.000	0.92	0.88	0.66
		11.379	2.177	-4.254	-2.519	-3.333	-1.964	-1.455	-0.833	2.221	0.000	0.93	0.87	0.53
V	S	1.166	3.495	-4.935	0.000	0.000	0.000	0.000	0.000	0.000	0.83	0.82	0.78	
		0.730	3.280	-4.909	-0.604	1.607	0.000	0.000	0.000	0.000	0.000	0.84	0.80	0.75
		-1.667	2.817	-5.741	-0.234	0.862	4.642	0.655	0.000	0.000	0.000	0.86	0.80	0.49
		-2.841	3.397	-5.190	0.552	4.934	4.095	1.133	-6.367	0.009	0.000	0.90	0.84	0.61
I		0.137	3.260	-3.529	0.000	0.000	0.000	0.000	0.000	0.000	0.81	0.80		
		2.485	2.968	-4.434	-0.821	-0.769	0.000	0.000	0.000	0.000	0.000	0.84	0.82	
		3.175	3.019	-4.387	-0.663	-0.738	-0.322	-0.863	0.000	0.000	0.000	0.85	0.82	
		4.130	3.111	-4.476	-0.917	-0.756	-0.333	-0.741	-0.465	-0.076	0.000	0.86	0.81	

Fig. 12

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP2013/076918

5	A. CLASSIFICATION OF SUBJECT MATTER G01N33/53(2006.01) i	
	According to International Patent Classification (IPC) or to both national classification and IPC	
10	B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) G01N33/53	
15	Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched Jitsuyo Shinan Koho 1922-1996 Jitsuyo Shinan Toroku Koho 1996-2013 Kokai Jitsuyo Shinan Koho 1971-2013 Toroku Jitsuyo Shinan Koho 1994-2013	
	Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) JSTPlus/JMEDPlus/JST7580 (JDreamIII)	
20	C. DOCUMENTS CONSIDERED TO BE RELEVANT	
	Category*	Citation of document, with indication, where appropriate, of the relevant passages
25	X	JP 2012-13415 A (Nagoya University), 19 January 2012 (19.01.2012), claims 1, 3; paragraphs [0030], [0031], [0006]; claims 7, 11; paragraph [0043] (Family: none)
30	A	JP 2009-510395 A (The Regents of the University of California), 12 March 2009 (12.03.2009), paragraph [0071] & US 2007/0117123 A1 & EP 1934373 A
35		Relevant to claim No. 1-8, 14, 15 1-8, 14, 15
40	<input type="checkbox"/> Further documents are listed in the continuation of Box C. <input type="checkbox"/> See patent family annex.	
45	* Special categories of cited documents: "A" document defining the general state of the art which is not considered to be of particular relevance "E" earlier application or patent but published on or after the international filing date "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) "O" document referring to an oral disclosure, use, exhibition or other means "P" document published prior to the international filing date but later than the priority date claimed "I" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family	
50	Date of the actual completion of the international search 16 October, 2013 (16.10.13)	Date of mailing of the international search report 29 October, 2013 (29.10.13)
55	Name and mailing address of the ISA/ Japanese Patent Office	Authorized officer
	Facsimile No.	Telephone No.

Form PCT/ISA/210 (second sheet) (July 2009)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP2013/076918

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: 9-13
because they relate to subject matter not required to be searched by this Authority, namely:
(See extra sheet)
2. Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.
3. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

- Remark on Protest**
- The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet (2)) (July 2009)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/JP2013/076918

Continuation of Box No.II-1 of continuation of first sheet(2)

5

Claims 9 to 13 pertain to "examination methods of integration disorder syndrome" that correspond to diagnostic methods to be practiced on the human body and thus relate to a subject matter which this International Searching Authority is not required, under the provisions of Article 17(2)(a)(i) of the PCT and Rule 39.1(iv) of the Regulations under the PCT, to search.

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REFERENCES CITED IN THE DESCRIPTION

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

Patent documents cited in the description

- JP 2012228417 A [0001]
- JP 2012013415 A [0005]

Non-patent literature cited in the description

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专利名称(译)	整合功能障碍综合征标志物的设定和利用		
公开(公告)号	EP2908134A4	公开(公告)日	2016-06-08
申请号	EP2013846893	申请日	2013-10-03
[标]申请(专利权)人(译)	国立大学法人名古屋大学		
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IPC分类号	G01N33/53 G01N33/68		
CPC分类号	G01N33/6893 G01N33/6896 G01N2800/302 G01N2800/50 G01N2800/60		
优先权	2012228417 2012-10-15 JP		
其他公开文献	EP2908134A1		
外部链接	Espacenet		

摘要(译)

本发明的目的是提供一种生物标志物的组合，其允许高度准确地区分精神分裂症及其利用。精神分裂症标记组的组合，包括选自由三官能嘌呤生物合成蛋白腺苷-3，尿卟啉原脱羧酶，干扰素诱导的GTP结合蛋白Mx1，谷氧还蛋白-3，微管相关蛋白RP组成的组中的两种或更多种蛋白质分子的组合。/ EB家族成员1，微管蛋白折叠辅因子B，免疫球蛋白μ链C区和热休克70kDa蛋白4L。另外，提供了一种使用样本中设置的标记物的水平作为指标来检查精神分裂症的方法。