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(57) Abstract: A method for preparing a biologically active complex, said method comprising a recombinant protein having the sequence of α -lactalbumin, such as human α -lactalbumin or a fragment thereof but which lacks intra-molecular disulfide bonds, and oleic acid, and process for preparing this are described and claimed. The recombinant protein suitably has cysteines found in the native protein changed to other amino acids, such as alanine. Improvements in recombinant expression, process rationalisation and yields of biologically active complexes, as well as the complexes obtained are also described and claimed.



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Complex and Production Process

The present invention relates to a process for the preparation of a therapeutic protein complex, and to apparatus and reagents for use in the process.

5 Mutated forms of recombinant α -lactalbumin are known in the art, and although many of the properties found for the folded and molten globular forms have been shown to be similar to the native protein, it is generally accepted that there is generally a reduction in stability in the mutated forms. α -Lactalbumin itself in a partially unfolded or molten globule state has been used previously to form biologically active complexes, (Svensson et al. Proc. Natl. Acad. Sci. USA (2000) 10 97(8) 4221-4226).

Any discussion of documents, acts, materials, devices, articles or the like which has been included in the present specification is not to be taken as an admission that any or all of these matters form part of the prior art base or were common general knowledge in the field relevant to the present disclosure as it 15 existed before the priority date of each claim of this application.

However, the applicants have found that a particular type of recombinant protein, can be used to produce therapeutically active complexes with unique compositional features and structures, as demonstrated by n.m.r.. The complexes retain useful biological and activity in spite of these differences and furthermore can 20 be prepared efficiently.

Thus according to the present invention there is provided a method of producing a biologically active complex, said method comprising contacting a recombinant protein having the sequence of α -lactalbumin or a fragment thereof but which lacks intra-molecular disulfide bonds or cross-links, with oleic acid under 25 conditions in which a biologically active complex is formed and isolating the complex.

Throughout this specification the word "comprise", or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated element, integer or step, or group of elements, integers or steps, but not the 30 exclusion of any other element, integer or step, or group of elements, integers or steps.

By ensuring that the recombinant protein lacks intra-molecular disulfide crosslinks, the molecule will be three-dimensionally non-native and completely inactive in terms of its original endogenous biological activity. This may be achieved for example by changing cysteine residues in the native α -lactalbumin to other residues, in particular alanine residues, although other means, for example by adding thiol compounds, or altering the pH of the protein may be considered. Preferably all cysteine residues will be changed to other residues, such as alanine residues.

The expression "biologically active" as used herein means that the complex is able to induce tumour cell death, in particular by apoptosis in tumour cells

and/or has a bactericidal effect not seen with the native monomeric α -lactalbumin forms.

The term "fragment thereof" refers to any portion of the given amino acid sequence which will form a complex with the similar activity to complexes
5 including the complete α -lactalbumin amino acid sequence. Fragments may comprise more than one portion from within the full-length protein, joined together. Portions will suitably comprise at least 5 and preferably at least 10 consecutive amino acids from the basic sequence.

Suitable fragments will be deletion mutants comprising at least 20 amino
10 acids, and more preferably at least 100 amino acids in length. They include small regions from the protein or combinations of these.

Suitable fragments will include the region which forms the interface between the alpha and beta domains is, in human α -lactalbumin, defined by amino acids 34-38 and 82-86 in the structure. Thus suitable fragments will include these
15 regions, and preferably the entire region from amino acid 34-86 of the native protein. However, other active fragments may be found.

In particular the recombinant protein is based upon the sequence of human α -lactalbumin but α -lactalbumin from other sources, including bovine or ovine α -lactalbumin may be used to derive the recombinant protein.

20 Methods that may be used to convert recombinant protein and oleic acid to biologically active complex are analogous to those described for example in WO99/26979 and WO2008/138348, the content of which is incorporated herein by reference. However, in accordance with the method of the invention, a distinct biologically active product is more readily obtainable in good yield.

25 In particular, when using the method of the invention, high yields of biologically active complex are obtained conveniently, in particular from a single fraction eluting from a column and without the need for a prolonged folding process.

The recombinant protein as defined above is suitably contacted with the
30 oleic acid under conditions which allow ion exchange to take place in particular on an ion exchange column, specifically an anion exchange column such as a DEAE-Trisacryl M column (available from BioSeptra, Ville-neuf, France). The column is suitably "pre-conditioned" with oleic acid before the recombinant protein is

applied to it. This may be achieved by eluting or conditioning the column first with oleic acid. Suitably the oleic acid is eluted through a column containing new unused ion exchange material such as DEAE Trisacryl. Suitable elution buffers include Tris-HCl with a pH of 8.5. The amount of oleic acid composition applied to the column in this way may be small depending upon factors such as the size of the column and the volume of recombinant protein required to be converted to biologically active complex. For example, it has been found that only 10mg of oleic acid can be used to condition a column of 14cm x 1.6cm.

After the recombinant protein has been applied to the column (for example in solution in a suitable buffer), it is then eluted with a linear salt gradient, and the fraction eluting at high salt (1M NaCl or equivalent) is isolated. Using the method of the invention, substantially all the product is obtainable from this one peak, whereas previously, two peaks have always been required to be isolated.

This provides a significant enhancement of production efficiency and purity of product since there is no need to fold the expressed protein to the native state and no need to obtain and pool multiple fractions.

Thus in a particular embodiment, the invention provides a method of producing a biologically active complex, said method comprising contacting a recombinant protein having the sequence of α -lactalbumin or a fragment thereof but which lacks intra-molecular disulfide bonds (crosslinks), with oleic acid on an anion exchange column under conditions in which a biologically active complex is formed, eluting the column with a salt gradient and isolating the complex from a single fraction eluting at high salt concentration.

The expression "high salt concentration" refers to concentrations of salts with cations such as halides and in particular chlorides at concentrations in excess of 0.5M, for example in excess of 0.75M and in particular at about 1M. The concentration required may vary depending upon the salt used, but in a particular embodiment, the salt is NaCl, and suitably 1M NaCl.

In accordance with the invention, the "recombinant protein having the sequence of α -lactalbumin" comprises a protein having the sequence of native mature α -lactalbumin but which has all of the cysteines found at positions 6, 28, 61, 73, 77, 91, 111 and 120 in the full length sequence of mature human α -lactalbumin mutated to other amino acids, such as alanine, which do not give rise

to disulphide bridges. Thus a particular of a protein that may be utilised in accordance with the invention comprises a protein of SEQ ID NO 1.

KQFTKAELSQLLKDIDGYGGIALPELIATMFHTSGYDTQAIVENNESTEYGL
5 FQISNKLWAKSSQVPQSRNIADISADKFLDDDDITDDIMAAKKILDIKGIDYW
LAHKALATEKLEQWLAEKL (SEQ ID NO 1)

where the bold type indicates positions of mutations of cysteines in native human α -lactalbumin.

10 The applicants have found that some amino acid residues, for example up to 20 amino acids, may be attached at the terminal ends of the protein, if convenient, for example for expression purposes. Thus in particular, a recombinant protein as shown in SEQ ID NO. 1 but with an additional methionine at the N-terminus (SEQ ID NO 2 shown below) has been used in the method of the
15 invention. The complex obtained using this sequence has been designated Cys567OA. This complex shows unique properties when examined by n.m.r. and thus it forms a particular aspect of the invention.

The recombinant protein used in the method is suitably produced in pure form, using conventional recombinant expression methods. In particular, DNA
20 encoding the required recombinant α -lactalbumin can be inserted into suitable expression vectors such as plasmids, which can then be employed to transform host cells, for example, prokaryotic cells such as *E. coli* or eukaryotic cells such as particular insect cells using conventional methods.

By using the recombinant protein as described above, there is no need for
25 pretreatment steps, for example by treatment with a calcium chelating agent such as EDTA (ethylene diamine tetraacetic acid), subjecting the material to low pH or high temperature, in order to remove calcium and increase the amount of molten globule-like material present. Such a step is generally preferable when using native human α -lactalbumin or modified forms in which some cysteine residues
30 remain in order to generate a biologically active complex.

Suitably the oleic acid used in the process is in pure form although a casein containing fraction of human milk can provide a convenient source of this material and may be used in the process as has been demonstrated previously.

A pre-treated column can be used repeatedly to convert numerous fractions of a recombinant protein having the sequence of α -lactalbumin or a fragment thereof to biologically active complex as described above. Once the column is exhausted or the conversion rate drops to unacceptable levels, the pre-treatment step can be repeated in order to restore the complex production activity.

The product obtained using the process of the invention is novel and therefore forms a further aspect of the invention.

Thus, the invention further provides a biologically active complex of a recombinant protein having the sequence of α -lactalbumin or a fragment thereof as described above, and oleic acid. In particular the invention provides a biologically active complex comprising a recombinant protein of SEQ ID NO 2 and oleic acid, that has been designated Cys567OA.

MKQFTKAELSQLLKDIDGYGGIALPELIATMFHTSGYDTQAIVENNESTEY
GLFQISNKLWAKSSQVPQSRNIADISADKFLDDDDITDDIMAAKKILDIKID
YWLAHKALATEKLEQWLAEKL (SEQ ID NO 2)

The complex has been found to be biologically active in that it has activity in inducing tumour cell-death for instance by apoptosis and/or have a bactericidal effect that is at least equal to that obtained with other biologically active complexes such as HAMLET.

Thus, it may be formulated into useful pharmaceutical compositions by combining it with pharmaceutically acceptable carriers in the conventional manner. Such compositions form a further aspect of the invention.

The invention further provides a pharmaceutical composition comprising a complex according to the present invention in combination with a pharmaceutically acceptable carrier.

The compositions in accordance with this aspect of invention are suitably pharmaceutical compositions in a form suitable for topical use, for example as creams, ointments, gels, or aqueous or oily solutions or suspensions. These may include the commonly known carriers, fillers and/or expedients, which are

pharmaceutically acceptable.

Topical solutions or creams suitably contain an emulsifying agent for the protein complex together with a diluent or cream base.

5 The daily dose of the complex varies and is dependant on the patient, the nature of the condition being treated etc. in accordance with normal clinical

practice. As a general rule from 2 to 200 mg/dose of the biologically active complex is used for each administration.

In a further aspect of the invention, there is provided a method for treating cancer which comprises administering to a patient in need thereof, a biologically
5 active complex as described above.

In particular, the complex may be used to treat cancers such as human skin papillomas, human bladder cancer and glioblastomas. In the latter case, administration may be by infusion as is known in the art.

The invention further provides the biologically active complex as defined
10 above for use in therapy, in particular in the treatment of cancer.

That the elimination of cysteine residues would lead to an enhanced yield of biologically active complex is unexpected.

Thus, yet a further aspect of the invention provides a method for increasing the yield of a biologically active complex obtainable by a process comprising
15 contacting α -lactalbumin or a fragment thereof and oleic acid under ion exchange conditions, said method comprising using a recombinant protein having the sequence of α -lactalbumin or a fragment thereof but which lacks at least some of the intra-molecular disulfide crosslinks found in the native protein in said process.

As before, the disulfide cross-links are suitably eliminated by changing
20 cysteine residues to other amino acids. In particular, all disulfide crosslinks are eliminated, for example by changing all cysteine residues to different amino acids, for instance alanine.

Furthermore, the invention provides the use of a recombinant protein having the sequence of having the sequence of α -lactalbumin or a fragment
25 thereof but which lacks intra-molecular disulfide bonds or crosslinks, in the preparation of biologically active complexes. In particular, the recombinant protein has the sequence of human α -lactalbumin or a fragment thereof in which cysteine residues and in particular all cysteine residues are changed to different amino acids.

30 Recombinant proteins used in these aspects of the invention may contain additional amino acids as described above.

The invention will now be particularly described by way of example with reference to the accompanying diagrammatic drawings in which:

Figure 1 relates to the structure of α -lactalbumin and conversion of recombinant protein as described above and native α -lactalbumin to biologically active complex on an oleic acid-conditioned matrix. (A) shows the structure of α -Lactalbumin containing eight cysteines, which form four disulfide bonds located throughout the protein. The disulfide bonds are shown in black and the residue numbers of cysteines involved are marked. The calcium ion is shown in black. The ribbon structure was obtained from PDB accession number 1HML (10) and modified by MOLMOL (Anderson et al., Biochemistry 1997 36 (39) 11648-11654. (B) This is a graph showing the elution of complex over time at low salt (Fraction 1) and high salt (Fraction 2). To form the complex, recombinant protein of SEQ ID NO 2 was applied to an oleic acid conditioned ion exchange column and the complex was eluted with a NaCl gradient (conductivity trace in light grey). Human α -lactalbumin with EDTA or without EDTA was used as control. (C) This is a table showing conversion yields as determined as the area under the curve from (B) 0-110 min (fraction 1) and 110-140 min (fraction 2).

Figure 2. shows the results of circular dichroism spectroscopy of α -lactalbumin and various complexes. (A) The tertiary structure of the recombinant protein having the sequence of α -lactalbumin in which all cysteines have been converted to alanines (black solid line) and the biologically active complex obtained therefrom (designated Cys567OA) (black dashed line) was examined by near-UV CD spectroscopy. The spectra were recorded at 70 μ M in 5 mM Tris, pH 8.5 with native α -lactalbumin (grey solid line), apo α -lactalbumin (grey cross) and HAMLET (grey dashed line) as controls. The spectra of human α -lactalbumin, α -lactalbumin^{All-Ala} and HAMLET have been described previously. (B) The secondary structure of HAMLET (grey dashed line) and Cys567OA (black dashed line) was examined with far-UV CD spectroscopy. The recorded spectra of the controls, α -lactalbumin (grey solid line) and α -lactalbumin^{All-Ala} (black solid line), were consistent with previous reports. The spectra were recorded at 28 μ M in 5 mM Tris, pH 8.5.

Figure 3. compares the effect of HAMLET and the biological complex of the present invention in killing tumor cells. (A) L1210, (B) Jurkat, (C) HeLa and (D) A549 cells were exposed to HAMLET or Cys567OA for 6 hours. The lymphoma cells (L1210 and Jurkat) were treated with 7, 14 and 21 μ M of HAMLET and the carcinoma cells (A549 and HeLa) with 14, 28 and 42 μ M. Cell death was determined by Trypan blue exclusion, in percent of untreated cells, and shown in the left panel. The decrease in ATP levels by HAMLET (black triangle) and Cys567OA (black circle) are shown in the right panel, in percent of the medium control. Averages of two to five experiments are shown with standard deviation as error bars. α -Lactalbumin (grey triangle) and α -lactalbumin^{All-Ala} (grey circle) proteins were used as controls. Cys567OA was shown to be as biologically active as HAMLET, and particularly more active in HeLa and A549 cell lines.

Figure 4 illustrates cellular internalization of Alexa-labeled complexes. The internalization of the biological complex of the invention (Cys567OA) by A549 cells was examined by confocal microscopy using Alexa-fluor labeled complex. α -Lactalbumin, recombinant protein having the sequence of α -lactalbumin with all cysteines substituted by alanines and HAMLET were used as controls. The cells were treated for 15 min and 3 hours with 35 μ M. (A) HAMLET was rapidly internalized by the tumor cells after 15 minutes and after 3 hours a further internalization had occurred. (B) Cys567OA was internalized more slowly than HAMLET, but after 3 hours similar amounts were present in the cells. (C) α -Lactalbumin or (D) α -lactalbumin^{All-Ala} were not internalized by the cells.

Figure 5 shows the result of TUNEL staining of human lung carcinoma cells treated with biologically active complexes including the complex of the present invention. Evidence of DNA damage in (A) L1210, (B) Jurkat, (C) HeLa and (D) A549 cells after HAMLET and Cys567OA exposure was examined using TUNEL staining. HAMLET and Cys567OA (14 μ M in lymphoma cells, 28 μ M in carcinoma cells) caused nuclear DNA damage in the four cell lines, indicated by positive TUNEL staining. α -Lactalbumin and α -lactalbumin^{All-Ala} (21 μ M in lymphoma cells, 42 μ M in carcinoma cells) did not cause DNA damage.

Figures 6 and 7 show the results of *NMR spectroscopy* of human α -lactalbumin (*HLA*), recombinant human α -lactalbumin as described in below (rHLA^{all-Ala}) and protein-oleic acid complexes.

5 Example 1

Protein expression and purification

Wild-type α -lactalbumin contains eight cysteines at positions 6, 28, 61, 73, 77, 91, 111 and 120, forming four disulfide bonds, which stabilize the native state (Figure 1A). Two disulfide bonds are present in the α -domain [6-120, 28-111], one
10 in the β -domain [61-77] and one in the interface between the two domains [73-91]. The protein is also stabilized by a calcium ion, which if removed, makes α -lactalbumin lose its well-defined tertiary structure and adopt a molten globule state.

A vector encoding a recombinant protein having the sequence of human α -lactalbumin in which all cysteines were changed to alanines, pALAALA, obtained
15 by incorporating point mutations in the wildtype vector, pALA, the α -lactalbumin gene cloned into the T7-polymerase-based expression vector pAED4 (HUFF M.E. Curr Opin. Struct. Biol. (2003) 13 (6), 674-682) was used. The vector was transformed into *Escherichia coli* BL-21*, the recombinant protein expressed and purified as described previously described (Peng Z.Y. et al., Biochemistry (1995)
20 34(104),3241-3252; Schulman B. et al., J. Mol. Biol. 253, 651-657) but with some modifications. Inclusion bodies were solubilized in urea buffer (10 mM Tris, 8 M urea, 5 mM reduced glutathione, pH 8.0) and loaded onto a DEAE-cellulose (Whatman, Brentford, UK) column equilibrated with 20 mM Tris, pH 8.0. The column was washed with 25 mM Tris, 10 mM reduced glutathione, 0.25 M NaCl,
25 pH 8.0 and the protein eluted with 25 mM Tris, 7 M urea, 0.5 M KCl at pH 8.0. Fractions were pooled and dialysed against still tap water for 24 hours and flowing tap water for at least 48 hours (Spectra/Pore, Laguna Hills, CA, molecular weight cutoff 3.5 kDa). In case of precipitation during dialysis, the precipitate was dissolved in 5 M urea, then dialysed against flowing tap water and lyophilized. The
30 dialyzed sample was loaded onto a DEAE-Sephacel (Amersham Biosciences, Uppsala, Sweden) column equilibrated with 25 mM Tris, 0.2 mM CaCl₂ at pH 7.8 then eluted with a linear salt gradient (25 mM Tris, 0.2 mM CaCl₂, 0-0.4 M NaCl

pH 7.8). Fractions were pooled, dialyzed against distilled water at pH 7 (molecular weight cutoff 3.5 kDa), and lyophilized. The purified mutant protein is of SEQ ID No 2 which is the sequence of human α -lactalbumin but contains an extra N-terminal methionine residue, which was not removed.

5 The recombinant protein was expressed in *E. coli* BL21* with relatively high yields (100 mg/L culture) and purified to homogeneity. Since, the recombinant protein substitutes all cysteines for alanines, it thereby contains no disulfide bonds. However the native-like topology is known to be preserved. The mutant adopts a molten globule-like conformation, as shown by near-UV CD
10 spectroscopy and by NMR with a retained secondary structure shown by far-UV CD spectroscopy. This protein was designated rHLA^{all-Ala}.

Example 2

Complex formation with oleic acid by ion exchange chromatography

15 A column (14 cm x 1.6 cm) was packed with 10 ml of DEAE-Trisacryl M (BioSeptra, Ville-neuf, France) and conditioned with oleic acid (C18:1:9cis) (Larodan, Malmö, Sweden) as previously described (Svensson et al. Proc. Natl. Acad. Sci. USA (2000) 97(8) 4221-4226 and Pettersson J. et al., Biochem. Biophys. Res. Commun. (2006) 345(1) 260-270). Essentially, ten milligrams of
20 oleic acid was dissolved in 500 μ l of 99.5% ethanol by sonication. After addition of 10mM Tris-HCl pH 8.5 (10ml), the solution was applied to the column. Five milligrams of protein, (the recombinant protein rHLA^{all-Ala} obtained as described in Example 1), or controls comprising native α -lactalbumin or native α -lactalbumin pre-incubated with excess EDTA) were dissolved in buffer (50 mM Tris/HCl pH
25 8.5, 0.1 M NaCl) and added to the column individually.

Fractions were collected after applying a NaCl gradient.

The column was eluted with an NaCl gradient, (Buffer A comprising 10mM Tris HCL(pH 8.5) followed by Buffer B which was Buffer A containing 1M NaCl) and the fractions eluting before (fraction 1, t = 0-110 min) or after high salt
30 (fraction 2, t = 110-130 min) were examined (Fig. 1B). The complex obtained using the recombinant protein rHLA^{all-Ala} of Example 1, (Cys567OA) eluted as a sharp peak at the same position as HAMLET. In contrast, wild type α -lactalbumin does not produce any significant complex that eluted after applying high salt (Fig.

1B and C). In fact, the recombinant protein rHLA^{all-Ala} of Example 1 was found to convert to a biologically active complex more efficiently than EDTA-treated α -lactalbumin with a recovery yield of 99% of applied protein (range 87-99%, SD 4.5, n=6) compared to 71% (range 67-94%, SD 11.3, n=5), respectively (Fig. 1C).

5 This may reflect the greater structural homogeneity of the mutant protein's conformation, where a greater proportion of the recombinant protein rHLA^{all-Ala} of Example 1 more readily adopt the molten globule state under the conditions of the chromatographic conversion to the fatty acid-bound complex.

Salt was removed by dialysis against distilled water (Spectra/Pore,
10 membrane cut off 3.5 kDa) followed by lyophilization.

Example 3

Circular dichroism spectroscopy on the α -lactalbumin variants

Far- and near-UV CD spectra were collected on α -lactalbumin, the
15 recombinant protein rHLA^{all-Ala} of Example 1, HAMLET and the Cys567OA obtained using the recombinant protein rHLA^{all-Ala} of Example 1 at 25°C. Lyophilized material was dissolved in 5 mM Tris, pH 8.5 to 70 and 28 μ M for near- and far-UV CD spectra, respectively. Near-UV spectra were obtained between 240 and 320 nm and far-UV spectra between 190 and 250 nm. The
20 wavelength step was 1 nm, the response time was 8 sec and scan rate at 10 nm/min. An average of six scans is presented where the mean residue ellipticity, θ_m in deg \cdot cm² \cdot dmol⁻¹, was calculated as described previously (Svensson M. et al., J. Biol. Chem. (1999) 274 (10), 6388-6396).

Substantial weakening of the tertiary interactions in the recombinant protein
25 rHLA^{all-Ala} of Example 1 was detected by near-UV CD spectroscopy (Fig. 2A), in agreement with the molten globule cases of α -lactalbumin. In fact, at room temperature, apo- α -lactalbumin is not completely molten globular (Fig. 2A), and instead a significant partitioning of the population of protein molecules into native and molten globule states is found, coexisting in equilibrium and resulting in the
30 averaging of spectra. Thus, under identical conditions, a greater proportion of recombinant protein rHLA^{all-Ala} of Example 1 molecules are in the authentic molten globule state, which may contribute to the observed increased conversion yield of

the recombinant protein rHLA^{all-Ala} of Example 1 with oleic acid described above. After conversion to a biologically active complex, the near-UV spectrum of the complex was nearly identical to the mutant protein-only spectrum, showing that the binding of oleic acid did not increase the amount of detectable tertiary structure (Fig. 2A).

With regards to secondary structure, the recombinant protein rHLA^{all-Ala} of Example 1 and the biologically active complex obtained therefrom (Cys567OA) both retained a qualitatively similar content of secondary structure with the wild type protein as shown by far-UV CD spectroscopy (Fig. 2B), again correlating well with previous studies.

Example 4

Cell death assays

Mouse lymphoma cells (L1210, ATCC, CCL-219), human lymphoma cells (Jurkat, ATCC, TIB-152), human lung carcinoma cells (A549, ATCC, CCL-185) and human cervical carcinoma cells (HeLa, ATCC, CCL-2) were used for examining the tumoricidal activity of Cys567OA. The cells were harvested, washed and resuspended in RPMI 1640 medium (PAA Laboratories GmbH, Pasching, Austria) in the absence of fetal calf serum. For adherent cells, versene (140 mM NaCl, 2.4 mM KCl, 8 mM Na₂HPO₄, 1.6 mM KH₂PO₄, 0.5 mM EDTA, pH 7.2) was used for detachment. The cells were seeded into 24 well plates at 1x10⁶ cells/well (TPP, Trasadingen, Switzerland). The lyophilized material was dissolved at 0.7 mM (MW 14,200 g/mol) in phosphate-buffered saline (PBS) and added to wells to a final concentration between 7 and 42 µM. The stated concentration of HAMLET and Cys567OA refer to the molarities of the protein moiety. Cells were incubated 37°C in 5% CO₂ atmosphere and foetal calf serum was added to each well to a final concentration of 5% after 1 hour. Cell viability was determined after 6 hours using Trypan blue exclusion with interference contrast microscopy (Laborlux 12, Leitz Wetzlar, Germany). ATP levels were determined using ATP Lite (Luminescence ATP detection assay system, PerkinElmer, Boston, MA) and luminescence was detected using a luminometer (LUMIstar, BMG Labtech, Offenburg, Germany).

The loss of viability after 6 hours was quantified as the decrease in ATP levels and the increase in Trypan blue staining (Fig. 3). Cys567OA was shown to kill the tumor cells in a dose-dependent manner. More than 80% of all cells were killed after 6 hours of exposure to the highest concentration tested (21 μ M for lymphoma cells and 42 μ M for carcinoma cells). Similar results were obtained for HAMLET, with more than 60% of the cells killed after 6 hours exposure to the highest concentration. There was no statistically significant difference in tumoricidal activity between the two complexes ($p > 0.05$, one-way ANOVA). The results show that the Cys567OA is as active as HAMLET.

In addition, similar to the native protein-only control, the recombinant protein rHLA^{all-Ala} of Example 1 alone did not reduce cell viability (Fig. 3). A statistically significant difference in viability of cells treated with the complex obtained as described above and the fatty acid-free recombinant protein rHLA^{all-Ala} of Example 1 was observed ($p < 0.005$, one-way ANOVA). Many studies have suggested that partial unfolding of proteins followed by oligomerization and aggregation result in amyloid structures with cytotoxic properties. In the case of the acidic molten globule form of α -lactalbumin (the "A-state"), amyloid fibrils are indeed known to form in the presence of high concentrations of salt. However, such solution conditions are not used here with the recombinant protein rHLA^{all-Ala} of Example 1, thereby showing that partial unfolding to the molten globule form alone does not make the protein cytotoxic.

Differences in effect on cell viability were compared using one-way analysis of variance (ANOVA) followed by the Bonferroni Multiple Comparisons test. Analyses were performed using GraphPad InStat3 for Macintosh version 3.0b.

Example 5

Uptake of Cys567OA in tumor cells

The cellular uptake of the recombinant protein and Cys567OA obtained therefrom was studied using AlexaFluor 568-labeled protein (Molecular Probes, Invitrogen, Carlsbad, CA). Human lung carcinoma cells (A549) were seeded onto 8-well chamber slides (Nunc, Rochester, NY) to a density of 50,000 cells per well and incubated overnight at 37°C in 5% CO₂. ALEXA-labeled and unlabeled protein was mixed to a 1:10 ratio and applied to the cells to a final concentration of

35 μM in absence of fetal calf serum. Cells were incubated in 37°C , 5% CO_2 and cells were fixated in 3.7% formaldehyde after 15 min. When incubating for 3 h, fetal calf serum was added after one hour to a final concentration of 5%. Cellular uptake was analyzed by confocal microscopy (LSM510 META confocal system, Carl Zeiss, Jena, Germany) and the result shown in Fig. 4. HAMLET – obtained using native α -lactalbumin as described in Example 2 above was used as a control.

As expected, HAMLET was rapidly internalized by the tumor cells, as shown after 15 minutes of exposure (Fig. 4A). After 3 hours a further increase had occurred. Cys567OA showed a similar pattern with rapid internalization followed by a translocation to the nuclei (Fig. 4B). Uptake was weak after 15 minutes when compared with HAMLET, but after 3 hours a similar number of cells had taken up Cys567OA. The reason for the slight difference in uptake kinetics was not immediately obvious, however it is thought that the relatively greater flexibility of the recombinant protein within the Cys567OA complex may bear some responsibility in delaying the initial uptake.

Internalization of the mutant protein without oleic acid was also compared to Cys567OA (35 μM of Cys567OA or of the recombinant protein rHLA^{all-Ala} of Example 1) (Fig. 4C and D). The mutant protein bound to the cell surface but was not internalized by the tumor cells. Large aggregates of the recombinant protein were formed and some remained adherent to the cell surface at 15 minute and 3 hours (Fig. 4D).

The results show that internalization into tumor cells is a general feature of HAMLET and Cys567OA, suggesting that the fatty acid cofactor is needed for uptake into tumor cells as well as for the tumoricidal activity. Furthermore, there was no evidence that the recombinant protein itself could be internalized.

Example 6

TUNEL staining

HAMLET has been shown to cause DNA damage in tumor cell lines and *in vivo* in human tumors using the TUNEL assay (Mossberg et al. Int. J. Cancer (2007) 121(6) 1352-1359). To examine the extent of DNA damage in response to Cys567OA, the four tumor cell lines used in Example 4 were exposed to the complex for 6 hours (14 μM for lymphoma cells and 28 μM for carcinoma cells).

HAMLET, recombinant protein rHLA^{all-Ala} of Example 1 and α -lactalbumin were used as controls.

Cells were harvested by centrifugation and fixed in 4% paraformaldehyde diluted in PBS. The cells were centrifuged onto L-lysine coated microscope slides (25 x g, 5 min, Cytospin 3, Shandon, Cheshire, GB) and stored at -20°C. Cells with nuclear DNA damage were identified by the TUNEL assay (Roche, Basel, Switzerland). Briefly, the slides were thawed at room temperature, washed twice in PBS and permeabilized with 0.1% sodium citrate, 0.1% Triton X-100. TUNEL reaction mixture was applied and the slides were incubated at 37°C in 5% CO₂ for 1h. Slides were washed three times with PBS, mounted with coverslip and mounting medium (Sigma-Aldrich, St Louise, MO, USA) and examined by confocal microscopy.

Cys567OA caused DNA damage detected by TUNEL staining in all cell types (Fig. 5). The frequency of TUNEL positive cells was similar to that in HAMLET-treated cells. In contrast, the recombinant protein rHLA^{all-Ala} of Example 1 and α -lactalbumin did not influence TUNEL staining. The results show that the cytotoxic effect of both the oleic acid/molten globule complexes includes damage of nuclear DNA.

In summary, the recombinant protein rHLA^{all-Ala} of Example 1 having the sequence of α -lactalbumin in which all eight cysteine residues are substituted for alanines, rendering the protein non-native under all conditions is readily converted to a biologically active complex in the presence of oleic acid. In fact, the production process was surprisingly good, giving an enhanced yield in a single peak. This is particularly advantageous in manufacturing terms. Furthermore the complex obtained exhibited strong tumoricidal activity against lymphoma and carcinoma cell lines. By confocal microscopy, it was shown to accumulate within the nuclei of tumor cells, thus reproducing the cellular trafficking pattern of HAMLET with identical tumoricidal activity. Therefore, Cys567OA represents a particularly preferred drug candidate.

Example 7

Structural study of Cys567OA

(Experimental procedure)

¹H NMR spectroscopy – recombinant human α -lactalbumin rHLA^{all-Ala} as described in Example 1, HAMLET and Cys567OA were solvent-exchanged to sodium phosphate buffer, pH 7.0 with 2.0 M urea using a 2.0 ml Zeba spin desalting column (Thermo Scientific). Human HLA, which contains a bound Ca²⁺ ion, was solvent-exchanged to 2.0 M urea in distilled water, and the pH adjusted to 7. In all cases, the solvents contained 10% D₂O. One-dimensional ¹H NMR spectroscopy of the four samples were acquired on a 600 MHz Ultrashield spectrometer with an indirect detection cryoprobe (Bruker BioSpin). Temperatures of 20 °C, 30 °C, 40 °C, 50 °C, and 55 °C were maintained with a variable temperature unit.

Apart from HLA, the one-dimensional ¹H NMR spectra of the rHLA^{all-Ala}, HAMLET and Cys567OA were poorly resolved and highly broadened as would be found with molten globule species of α -lactalbumin (Figs 6A-D). One of the key spectral features of native or native-like three-dimensional structure in α -lactalbumin is the intense upfield-shifted methyl resonances corresponding to the δ CH₃ protons of Ile95 (-0.7 ppm at 30°C) and the γ CH₃ protons of Val92 (-0.5 ppm at 30°C) (Fig 6B and 7A). Using this criterion, it was immediately apparent that HAMLET, despite its broad peaks throughout the spectrum in general, still contained considerable native-like structure (Fig 7A), albeit at a much lower population than folded HLA. This was consistent with the near-UV CD spectrum, where the ellipticity amplitudes of HAMLET was intermediate of apo-HLA and rHLA^{all-Ala}/Cys567OA. As a means to further distinguish the samples, each protein or protein-fatty acid complex was subjected to gradually higher temperatures in the presence of 2.0 M urea. The reason for adding urea was two-fold: first to aid in the solubility of the proteins, especially for rHLA^{all-Ala}, and second, to subtly increase the dynamic properties of the molecules to distinguish between conformational fluctuations on the microsecond to millisecond timescale (those that are observed in molten globules) from faster timescales (those that are observed with unfolded, highly dynamic molecules). It was noted that the addition of 2M urea did not strip the oleic acid from the proteins, nor does its presence negatively affect the cytotoxic activity of HAMLET and Cys567OA (30 min incubation with 2M urea and phosphate buffered saline; data not shown).

For the case of HLA, starting from a wide dispersion of chemical shifts and well-defined peaks as a result of a fully folded, native structure (20°C and 30°C), the peaks gradually broadened while the chemical shift dispersion appeared to narrow in range (40°C to 55°C) (Fig 6B). The characteristic upfield-shifted methyl resonances were still present at high temperature, however the peak heights become increasingly smaller as they broadened (Fig 7A,B), suggesting that there existed a significant population of molten globule molecules at 55°C in the presence of 2.0 M urea. For comparison, the conditions for the classical high-temperature molten globule state of α -lactalbumin is approximately 90 °C (pH 7, no chemical denaturant). In contrast, the spectrum of rHLA^{all-Ala} begins with poor chemical shift dispersion and broad peaks (20°C and 30°C), but at higher temperatures, even as the chemical shifts narrows further, the peaks gradually sharpen (40°C to 55°C) (Fig. 6A). This indicates that the protein is undergoing a transition from the molten globule state to an increasingly loose, unfolded state. One important aspect is that there are absolutely no upfield-shifted methyl resonances at any temperature in this variant (Fig. 7A,B), suggesting that rHLA^{all-Ala} lacks strong inter-residue side-chain interactions at all temperatures, as also suggested by the features found in the near-UV CD spectrum (not shown).

As noted above, the spectra of HAMLET (20°C and 30°C; Fig 7) displayed the δ CH₃ protons of Ile95 (-0.7 ppm at 30°C) and the γ CH₃ protons of Val92 (-0.5 ppm at 30°C), indicative of a presence of native-like three-dimensional structure albeit at lower populations than HLA. Upon increasing the temperature, as many of the peaks sharpen (Fig 6D) these upfield resonances vanish (Fig 7B), suggesting that although partially native-like at lower temperatures, HAMLET's overall behaviour was markedly different from that of native HLA. In fact, the upfield NMR spectrum of HAMLET is found to be identical to that of Cys567OA at 55°C (Fig 7B), where there are no upfield resonances except for a very small peak at 0.05 ppm. Surprisingly for Cys567OA, as the temperature is increased and the peaks sharpen as expected of molten globules (Fig 6C), there is no change in the upfield region (Fig 7A,B).

In this series of experiments, temperature-varied ¹H NMR spectroscopy has been exploited to differentiate (i) the spectrally well-dispersed, narrow peak-

exhibiting native state, (ii) the spectrally poorly-dispersed, broad peak-exhibiting molten globule states, and (iii) the spectrally poorly-dispersed, narrow peak-exhibiting unfolded states of rHLA^{all-Ala}, HLA, HAMLET and Cys567OA. Significant work on the backbone dynamics has been done with greater detail on

5 α -lactalbumin and its varied molten globule states, as well as other archetypal proteins such as apomyoglobin. These bodies of work show the intricacies and nuances of backbone dynamics with regards to different structural regions under different experimental conditions. One of the key conclusions reached from this work is firstly that Cys567OA is clearly structurally different from HAMLET

10 under physiological conditions. Furthermore, whereas HAMLET contains a population of native-like molecules, Cys567OA is completely devoid of native-like side-chain packing, but nevertheless exhibits equivalent cytotoxic activity as HAMLET. Hence, unlike amyloid fibril examples, deliberately engineered, non-native, and partially unfolded structural ensembles can confer independent

15 beneficial effects to the cells depending on the environment.

Claims

1. A method for producing a biologically active complex, said method comprising contacting a recombinant protein having the sequence of α -lactalbumin or a fragment thereof but which lacks intra-molecular disulfide bonds, with oleic acid under conditions in which a biologically active complex is formed and isolating the complex.
2. A method according to claim 1 wherein the recombinant protein comprises α -lactalbumin in which all the cysteine residues have been changed to other amino acids.
3. A method according to claim 2 wherein the cysteine residues in the α -lactalbumin have been changed to alanine residues.
4. A method according to any one of the preceding claims wherein the α -lactalbumin is human α -lactalbumin.
5. A method according to any one of the preceding claims wherein a recombinant protein having the sequence of α -lactalbumin or a fragment thereof as defined in claim 1 is contacted with the oleic acid on an ion exchange column, specifically an anion exchange column.
6. A method according to claim 5 wherein the column is eluted with a linear salt gradient, and biologically active complex is isolated from a single fraction eluting at high salt concentration.
7. A method according to claim 6 wherein the high salt concentration is 1M NaCl or equivalent.
8. A method according to any one of the preceding claims wherein the recombinant protein comprises SEQ ID NO. 1

KQFTKAELSQLLKDIDGYGGIALPELIATMFHTSGYDTQAIVENNESTEYGL
 FQISNKLWAKSSQVPQSRNIADISADKFLDDDDITDDIMAAKKILDIKGIDYW
 LAHKALATEKLEQWLAEKL (SEQ ID NO 1)

optionally with up to 20 amino acids attached at the terminal ends of the protein.

5

9. A method according to claim 8 wherein the recombinant protein is of SEQ ID No 2

MKQFTKAELSQLLKDIDGYGGIALPELIATMFHTSGYDTQAIVENNESTEY
 GLFQISNKLWAKSSQVPQSRNIADISADKFLDDDDITDDIMAAKKILDIKGID

10 YWLAHKALATEKLEQWLAEKL (SEQ ID NO 2)

10. A biologically active complex comprising a recombinant protein having the sequence of α -lactalbumin but which lacks intra-molecular disulfide bonds, or a fragment thereof and oleic acid.

15

11. A biologically active complex of claim 10 wherein the recombinant protein is of SEQ ID NO 1 or SEQ ID NO 2.

20 12. A pharmaceutical composition comprising a complex according to claim 10 or claim 11 in combination with a pharmaceutically acceptable carrier.

13. A biologically active complex according to claim 10 or claim 11 for use in therapy.

25

14. A biologically active complex according to claim 13 for use in the treatment of cancer.

15. A method for increasing the yield of a biologically active complex obtainable by a process comprising contacting α -lactalbumin or a fragment thereof and oleic acid under ion exchange conditions, said method comprising using a recombinant protein having the sequence of α -lactalbumin or a fragment thereof but which lacks at least some intra-molecular disulfide bonds, in said process.

30

16. A method according to claim 16 wherein at least some cysteine residues are changed to different amino acids.
17. The use of a recombinant protein having the sequence of α -lactalbumin or a fragment thereof but which lacks intra-molecular disulfide bonds, for instance in which cysteine residues, and in particular all cysteine residues, are changed to different amino acids, in the preparation of biologically active complexes.
18. The method of claim 1 or 15, the biologically active complex of claim 10, or the pharmaceutical composition of claim 12, or the use of claim 17, substantially as herein described with reference to the figures and/or examples, excluding comparative examples.

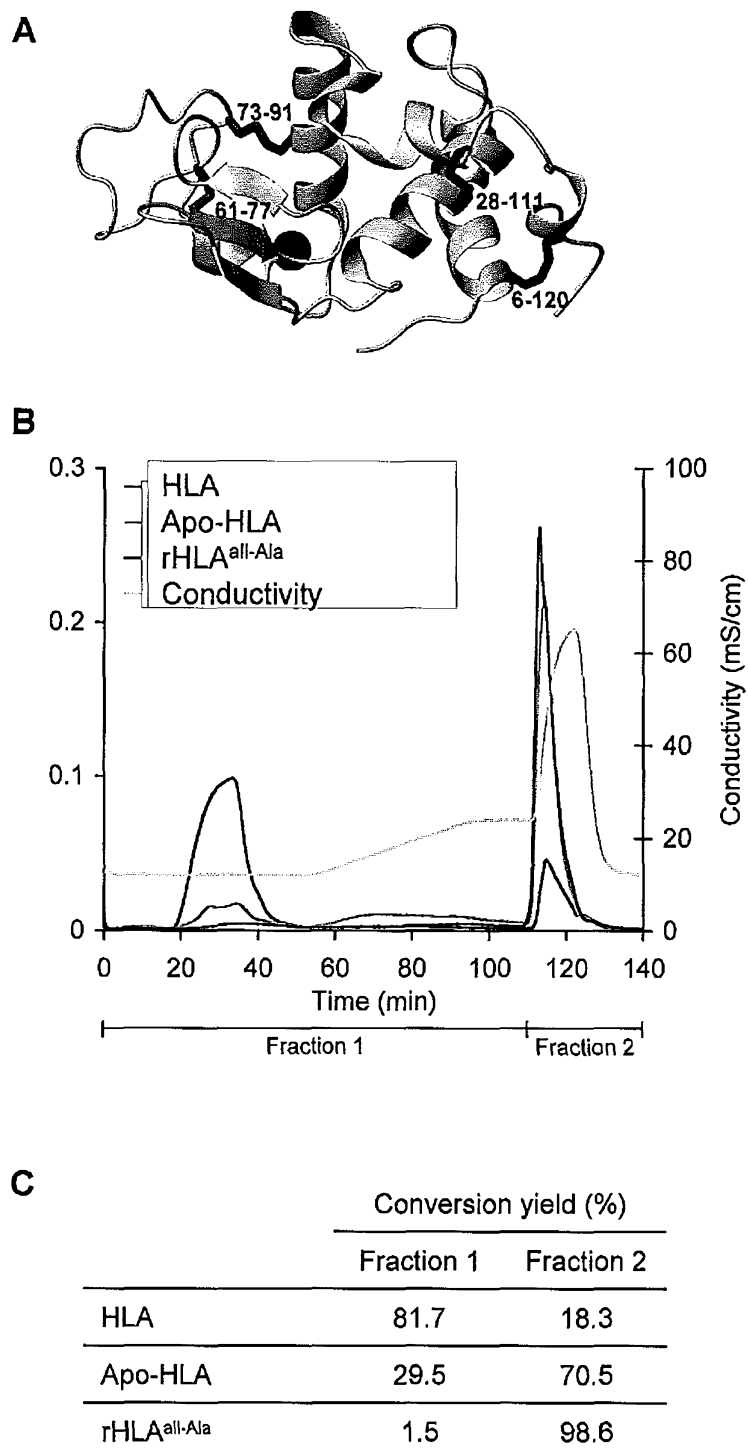
Figure 1

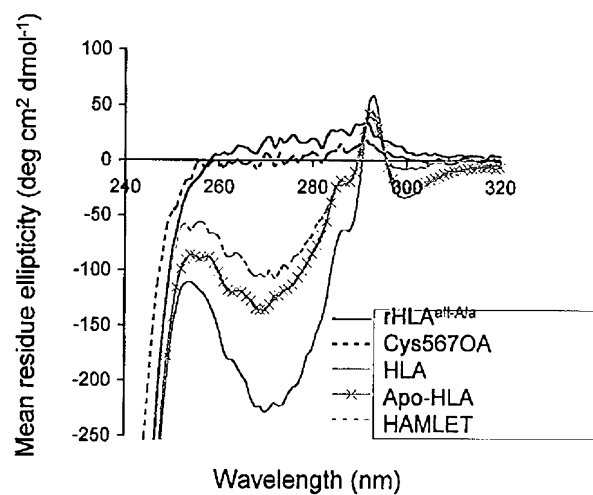
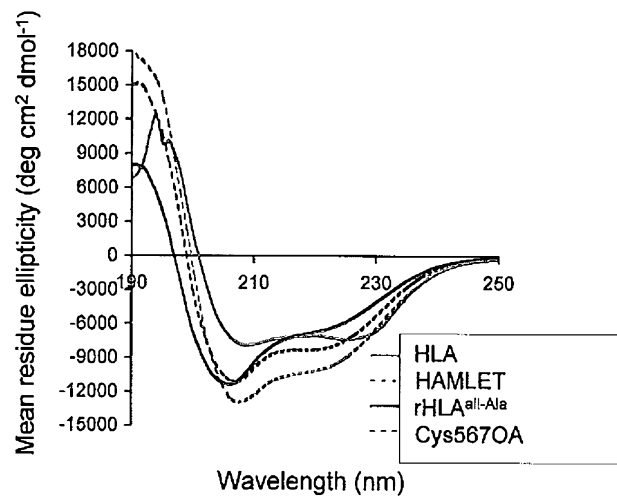
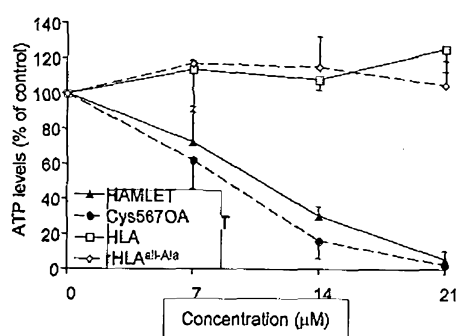
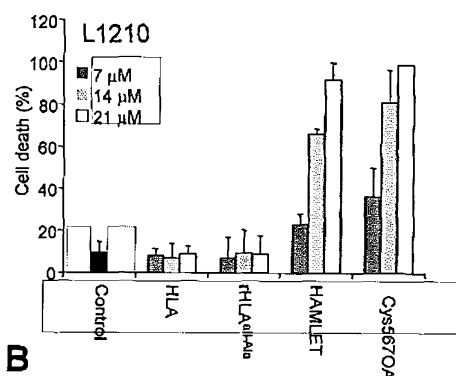
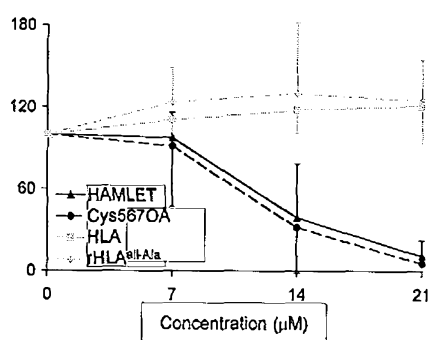
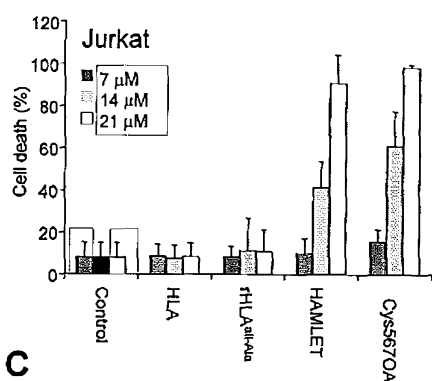
Figure 2**A****B**

Figure 3

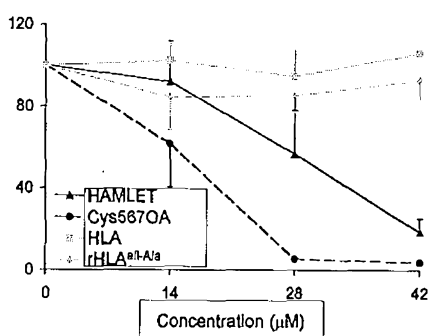
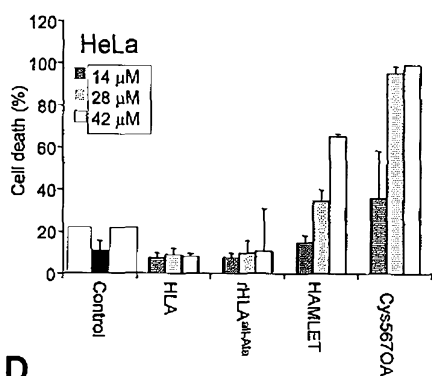
A



B



C



D

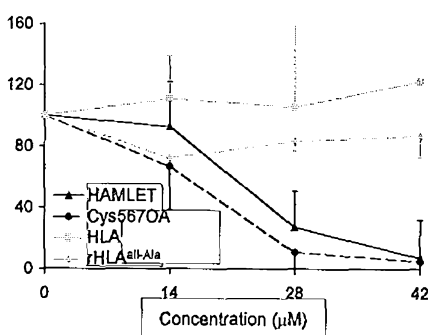
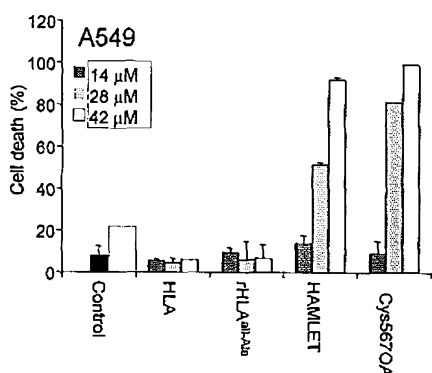


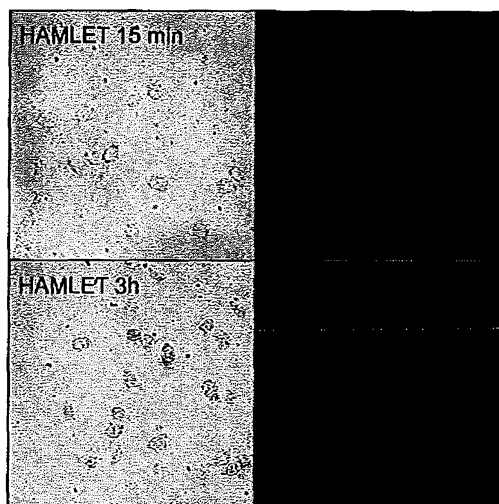
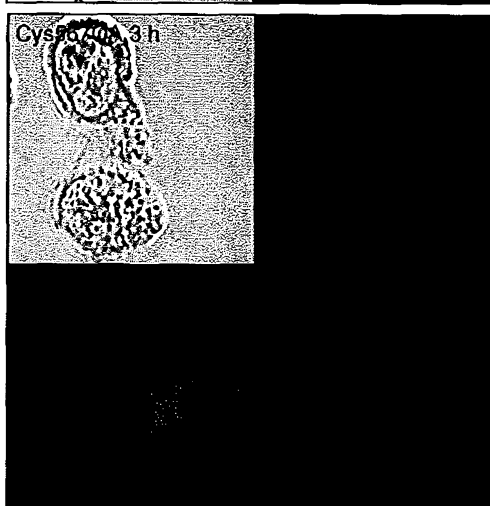
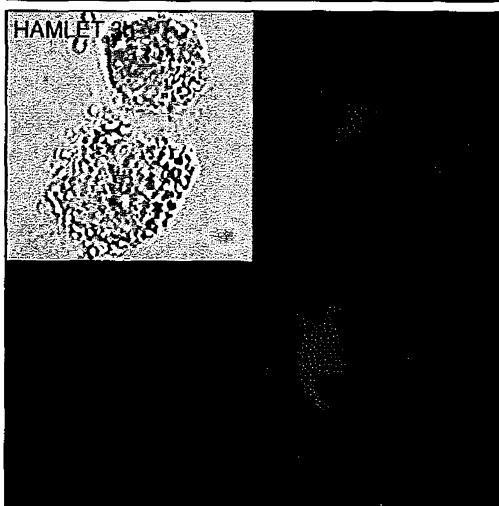
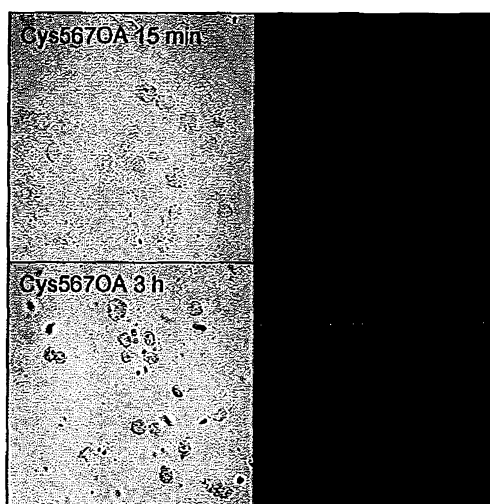
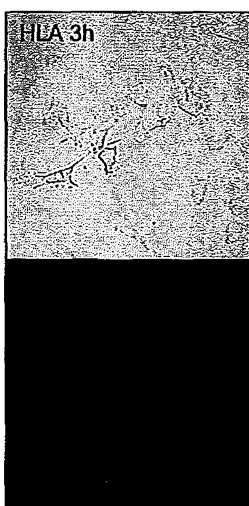
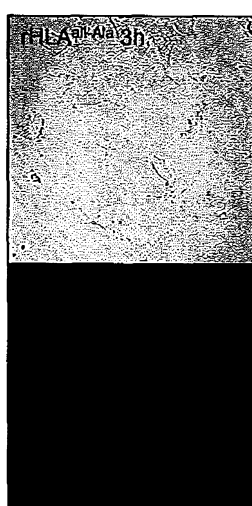
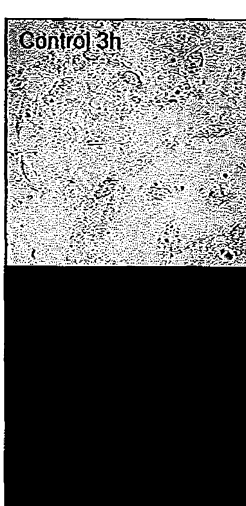
Figure 4**A****B****C****D****E**

Figure 5

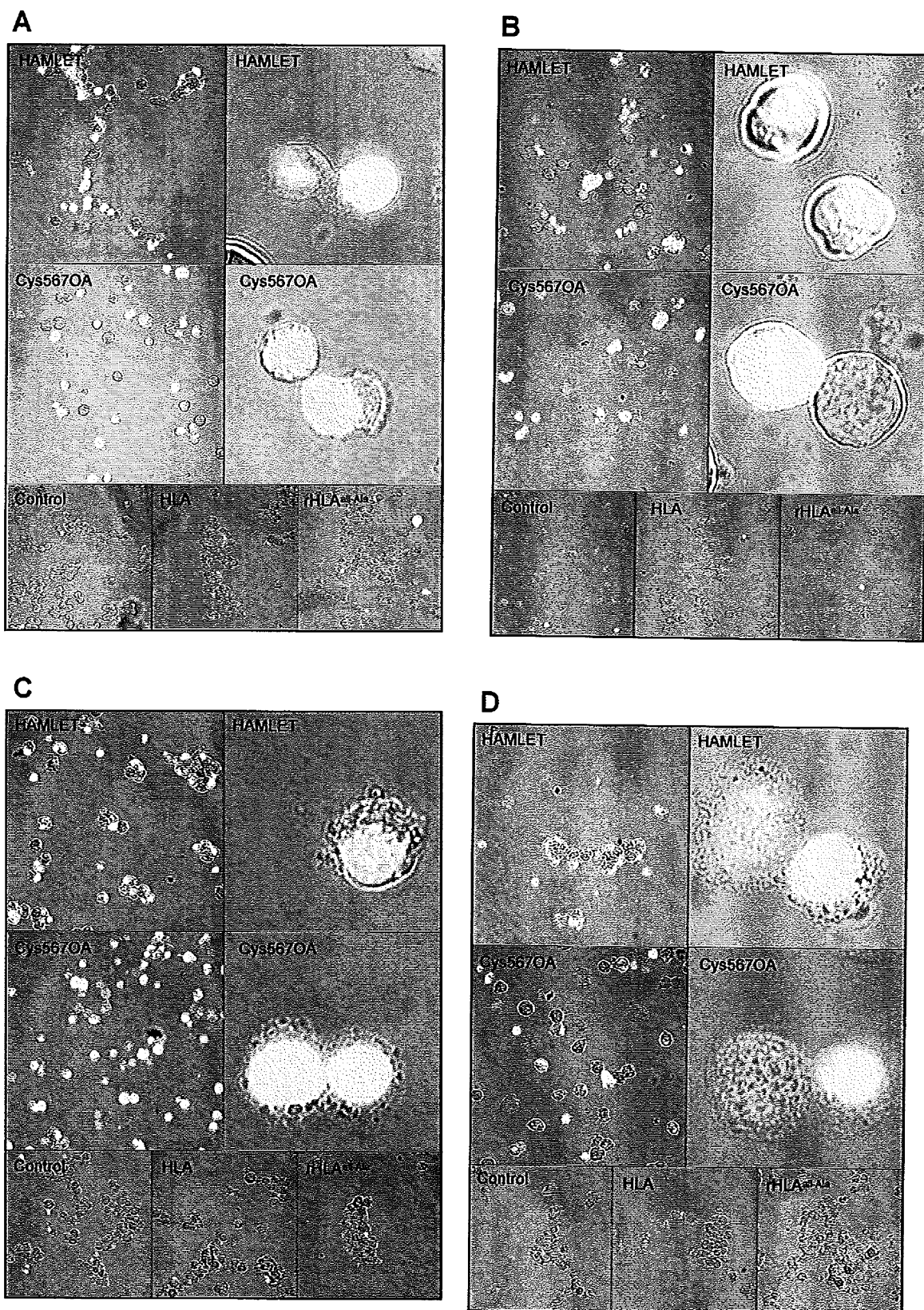


Figure 6

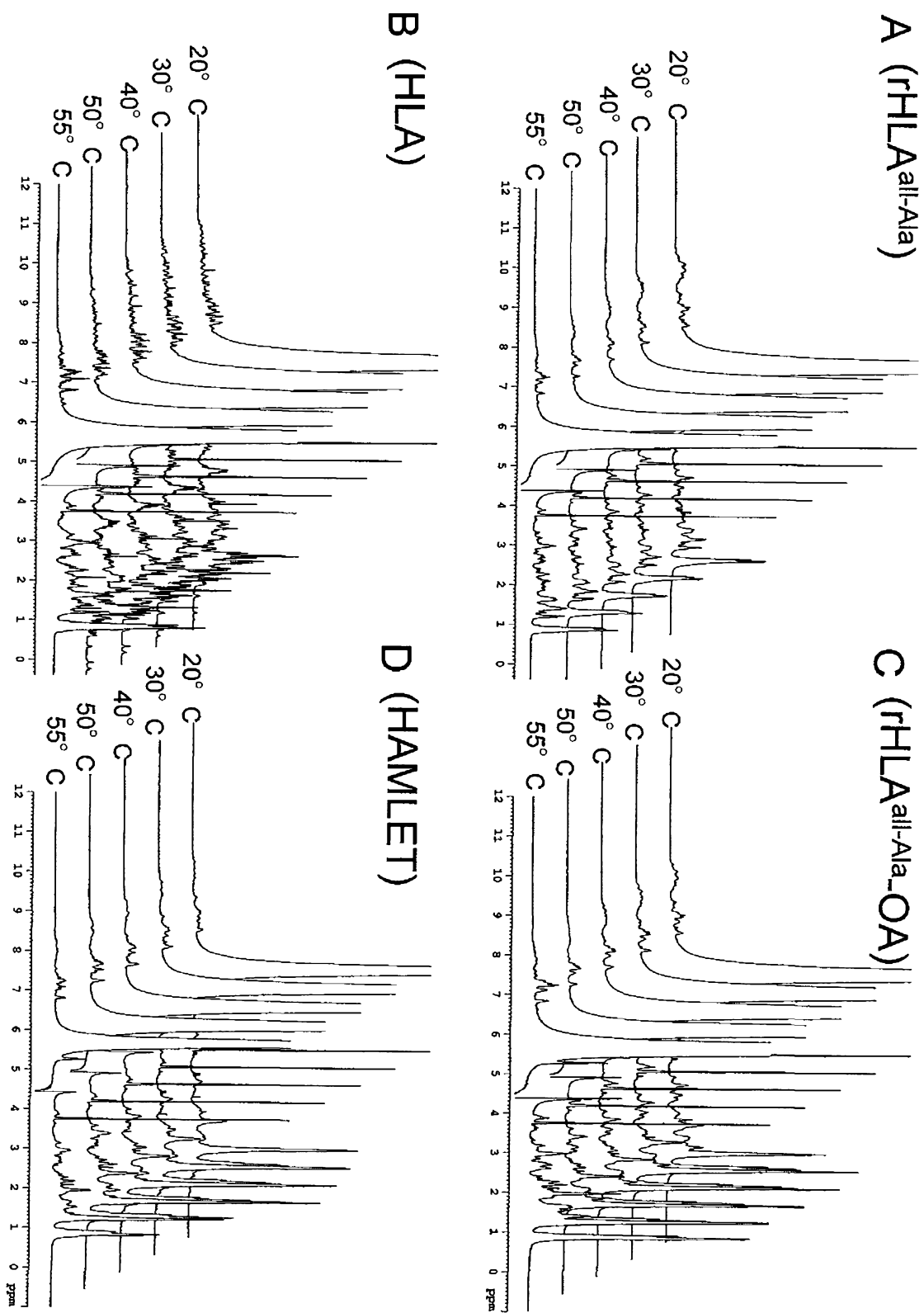


Figure 7

