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(54) Titre : IDENTIFICATION D'INTERACTIONS COMPOSE-PROTEINE AU MOYEN DE BANQUES DE MOLECULES  
DE FUSION PROTEINE-ACIDE NUCLEIQUE  
(54) Title: IDENTIFICATION OF COMPOUND-PROTEIN INTERACTIONS USING LIBRARIES OF PROTEIN-NUCLEIC  
ACID FUSION MOLECULES

(57) Abrégé/Abstract:

Disclosed herein is a method for detecting a compound-protein interaction, involving: (a) providing a compound library in which each member of the compound library is immobilized on a solid support; (b) contacting each member of the immobilized compound library in a single reaction chamber with each member of a protein-nucleic acid fusion library under conditions which allow the formation of compound-fusion complexes; (c) isolating the immobilized compound-fusion complexes; and (d) detecting a compound-fusion complex as an indication that the protein of the fusion interacts with the compound. In preferred embodiments, the protein is identified by reading the nucleic acid portion of the fusion, and the compound is identified by reading a detectable tag bound to either the compound or the solid support.

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(54) Title: IDENTIFICATION OF COMPOUND-PROTEIN INTERACTIONS USING LIBRARIES OF PROTEIN-NUCLEIC ACID FUSION MOLECULES

## (57) Abstract

Disclosed herein is a method for detecting a compound-protein interaction, involving: (a) providing a compound library in which each member of the compound library is immobilized on a solid support; (b) contacting each member of the immobilized compound library in a single reaction chamber with each member of a protein-nucleic acid fusion library under conditions which allow the formation of compound-fusion complexes; (c) isolating the immobilized compound-fusion complexes; and (d) detecting a compound-fusion complex as an indication that the protein of the fusion interacts with the compound. In preferred embodiments, the protein is identified by reading the nucleic acid portion of the fusion, and the compound is identified by reading a detectable tag bound to either the compound or the solid support.

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IDENTIFICATION OF COMPOUND-  
PROTEIN INTERACTIONS USING LIBRARIES  
OF PROTEIN-NUCLEIC ACID FUSION MOLECULES

Background of the Invention

In general, the invention features screening methods involving nucleic acid-protein fusions.

Screening is considered to be an efficient tool to identify binding interactions between proteins and small molecule compounds derived from large pharmaceutically-based collections, new synthetic approaches such as combinatorial chemistry, or natural sources (TIBTECH, vol. 13, p. 115, 1995). However, the multidisciplinary nature of most screening techniques poses significant challenges. The most important challenge of such techniques is maintaining a ready supply of materials for the screen. Screening of small molecule compound libraries with different protein targets requires sufficient amounts of compound. Alternatively, screening of large compound libraries (for example, having  $10^6$  members or greater) requires large amounts of recombinant protein. Another challenge is to operate the screen rapidly and cost effectively. Screening of compound libraries with different protein targets is generally time consuming if carried out in a sequential fashion.

Lately, a method has been described for the isolation of proteins with desired properties out of a pool of proteins (Szostak et al., Selection of Proteins Using RNA-Protein Fusions, U.S.S.N. 09/007,005, January 14, 1998, and U.S.S.N. 09/247,190, February 9, 1999; and Roberts & Szostak, Proc. Natl. Acad. Sci. USA (1997) vol. 94, p. 12297-12302). This technique is accomplished by means of protein-RNA fusion molecules where each protein is covalently linked to its encoding RNA. The protein-RNA fusion technology may be used to screen cDNA libraries and to clone new genes on the basis of protein-protein interactions (see, for example, Szostak et al., Selection of

Proteins Using RNA-Protein Fusions, U.S.S.N. 09/007,005, January 14, 1998, and U.S.S.N. 09/247,190, February 9, 1999).

### Summary of the Invention

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Various embodiments of this invention provide a method for detecting a compound-protein interaction, said method comprising: (a) providing a coded or addressable compound library which comprises a plurality of different compounds, wherein said compounds are immobilized on a solid support; (b) simultaneously 10 contacting said different immobilized compounds in a single reaction chamber with each member of a protein-nucleic acid fusion library under conditions which allow the formation of compound-fusion complexes; (c) isolating said immobilized compound-fusion; and (d) detecting said compound-fusion complex as an indication that the protein of said fusion interacts with said compound.

15

Various embodiments of this invention provide a method for detecting a compound-protein interaction, said method comprising: (a) providing a coded or addressable compound library which comprises a plurality of different compounds, wherein said compounds are immobilized on a solid support; (b) simultaneously contacting said library of different immobilized compounds with a protein-nucleic 20 acid fusion library under conditions which allow fusions of said protein-nucleic acid fusion library to bind to said compounds; and (c) detecting a bound protein-nucleic acid fusion as an indication that the protein of said protein-nucleic acid fusion interacts with a compound of said compound library.

25

The purpose of the present invention is to efficiently identify protein-compound binding interactions (and, particularly, protein-small molecule interactions) by screening small molecule compounds with libraries of protein-nucleic acid fusions (for example, protein-RNA fusions) in a parallel fashion, thus providing a catalogue of small molecule-protein pairs.

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Accordingly, in a first aspect, the invention features a method for detecting a compound-protein interaction, the method involving: (a) providing a compound library in which each member of the compound library is immobilized on a solid support; (b) contacting each member of the 5 immobilized compound library in a single reaction chamber with each member of a protein-nucleic acid fusion library under conditions which allow the formation of compound-fusion complexes; (c) isolating the immobilized compound-fusion complexes; and (d) detecting the compound-fusion complex as an indication that the protein of the fusion interacts with the compound.

10 In preferred embodiments, the protein-nucleic acid fusion is either a protein-RNA fusion, a protein-DNA fusion, or a protein fused to a DNA-RNA hybrid; the solid support is a bead; each bead is coded with a unique detectable label; the compound of the complexed protein-nucleic acid fusion is identified by the unique detectable label associated with the bead; the detectable label is a 15 peptide label, a nucleic acid label, a chemical label, a fluorescent label, or a radio frequency tag; the solid support is a chip and the compound library is immobilized on the chip in an addressable array; each member of the protein-nucleic acid fusion library is detectably labeled; the compound-fusion complex, or the components thereof, are recovered by release from the solid support; the

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method further involves recovering the protein-nucleic acid fusion from the solid support and identifying the protein; the identity of the protein is determined from the sequence of the nucleic acid portion of the protein-nucleic acid fusion; and the compound is a small molecule.

5 In a related aspect, the invention features a method for detecting a compound-protein interaction, the method involving: (a) providing a compound immobilized on a solid support; (b) contacting the immobilized compound with a protein-nucleic acid fusion library under conditions which allow the fusion to bind to the compound; and (c) detecting a bound protein-nucleic acid fusion as  
10 an indication that the protein of the protein-nucleic acid fusion interacts with the compound.

In preferred embodiments, the protein-nucleic acid fusion is either a protein-RNA fusion, a protein-DNA fusion, or a protein fused to a DNA-RNA hybrid; the protein-nucleic acid fusion is detectably labeled and the interaction  
15 is indicated by the association of the detectable label with the solid support; the bound protein-nucleic acid fusion is recovered by release from the solid support; the method further involves recovering the protein-nucleic acid fusion from the solid support and identifying the protein; the identity of the protein is determined from the sequence of the nucleic acid portion of the protein-nucleic  
20 acid fusion; the solid support is a column, glass slide, chip, or bead; and the compound is a small molecule.

As used herein, by a "library" is meant a collection of at least two molecules (for example, molecules such as compounds or protein-nucleic acid fusions). A compound library preferably includes at least  $10^2$  or  $10^3$  members, and, more preferably, at least  $10^4$ ,  $10^5$ , or  $10^6$  members. A protein-nucleic acid library (for example, a protein-RNA library) preferably includes at least  $10^2$  or  $10^3$  members, more preferably, at least  $10^4$ ,  $10^5$ , or  $10^6$  members, and, most preferably, at least  $10^{10}$  or  $10^{12}$  members.

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By a "DNA-RNA hybrid" is meant a DNA strand hybridized to a complementary RNA strand. Typically, the DNA strand is generated by reverse transcription of the RNA molecule.

By "addressable array" is meant a fixed pattern of immobilized 5 objects on a solid surface in which the identity of the objects is known or can be readily determined.

By a "small molecule" is meant a compound with a molecular weight of less than or equal to 10,000 Daltons, preferably, less than or equal to 1000 Daltons, and, most preferably, less than or equal to 500 Daltons.

10 The present invention provides a number of advantages. For example, the present methods reduce the amount of material required for a screen. In standard screens, considerable amounts of protein and small molecule compounds are required because each compound is screened with a single protein in a spatially segregated chamber. A library of protein-nucleic 15 acid fusion molecules, however, can be screened for binding interactions with small molecule compounds in the same reaction chamber in a parallel fashion. In addition, the protein target need not be cloned, overexpressed, or isolated, but rather is screened as a protein-nucleic acid fusion molecule and identified by its coding nucleic acid. Moreover, material costs may be further reduced by 20 miniaturization, which is facilitated by the present methods and is limited solely by the choice of detection method for the identification of small molecule-fusion complexes.

In addition, the present invention provides advantages in terms of the time required to carry out a compound screen. In particular, the methods 25 described herein accelerate the identification of ligands (for example, small molecule ligands) by screening a library of protein targets with a library of potential ligands in a parallel fashion. In contrast to standard screens, where a

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small compound library is screened for binding to different proteins in a sequential fashion, small molecule compounds may be screened, in the present techniques, with a library of protein-nucleic acid fusions in a single assay. Consequently, the present invention facilitates the screening of members of a 5 library of small molecule compounds for binding to the members of a library of proteins in a highly efficient manner.

Other features and advantages of the invention will be apparent from the following detailed description, and from the claims.

#### Brief Description of the Drawings

10 FIGURE 1 is a schematic illustration of an exemplary approach to screening a compound immobilized on a solid support with a library of protein-nucleic acid fusions.

15 FIGURE 2 is a schematic illustration of an exemplary approach to screening a library of compounds immobilized to beads with a library of protein-nucleic acid fusions.

FIGURE 3 is a schematic illustration of an exemplary approach to screening an addressable array of compounds immobilized on a microchip with a library of protein-nucleic acid fusions.

20 FIGURE 4 is a graph illustrating compound binding to an RNA-protein fusion on a bead solid support.

#### Detailed Description

The methods of the present invention facilitate the efficient identification of protein-compound (and, preferably, protein-small molecule) binding interactions by screening such compounds with libraries of protein-nucleic acid fusions (for example, protein-RNA fusions), thus providing a 25 catalog of compound-protein pairs. If desired, libraries of compounds may be

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screened against libraries of protein-nucleic acid fusions in a single screen. In preferred embodiments, either the compounds or the fusions are immobilized on a solid support (for example, a bead, chip, glass slide, or column) to simplify the screen and/or result readings. In addition, to facilitate the identification of 5 compound-protein pairs, the compound (or the solid support to which it is immobilized) may be tagged with a detectable label characteristic of that particular compound or compound family.

Any compound may be screened by the methods of the invention, although small molecules represent preferred targets for screening.

10 These and other aspects of the invention are now described in more detail below. These examples are provided for the purpose of illustrating the invention, and should not be construed as limiting.

### Screening Assays

15 As discussed above, screening of compounds against protein-nucleic acid fusions (for example, protein-RNA fusions) may be carried out in a number of different formats. One particular format is illustrated in Figure 1. By this approach, a single compound is immobilized on a column or any other solid surface using any one of a variety of standard methods. The solid phase-  
20 bound small molecule compound is then incubated with screening buffer containing BSA or another inert protein to reduce non-specific binding. Next, the buffer solution is removed, and the solid phase presenting the compound is incubated with a solution of a protein-nucleic acid fusion library, followed by washes with screening buffer to remove non-specifically bound fusion molecules. Specifically bound protein-nucleic acid fusions are then eluted (for example, by affinity elution using buffer containing free small molecule compound). “Reading” the nucleic acid (for example, RNA) portion of the 25 eluted fusion molecules provides an identification of the protein that bound the

small molecule compound. Such a "reading" may be carried out as described below.

Alternatively, multiple compounds may be screened simultaneously against multiple protein-nucleic acid fusions. Two exemplary formats for 5 carrying out this type of screen are shown in Figures 2 and 3. In these formats, an encoded (addressable) library of small molecules is immobilized on beads or any other surface, such as a chip. The solid phase-bound library is then incubated with screening buffer containing BSA or another inert protein to reduce non-specific binding. Subsequently, the buffer solution is drained, and 10 the small molecule compound library is incubated with a fusion library, followed by washes with screening buffer to remove non-specifically bound molecules. Protein-nucleic acid fusion molecules specifically binding to small molecules are then detected or, if a bead format is utilized, sorted and collected. A reading code (or tag or address) is used to identify the small molecule 15 compound, and reading of the nucleic acid portion of bound fusion molecules is used to identify the protein (as described below).

Protein-nucleic acid fusion molecules of different genotypes and different phenotypes can sometimes bind to the same small molecule compound. If desired, therefore, the bound fraction of fusion molecules may 20 be collected, amplified, and reincubated with an identified ligand under more stringent conditions (e.g., a lower concentration of protein-nucleic acid fusion). This process may be repeated any number of times, allowing for the isolation of a receptor with any desired ligand affinity (for example, selection for a receptor having the highest affinity).

25 In addition, once identified, a binding interaction between a solid phase-bound compound and a fusion molecule may be confirmed or analyzed by addition of free ligand or free protein to a compound-fusion complex in a standard binding assay.

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The present screens may be used to identify unknown compound-protein interactions or may be exploited in circumstances where some general knowledge of an interaction (for example, between a ligand and a receptor) is available. In the latter case, biased libraries may be used for screening. Such 5 libraries may contain particular classes of compounds (or proteins) or modifications of a single compound (or protein). In general, the biasing element tends to increase the average affinity of a ligand for a target receptor and to orient the ligand in a uniform way (see, for example, Chen et al., JACS (1993) vol. 115, p. 12591-12592). This type of approach facilitates the 10 identification, for example, of ligands which bind to a receptor at a targeted site.

#### Preparation of Protein-Nucleic Acid Fusions

As discussed above, the present techniques may be applied to any population of protein-nucleic acid fusions, including protein-RNA fusions, 15 protein-DNA fusions, and fusions between proteins and hybrid DNA-RNA molecules.

For use in the methods described herein, random libraries of protein-RNA fusion molecules may be prepared, for example, as described in Szostak et al., Selection of Proteins Using RNA-Protein Fusions, U.S.S.N. 09/007,005, 20 January 14, 1998, and U.S.S.N. 09/247,190, February 9, 1999; Roberts & Szostak, Proc. Natl. Acad. Sci. USA (1997) vol. 94, p. 12297-12302; or Kuimelis et al., Addressable Protein Arrays, U.S.S.N. 60/080,686, April 3, 1998, and U.S.S.N. 09/282,734, March 31, 1999). Alternatively, libraries of cellular RNA-protein fusion molecules may be prepared from mRNAs or 25 cDNAs that lack 3'-untranslated regions, for example, as described in Lipovsek et al. (Methods for Optimizing Cellular RNA-Protein Fusion Formation, U.S.S.N. 60/096,818, August 17, 1998) and Hammond et al. (Methods for Producing Nucleic Acids Lacking 3'-Untranslated Regions and Optimizing

Cellular RNA-Protein Fusion Formation, U.S.S.N. 09/374,962, August 16, 1999).

To label such protein-RNA fusions, any standard labeling method and any detectable label (including, for example, radioactive, fluorescent, and 5 chemiluminescent labels) may be utilized. If desired, fusions may be radioactively labeled by generating the fusion or fusion components in the presence of radioactive amino acids (for example, <sup>35</sup>S- or <sup>14</sup>C-labeled amino acids) or radioactive nucleotides (for example, <sup>35</sup>S- or <sup>32</sup>P-labeled nucleotides). Alternatively, fusion molecules may be fluorescently labeled. In one particular 10 example, the DNA linker (for example, the dA<sub>27</sub>dCdCP linker described in Roberts & Szostak, Proc. Natl. Acad. Sci. USA (1997) vol. 94, p. 12297-12302) may be modified with a fluorescein phosphoramidite marker (Glen Research, Sterling, VA), and this linker used for the synthesis of 15 fluorescent protein-RNA fusions. In yet another alternative, protein-RNA fusions prepared according to the method of Roberts & Szostak (Proc. Natl. Acad. Sci. USA (1997) vol. 94, p. 12297-12302; and Selection of Proteins Using RNA-Protein Fusions, U.S.S.N. 09/007,005, January 14, 1998, and 20 U.S.S.N. 09/247,190, February 9, 1999) or cellular RNA-protein fusions prepared according to the method of Lipovsek et al. (Methods for Optimizing Cellular RNA-Protein Fusion Formation, U.S.S.N. 60/096,818, August 17, 1998) or Hammond et al. (Methods for Producing Nucleic Acids Lacking 3'- 25 Untranslated Regions and Optimizing Cellular RNA-Protein Fusion Formation, U.S.S.N. 09/374,962, August 16, 1999) may be labeled by base pairing the fusion to a fluorescently-labeled oligonucleotide (for example, base pairing a fluorescent poly-dT oligonucleotide to the dA<sub>27</sub>dCdCP linker).

Alternatively, protein-DNA fusions may also be labeled using similar techniques. Such protein-DNA fusions may be generated as described, for example, in Lohse et al., DNA-Protein Fusions and Uses Thereof, U.S.S.N.

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60/110,549, December 2, 1998. In yet another alternative, the above labeling techniques may be used for fusions of proteins to hybrid DNA-RNA portions (i.e., one strand of each). Such hybrid fusions are generated, for example, by subjecting a RNA-protein fusion to a step of reverse transcription using  
5 standard techniques.

#### Preparation of Compounds

For carrying out the screening methods of the invention, any compound library may be utilized. Such libraries may be derived from natural products, synthetic (or semi-synthetic) extracts, or chemical libraries according  
10 to methods known in the art. Those skilled in the field of drug discovery and development will understand that the precise source of compounds is not critical to the screening procedure(s) of the invention. Examples of natural compound sources include, but are not limited to, plant, fungal, prokaryotic, or animal sources, as well as modification of existing compounds. Numerous  
15 methods are also available for generating random or directed synthesis (e.g., semi-synthesis or total synthesis) of any number of chemical compounds, including, but not limited to, saccharide-, lipid-, peptide-, and nucleic acid-based compounds. Synthetic compound libraries may be obtained commercially or may be produced according to methods known in the art.  
20 Furthermore, if desired, any library or compound is readily modified using standard chemical, physical, or biochemical methods.

In certain methods of the invention, interacting compounds are identified as a result of a detectable label, or "tag," bound to either the compound or its associated solid support (for example, bead). A coded library  
25 of small molecule compounds may be prepared on beads as described, for example, in Combs et al., JACS (1996) vol. 118, p. 287-288. In addition, a number of encoding schemes are available, including peptide and nucleic acid codes (Kerr et al., JACS (1993) vol. 115, p. 2529-2531; and Brenner & Lerner,

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Proc. Natl. Acad. Sci. USA (1992) vol. 89, p. 5381-5383); chemical tags (Ohlmeyer et al., Proc. Natl. Acad. Sci. USA (1993) vol. 90, p. 109222-10926; and Maclean et al., Proc. Natl. Acad. Sci. USA (1997) vol. 94, p. 2805-2810); fluorophore tags (Yamashita & Weinstock (SmithKline Beecham Corporation), 5 WO95/32425 (1995); and Sebestyen et al., Pept. Proc. Eur. Pept. Symp. 22nd 1992 (1993), p. 63-64); and radio frequency tags (Nicolaou et al., Angew. Chem. Int. Ed. Engl. (1995) vol. 34, p. 2289-2291; and Moran et al., JACS (1995) vol. 117, p. 10787-10788). Such labels may be read as described in the references above.

10 Alternatively, an addressable library of compounds (for example, small molecule compounds) may be prepared on a solid surface, such as a chip surface. A variety of techniques are available for immobilizing compounds on a chip surface, and any may be utilized. Preferable techniques include photolithography (Affymetrix, Santa Clara, CA), mechanical microspotting 15 (Schena et al., Science (1995) vol. 270, p. 467-470; Synteni, Fremont, CA) and ink jetting (Incyte Pharmaceuticals, Palo Alto, CA; and Protogene, Palo Alto, CA).

#### Identification of Compound-Fusion Interactions

20 To identify interactions between compounds (for example, coded compounds) and protein-nucleic acid fusions, any method may be utilized which provides a means for detecting a label associated with the compound or fusion or, if appropriate, for isolating and determining the identity or "address" of the compound-fusion pair.

25 In one particular example, compound-protein pairs (for example, small molecule-protein pairs) may be isolated and identified on beads. To detect a label associated with a bead, the bead resin is preferably plated out, followed by scanning, for example, for a fluorescent or radioactive label (using,

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for example, a Phosphorimager to detect a radioactive label). Protein-nucleic acid fusion molecules binding to small molecules presented on a bead may be isolated by physically sorting the beads. Alternatively, beads bound to fluorescently labeled fusion molecules may be sorted on a fluorescence activated cell sorter (FACS). Selected beads may be individually and spatially separated (for example, into the wells of a 96-well microtiter plate). For RNA-protein fusions, molecules bound to individual beads may then be identified by reverse transcription of the RNA portion, followed by sequencing of the DNA as described by Roberts & Szostak (Proc. Natl. Acad. Sci. USA (1997) vol. 94, 5 p. 12297-12302) and Szostak et al. (Selection of Proteins Using RNA-Protein Fusions, U.S.S.N. 09/007,005, January 14, 1998, and U.S.S.N. 09/247,190, 10 February 9, 1999). The tag coding for the compound (for example, the small molecule compound) on each individual bead may be read as described above.

Alternatively, ligand-receptor pairs on a chip surface may be 15 detected by scanning the chip surface for radioactivity or fluorescence. The address of the interacting pair on the chip reveals the identity of the compound (for example, the small molecule compound). The fusion molecule may be picked from the chip surface using an addressable microcollector or any other standard method (see, for example, Kuimelis et al., Addressable Protein Arrays, 20 U.S.S.N. 60/080,686, April 3, 1998, and U.S.S.N. 09/282,734, March 31, 1999). The retrieved fusion molecule may then be identified by characterizing the nucleic acid portion of the fusion as described above.

#### Compound Screening Utilizing a Bead Format

As described above, compounds may be immobilized on a bead solid 25 support and used to screen for protein-nucleic acid fusions, and specifically for RNA-protein fusions, which are capable of interacting with the compound. In one particular working example of this approach, the dihydrofolate reductase

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(DHFR) gene was cloned out of a human liver cDNA library (Maxim Biotech, South San Francisco, CA). The construct contained the entire DHFR gene with an added C-terminal DYKDDDDK-ASA peptide tag (SEQ ID NO: 1). RNA-protein fusions of DHFR were prepared by PCR amplification of the DHFR coding sequence followed by fusion formation as described in Roberts & Szostak (Proc. Natl. Acad. Sci. USA (1997) vol. 94, p. 12297-12302) and Szostak et al. (Selection of Proteins Using RNA-Protein Fusions, U.S.S.N. 09/007,005, January 14, 1998, and U.S.S.N. 09/247,190, February 9, 1999). The fusions were purified using oligo-dT-cellulose affinity chromatography (Edmonds et al., Proc. Natl. Acad. Sci. USA (1971) vol. 68:1336) and reverse transcribed with Superscript II reverse transcriptase according to the manufacturer's instructions. 100 fmol of DHFR fusion in 10  $\mu$ L 1 X buffer (Phosphate buffered saline, 1 M NaCl, 1 mg/ml BSA, 0.1 mg/ml sheared DNA, 1% v/v Triton X-100) was combined with 10  $\mu$ L pre-equilibrated methotrexate-agarose (as described in Kaufman, Methods Enzymol. (1974) vol. 34:272-81) in a 500  $\mu$ L eppendorf tube. The slurry was incubated for 30 minutes at ambient temperature with mixing every 5 minutes. The slurry was then centrifuged for 1 minute at 3000 rpm in an eppendorf microfuge. The liquid was removed, and the methotrexate-agarose was washed 3 times with 500  $\mu$ L of 1 x buffer. The fusions were then eluted by incubation of the methotrexate-agarose in 50  $\mu$ L 30  $\mu$ M methotrexate for 30 minutes at 37°C.

The results of this interaction assay are shown in Figure 4. In this figure, the percent of total fusion molecules was monitored by measuring  $^{35}$ S-methionine label incorporated into the fusions during the translation step. As indicated, the third wash contained no significant amount of fusion molecules. In addition, of the total amount of fusion included within the matrix, 86% flowed through the bead column, and the other 14% was efficiently eluted with methotrexate.

Use

The present methods provide an efficient means for screening either small or large libraries for compound-protein binding interactions. In addition, these methods may be utilized to screen protein-nucleic acid fusions against

5 one compound or against a library of compounds.

Commercial uses for screening a library of fusion molecules against a single compound include, without limitation, identification of a protein binder for a desired small molecule from a random pool of fusion molecules, rationalization of the mechanism of action of a given drug by isolating the

10 cellular target from a pool of cellular mRNA-protein fusion molecules (or a pool of the DNA-protein fusion or hybrid fusion derivatives), and rationalization of the side effect profile of a given drug by isolating most or all target proteins from a pool of cellular mRNA-protein (or DNA-protein or hybrid-protein) fusion molecules, leading to an improved drug with reduced

15 side effects.

Uses for screening a library of fusion molecules against an encoded (addressable) library of compounds include, without limitation, screening a library of small molecule compounds with a library of nucleic acid-protein (for example, cellular mRNA-protein) fusion molecules for potential new lead

20 compounds (for example, ligands or enzyme inhibitors), screening a library of nucleic acid-protein (for example, cellular mRNA-protein) fusion molecules with a library of small molecule compounds for potential targets (for example, receptors or enzymes), and mapping of binding interactions between the members of a protein library and the members of a small molecule compound

25 library, thus providing a catalogue of ligand-protein pairs.

Other embodiments are within the claims.

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## SEQUENCE LISTING

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<120> IDENTIFICATION OF COMPOUND-PROTEIN INTERACTIONS USING LIBRARIES  
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&lt;151&gt; 1998-08-17

&lt;160&gt; 1

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic affinity tag

&lt;400&gt; 1

Asp Tyr Lys Asp Asp Asp Asp Lys Ala Ser Ala

1

5

10

**What is claimed is:**

1. A method for detecting a compound-protein interaction, said method comprising:
  - (a) providing a coded or addressable compound library which comprises a plurality of different compounds, wherein said compounds are immobilized on a solid support;
  - (b) simultaneously contacting said different immobilized compounds in a single reaction chamber with each member of a protein-nucleic acid fusion library under conditions which allow the formation of compound-fusion complexes;
  - (c) isolating said immobilized compound-fusion; and
  - (d) detecting said compound-fusion complex as an indication that the protein of said fusion interacts with said compound.
2. The method of claim 1, wherein said protein-nucleic acid fusion is a protein-RNA fusion, a protein-DNA fusion, or a protein fused to a DNA-RNA hybrid molecule.
3. The method of claim 1 or 2, wherein said solid support is a bead.
4. The method of claim 3, wherein each said bead is coded with a unique detectable label.
5. The method of claim 4, wherein said compound-fusion complex is identified by said unique detectable label associated with said bead.
6. The method of claim 4 or 5, wherein said detectable label is a peptide label, a nucleic acid label, a chemical label, a fluorescent label, or a radio frequency tag.
7. The method of claim 1 or 2, wherein said solid support is a chip and said compound library is immobilized on said chip in an addressable array.
8. The method of claim 7, wherein each member of said protein-nucleic acid fusion library is detectably labeled.

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9. The method of any one of claims 1 to 8, wherein said compound-fusion complex, or the components thereof, are recovered by release from said solid support.

10. The method of any one of claims 1 to 9, wherein said method further comprises recovering said protein-nucleic acid fusion from said solid support and identifying said protein.

11. The method of claim 10, wherein the identity of said protein is determined from the sequence of the nucleic acid portion of said protein-nucleic acid fusion.

12. The method of any one of claims 1 to 11, wherein each of said compounds has a molecular weight of less than or equal to 10,000 Daltons.

13. A method for detecting a compound-protein interaction, said method comprising:

(a) providing a coded or addressable compound library which comprises a plurality of different compounds, wherein said compounds are immobilized on a solid support;

(b) simultaneously contacting said library of different immobilized compounds with a protein-nucleic acid fusion library under conditions which allow fusions of said protein-nucleic acid fusion library to bind to said compounds; and

(c) detecting a bound protein-nucleic acid fusion as an indication that the protein of said protein-nucleic acid fusion interacts with a compound of said compound library.

14. The method of claim 13, wherein said protein-nucleic acid fusion is a protein-RNA fusion, a protein-DNA fusion, or a protein fused to a DNA-RNA hybrid molecule.

15. The method of claim 13 or 14, wherein said protein-nucleic acid fusion is detectably labeled and said interaction is indicated by the association of said detectable label with said solid support.

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16. The method of claim 13, 14 or 15, wherein said bound protein-nucleic acid fusion is recovered by release from said solid support.

17. The method of any one of claims 13 to 16, wherein said method further comprises recovering said protein-nucleic acid fusion from said solid support and identifying said protein.

18. The method of claim 16 or 17, wherein the identity of said protein is determined from the sequence of the nucleic acid portion of said protein-nucleic acid fusion.

19. The method of any one of claims 13 to 18, wherein said solid support is a column, glass slide, chip, or bead.

20. The method of any one of claims 13 to 19, wherein each of said compounds has a molecular weight of less than or equal to 10,000 Daltons.

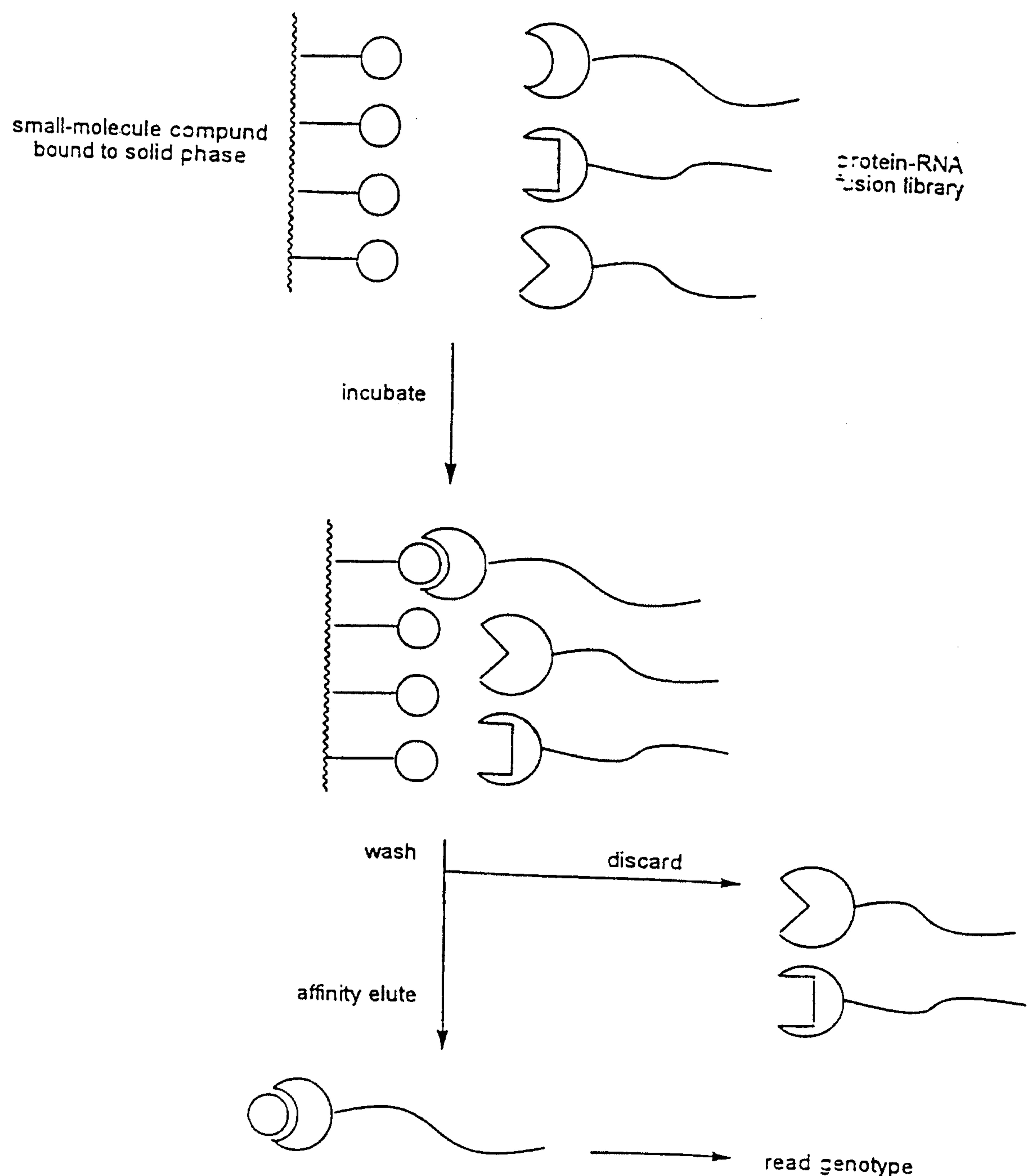


FIGURE 1

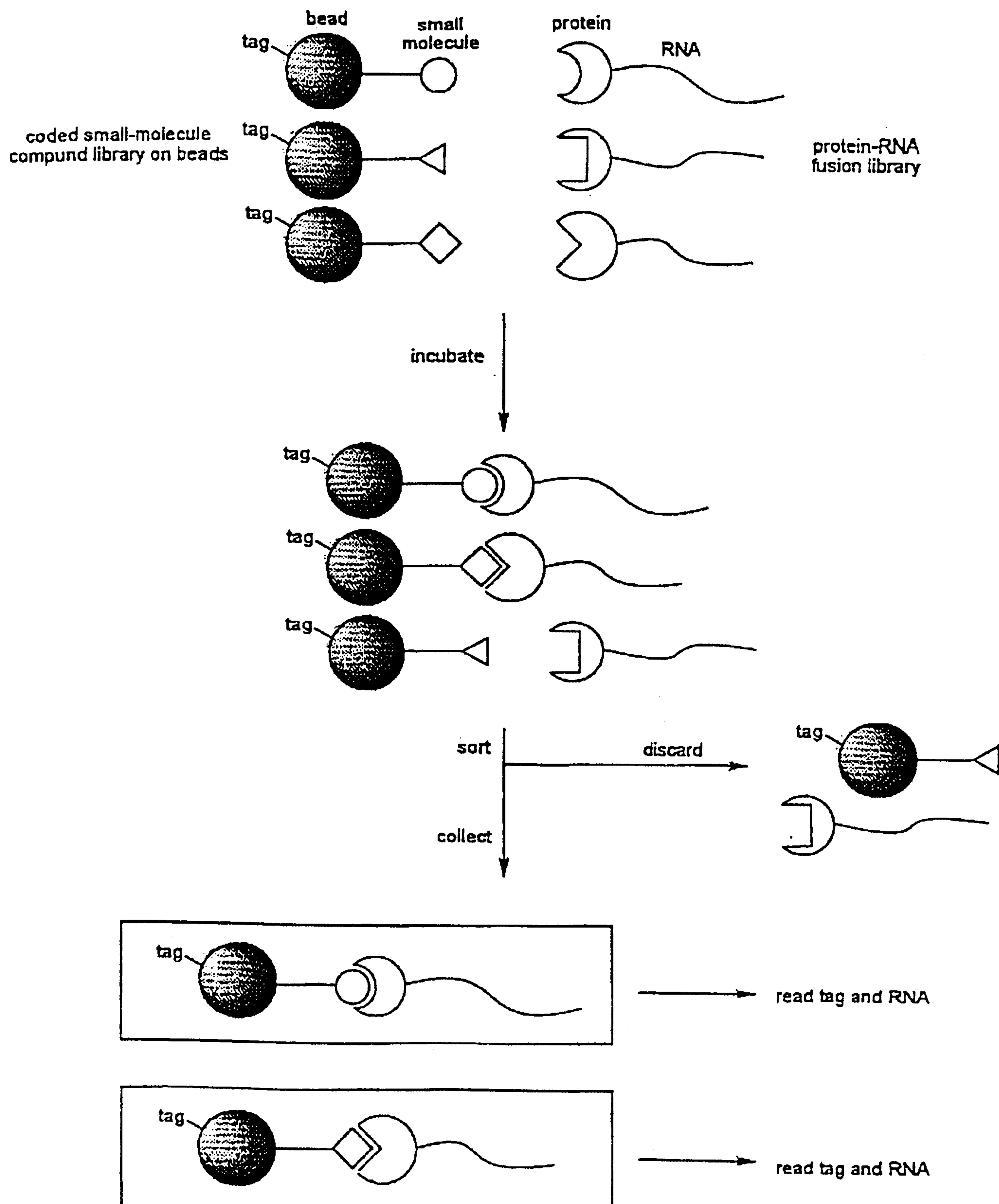


FIGURE 2

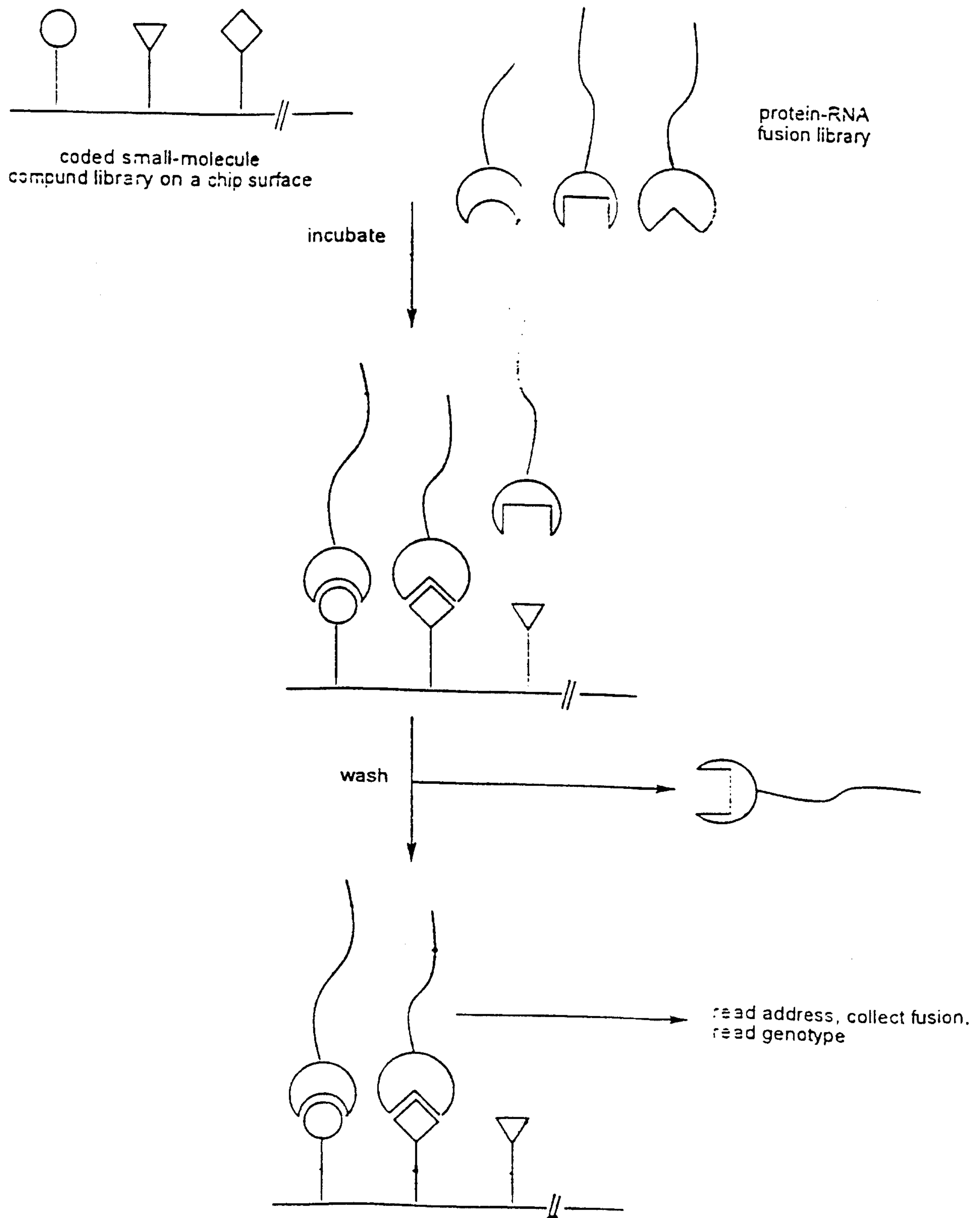


FIGURE 3

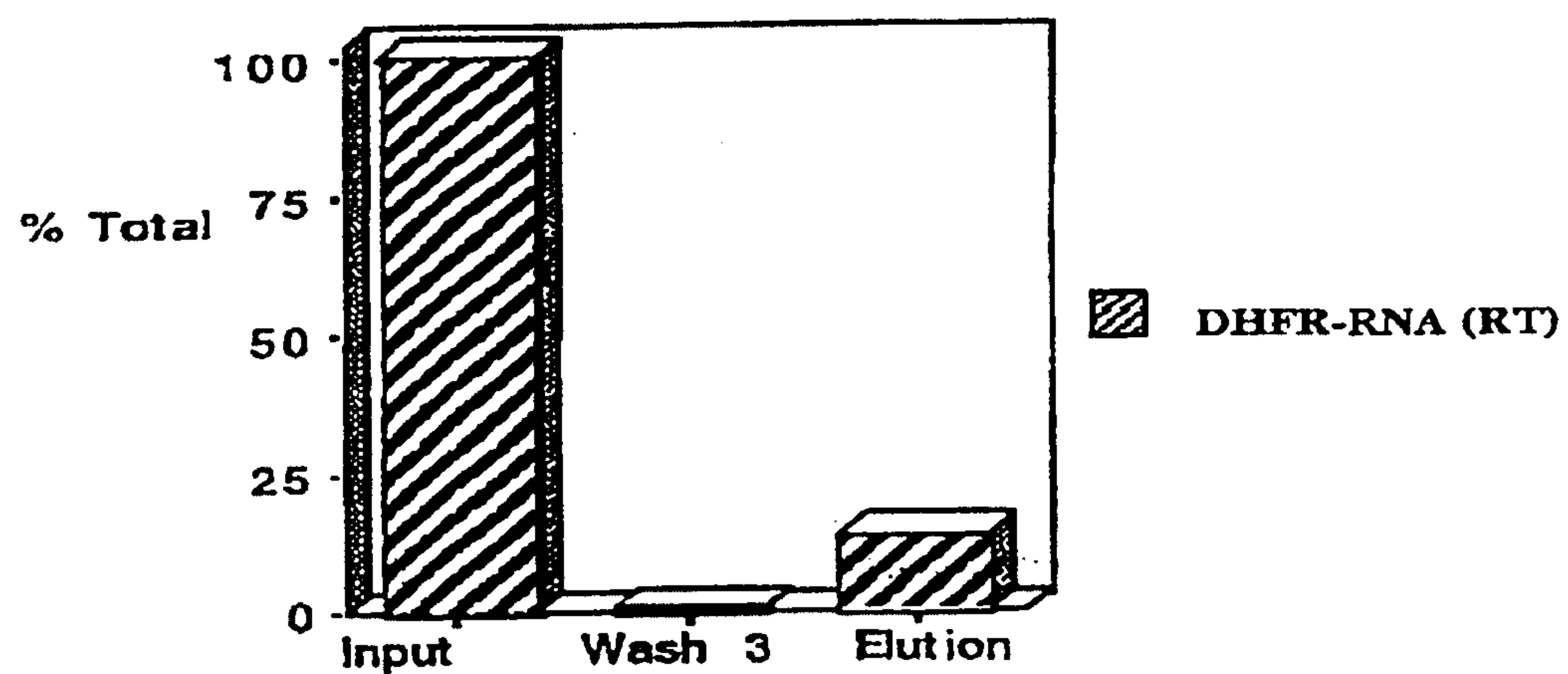


FIGURE 4