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Fortsættes ...



# DESCRIPTION

## Field of the Invention

[0001] The present invention relates to a preparation method which is performed by expressing the recombinant carrier proteins in *Escherichia coli* and purification thereof. More particular, the invention relates to an industrially scalable process for the recovery of recombinant carrier proteins.

## Background of the Invention

[0002] The role of the carrier protein is to enhance immunogenicity by providing T-cell epitopes via MHC Class II presentation to T-helper cells. Carrier proteins also increase the magnitude of the immune response as well as engender B-cell 'memory'. The number of carrier proteins used in licensed vaccines is relatively limited, which include tetanus toxoid (TT), diphtheria toxoid (DT), Cross Reactive Material 197 (CRM<sub>197</sub>), *Haemophilus influenzae* protein D, Neisseria outer membrane protein, Pertussis toxin (PT), Pertactin (PRN) and Filamentous Hemagglutinin (FHA). Access to clinically-proven, safe and efficacious carrier proteins is critical for research in the field of conjugate vaccines. Thus, purification of native, soluble and functional form of carrier proteins is very important and crucial step in conjugate vaccine production. Absence of toxicity and strong immunogenicity makes carrier proteins such as tetanus toxoid (TT), diphtheria toxoid (DT), Cross Reactive Material 197 (CRM<sub>197</sub>), *Haemophilus influenzae* protein D, Neisseria outer membrane protein, Pertussis toxin (PT), Pertactin (PRN) and Filamentous Hemagglutinin (FHA), a robust candidate as a carrier for poor immunogens like peptides, oligosaccharides, polysaccharides and even nucleic acids. Since the said carrier proteins are well characterized hence they are preferred over other carrier proteins and therefore widely used in commercially available vaccines.

[0003] CRM<sub>197</sub>, a mutant form of DT was isolated in the early 1970's. It also contributed to the understanding of the A and B chain structure and function of DT. Uchida et al described the isolation and properties of several mutants including CRM<sub>197</sub> (Uchida *et al* 1973). CRM<sub>197</sub> is a non-toxic DT mutant that contains a lesion in the A chain which blocks ADP-ribosylation. CRM<sub>197</sub> results from a single base change in the structural gene resulting in the substitution of glutamic acid for glycine at position 52. It is a single polypeptide consisting of 535 amino acids and on SDS gels this protein migrates as a single major band of approximate molecular weight of 58.4Kda. While CRM<sub>197</sub> shows no enzymatic activity (except endonuclease), it is immunologically indistinguishable from DT. CRM<sub>197</sub> has the advantage of being a well-defined protein in contrast to formaldehyde treated toxin (toxoid) which is non-specifically cross linked and subject to rearrangement.

**[0004]** Although *Escherichia coli* is one of the most widely used hosts for the production of recombinant proteins, insoluble expression of heterologous proteins is a major bottleneck in production of these recombinant proteins (Baneyx F, 1999 ;Peternel S *et al*,2011). A major pathway of product loss during the refolding step is aggregation. These insoluble protein aggregates or inclusion bodies (IB's) can be used only after refolding *in vitro* into soluble form having its native conformation. The inclusion bodies of different proteins have different characteristics and require a lot of optimization for refolding individual protein. In most cases, a significant amount of precipitation is observed while refolding the proteins (Singh S *Met al*, 2005). This results in a great loss of overall yield of the target proteins, with approximately 40% being refolded to soluble and biologically active form. Several approaches have been described for *in vitro* refolding; most of them involve the use of additives for assisting correct folding. These additives or co-solutes play a major role in refolding process and can be classified according to their function as aggregation suppressors or folding enhancers (Hamada H *et al*, 2009).

**[0005]** US Patent No. 4,961,969 disclosed an approved procedure for the purification and renaturation of biologically active, bacterially produced IFN- $\beta$  is described. The partially purified material obtained by solubilization of isolated refractile bodies from the recombinant cells is treated to obtain reduction of the protein in the presence of a chaotropic environment and then oxidized after removal of the reducing agent. However, the chaotropic environment is retained during the oxidation. Upon removal of the chaotropic environment, a solubilizing additive is supplied to maintain the IFN- $\beta$  in solution. Further purification by conventional means may also be effected.

**[0006]** US patent publication No. 2007/0027305 describes a method of recovering a refolded protein such as Interferon  $\beta$ , which involves solubilizing inclusion bodies (IBs) with chaotropic reagents such as 6M guanidine-hydrochloride (GuHCL) or 8M urea, static mixing a concentrated solution of a denatured protein with a refolding diluent to obtain the refolded protein.

**[0007]** US patent publication No. 2015/0133636 describes a processes for purifying a target molecule from a sample comprising the steps of: (a) providing a sample comprising the target molecule and one or more impurities; (b) adding at least one precipitant to the sample and removing one or more impurities, thereby to recover a clarified sample; (c) subjecting the clarified sample from step (b) to a bind and elute chromatography step comprising at least two separation units, thereby to obtain an eluate comprising the target molecule; and (d) subjecting the eluate to flow-through purification comprising use of two or more media; where at least two steps are performed concurrently for at least a duration of their portion, and wherein the process comprises a single bind and elute chromatography step. It is further disclosed that the process comprises a virus inactivation step between steps (c) and (d) above, using use of one or more in-line static mixers.

**[0008]** The above methods disclosed recovery of proteins, however, there is no specific method disclosed for carrier proteins such as tetanus toxoid (TT), diphtheria toxoid (DT), Cross

Reactive Material 197 (CRM<sub>197</sub>), *Haemophilus influenzae* protein D, Neisseria outer membrane protein, Pertussis toxin (PT), Pertactin (PRN) and Filamentous Hemagglutinin (FHA). Thus an appropriate method is required which minimizes the loss with improved purity during the refolding step in preparation of carrier proteins.

**[0009]** A. Stefan et al. (J. Biotech. 2011, 156, 245-252) describes the overexpression, isolation and purification of diphtheria toxin variant CRM<sub>197</sub> in *Escherichia coli*. WO 2014/126884 A1 relates to methods for refolding denatured proteins present in the form of inclusion bodies at high pH values, without using a denaturing or chaotropic agent. EP 1 845 103 A1 describes a method for refolding a protein by mixing the denatured protein with a refolding buffer at specific mixing conditions. S. Singh et al. (J. Chem. Technol. Biotechnol. 2008, 83, 1126-1134) relates to the recovery of proteins from inclusion bodies of *Escherichia coli* by mild solubilisation at an alkaline pH value. WO 2007/016272 A1 describes a method of recovering a refolded protein involving static mixing of a concentrated solution of a denatured protein with a refolding diluent.

### **Objective of the Invention**

**[0010]** It is the objective of the present invention to provide an industrially scalable process for the preparation of carrier proteins selected from tetanus toxoid (TT), diphtheria toxoid (DT), Cross Reactive Material 197 (CRM<sub>197</sub>), *Haemophilus influenzae* protein D, Neisseria outer membrane protein, Pertussis toxin (PT), Pertactin (PRN) and Filamentous Hemagglutinin (FHA) which are useful in the preparation of vaccine.

**[0011]** Yet another objective of the present invention is to provide an improved method suitable for large-scale production of carrier proteins selected from tetanus toxoid (TT), diphtheria toxoid (DT), Cross Reactive Material 197 (CRM<sub>197</sub>), *Haemophilus influenzae* protein D, Neisseria outer membrane protein, Pertussis toxin (PT), Pertactin (PRN) and Filamentous Hemagglutinin (FHA) which is simple with low cost and high yield.

### **Summary of the Invention**

**[0012]** The present invention provides a process for the preparation of carrier proteins selected from tetanus toxoid (TT), diphtheria toxoid (DT), Cross Reactive Material 197 (CRM<sub>197</sub>), *Haemophilus influenzae* protein D, Neisseria outer membrane protein, Pertussis toxin (PT), Pertactin (PRN) and filamentous hemagglutinin (FHA), which comprises the steps of:

1. a) transformation of *Escherichia coli* with the desired gene coding for the carrier protein using a plasmid vector,
2. b) culturing the transformed *Escherichia coli* in suitable culture medium under suitable conditions,

3. c) isolation and purification of Inclusion bodies,
4. d) denaturation and solubilization of inclusion bodies at high pH value ranging from 9 to 14,
5. e) followed by pH adjustment within a range of 6 to 8.5 of the solubilized protein using in-line static mixer for a period of 0.1 to 200 msec, to produce refolded protein,
6. f) intermediate purification of the refolded protein using ion exchange chromatography to obtain >90 % pure and native carrier protein and
7. g) further purification of the semi purified protein obtained in step (f) by one or more chromatographic separations using anion exchange chromatography, hydrophobic interaction chromatography, metal & dye affinity chromatography, affinity chromatography, multimodal chromatography, hydroxyapatite chromatography and size exclusion chromatography to obtain purified carrier protein.

**[0013]** The present invention also provides a process for the preparation of recombinant carrier proteins as described in the text below.

**[0014]** Preferred embodiments of the present invention are described in the text below.

#### **Brief Description of the Drawings:**

##### **[0015]**

Figure 1: Ion Exchange chromatogram wherein refolded protein sample was loaded on first anion exchange resin at the flow rate of 150 - 300 cm per hour. Flow - through and equilibration wash consists of aggregates and other cellular impurities. Elution step is performed to recover refolded target followed by column regeneration. This chromatography is used as capture chromatography, wherein Y-axis represents absorbance at 280 (mAU) and X-axis represents retention volume (ml).

Figure 2: Ion Exchange chromatogram elute from first chromatography is concentrated and diafiltered. This protein sample was loaded on second anion exchange resin at the flow rate of 150 - 300 cm per hour. Flow - through and equilibration wash consists of low molecular weight impurities and other remaining cellular impurities. Linear gradient elution is performed to recover rCRM from fusion protein followed by column regeneration. This chromatography is used as intermediate purification chromatography. Wherein Y-axis represents absorbance at 280 (mAU) and X-axis represents retention volume (ml).

Figure 3: HIC chromatogram elute from Second chromatography is concentrated and diafiltered. This protein sample was loaded on hydrophobic interaction resin at the flow rate of 150 - 300 cm per hour. Flow - through and equilibration wash consists of endotoxins, host cell nucleic acids and remaining cellular impurities. Gradient elution step is performed to recover rCRM followed by column regeneration. This chromatography is used as polishing

chromatography wherein Y-axis represents absorbance at 280 (mAU) and X-axis represents retention volume (ml).

Figure 4: SDS - Reducing SDS - PAGE analysis was performed to check purity and nicking by loading various amount of purified rCRM<sub>197</sub> wherein Lane 8, 6, 4 and are blank. Lane 1, 3, 5, 7, and 9 are loaded with purified rCRM<sub>197</sub> with increasing concentrations (2.5 µg, 5 µg, 7.5 µg & 10 µg). Protein low molecular weight marker (BioRad) was loaded in Lane 10.

Figure 5: Western Blot of purified CRM<sub>197</sub> wherein Lane 1 loaded with StdCRM<sub>197</sub> and lane 3 loaded with rCRM<sub>197</sub>.

Figure 6: SEC - HPLC chromatogram of purified CRM<sub>197</sub> wherein X-axis represents retention time (min) and Y-axis milli absorbance unit (mAU) at 280 nm.

Figure 7: Impact of inline mixing on refolding of rCRM<sub>197</sub>. Y-axis represents % refolding & % aggregation and X-axis represent time in milliseconds.

### Detailed Description of the Invention

**[0016]** The present invention relates to an industrially scalable process for the preparation of carrier proteins selected from but are not limited to tetanus toxoid (TT), diphtheria toxoid (DT), Cross Reactive Material 197 (CRM<sub>197</sub>), *Haemophilus influenzae* protein D, Neisseria outer membrane protein, Pertussis toxin (PT), Pertactin (PRN) and filamentous hemagglutinin (FHA) in a prokaryotic host wherein the target protein is expressed as inclusion bodies in *Escherichia coli*, inclusion bodies are isolated and purified and the purified inclusion bodies are denatured followed by refolding as defined in the claims. Further purification is performed using chromatographic separation to obtain pure and native carrier proteins.

**[0017]** *Escherichia coli* strain used is selected from but not limited to BL21DE3, Origami2, BL21A1, W3110, HMS174, C43, ER2566, MAX, B834.

**[0018]** Inclusion bodies are refractile, intracellular protein aggregates usually observed in bacteria upon targeted gene overexpression. In general solubilisation agents and refolding buffers are used are for solubilizing the inclusion bodies and refolding of the protein, wherein the solubilisation agent is removed during refolding. Protein refolding from denatured proteins is influenced by several factors, including solubility of protein, removal of denaturant, and assistance of refolding by co-solute or additives.

**[0019]** Chaotropic agents are cosolutes that can disrupt the hydrogen bonding network between water molecules and reduce the stability of the native state of proteins by weakening the hydrophobic effect. Hence in the present invention solubilisation of inclusion bodies are

being carried out at high pH value ranging from 8 to 14 without the use of chaotropic agent which are associated with challenges like they are corrosive, risk of powder handling in graded area, disposal and waste management and impact on protein integrity (carbamylation).

**[0020]** The solubilizing of inclusion bodies is carried out using buffers selected from carbonate, bicarbonate, Tris, borate, Glycine and NaOH, preferably Tris buffer. The concentration used during the solubilisation of inclusion bodies (IBs) may range from 50 to 200 mM.

**[0021]** The present invention also provides a process for the preparation of carrier proteins wherein the refolding step has been optimized using in-line static mixer by rapid pH adjustment without using refolding buffers for a period of 0.1 to 200 microseconds.

**[0022]** Accordingly, the main embodiment of the invention provides cost effective, robust, industrial scale chromatography based process for preparation of recombinant carrier proteins selected from tetanus toxoid (TT), diphtheria toxoid (DT), Cross Reactive Material 197 (CRM<sub>197</sub>), *Haemophilus influenzae* protein D, Neisseria outer membrane protein, Pertussis toxin (PT), Pertactin (PRN) and Filamentous Hemagglutinin (FHA) from a prokaryotic expression system, wherein protein is expressed as inclusion bodies which comprises:

1. a. transformation of bacterial cells with the desired gene coding for carrier proteins using a plasmid vector,
2. b. culturing the transformed bacterial cells in chemically defined media supplemented with glucose as carbon source wherein pH is maintained at 5-9 and at temperature of 20-40°C;
3. c. lysing bacterial cells by mechanical means above 800-1200 bars thereby producing a lysate containing inclusion bodies and cellular components;
4. d. clarifying the aqueous cell lysate by separating solids from the solution;
5. e. isolation and purification of inclusion bodies (IBs) by using buffers selected from carbonate, bicarbonate, Tris, borate, Glycine and NaOH to remove cellular contaminants to form a pellet of purified IBs;
6. f. denaturation and solubilization of inclusion bodies (IB) at high pH value ranging from 9 to 14 using buffers selected from carbonate, bicarbonate, Tris, borate, Glycine and NaOH buffer;
7. g. rapid pH adjustment within a range of 6 to 8.5, preferably at 8, of solubilized carrier proteins using acid containing redox systems and in-line static mixer for a period of 0.1 to 200 msec, to produce refolded protein,
8. h. intermediate purification of the refolded protein using ion exchange chromatography to obtain >90 % pure and native carrier protein and
9. i. further purification of the semi purified protein obtained in step (h) by one or more chromatographic separations using anion exchange chromatography, hydrophobic interaction chromatography, metal & dye affinity chromatography, affinity chromatography, multimodal chromatography, hydroxyapatite chromatography and size exclusion chromatography to obtain purified carrier protein.

**[0023]** Rapid pH adjustment of solubilized carrier proteins is carried out using organic or inorganic acids like HCl, orthophosphoric acid, acetic acid, citric acid containing redox system like cysteine and cysteine, using inline static mixer thus affecting refolding; wherein the purified inclusion bodies are denatured followed by pH adjustment of the solubilized protein using in-line static mixer for a period of 0.1 to 200 msec, to produce refolded protein.

**[0024]** In a preferred embodiment, HCl is used for rapid pH adjustment during refolding step (g) and the concentration may range from 100 to 500 mM HCl and cysteine may range from 2 to 20 M and cysteine from 1 to 10 M.

**[0025]** In an embodiment of the present invention, the refolding step is carried out using static mixer by rapid pH adjustment within a range of 6 to 8.5, preferably at 8 in microseconds wherein pH being the most critical factor having no significant influence on the target protein concentration during refolding.

**[0026]** The refolding may be performed at a temperature in the range to 2 to 10°C, preferably, at 4°C. The dilution ratio of the HCl and inclusion bodies may be kept constant or the dilution ratio may be selected from 0 to 5: 1 to 5.

**[0027]** In an embodiment of the present invention, use of low dilution in the pH range of 6 to 8.5 during the refolding step is carried out which gives major advantages in the facility requirement and hence makes the process economical.

**[0028]** In another embodiment, the purified inclusion bodies was renatured followed by pH adjustment of the solubilized protein using in-line static mixer for a period of 0.1 to 200 msec, to produce refolded protein. The above mentioned inclusion bodies was solubilized in 100 mM Tris buffer. The pH of the solubilized inclusion bodies was adjusted to 8 by 300 mM HCl containing 2 to 20 mM cysteine & 1 to 10 mM cysteine. The temperature of all the solutions is maintained between 0 - 6 °C.

**[0029]** The purified CRM<sub>197</sub> prepared according to the present invention meets all the specifications as laid in Table I below.

**Table I**

S.No.	Description	Specifications
1	Identity	Western blot: a major immunoreactive band of mass 58kD ± 10%(Figure 5)
2	Purity	SDS PAGE; CRM <sub>197</sub> NLT 90%(Figure 4)
3	Nicked CRM (A and B Chain)	SDS PAGE: Reducing gel Commassie Blue; A and B chain content NMT 10% (total) of total CRM <sub>197</sub> (Figure 4)
4	Dimer/ higher mol. Weight SEC - HPLC	NMT 15% (Figure 6)

S.No.	Description	Specifications
5	Endotoxin	NMT 100EU/100ug

**[0030]** In yet another embodiment of the invention, purification by chromatography is carried out using single or multi step chromatography selected from i) direct ion exchange followed by ion exchange followed by hydrophobic interaction chromatography and ii) Ion exchange followed by hydrophobic interaction chromatography (HIC). Further the said ion exchange chromatography is an anion exchange chromatography. The anion exchange resins are selected from the group but not limited to consisting of DEAE cellulose, MonoQ, Capto Q, Eshmino Q, Gigacap Q 650M, Nuvia-Q, Cellufine Q-h, MiniQ, Source 15Q and 30Q, Q, DEAE Sepharose Fast Flow, Q Sepharose high Performance, QAE SEPHADEX™ and FAST Q SEPHAROSE™ (GE Healthcare), UNOsphere Q, Macro-Prep DEAE and Macro-Prep High Q from Biorad, Ceramic HyperD Q, ceramic HyperD DEAE, Toyopearl SuperQ-650S, 650M and 650C, QAE-550C and 650S, DEAE-650M and the like.

**[0031]** The anion exchange column is eluted at 10 to 60% of 1M NaCl in Tris - HCl buffer and the concentration of the buffer may range from 10mM to 300mM. The anion exchange column runs in the pH range of 6 to 9, preferably 8 to 9.

**[0032]** The hydrophobic interaction chromatography support is selected from the group but not limited to butyl-, phenyl-, octyl-agarose, butyl-, phenyl-, ether- organic polymer resin and phenyl sepharose and the like.

**[0033]** The hydrophobic interaction chromatography column runs in the pH range of 5 to 8, preferably 6 to 7.6.

**[0034]** The buffer used for hydrophobic interaction chromatography may be sodium or potassium phosphate containing sodium chloride ranging from 2M to 5M concentration or only sodium sulphate salt from 2M to 3M concentration.

**[0035]** In the specific embodiment, the carrier protein is CRM<sub>197</sub> and the yield of soluble CRM<sub>197</sub> is about 0.01 g/l, 0.1 g/l, 0.25 g/L, 0.5 g/L, about 1 g/L, about 1.5 g/L, about 2 g/L, about 2.5 g/L, about 3 g/L, about 3.5 g/L, about 4 g/L, about 4.5 g/L, about 4.5 g/L, about 5 g/L.

**[0036]** In another specific embodiment, the carrier protein is CRM<sub>197</sub> and the yield of insoluble CRM<sub>197</sub> is about 0.1 g/l, 0.25 g/L, 0.5 g/L, about 1 g/L, about 1.5 g/L, about 2 g/L, about 2.5 g/L, about 3 g/L, about 3.5 g/L, about 4 g/L, about 4.5 g/L, about 4.5 g/L, about 5 g/L.

**[0037]** The invention thus involves more than one subsequent purification steps, and also exploits pI value of CRM<sub>197</sub> in an ion exchange chromatographic step, whereby it is separated from other contaminating proteins. Finally, the quantity of CRM<sub>197</sub> was quantified by

BCA/Bradford/Lowry Assay and visualised in 10-12% acrylamide gel (SDS-PAGE). The identification of polypeptide is done by Western blot and similar immunoassays. The purity and integrity of purified polypeptide is measured by SDS-PAGE and HPLC methods. The yield of the protein thus expressed was 500-3000 mg/L of the culture medium and can be subsequently varied by modulating the culture additives and conditions, as well as purification steps. The method of invention provides an industrially applicable method of tuning the induction time and subsequently modulating the pH and temperature of the chromatographic steps provides simple, inexpensive, and is not laborious. It excludes need of extensive steps involving preparation of buffers or kit or working solution thereof.

**[0038]** In the particular embodiment the purified CRM<sub>197</sub> polypeptide readily lacked the first Met amino acid, whose presence is not desired in the final CRM<sub>197</sub> protein and removal of which entails requirement for additional purification steps. The polypeptide thus obtained is in active and native form; it readily lacks the undesired methionine as first amino acid without the need of additional steps. CRM<sub>197</sub> amino acid sequence was analyzed by Insilico/bioinformatics tools; showed about 38.4% hydrophobicity in the protein. The isoelectric point of CRM<sub>197</sub> was found about 5.81. CRM<sub>197</sub> protein contained 4 cysteine amino acid residue and 21 proline residues. The refolding of polypeptide is confirmed by functional assays by measuring endonuclease activity over DNA. Biophysical confirmation was done by Circular Dichroism (CD) analysis of polypeptide and compared with commercially available polypeptides.

**[0039]** The carrier proteins prepared according to the present invention is used to conjugate with polysaccharide molecules isolated from *Pneumococcus*, *Haemophilus influenzae*, *Meningococcus*, *Streptococcus pneumoniae* and other pathogenic bacteria.

**[0040]** In another embodiment, the carrier proteins prepared according to the present invention is used as a conjugated carrier for vaccines such as those against *Pneumococcus*, *Haemophilus influenzae*, *Meningococcus*, *Streptococcus pneumoniae* and other pathogenic bacteria.

**[0041]** The process of the present invention does not require chaotropic agents nor refolding buffers (classical dilution based methods), which makes the process simple and commercially feasible.

**[0042]** A very high amount and pure form of carrier proteins can be achieved by the process disclosed and illustrated herein.

**[0043]** Carrier proteins prepared according to the process of the present invention are economical and requires less time.

**[0044]** The present invention is more specifically illustrated with reference to the examples given below. However, it should be understood that the present invention is not limited by an example in any manner but includes other carrier proteins and variations thereof within the

parameters described herein, as can be known to those well-versed in the art.

**Example I:**

**Step (i): Synthesis of CRM<sub>197</sub> gene:**

**[0045]** Full length CRM<sub>197</sub> gene was optimized according to *Escherichia coli* codon usage. The following parameters were used for CRM<sub>197</sub> gene optimization: Codon Usage Bias, GC content, mRNA Secondary Structure, Custom Desired Patterns, Custom Undesired Patterns, Repeat Sequences (direct repeat, inverted repeat, and dyad repeat), Restriction Enzyme Recognition Sites (deletion or insertion).

**[0046]** Optimized CRM<sub>197</sub> gene was cloned at multiple cloning site of pUC57 plasmid vector using BamHI and SapI restriction sites, generating pUC57\_CRM<sub>197</sub>. The vectors containing CRM<sub>197</sub> gene was transformed in *Escherichia coli* DH5α host and clones was selected on LB+Kanamycin<sup>r</sup> plate. The presence and correctness of CRM<sub>197</sub> gene in pUC57 was confirmed by restriction digestion of pUC57\_CRM<sub>197</sub> plasmid by Age I (located in CRM<sub>197</sub> gene) and Nde I (located in pUC57 plasmid). Further the sequence of CRM<sub>197</sub> was confirmed by PCR and DNA sequencing.

**Step (ii): Insertion of CRM<sub>197</sub> into expression vector pTWIN1**

**[0047]** *Escherichia coli* DH5α carrying pUC57\_CRM<sub>197</sub> was grown over night in LB+Kanamycin in 50 ml volume. Bacteria was centrifuged and pellet was used for plasmid isolation. Isolation of plasmid was done by using Qiagen plasmid mini-prep kit using manufacturer instructions. Isolated plasmid was quantified by nono-drop.

**[0048]** CRM<sub>197</sub> from pUC57 was excised, 5μg plasmid was digested with restriction endonucleases BamHI and SapI. The digested plasmid was run on 1% agarose gel and band corresponding to CRM<sub>197</sub> gene was purified by using Qiagen Gel extraction kit using manufacturer's instructions. Subsequently the 5 μg of expression plasmid pTWIN1 was also digested with BamHI and SapI to generate restriction sites in it that is compatible with CRM<sub>197</sub> gene. The digested pTWIN1 was also purified from gel using Qiagen Gel extraction kit with manufacturer's instructions.

**[0049]** The digested CRM<sub>197</sub> gene was ligated in pTWIN1 using T4 ligase based DNA ligation kit (Promega) using manufacturer's instructions. Vector (pTWIN1) and Insert (CRM<sub>197</sub>) was mixed in 1:3, 1:4, 1:5 ratio in the presence of T4 DNA ligase and buffers in a 20μl reaction

volume. Ligation mixture was incubated overnight at 16°C. Next morning 5µl of ligation mixture was added/transformed in BL21-DE3 *Escherichia coli* expression host. BL21 was transformed by using chemical transformation protocol. The ligation+ BL21 cells were incubated in ice for 30 min. After incubation heat shock was given for 45 seconds at 42°C. Sample was cooled at room temperature and 500µl SOC medium was added into it. The tube with transformants was incubated for 2 hours at 37°C with 200 rpm. From which 100µl mixture was plated on LB+Ampicillin plate for screening of transformants.

**[0050]** CRM<sub>197</sub> expression BL21-DE3 transformants were selected next morning from Luria Broth+Ampicillin plates. Of these 5 clones growing on Luria Broth+Ampicillin were selected and grown in 10 ml Luria Broth+Ampicillin media for overnight at 37°C, 200 rpm. Culture was centrifuged and plasmid was extracted from cell pellet using Qiagen plasmid extraction kit.

**[0051]** To verify the correctness of clone, 2µg plasmid was digested with AgeI and ApaI restriction endonuclease, respectively. AgeI site is present in CRM<sub>197</sub> and ApaI is in pTWIN1. Therefore double digestion with both the enzymes used for confirmation of correct clone. The clone was designated as pTWIN1\_ CRM<sub>197</sub> (BL21-DE3). Furthermore clones were confirmed by PCR using CRM<sub>197</sub> gene specific primers and DNA sequencing. The glycerol stock of BL21 expressing CRM<sub>197</sub> was made by growing bacteria in 10ml Luria Broth+Ampicillin overnight. Next morning 40% sterilized Glycerol was added into culture and 1ml aliquot was dispensed into cryovial. Vials were stored at -80°C for further use in expression analysis.

**Step (iii): Confirmation of expression of CRM<sub>197</sub>:**

**[0052]** BL21 clone stored at -80°C was streaked on Luria Broth+Ampicillin plate. Plate was incubated overnight at 37°C. Single colony was picked up and inoculated in 50ml Luria Broth+Ampicillin media in 150ml flask. Flask was incubated at 37°C, 200 RPM until OD<sub>600</sub>= 1. Once OD reaches to desired point, 5 ml culture was drawn which is used as uninduced culture. Uninduced culture was kept on ice until use. To induce the expression of CRM<sub>197</sub> gene 0.5mM IPTG was added to remaining 45 ml culture and flask was further incubated for additional 4 hours at 30°C and 200 rpm rotation. Induced culture was harvested after 4 hours and expression of CRM<sub>197</sub> was examined by SDS-PAGE (Figure 1) and Western Blot (Figure 2).

**[0053]** For SDS-PAGE analysis 1ml culture of induced and uninduced culture (both normalized for OD<sub>600</sub>=1) was taken into 1.5ml Eppendorf tube. The tube was centrifuged and pellet was resuspended into 50µl PBS. In this suspension 50 µl SDS-PAGE loading buffer with reducing agent (2x) was added. The mixture was boiled at 100°C for 5 min. Sample was cooled at room temperature and 20 µl of uninduced and induced culture was loaded in the 4-12% Tris Glycine gel. The gel was run for 1.5 hours at 150 volts. Gels were taken out and incubated in Coomassie Brilliant Blue dye for 1 hour. After staining gel was detained in destaining solution containing 40% methanol=10 % acetic acid for 3 hours. The CRM<sub>197</sub> expression was visualized

as ~58KD protein that is only visible in induced culture. For western blot a separate set of gel was run in the same manner as SDS-PAGE and gel was blotted on PVDF (polyvinylidenedifluoride membrane). The membrane was immunoblotted by anti-CRM<sub>197</sub> antibody. In the western blot CRM<sub>197</sub> appeared as single immunoreactive band at ~58 Kd. No CRM<sub>197</sub> specific band was observed in uninduced culture. This experiment confirms that the clone generated in the present study can express rCRM<sub>197</sub> protein. These clone were further used for large scale production and purification of CRM<sub>197</sub>.

#### **Step (iv): Inclusion bodies preparation**

**[0054]** One ml vial of BL21 *Escherichia coli* cells was inoculated into 50 ml LB+Amp media and grown overnight at 37°C, 200 rpm. Fermentation was done at 20L scale. *Escherichia coli* cells were inoculated to the fermenter and cultivated at 30°C centigrade. The culture was induced with 0.5 mM IPTG at OD<sub>600</sub>=20. After 12 hours post induction fermentation culture was harvested and cell pellet was prepared by centrifugation. Cell pellet was lysed mechanically in homogenizer. Inclusion body (which contains the desired protein CRM<sub>197</sub>) was isolated by centrifugation of cell lysates. Supernatant was discarded and pellet was retained which contains Inclusion body (IBs).The isolated inclusion bodies are purified using three wash buffers wherein first containing 20mM Tris + 250mM NaCl, second containing 20mM Tris + 2M Urea + 1% Triton X-100 and third one containing 20mM Tris to obtain purified rCRM inclusion bodies.

#### **Example II**

**[0055]** 100g CRM<sub>197</sub> protein inclusion bodies were denatured by high pH, dissolved by stirring at 120min, clarified by centrifugation for 40minutes, the supernatant was collected and further clarified by 0.8 - 0.45 µ filter. Wherein said denaturing solution contained 100mM Tris-, pH 12.0. Refolding was performed by adjusting pH to 8 using 100 - 250 mM HCl containing 10mM Cystine, 20mM Cysteine pH 2.0 without any dilution by passing through static mixer (Sulzer and Koflow are the two manufacturers of in-line static mixer) for <10 milli seconds.

**[0056]** Anion exchange column (Capto Q, first anion exchange step) equilibrated with 50mM Tris-HCl, pH8.0 buffer contacted with refolded protein solution, followed by elution with 20 - 50mM NaCl in 50mM Tris-HCl, pH8.0 buffer.

**[0057]** The protein elute subjected to 10 kDa UF/DF (1<sup>st</sup> UF/DF) step to remove salt and concentrate the protein solution.

**[0058]** The above concentrated and diafiltered protein elute contacted with second anion exchange column (Source 30Q) equilibrated with 50mM Tris-HCl, pH8.0 buffer, followed by

linear gradient elution with 10 - 15mM NaCl in 50mM Tris-HCl, pH8.0 buffer.

**[0059]** The protein elute subjected to 10 kDa UF/DF (2<sup>nd</sup> UF/DF) step to remove salt and concentrate the protein solution.

**[0060]** The above concentrated and diafiltered protein elute toned with 3M NaCl by adding calculated solid NaCl and contacted with hydrophobic interaction column (Phenyl Sepharose FF) equilibrated with 50mM Tris-HCl, 3M NaCl pH8.0 buffer, followed by elution with 10mM potassium phosphate, pH7.2 buffer.

**[0061]** The protein elute subjected to 10 kDa UF/DF (1<sup>st</sup> UF/DF) step to remove salt and concentrate the protein solution. The protein solution is diafiltered with 10mM potassium phosphate, 5% sucrose pH7.2 buffer.

**[0062]** The concentrated and diafiltered protein elute filtered through 0.22 $\mu$  filtered and frozen at -70 °C.

**[0063]** Intermediate purification of the refolded protein (Figure 1) using ion exchange chromatography is carried out to obtain >90 % pure and native carrier protein and the semi purified protein obtained as a result of intermediate purification is subjected to further chromatographic separation (Figure 2 and 3) to obtain purified carrier proteins

**[0064]** Impact of mixing time on pH was evaluated for refolding of rCRM<sub>197</sub>. The pH based refolding was performed at 4°C, the dilution ratio was kept constant. The mixing time was changed from 2000 milli seconds to 60 milli seconds using inline static mixer. Table II shows the impact of reduction in mixing time is directly proportional to % rCRM refolding.

**Table II - Impact of inline mixing on refolding of rCRM<sub>197</sub>. (Figure 7)**

S. No.	Dilution Fold	Mixing Time (milli seconds)	% Aggregation	% rCRM Refolding
1	1.5x	60	30	38
2	1.5x	80	46	30
3	1.5x	120	52	26
4	1.5x	240	55	22
5	Traditional mixing	2000	77	11

**[0065]** Refolding parameters of the CRM197 prepared according to above described procedure is compared with the CRM197 prepared according to the conventional refolding process described herein.

**[0066]** Inclusion body based proteins are solubilized using chaotropic salts. The refolding is

performed by lowering the concentration of the chaotropic salt, this is achieved by dilution (over 100 fold). The dilution results in lowering the protein concentrations below 200 microgram / ml. The conventional dilution based refolding is not feasible in large scale manufacturing due to requirement of very large scale refolding vessels.

[0067] Comparison of the conventional refolding process with the process of the present invention is laid in Table III below.

**Table III**

Parameters	Conventional Refolding Process	Process of the present Invention
Target Protein conc (mg/ml)	~ 0.2	~ 5
Dilution required	~ 40X	~ 1.5X
Refolding Volume	~ 40L	~ 1.5L
Facility requirement	High volume vessels	Low volumes
Further process time	very high	Minimal process time

[0068] Various batches of CRM<sub>197</sub> with similar conditions described in the Example 2 have been prepared. The yield of CRM197 obtained from 3 different batches. The data disclosed in Table IV indicates the consistency in the refolding.

**Table IV - Yield of rCRM197**

Batch No.	Inclusion body rCRM <sub>197</sub> content (mg/L)	% Refolding	Refolded & purified rCRM <sub>197</sub> Productivity (mg/L)
TD/CRM/CRM-P/012-002/15	2400	19.4	340
TD/CRM/CRM-P/013-004/15	2200	17.49	347
TD/CRM/CRM-P/013-005/15	2900	18.2	342

## REFERENCES CITED IN THE DESCRIPTION

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- [US20070027305A](#) [0006]
- [US20150133636A](#) [0007]
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- [EP1845103A1](#) [0009]
- [WO2007016272A1](#) [0009]

**Non-patent literature cited in the description**

- **A. STEFAN et al.**J. Biotech., 2011, vol. 156, 245-252 [0009]
- **S. SINGH et al.**J. Chem. Technol. Biotechnol., 2008, vol. 83, 1126-1134 [0009]

**Patentkrav**

- 1.** Fremgangsmåde til fremstillingen af bærerproteiner valgt fra tetanus toxoid (TT), difteritoksoid (DT), tværreaktivt materiale 197 (CRM<sub>197</sub>), *Haemophilus influenzae* protein D, Neisseria ydermembranprotein, Pertussis toksin (PT),
- 5 Pertactin (PRN) og filamentøs hæmagglutinin (FHA), hvilken omfatter trinnene:
- a) transformation af *Escherichia coli* med den ønskede gen der koder for bærerproteinet under anvendelse af en plasmidvektor,
  - b) dyrkning af den transformerede *Escherichia coli* i egnet dyrkningsmedium under egnede betingelser,
  - 10 c) isolering og oprensning af inklusionslegemer,
  - d) denaturering og solubilisering af inklusionslegemer ved høj pH-værdi i området fra 9 til 14,
  - e) efterfulgt af pH-justering indenfor et område fra 6 til 8,5 af det solubilerede protein under anvendelse af in-line statisk blander i en
  - 15 periode på 0,1 til 200 millisekunder, til fremstilling af genfoldet protein,
  - f) mellemliggende oprensning af det genfoldede protein under anvendelse af ionbytterkromatografi for at opnå >90 % ren og nativ bærerprotein og
  - g) yderligere oprensning af det semioprensede protein opnået i trin (f) ved
  - 20 en eller flere kromatografiske separationer under anvendelse af anionbytterkromatografi, hydrofobisk interaktionskromatografi, metal- og farvestoffsaffinitetskromatografi, affinitetskromatografi, multimodal kromatografi, hydroxyapatitkromatografi og
  - 25 størrelseseksklusionskromatografi for at opnå oprenset bærerprotein.
- 2.** Fremgangsmåden ifølge krav 1, hvor pH-justeringen er ved 8.
- 3.** Fremgangsmåden ifølge krav 1 eller 2, hvor bærerproteinet er tværreaktivt materiale 197 (CRM<sub>197</sub>) og hvor den ønskede gen der koder for bærerproteinet i trin a) er genet der koder for CRM<sub>197</sub>, det semioprensede protein opnået i trin (f)
- 30 er >90 % ren nativ CRM<sub>197</sub> og det oprensede bærerprotein opnået i trin g) er oprenset CRM<sub>197</sub>.

**4.** Fremgangsmåden ifølge et hvilket som helst af kravene 1 og 3, hvor genfoldningstrinnet e) er blevet optimeret under anvendelse af in-line statisk blander ved hurtig pH-justering indenfor et område fra 6 til 8,5 for en periode på 1 til 200 mikrosekunder.

5

**5.** Fremgangsmåden ifølge krav 4, hvor den hurtige pH-justering er ved 8.

**6.** Fremgangsmåden ifølge et hvilket som helst af kravene 1, 3 og 4, hvor fremgangsmåden ikke involverer anvendelsen af genfoldningsbuffer og er  
10 optimeret under anvendelse af in-line statisk blander ved hurtig pH-justering indenfor et område fra 6 til 8,5 for en periode på 10 til 200 mikrosekunder.

**7.** Fremgangsmåden ifølge krav 6, hvor den hurtige pH-justering er ved 8.

15 **8.** Fremgangsmåden ifølge et hvilket som helst af kravene 1 til 3, hvor solubiliseringen af inklusionslegemer udføres ved høj pH-værdi i området fra 9 til 14 uden anvendelsen af kaotropisk stof.

**9.** Fremgangsmåden ifølge et hvilket som helst af kravene 1 til 8, hvor udbyttet af  
20 uopløseligt CRM<sub>197</sub> er fra omkring 0,01 til 5 g/l.

**10.** Fremgangsmåden ifølge et hvilket som helst af kravene 1 til 8, hvor udbyttet af opløseligt CRM<sub>197</sub> er fra omkring 0,01 til 5 g/l.

25 **11.** Fremgangsmåde til fremstilling af rekombinante bærerproteiner valgt fra tetanus toxoid (TT), difteritoksoid (DT), tværreaktivt materiale 197 (CRM<sub>197</sub>), *Haemophilus influenzae* protein D, Neisseria ydermembranprotein, Pertussis toksin (PT), Pertactin (PRN) og filamentøs hæmagglutinin (FHA) fra et prokaryotisk ekspressionssystem, hvor protein udtrykkes som inklusionslegemer,  
30 hvilken omfatter:

a. transformation af bakterieceller med den ønskede gen der koder for bærerproteiner under anvendelse af en plasmidvektor,

- b. dyrkning af de transformerede bakterieceller i kemisk defineret medie suppleret med glukose som karbonkilde, hvor pH opretholdes ved 5-9 og ved temperatur på 20-40 °C;
- 5 c. lysning af bakterieceller med mekanisk organ over 800-1200 bar for derved at fremstille et lysat indeholdende inklusionslegemer og cellulære komponenter;
- d. rensning af det vandige cellelysat ved at separere faststoffer fra opløsningen;
- 10 e. isolering og oprensning af inklusionslegemer (IBs) ved anvendelse af buffere valgt fra karbonat, bikarbonat, Tris, borat, Glycin og NaOH til at fjerne cellulære forurenede stoffer for at danne en pellet af oprenset IBs;
- f. denaturering og solubilisering af inklusionslegemer (IBs) ved høj pH-værdi i området fra 9 til 14 under anvendelse af buffere valgt fra karbonat-, bikarbonat-, Tris-, borat-, Glycin- og NaOH-buffer;
- 15 g. hurtig pH-justering indenfor et område fra 6 til 8,5 af solubiliserede bærerproteiner under anvendelse af syre indeholdende redoxsystemer og in-line statisk blander for en periode på 0,1 til 200 millisekunder, til fremstilling af genfoldet protein,
- 20 h. intermediær oprensning af det genfoldede protein under anvendelse af ionbytterkromatografi for at opnå >90 % ren og nativ bærerprotein og
- i. yderligere oprensning af det semioprensede protein opnået i trin (h) ved en eller flere kromatografiske separationer under anvendelse af anionbytterkromatografi, hydrofobisk interaktionskromatografi, metal- og farvestofaffinitetskromatografi, affinitetskromatografi, multimodal
- 25 kromatografi, hydroxyapatitkromatografi og størrelseseksklusionskromatografi for at opnå for at opnå oprenset bærerprotein.

**12.** Fremgangsmåden ifølge krav 11, hvor den hurtige pH-justering er ved 8.

# DRAWINGS

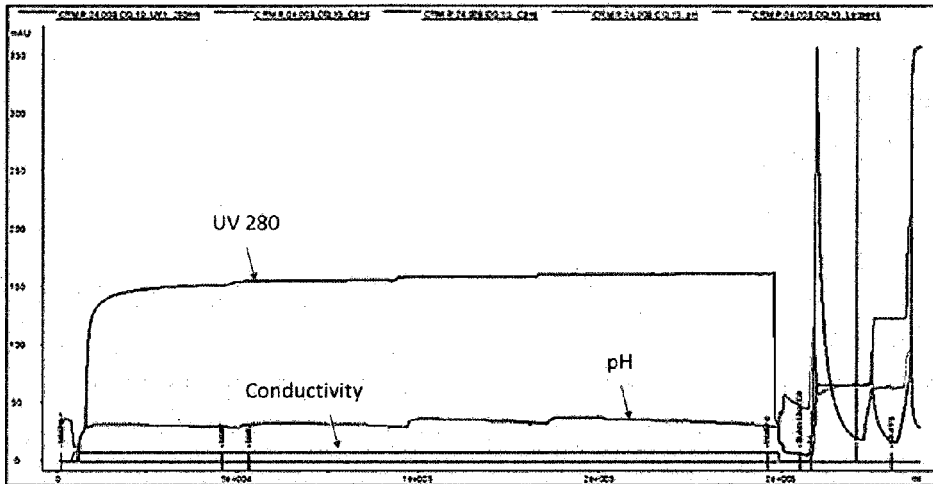


FIGURE 1

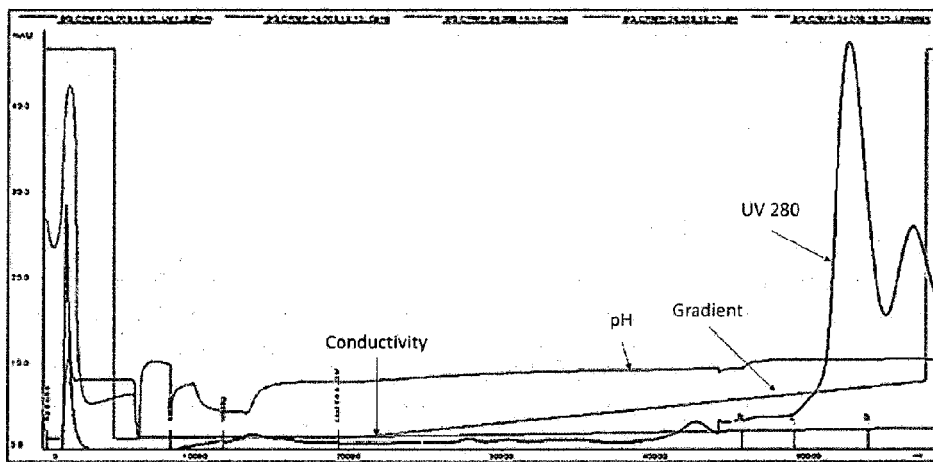


FIGURE 2

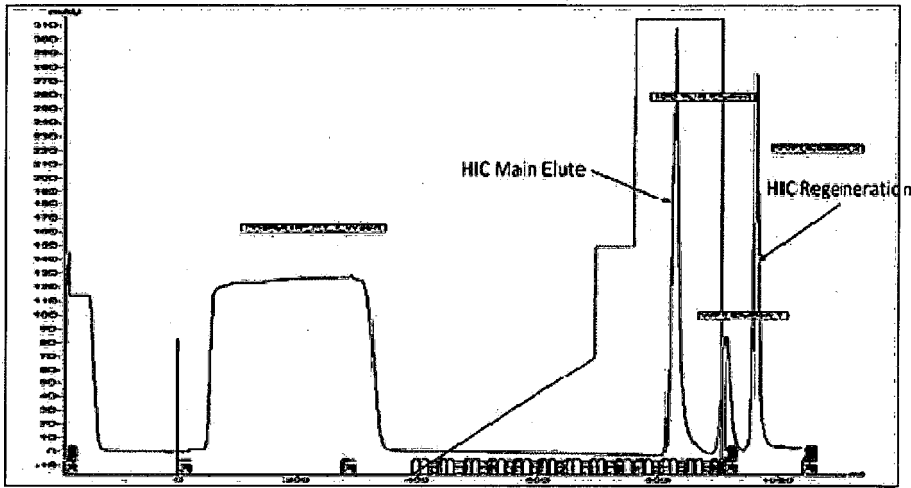


FIGURE 3

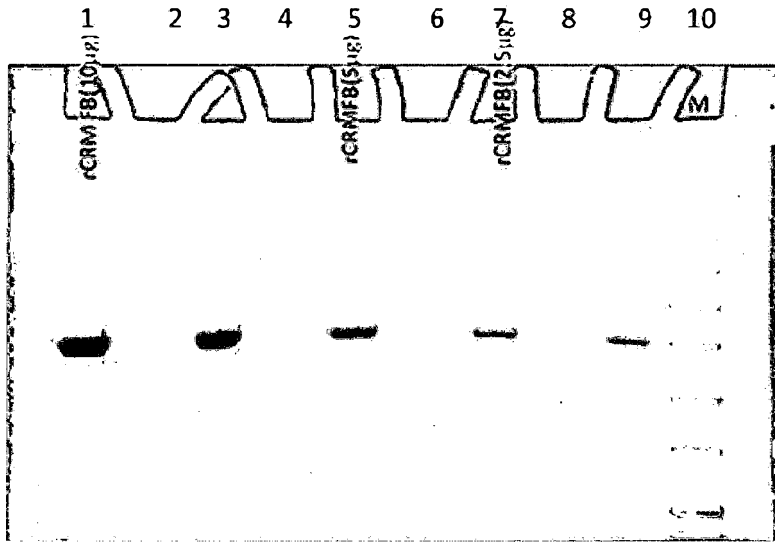


FIGURE 4

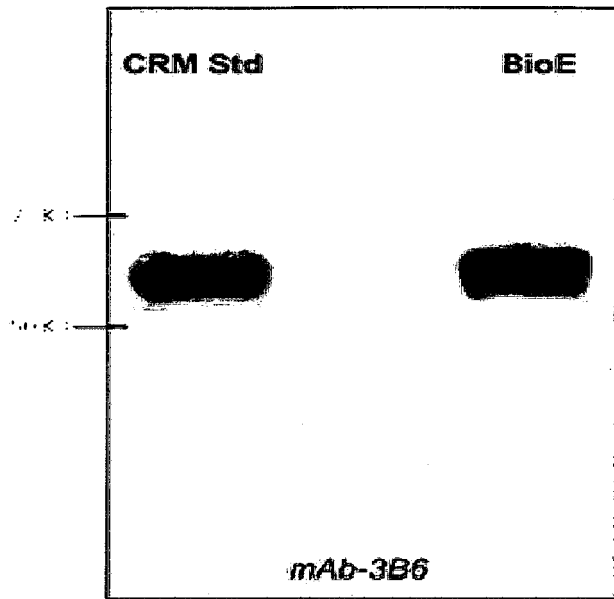


FIGURE 5

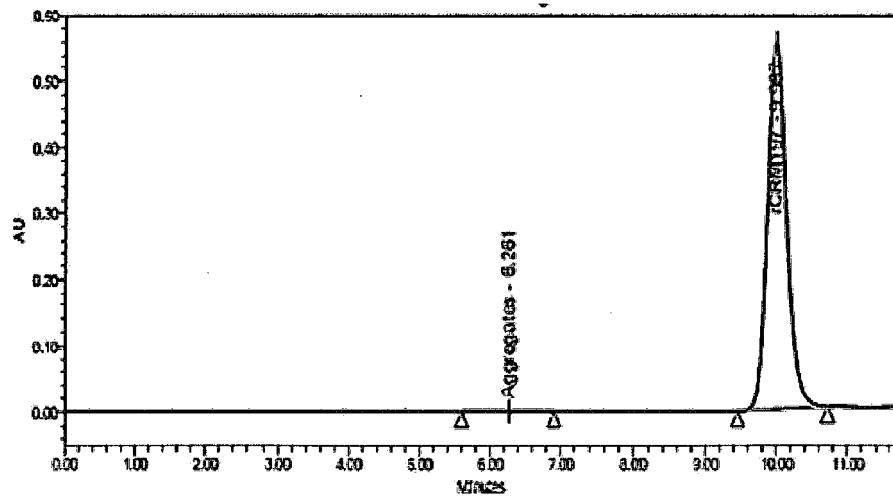


FIGURE 6

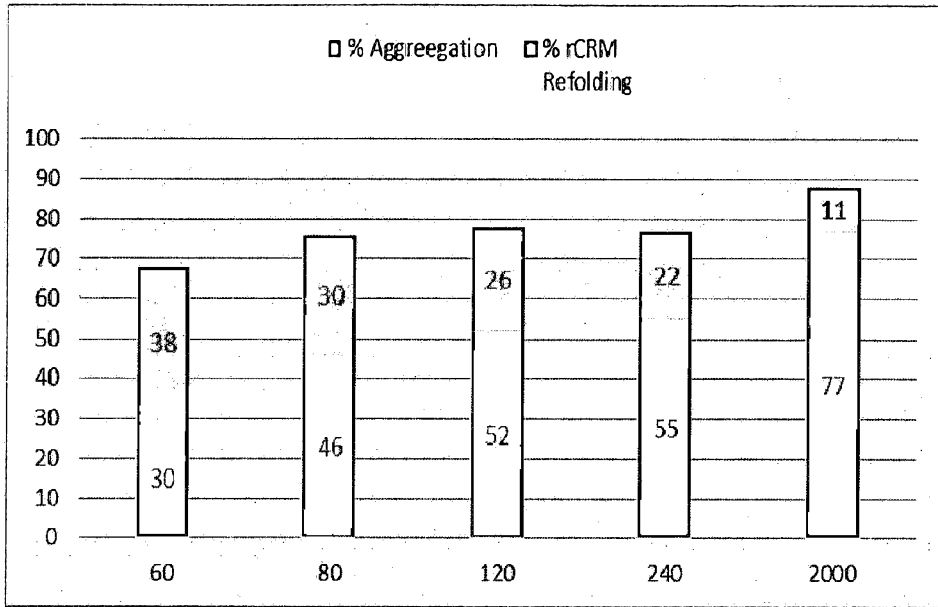


FIGURE 7