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(54) **Title**: METHOD AND APPARATUS FOR DETERMINING DIFFUSION PROPERTIES OF A SAMPLE

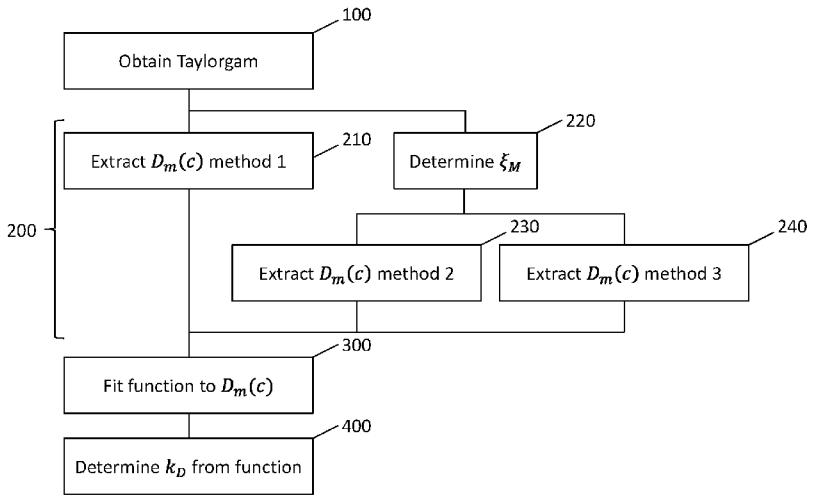

Figure 2

(57) **Abstract**: A method of determining a relationship between a mutual diffusion co-efficient D_m and the concentration c of a solute within a solvent. The method comprises: obtaining a Taylorgram (100) comprising a plurality of measurements of solute concentration c; and deriving from the Taylorgram (200) a plurality of mutual diffusion coefficient values D_m corresponding with a plurality of different concentrations c of solute in the solvent.

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METHOD AND APPARATUS FOR DETERMINING DIFFUSION PROPERTIES OF A SAMPLE

The invention relates to a method of determining diffusion properties of a sample, and more particularly doing so from a Taylorgram.

Developing a biopharmaceutical product that is stable against protein aggregation is a major challenge for the biopharmaceutical industry. Consequently, a significant body of research has been undertaken to understand the mechanisms governing protein self-association or aggregation and how to prevent or mitigate their occurrence. Weak or non-specific protein-protein interactions (PPIs), whose effects become more significant in concentrated protein solutions, have been identified as one pathway for the formation of non-reversible aggregates (*Lehermayr et al, 2011, Assessment of net charge and protein-protein interactions of different monoclonal antibodies, Journal of Pharmaceutical Sciences, 100(7): 2551-2562; Connolly et al, 2012, Weak interactions govern the viscosity of concentrated antibody solutions: high-throughput analysis using the diffusion interaction parameter, Biophysical Journal, 103:69-78*).

The relationship between interactive forces in dilute protein solutions and the propensity for protein aggregation in a final formulation is not straightforward and is a product of a complicated interplay between solute and solvent properties e.g. concentration, ionic strength and pH (*Saluja et al, 2008, Nature and consequences of protein-protein interactions in high protein concentration solutions, International Journal of Pharmaceutics, 358:1-15*). This relationship is further complicated by the presence of excipients and means that empirical determination of the protein-protein interactions is necessary for each formulation under development; and this can amount to hundreds of different combinations.

The diffusion interaction parameter (k_D) is one metric that describes the interactive forces between solute molecules in a given medium and a growing body of evidence has shown that it can successfully predict the aggregation propensity of formulations (*Saluja et al, 2010, Diffusion and sedimentation interaction parameters for measuring the second virial coefficient and their utility as predictors of protein aggregation, Biophysical Journal, 99:2657-2665*). The most widely used technique for determining k_D is Dynamic Light Scattering (DLS) because it allows the relatively trivial

measurement of the mutual diffusion coefficient (D_m); a critical parameter in k_D elucidation. To determine k_D, one measures the mutual diffusion coefficient at a series of solute concentrations and a plot of this value as a function of concentration yields k_D from the slope (Equation 1). The self-diffusion coefficient (D_0), which describes the diffusion of molecules at infinite dilution and is a measure of the Brownian motion of a single molecule, can also be extracted from the y-intercept.

$$D_m = D_0(1 + k_D C) \quad \text{(Eq. 1)}$$

More positive k_D values indicate that repulsive forces between protein molecules dominate within the solution; whereas increasingly negative values suggest that interactions have attractive tendencies, and thus indicate destabilising conditions.

Although the act of data collection is simple and the technique readily amenable to high-throughput screening via a plate reader, k_D determination by DLS may be made more difficult by methodological problems. The first such difficulty relates to the biased scattering intensities exhibited by differently sized particles; whereby the scattering intensity is approximately proportional to the sixth power of the molecular radius (r^6). Since it is the average diffusion coefficients that are reported, the resulting values may be susceptible to skew by larger particles. At worst, results can be rendered unusable in the presence of high-order aggregates or dust. In practice, this means that samples must be relatively pure and stable over the duration of the measurement. This may require clean-up procedures, such as filtering, which may be neither desirable nor appropriate for some types of sample. The second issue concerns the potential impact of solute concentration on bulk viscosity of the sample which in turn may affect the diffusion of a molecule in that environment. An increase in viscosity works to restrict diffusion and thus particles would appear to be larger than they truly are. For DLS, this means that the viscosity at all concentrations must be known in order to determine a corrected diffusion coefficient for datapoints where restricted diffusion occurs or the researcher is limited to working in conditions which are no longer representative or relevant.

Nuclear magnetic resonance (NMR) is a second technique that can be used to determine the k_D; however, such determinations are non-trivial. The use of specialised solvents or sample constructs may introduce complexities into sample

preparation and the conditions of measurement may be different from those in final formulations. In NMR measurements, molecular diffusion must also happen within a specific relaxation regime and, in particular, this makes obtaining accurate diffusion coefficients for larger molecules is more challenging. Consideration must also be given to possible misinterpretation due to presence of contamination, and to overly complicated spectra that may require dedicated personnel to make meaningful analyses. In addition, using NMR to determine diffusion coefficients is extremely time-consuming, as well as financially costly, and thus not applicable to large scale screening.

Sedimentation velocity ultracentrifugation (SV-AUC) and self-interaction chromatography (SIC) cannot directly measure k_D but can measure analogous parameters such as the sedimentation interaction parameter (k_S) and second virial coefficient (A_2), respectively.

Taylor dispersion analysis can be used to infer a mutual diffusion coefficient. For example, the width of a Gaussian distribution found from a best fit to a pulse Taylorgram can be used to determine a mutual diffusion coefficient for the injected sample. The concentration corresponding with such a single value of mutual diffusion coefficient is generally assumed to be the concentration of the sample at injection, without taking account of any reduction in concentration due to dispersion. A sequence of such measurements at different sample injection concentrations would be required to determine a relationship between concentration and mutual diffusion coefficient.

The above-mentioned techniques require the preparation and measurement of multiple samples at precisely known concentrations (as well as viscosities). Working with a single intact and unmodified sample would be more favourable when trying to correlate parameters with properties.

A method for investigating diffusion properties of a sample, for example the variation in mutual diffusion coefficient with solute concentration, and the diffusion interaction parameter, that overcomes or ameliorates at least some of these problems is desirable.

According to a first aspect of the invention, there is provided a method of determining a relationship between a mutual diffusion co-efficient D_m and the concentration c of a solute within a solvent. The method comprises obtaining a Taylorgram comprising a plurality of measurements of solute concentration c; and deriving from the Taylorgram a plurality of mutual diffusion coefficient values D_m corresponding with a plurality of different concentrations c of solute in the solvent.

Deriving a plurality of mutual diffusion coefficients corresponding with a plurality of different solute concentrations from a (single) Taylorgram avoids the need for preparing a plurality of samples at different concentrations and obtaining a Taylorgram for each of the plurality of samples. The preparation and separate analysis (whether by DLS or TDA) of a plurality of samples at different (initial) concentrations represents the prior art approach for determining the relationship between the mutual diffusion coefficient D_m and concentration c. Since embodiments of the present disclosure enable determining the relationship between mutual diffusion coefficient D_m and concentration c from a single Taylorgram (and therefore a single sample), the present disclosure represents a significant advance over the prior art.

The method may further comprise fitting a function to the Taylorgram.

The function may be of the form:

$$c = 0.5c_0 erfc(u) \text{ where } u = 0.5\frac{y(t \pm t_M)}{\sqrt{t}},$$

wherein t is the measurement time; c is the concentration; and t_M, y and c_0 are parameters to be determined from the fit.

The method may further comprise differentiating the Taylorgram to determine a rate of change of concentration with respect to time $\frac{dc}{dt}$.

The mutual diffusion coefficient values D_m may be derived from the function that is fitted to the Taylorgram and from the rate of change of concentration with respect to time.

The mutual diffusion coefficient values D_m may be determined using the following expression:

$$D_m(c) = \frac{\left[-4\frac{dc\sqrt{\pi}t^{3/2}e^{u^2}}{dt(t+t_M)\sqrt{t_M}}\right]^2 r^2 t_M}{48}$$

where r is the radius of the capillary.

The method may further comprise performing a transform on the Taylorgram to find a relationship between ξ and concentration c, where $\xi = \frac{x}{2\sqrt{t}}$.

The method may further comprise determining an interface ξ_M from the equation $\xi_M = \frac{1}{c_L - c_R}\int_{c_R}^{c_L} \xi dc$, where c_L is the higher limit of concentration c, and c_R is the lower limit of concentration c, or where c_L is the lower limit of concentration c, and c_R is the higher limit of concentration.

The method may further comprise:

determining a value of u corresponding with each concentration value c, from the relationship $c = 0.5c_0 erfc(u)$;

determining parameters h and m by fitting a straight line to the relationship between u and ξ, using the relationship $u = h(\xi - \xi_M) + m$;

wherein deriving the plurality of mutual diffusion coefficient values D_m corresponding with a plurality of different concentrations c of solute in the solvent comprises using the relationship $\frac{1}{h^2} + \frac{m\sqrt{\pi}}{h^2} erfc(u)\exp(u^2) = \frac{r^2 v^2}{48 D_m(c)}$.

Deriving the plurality of mutual diffusion coefficient values D_m may be performed by numerically determining a plurality of values of the differential $\frac{d\xi}{dc}$ and a plurality of values of the integral $\int_0^c \xi - \xi_M dc$, corresponding with different concentrations c, and using the expression $-\frac{1}{2}\frac{d\xi}{dc}\int_0^c \xi - \xi_M dc = \frac{r^2 v^2}{48 D_m(c)}$.

The method may further comprise determining a diffusion interaction parameter k_D of the solute in the solvent from the relationship $D_m(c)$ between the mutual diffusion coefficient values D_m and the corresponding concentrations c.

The method may further comprise determining the second virial coefficient A_2 from the diffusion interaction parameter k_D and an estimate of the coefficient of friction k_f and an estimate of the partial specific volume v_2 of the solute.

The method may further comprise estimating a measure of aggregation of solute particles from the values of the mutual diffusion coefficient over the duration of the Taylorgram.

According to a second aspect, an apparatus is provided, comprising a processor, configured to perform the method of the first aspect.

The apparatus may further comprise an instrument for performing a Taylor dispersion analysis, so as to obtain a Taylorgram.

According to a third aspect, there is provided a machine readable medium, comprising instructions for configuring a processor to perform the method according to the first aspect.

Examples will now be described, with reference to the accompanying drawings, in which:

Figure 1 is a schematic of a method for investigating diffusion properties;

Figure 2 is a schematic showing the outline of three alternatives for extracting a relationship between mutual diffusion coefficient and concentration;

Figure 3 is a schematic showing the first of three alternative methods for extracting a relationship between mutual diffusion coefficient and concentration;

Figure 4 is a schematic showing the second of three alternative methods for extracting a relationship between mutual diffusion coefficient and concentration;

Figure 5 is a schematic showing the third of three alternative methods for extracting a relationship between mutual diffusion coefficient and concentration;

Figure 6 is a graph showing a concentration plotted against ξ;

Figure 7 is schematic of an apparatus according to an embodiment;

Figure 8 is a frontal Taylorgram of BSA in iodide solution, which can be used in an embodiment to determine the relationship between mutual diffusion coefficient and concentration; and

Figure 9 is a graph showing a series of DLS measurements used to obtain estimates for self-diffusion coefficient D_0 and diffusion interaction parameter k_D for comparison with estimates obtained from a Taylorgram, according to an embodiment.

Taylor dispersion is a process by which shear flow is used to enhance the effective diffusivity of a sample. Laminar flow in a capillary results in a variation in flow velocity with radial location. Near the walls, the flow is substantially stationary, and flow velocity is at a maximum at the centre. This results in shearing of the adjacent lamina, which acts to enhance dispersion of a sample.

Taylor dispersion analysis (TDA) can be used to analyse properties of species within a sample. A plug of the sample may be injected into a microbore capillary and subsequently disperse as it traverses along the capillary within a laminar flow regime. The injected plug of the sample may be narrow (having a short duration) this being referred to as a pulse of the sample, resulting in a pulse Taylorgram. Alternatively the injected plug of the sample may be long (i.e. having a longer duration) this may be referred to as a slug of the sample, resulting in a frontal Taylorgram. The degree of dispersion exhibited by the plug is dependent on the diffusivity of the molecules within the plug and can be measured at one or multiple points downstream of the injection site. A concentration detector, responsive to the species of the sample, may be positioned at one or more locations downstream of the injection location. The concentration detectors (e.g. a UV-Visible spectrometer) may thereby produce a signal that is proportional to the concentration of the molecules in each cross-section of the flow past the detector. The resultant signal from the detector, typically referred to as a Taylorgram, corresponds to a temporally-resolved distribution of molecular concentration whose width is related to the hydrodynamic radius of the sample species.

Referring to Figure 1, a method according to an example embodiment comprises obtaining a Taylorgram at step 100, and then extracting (or determining) from the Taylorgram a relationship $D_m(c)$ between the mutual diffusion coefficient D_m and the concentration c, at step 200, for example by calculating a plurality of values of mutual diffusion coefficient at a corresponding plurality of different concentration values. Significantly, the methods disclosed more fully hereinafter can determine the relationship between mutual diffusion coefficient and concentration from a single Taylorgram.

The Taylorgram obtained at 100 may be generated from a plug or pulse injection, and may comprise a single detection point or multiple detection points.

Once $D_m(c)$ has been obtained, in step 300 a function may be fitted to $D_m(c)$, for example by plotting $D_m(c)$ and fitting a straight line to the relationship. In step 400, the parameters of the function may then be extracted and used to determine the diffusion interaction parameter, k_D.

In optional step 600, the relationship $D_m(c)$ between the mutual diffusion coefficient and concentration may be used to determine an aggregation % over the course of the Taylorgram. For example, aggregation will result in a change in the mutual diffusion coefficient, so a discontinuity in the mutual diffusion coefficient $D_m(c)$ may indicate aggregation of particles.

In optional step 500, the diffusion interaction parameter k_D may in turn be used to determine the second virial coefficient A_2, for instance using estimates of the molecular weight, coefficient of friction and the partial specific volume of the solute.

Referring to Figure 2, three different example methods are schematically illustrated for determining the relationship $D_m(c)$ between the mutual diffusion coefficient D_m and concentration, c. Step 200, in which $D_m(c)$ is extracted, is expanded into three different methods. The first of these methods 210, is different from the second method 230 and third method 240. Both of the second and third method 230, 240, involve determining an interface ξ_M, at step 220.

Each of the methods will now be described in more detail. The present invention is suitable for determining the diffusion in interaction parameter k_D from a Taylorgram generated from a single measurement. The sample may be injected in a slug, so as to create a frontal Taylorgram, or in a pulse, to create a pulse Taylorgram. The mathematics in the example methods deal with a frontal Taylorgram, but the skilled person will appreciate that it is straightforward to adapt the method for a pulse Taylorgram. The method uses the inherent variation in concentration over the course of a Taylorgram to provide a concentration series in which the state of interaction between the molecules is determined with reference to the concentration dependence of the mutual diffusion coefficient D_m.

Although UV absorption is typically used to determine concentration in a Taylorgram, the method will also work with any detection method that produces signals in which the concentration and signal from a particle can be rationally correlated, for example, based on any of: refractive index, fluorescence via an extinction coefficient). Each point in a Taylorgram represents a concentration, so a single Taylorgram provides a plurality of solute concentrations.

Method 1 – Explicit differential method

This method 210 is illustrated schematically in Figure 3. First, in step 211 a function is fitted to the Talorgram. The function may be of the form:

$$c = 0.5c_0 erfc(u) \qquad \text{(Eq. 2)}$$

where

$$u = 0.5\frac{y(t \pm t_M)}{\sqrt{t}} \qquad \text{(Eq. 3)}$$

In which t is the measurement time, and t_M is a parameter to be determined from the fit. Plus or minus signs in the $t \pm t_M$ term are used to designate analyses for the leading and trailing edges of a frontal Taylorgram, respectively. Note, that although y is estimated, it may be redundant in this method.

Next, in step 212, the Taylorgram (or the function fitted to the Taylorgram) is differentiated, for instance using Savitzy-Golay differentiation (or the difference method), to obtain $\frac{dc}{dt}$.

Next, from , $\frac{dc}{dt}$ determine h' from equation 4, below:

$$h'(C) = -4\frac{dc}{dt}\frac{\sqrt{\pi}t^{3/2}e^{u^2}}{(t+t_M)\sqrt{t_M}} \quad \text{(Eq. 4)}$$

A value of h' can be determined for each datapoint in the Taylorgram. Note that the determination of h' is not an essential step, but merely provides for a more elegant description of the calculation. In some embodiments the expression for h' may be substituted into Eq. 5 below, and $D_m(c)$

Finally, determine the mutual diffusion coefficient $D_m(c)$ using the following expression:

$$D_m(c) = \frac{h\prime(c)^2 r^2 t_M}{48} \quad \text{(Eq. 5)}$$

Common features of Methods 2 and 3

Both the second and third example methods share the steps 220 for determining a reference value, ξ_M, as shown in Figures 2, 4 and 5.

The Taylor dispersion relation for a sample plug in a buffer flowing at a mean speed of v in a capillary of radius r is given by

$$\frac{\partial c}{\partial t} = \frac{\partial}{\partial x}\left[k(c)\frac{\partial c}{\partial x}\right] \quad \text{(Eq. 6)}$$

where c is the concentration, x is the distance dispersed relative to the initial edge of the plug, k is the dispersion coefficient which is given by $\frac{r^2 v^2}{48 D_m(c)}$.

Using the Boltzmann transformation

$$\xi = \frac{x}{2\sqrt{t}} \quad \text{(Eq. 7)}$$

equation 6 can be rearranged to give:

$$-2\xi \frac{dc}{d\xi} = \frac{d}{d\xi}\left[k(c)\frac{dc}{d\xi}\right] \quad \text{(Eq. 8)}$$

This can be solved to give:

$$k(c) = -\frac{1}{2}\frac{d\xi}{dc}\int_0^c \xi - \xi_m dc = \frac{r^2 v^2}{48 D_m(c)} \quad \text{(Eq. 9)}$$

In which ξ_m defines a reference point, which must be properly determined for the mutual diffusion coefficients to be physically representative. The reference point is constrained by the requirement:

$$\int_{c_R}^{c_L}(\xi - \xi_M)dc = 0 \quad \text{(Eq. 10)}$$

where c_L and c_R are the limits of the concentrations to the left and right of the Taylorgram (i.e. corresponding with a maximum and minimum value of the concentration, depending on whether the method is performed on a leading edge or trailing edge of a frontal Taylorgram). The reference point ξ_M may define an interface, and is not in general and may not be co-incident with $\xi = 0$.

However for constant volume dispersion (as is the case in Taylor dispersion), the interface may be coincident with $\xi = 0$ (i.e. corresponding with an initial edge of the plug). Typically, this edge is ill-defined after considerable dispersion, but can be determined from the following relation:

$$\xi_M = \frac{1}{c_L - c_R}\int_{c_R}^{c_L} \xi dc \quad \text{(Eq.11)}$$

Hence, given a concentration profile of c as a function of ξ as well as the reference point ξ_M, the values of k as a function of c can be determined. This can be achieved via either of the second or third methods.

Method 2

This method considers the concentration profile c as a function of ξ, as shown in Figure 6.

The function:

$$C = 0.5C_0 erfc(u) \quad \text{(Eq. 12)}$$

is evaluated to obtain a value of u for each value c of the Taylorgram. The Boltzmann transformation (defined by equation 7) is used to determine a relationship between ξ and concentration c. Via the concentration c a relationship can subsequently be determined between u and ξ. A function can be fitted to describe this relationship, in accordance with the following (for instance by plotting u against ξ, and fitting a straight line):

$$u = h(\xi - \xi_M) + m \quad \text{(Eq. 13)}$$

Where h and m are parameters determined by the fit. Inserting equation 13 into equation 12, and then solving for $k(c)$ in equation 9 gives:

$$k(c) = \frac{1}{h^2} + \frac{m\sqrt{\pi}}{h^2} erfc(u) \exp(u^2) = \frac{r^2 v^2}{48 D_m(c)} \quad \text{(Eq. 14)}$$

from which it is straightforward to determine $D_m(c)$.

Method 3

This method can be performed numerically or graphically, and involves the estimation of evaluation of the integral $\int_0^c \xi - \xi_m dc$ and the differential $\frac{d\xi}{dc}$ in equation 9 directly from the transformed concentration profile $c(\xi)$. The skilled person will be aware that a wide range of techniques exist for approximating differentials and integrals from

such data, either numerically or graphically from a plot. Smoothing or filtering of the data may be performed before, or after performing the transform, for instance using a moving average, or by a Savitzky-Golay filter.

Second virial coefficient

Another, closely related, parameter suitable for measuring protein-protein interactions is the second virial coefficient, A_2 - also known as the osmotic virial coefficient (B_{22} or B_2). The second virial coefficient is linked to k_D by the following expression (Eq. 15); where M_W is the molecular weight of the protein, k_f is the coefficient of friction and v_2 is the partial specific volume.

$$k_D = 2M_W A_2 - k_f - 2v_2 \qquad \text{(Eq. 15)}$$

Here, positive and negative A_2 values are suggestive of repulsive and attractive forces between protein molecules, respectively.

Providing that the coefficient of friction and partial specific volume are known or can be otherwise estimated or determined, the A_2 parameter can also be extracted using k_D.

Aggregation

The mutual diffusion coefficient $D_m(c)$ provides a measure of the average size of the species under analysis. As the species transition through the capillary they are spatially distributed within the plug. With this knowledge and with the measurement of the diffusion coefficient at every data point collected over a certain time period a measure of aggregation can be estimated (e.g. a proportion or % aggregation) from the change in diffusion coefficient $D_m(c)$ over the Taylorgram.

Apparatus

Referring to Figure 7, an apparatus 40 is shown in accordance with an embodiment. The apparatus 40 comprises an instrument 50, processor 51, output means 52 and input means 53. The instrument 50 is operable to perform a Taylor dispersion analysis on a sample, so as to produce Taylorgram data 71. The processor 51 may be configured to estimate parameters for fitting a model (e.g. Gaussian, error function) to the Taylorgram data 71, in accordance with an embodiment (for instance as described

above). The processor 51 may provide an output 72 to the output means 52, which may comprise a display or printer. The output 72 may comprise model parameter estimates, and/or estimates of the properties of the sample analysed by the instrument 50, based on a model fitted to the data 71 by the processor 51. The processor 51 may be configured to use estimated model parameters (determined according to an embodiment) as a starting point for a numerical search for a best fit to the Taylorgram data 71 (for instance via regression analysis based on least squares). An input means 53 may be provided for controlling the processor 51 and/or instrument. The input means 53 may comprise a keyboard, mouse or other suitable user interface device.

The instrument 50 may comprise a capillary linking two containers . Liquid is driven (e.g. at constant pressure) from the first container to the second container. The first container contains a run (or carrier) solution so that the capillary is initially filled with the run solution. The first container is then disconnected from the capillary , and a third container is connected that contains a sample solution. The sample solution may be a pharmaceutical or biopharmaceutical species dissolved either in the run/carrier solution, or in a different medium . The different medium may differ from the run/carrier solution in having an excipient, e.g. a salt or a sugar, dissolved at a different concentration than in the run/carrier solution. This may be appropriate in formulations which are designed to stabilise active drug species.

A first and second window are spaced apart along the length of the capillary between the first and second containers. The capillary may be formed in a loop so that both the first and second windows may be imaged using a single optical assembly, for instance by arranging for them to be adjacent to one another in an area imaged by the pixel array of an area imaging detector. In other embodiments, a single window may be used, or the detector may comprise a single element, rather than a pixel array.

To inject a plug of the sample into the capillary the third container may be connected to the capillary and then disconnected after a suitable volume of the sample has been injected under pressure. The second container is connected the capillary when the third container is disconnected from the capillary. The detector captures a frame sequence comprising measures of the received light intensity at the detector as the pulse of sample solution or the flow front passes through each of the first and second

windows. The detector output thereby provides data on absorbance versus time: a Taylorgram.

Example results

The methodology described herein was applied to frontal Taylorgrams obtained from BSA (Bovine Serum Albumin) prepared in Iodide and Sulphate buffers at a final concentration of 30 mg/mL. Samples were injected into a microbore capillary (ID 75μm) at 140 mbar for a duration of 3 minutes and eluted using the same pressure. Taylorgrams were recorded using UV detection at a wavelength of 280 nm.

Figure 8 shows an example of a frontal Taylorgram 801 obtained from a sample of BSA in an iodide buffer solution from which a self-diffusion co-efficient D_0 and diffusion interaction parameter k_D can be obtained, in accordance with an embodiment.

Figure 9 shows diffusion co-efficient values for BSA in an iodide buffer 901 and a sulfate buffer 203, obtained by performing DLS on each of a plurality of sample concentrations, according to conventional prior art methodology for determining D_0 and k_D. A best fit 902, 904 can be used to determine D_0 and k_D (from equation 1).

Clearly, both sample preparation and analysis are considerably more laborious according to the prior art method, compared with embodiments of the present disclosure, which uses a single initial sample and a single Taylorgram. These comments also apply to determination of these parameters by prior art TDA methods, which would also require preparation of a similar series of sample concentrations for injection and analysis. Auto-dilution and automatic sample handling may reduce some of the drudgery, but would result in a more complex and expensive instrument, and performing this sort of series of measurements would still take a considerable amount of time and consume significant amounts of sample, which may be prohibitive in the context of early pharmaceutical development (where available quantities of sample may be very small/expensive).

The results are summarised in Table 1 below:

Table 1 – Summary of results. Determination of the self-diffusion coefficient and interaction parameter using the first, second and third example methods. Comparison with the traditional DLS method is also shown.

Buffer	Parameter	Method			DLS
		1	2	3	
Iodide	D_0 ($\mu m^2/s$)	54.55	54.67	56.16	59.3
	k_D	0.016	0.016	0.012	0.016
Sulfate	D_0 ($\mu m^2/s$)	54.68	54.70	54.94	58.4
	k_D	0.009	0.009	0.009	0.009

All methods are in good agreement with the results from DLS and with trends expected from the reverse Hofmeister effect.

A number of other variations are possible, within the scope of the invention, as defined by the appended claims.

CLAIMS

1. A method of determining a relationship between a mutual diffusion co-efficient D_m and the concentration c of a solute within a solvent, comprising:

obtaining a Taylorgram (100) comprising a plurality of measurements of solute concentration c;

deriving from the Taylorgram (200) a plurality of mutual diffusion coefficient values D_m corresponding with a plurality of different concentrations c of solute in the solvent.

2. The method of claim 1, wherein the method further comprises fitting a function (300) to the Taylorgram.

3. The method of claim 2, wherein the function is of the form:

$c = 0.5c_0 erfc(u)$ where $u = 0.5\frac{y(t \pm t_M)}{\sqrt{t}}$,

wherein t is the measurement time; c is the concentration; and t_M, y and c_0 are parameters to be determined from the fit.

4. The method of claim 3, further comprising differentiating the Taylorgram (212) to determine a rate of change of concentration with respect to time $\frac{dc}{dt}$.

5. The method of claim 4, wherein the mutual diffusion coefficient values D_m are derived (213) from the function that is fitted to the Taylorgram and from the rate of change of concentration with respect to time.

6. The method of claim 5, wherein the mutual diffusion coefficient values D_m are determined (213) using the following expression:

$$D_m(c) = \frac{\left[-4\frac{dc\sqrt{\pi}t^{3/2}e^{u^2}}{dt(t+t_M)\sqrt{t_M}}\right]^2 r^2 t_M}{48}$$

where r is the radius of the capillary.

7. The method of claim 1, further comprising performing a transform (221) on the Taylorgram to find a relationship between ξ and concentration c, where $\xi = \frac{x}{2\sqrt{t}}$.

8. The method of claim 7, comprising determining an interface ξ_M (222) from the equation $\xi_M = \frac{1}{c_L - c_R}\int_{c_R}^{c_L} \xi dc$, where c_L is the higher limit of concentration c, and c_R is the lower limit of concentration c, or vice-versa.

9. The method of claim 8, further comprising:

determining a value of u corresponding with each concentration value c, from the relationship $c = 0.5c_0 erfc(u)$;

determining parameters h and m by fitting a straight line to the relationship between u and ξ, using the relationship $u = h(\xi - \xi_M) + m$ (231);

wherein deriving the plurality of mutual diffusion coefficient values D_m corresponding with a plurality of different concentrations c of solute in the solvent (233) comprises using the relationship $\frac{1}{h^2} + \frac{m\sqrt{\pi}}{h^2} erfc(u) \exp(u^2) = \frac{r^2 v^2}{48 D_m(c)}$.

10. The method of claim 8, wherein deriving the plurality of mutual diffusion coefficient values D_m is performed (242) by numerically determining (241) a plurality of the differential $\frac{d\xi}{dc}$ and a plurality of the integral $\int_0^c \xi - \xi_M dc$, corresponding with different concentrations c, and using the expression $-\frac{1}{2}\frac{d\xi}{dc}\int_0^c \xi - \xi_M dc = \frac{r^2 v^2}{48 D_m(c)}$.

11. The method of any preceding claim, further comprising determining a diffusion interaction parameter k_D of the solute in the solution (400) from the relationship $D_m(c)$ between the mutual diffusion coefficient values D_m and the corresponding concentrations c.

12. The method of claim 11, further comprising determining the second virial coefficient A_2 (500) from the diffusion interaction parameter k_D and an estimate of the coefficient of friction k_f and an estimate of the partial specific volume v_2 of the solute.

13. The method of any preceding claim, further comprising estimating a measure of aggregation of solute particles (600) from the values of the mutual diffusion coefficient over the duration of the Taylorgram.

14. Apparatus (40), comprising a processor (51), configured to perform the method of any preceding claim.

15. The apparatus of claim 14, further comprising an instrument (50) for performing a Taylor dispersion analysis, so as to obtain a Taylorgram.

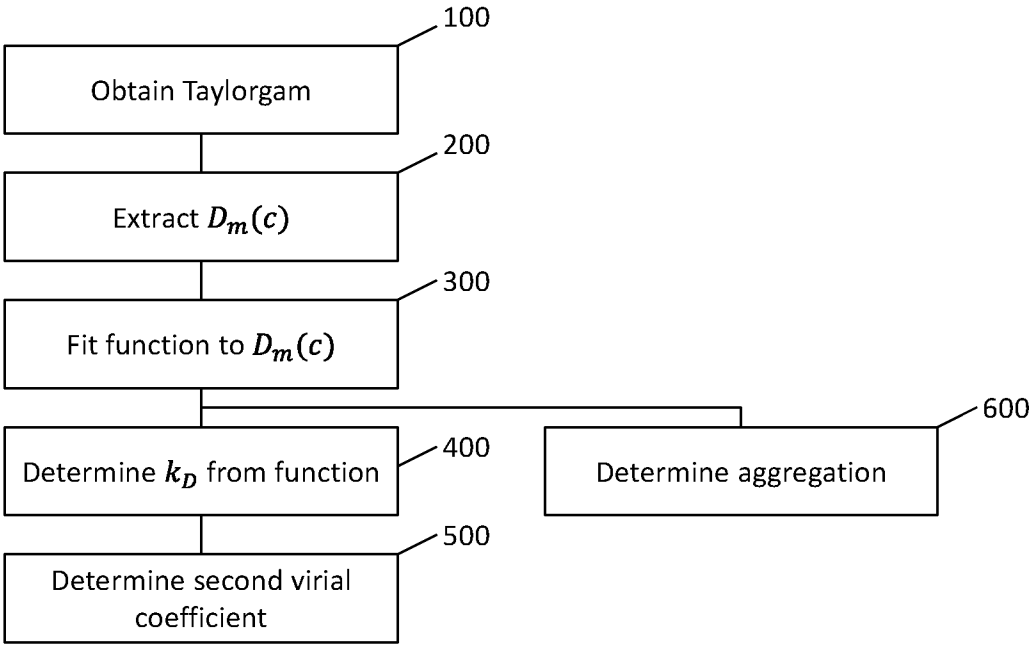

Figure 1

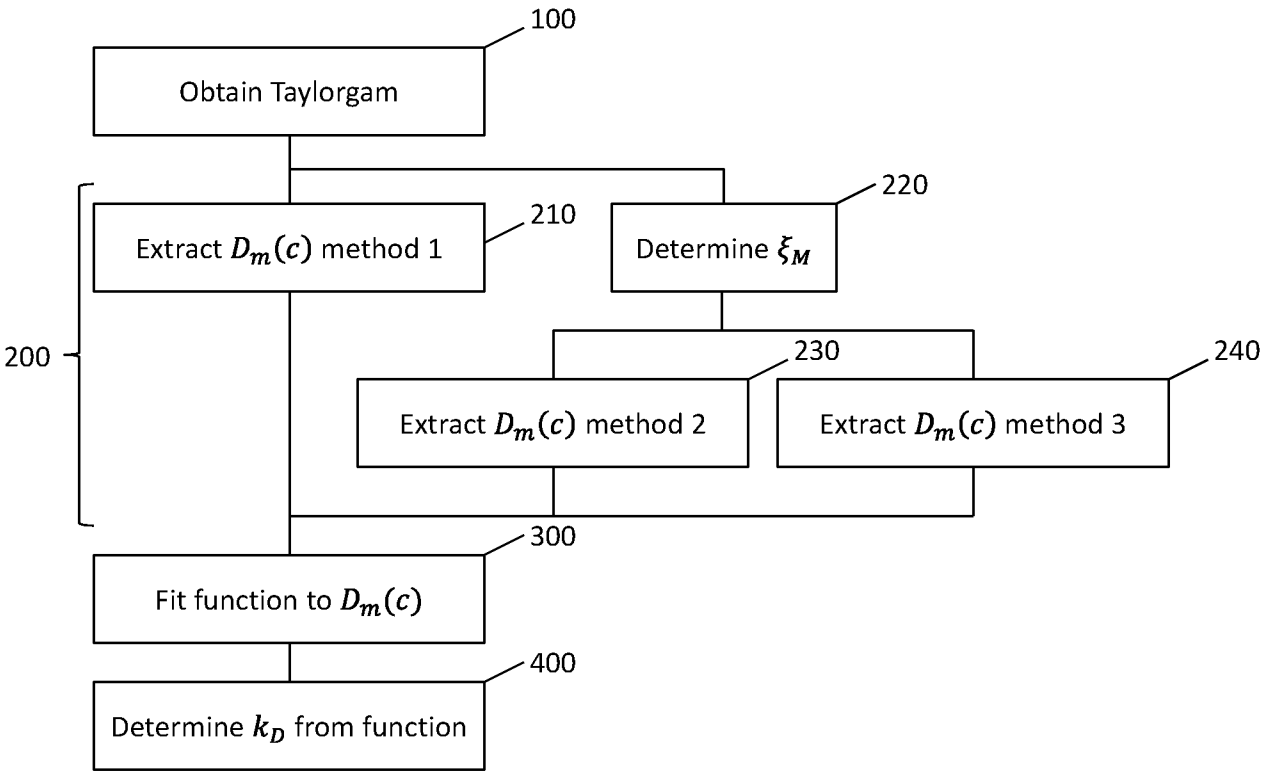

Figure 2

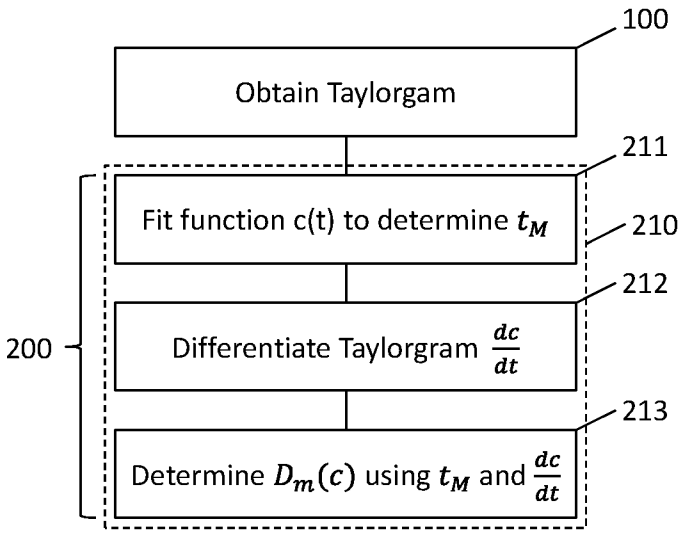

Figure 3

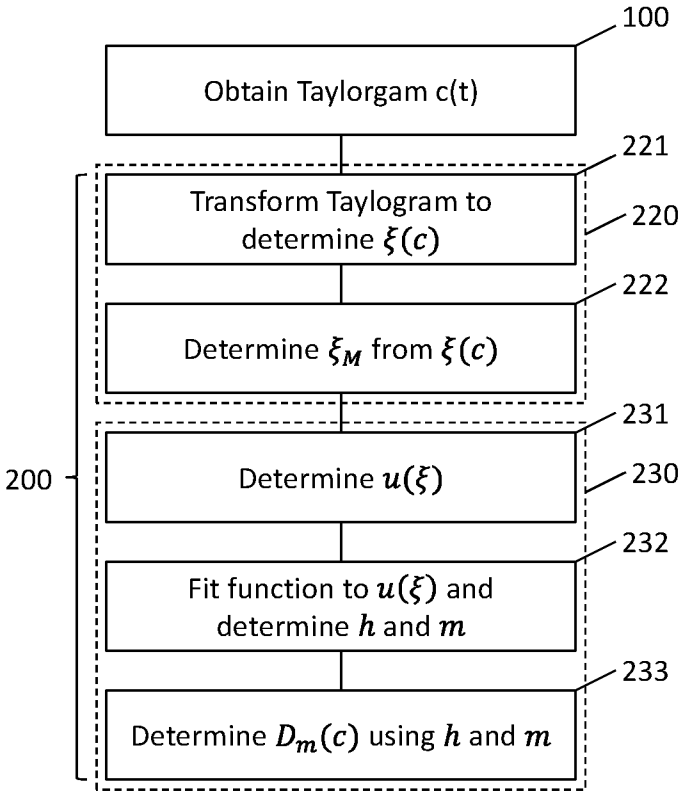

Figure 4

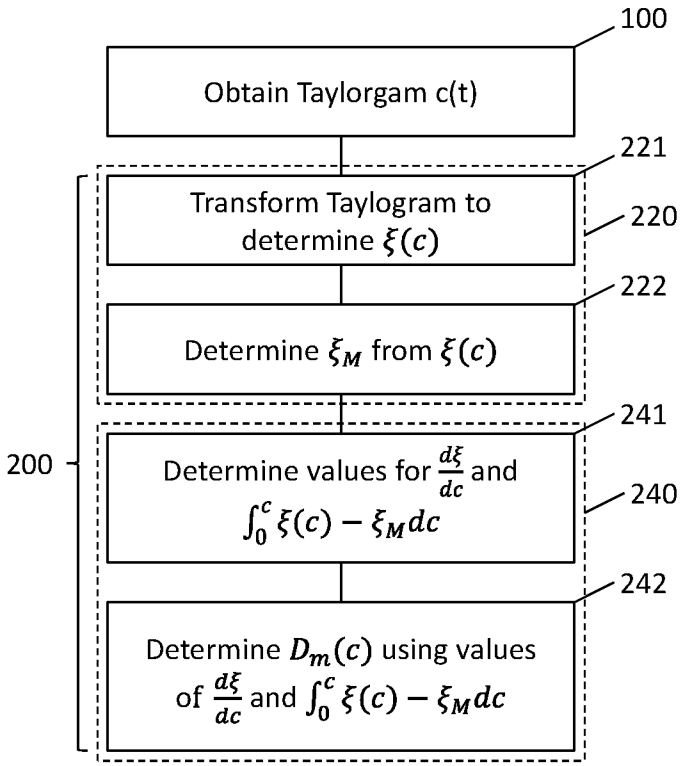

Figure 5

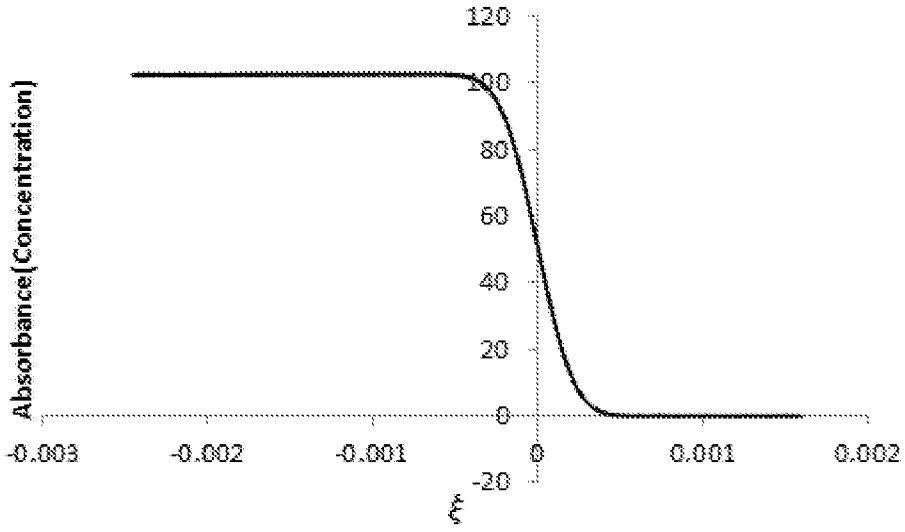

Figure 6

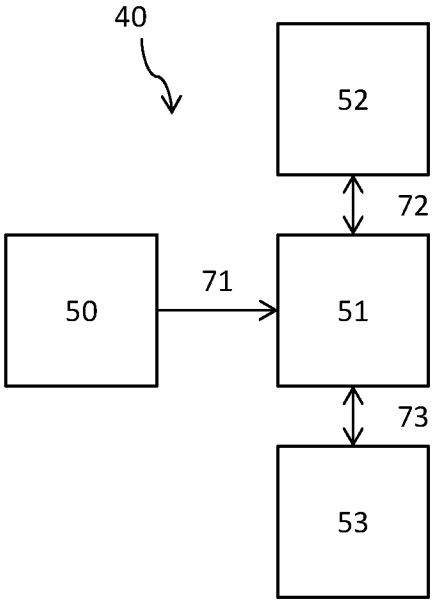

Figure 7

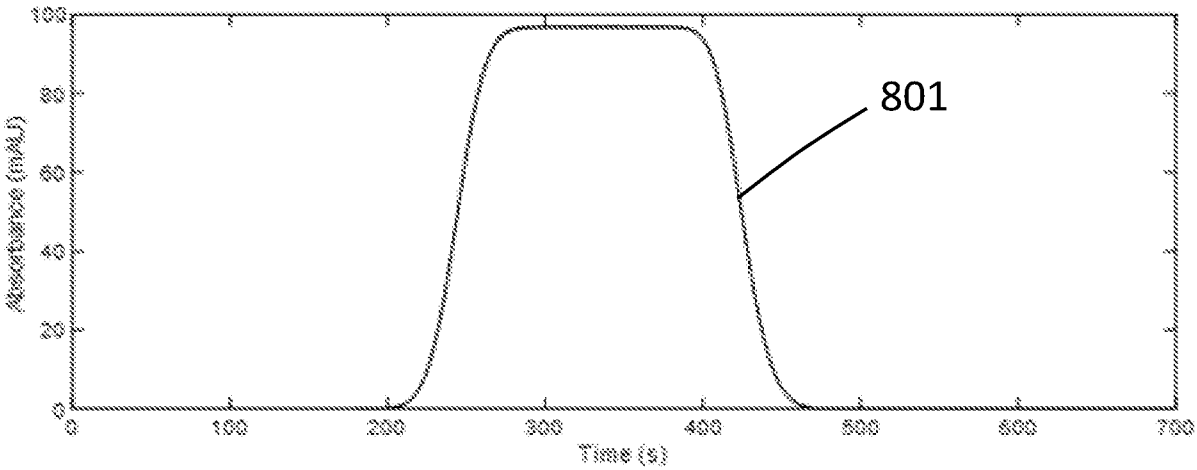

Figure 8

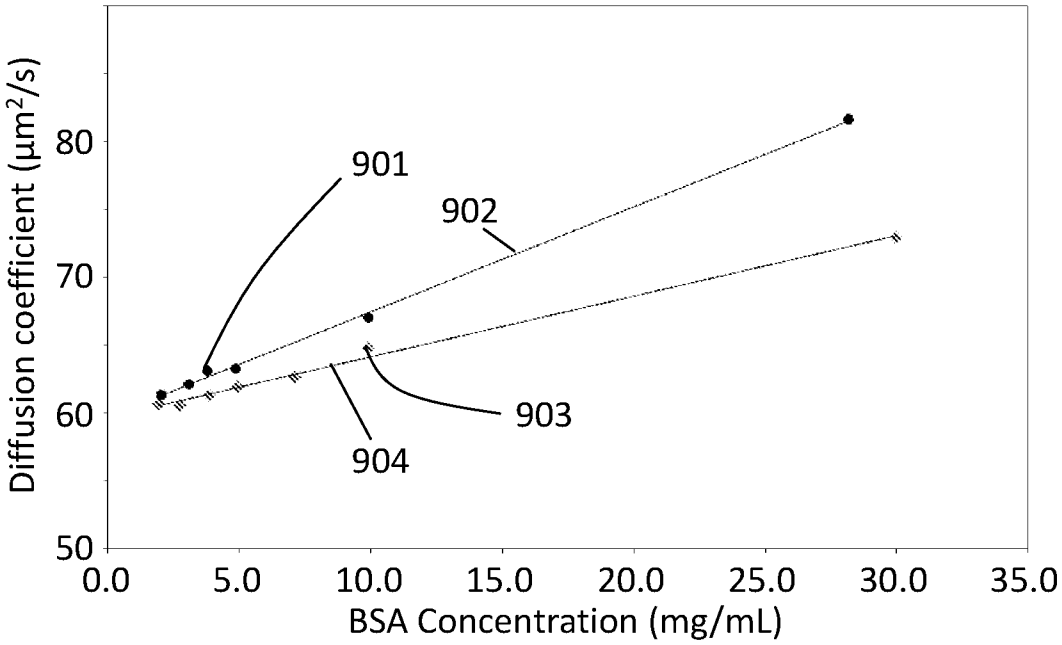
Diffusion coefficient (μm²/s)
80
70
60
50
0.0
5.0
10.0
15.0
20.0
25.0
30.0
35.0
BSA Concentration (mg/mL)
901
902
903
904

Figure 9

INTERNATIONAL SEARCH REPORT

International application No
PCT/GB2016/052025

A. CLASSIFICATION OF SUBJECT MATTER
INV. G01N15/06 G01N35/08
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	FR 2 992 423 A1 (CENTRE NAT RECH SCIENT [FR]; UNIV MONTPELLIER I [FR]; UNIV MONTPELLIER) 27 December 2013 (2013-12-27) claim 1; figure 1	1-15
X	US 7 039 527 B2 (TRIPATHI ANUBHAV [US] ET AL) 2 May 2006 (2006-05-02) column 10, line 63 - column 11, line 32	1-15

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[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

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"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

"T" 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

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"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
24 August 2016	01/09/2016

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Thomte, Peter

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INTERNATIONAL SEARCH REPORT

International application No
PCT/GB2016/052025

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	COTTET H ET AL: "Determination of dendrigraft poly-L-lysine diffusion coefficients by Taylor dispersion analysis", BIOMACROMOLECULES, AMERICAN CHEMICAL SOCIETY, US, vol. 8, no. 10, 1 October 2007 (2007-10-01), pages 3235-3243, XP002512116, ISSN: 1525-7797, DOI: 10.1021/BM070268J [retrieved on 2007-09-06] page 3235, paragraph 2	1
X	CN 101 907 549 A (UNIV NANJING) 8 December 2010 (2010-12-08) paragraph [0011]	1

1

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/GB2016/052025

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		WO 2014001409 A1	03-01-2014
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		WO 2005033672 A1	14-04-2005
CN 101907549 A	08-12-2010	NONE	