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(54) Titre : POLYPEPTIDE A ACTIVITE ASPARAGINASE, CASSETTE D'EXPRESSION, VECTEUR D'EXPRESSION, CELLULE HOTE, COMPOSITION PHARMACEUTIQUE, PROCEDES POUR PRODUIRE UN POLYPEPTIDE A ACTIVITE ASPARAGINASE ET POUR PREVENIR OU TRAITER LE CANCER, ET UTILISATION D'UN POLYPEPTIDE

(54) Title: POLYPEPTIDE WITH ASPARAGINASE ACTIVITY, EXPRESSION CASSETTE, EXPRESSION VECTOR, HOST CELL, PHARMACEUTICAL COMPOSITION, METHODS FOR PRODUCING A POLYPEPTIDE WITH ASPARAGINASE ACTIVITY AND FOR PREVENTING OR TREATING CANCER, AND USE OF A POLYPEPTIDE

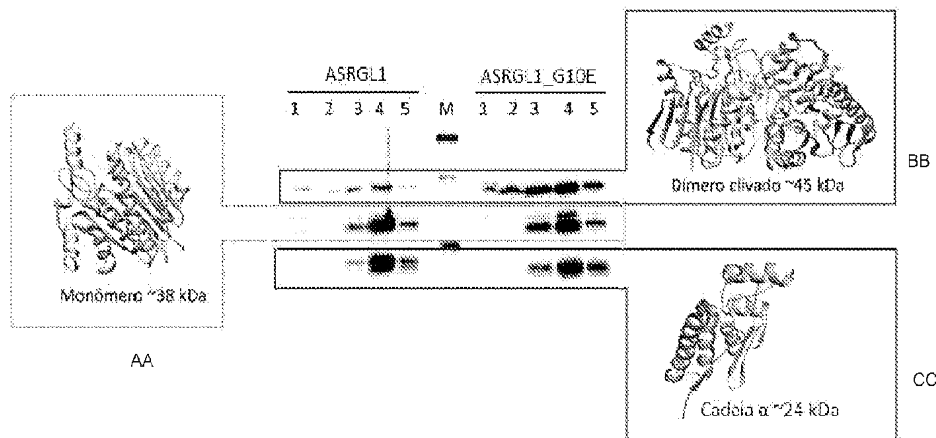

FIGURA 1

AA Monomer ~38 kDa
BB Cleaved dimer ~45 kDa
CC α chain ~24 kDa

(57) Abrégé/Abstract:
The present invention relates to polypeptides with asparaginase activity, which have an increased self-processing rate in comparison to wild-type human L-asparaginase (ASRGL1), said polypeptides having a mutation in the glycine-rich loop of ASRGL1, denominated the HGG (Histidine 8-Glycine 9-Glycine 10) loop. Polynucleotides encoding the polypeptides of the invention, expression cassettes comprising said polynucleotides, expression vectors, host cells, pharmaceutical compositions, uses of the polypeptide of the invention in manufacturing a medication for preventing or treating cancer, and methods for producing the polypeptide of the invention and for preventing or treating cancer are also described herein.

ABSTRACT

The present invention refers to polypeptides with asparaginase activity that have an increased rate of self-processing compared to human wild L-asparaginase (ASRGL1), with mutation in the ASRGL1 glycine rich loop called HGG loop (Histidine 8-Glycine 9-Glycine 10). Polynucleotides that encode the polypeptides of invention are also described here, expression cassettes comprising so-called polynucleotides, expression vectors, host cells, pharmaceutical compositions, uses of the invention polypeptide in the manufacture of a preventive medicine or cancer treatment and methods to produce the polypeptide of invention and to prevent or treat cancer.

POLYPEPTIDE WITH ASPARAGINASE ACTIVITY, EXPRESSION CASSETTE, EXPRESSION VECTOR, HOST CELL, PHARMACEUTICAL COMPOSITION, METHODS FOR PRODUCING A POLYPEPTIDE WITH ASPARAGINASE ACTIVITY AND FOR PREVENTING OR TREATING CANCER, AND USE OF A POLYPEPTIDE

FIELD OF INVENTION

[001] This invention relates to the field of oncology and biotechnology. More specifically, this invention relates to polypeptides with asparaginase activity useful in the prevention and treatment of cancer.

BACKGROUND OF THE INVENTION

[002] Leukemia is a malignant disease characterized by the excessive and unregulated proliferation of abnormal cells in the bone marrow, which are cells carrying an accumulation of mutations that prevent them from completing their differentiation, replace normal hematopoietic cells. Among the main consequences of leukemia on an individual are increased risk for anemia and bleeding, and the increased susceptibility to contraction of infections. In addition, leukemic cells can invade several other tissues through the circulation. Without effective treatment, leukemia is lethal.

[003] According to clinical and pathological parameters, leukemia is subdivided in two manners. The first division is based on time of development and includes the acute and chronicle forms. The second is related to the type of cell affected. Lymphoid and myeloid leukemias are characterized by neoplastic changes in lymphoid and myeloid progenitor cells, respectively.

[004] The world scenario in 2012 showed that 2.5% of all types of cancer are leukemia, totaling approximately 352,000 new cases this year. With a high mortality rate, 265,000 deaths from leukemia were expected in the world that same year. In Brazil, an estimated 10,070 new cases out of all

types of leukemia were reported for the year 2016, with acute lymphoid leukemia (ALL) being the most common cancer in childhood. This disease corresponds to 30% of all malignant neoplasms in children aged 0 to 14 years. (AMERICAN CANCER SOCIETY, 2016).

[005] The current treatment of ALL is composed of three phases. The protocol describing the stages of treatment was developed by the European group Berlin-Frankfurt-Munich (BFM) and has been used by INCA's Hematology System since 1982 (INCA, 2001). This protocol is based on the stratification of patients according to the different risk groups of recurrence of the disease. Patients in the low-risk group are those aged between 1 and 10 incomplete years, with a leukocyte count of less than 50,000/• L blood. Chromosomal or genetic changes in lymphocytes, variation in cell count after treatment initiation, presence of leukemic cells in the cerebrospinal fluid and the origin of leukemic cells (whether T or B lymphocytes) are factors that can also affect the prognosis (US Cancer Institute), 2015). In addition, this protocol combines different chemotherapy drugs in order to reduce patient resistance.

[006] The first phase is called induction, lasts from one to three months, and aims to achieve remission, when the cell counts in the blood return to normal and no leukemic cells are found in the bone marrow. A chemotherapeutic, steroid and asparaginase enzyme are used for induction. The second phase is consolidation, where an attempt is made to completely eliminate the remaining leukemic cells by preventing them from becoming resistant. For this purpose several chemotherapeutic drugs are used and asparaginase. This is the most intense phase of the treatment, lasting two months. After the complete remission of the leukemic cells, the maintenance phase begins, which can last from two to three 5 years and makes use of chemotherapy and steroids. (INCA, 2001; MÖRICKE *et al.*, 2008; INSTITUTO ONCOGUIA, 2015).

[007] In the last 40 years there have been notable advances in the treatment of infant ALL, resulting in a survival rate of up to 90% for patients (AMERICAN CANCER SOCIETY, 2016). The introduction of asparaginase in the treatment at the end of the 1970s contributed to an increase of at least 15% in the survival rate. However, significant challenges remain, such as the development of therapeutic approaches with lower toxicity.

[008] The efficacy of the use of asparaginase enzyme in the treatment of ALL is based on the deficiency presented by most leukemic cells: absence or reduction of asparagine synthase protein expression. Asparagine synthase performs the conversion from aspartate to asparagine. Being unable to synthesize asparagine again, leukemic cells are dependent on circulating asparagine. Tumor cells, especially in ALL, require a large amount of asparagine to maintain their abnormal growth characteristic of these malignant diseases. For this reason, the use of asparaginase against ALL becomes advantageous. Intramuscular or intravenous injection of asparaginase causes rapid depletion of the amino acid in plasma, leading to a reduction in the metabolism of leukemic cells and ultimately to death by apoptosis, while normal cells maintain their functions by being able to synthesize asparagine. Thus, asparaginase has a selective effect on neoplastic cells, unlike a chemotherapeutic agent, for example, which affects the proliferation process of both cancerous and normal cells.

[009] Asparagine is a non-essential amino acid important for the growth and development of all cells both healthy and neoplastic. By acting on protein biosynthesis, its depletion harms cell proliferation (AVRAMIS, 2012). The reduction of the circulating concentration of asparagine from 50 • M to 3 • M or less during treatment with asparaginase (AVRAMIS, 2012) prevents leukemic cells from continuing the cell cycle by activating apoptosis signaling. This is in line with evidence that depletion of an amino acid can lead to the induction of apoptosis or autophagia (SONG *et al.*, 2015). In other

types of cancer (ovarian cancer, chronic myeloid leukemia, and pulmonary adenocarcinoma), asparaginase has been reported to induce not only apoptosis, but also autophagy, given that asparagine acts as a negative modulator of this process.

[0010] Despite its primary use in the treatment of ALL, asparaginase has therapeutic potential for use in other types of cancer, such as acute myeloid leukemia (WILLEMS *et al.*, 2013), ovarian cancer (LORENZI *et al.*, 2008; YU *et al.*, 2012; PURWAHA *et al.*, 2014), brain cancer, prostate cancer, pulmonary adenocarcinoma (ZHANG *et al.*, 2016), non-Hodgkin's lymphoma, chronic lymphoid leukemia, and sarcomas such as lymphosarcoma, reticulosarcoma and melanosarcoma.

[0011] Currently, three asparaginases are used in the therapy of ALL: the native L-asparaginase II of *Escherichia coli, a* PEGuilated form of this enzyme, and the isolated L-asparaginase of Erwinia *chrysanthemi.* The selection of asparaginase that will compose the chemotherapy regimen depends on the country in which the treatment is performed. The choice of enzyme version to be used prioritizes the reduction of side effects and maintaining the effectiveness of the treatment. In Brazil, *E. coli* L-asparaginase II is used as first choice (MÖRICKE *et al.*, *2008*; PIETERS *et al.*, 2011).

[0012] *E. coli* L-asparaginase II is the most toxic and immunogenic among the three available. Even in the last BFM protocol update there was a 50% reduction in the dose of this enzyme due to its side effects. After administration, E. coli L-asparaginase II is *soon* recognized by the cells of the immune system as it does not diffuse into extracellular space. Once the immune response is activated, the enzyme will have its action neutralized. In 60% of the patients a hypersensitivity reaction associated with the inactivation of the drug is generated. However, the antibodies produced against *E. coli* L-asparaginase II are not always accompanied by the characteristic symptoms of

a hypersensitivity reaction (anaphylaxis, edema, serum disease, bronchospasm, urticaria and rash, itching and swelling of the extremities, erythema), in approximately 30% of patients a silent inactivation occurs (PIETERS *et al.*, 2011; AVRAMIS, 2012).

[0013] PEGuilded enzyme and *E. chrysanthemi* isolate are indicated as substitutes in these cases of hypersensitivity and/or inactivation. PEG-asparaginase is relatively less immunogenic. However, its administration after treatment with the native enzyme may result in silent inactivation because of a cross-reaction with anti paraginase antibodies already present in the patient. *E. chrysanthemi* L-asparaginase largely solves the problem of hypersensitivity since the chances of developing antibodies against this enzyme are 12-20%. However, it has a shorter half-life and studies report a significantly higher number of patients who do not achieve complete remission of leukemic cells (PIETERS *et al.*, 2011; RYTTING, 2012; AVRAMIS, 2012).

[0014] In addition to the effects resulting from the arousal of the immune response, the administration of multiple doses of asparaginase can generate toxic effects. The high toxicity of bacterial asparaginases is related to their hydrolytic non-specificity, leading also to the depletion of glutamine, which is converted to glutamate and ammonia by these enzymes. This non-specific hydrolysis is related to most of the side effects, such as liver disease, acute pancreatitis, hyperglycemia, glucosuria, ketoacidosis, central nervous system disorders, hypoalbuminemia, hypofibrinonemia, hypercoagulation, among other dysfunctions. It has been described that glutamine deprivation can activate intracellular mechanisms that reach the mitochondria and activate the apoptosis pathways, but this does not alleviate the toxic effects generated by glutamine hydrolysis and may still induce growth factor expression (AVRAMIS, 2012).

[0015] In addition to selectively leading leukemic cells to death, asparaginase enhances the antileukemic effect of steroids by further

improving treatment outcomes. Therefore, research with asparaginase has sought the production of an enzyme with a high affinity for asparagine and a long half-life. These characteristics can be found in a human asparaginase enzyme, an alternative treatment option to bacterial asparaginases.

[0016] The inclusion of human L-asparaginase in the treatment of acute lymphoid leukemia could solve many of the problems faced with bacterial enzymes. However, it is a challenging solution because the human enzyme is only active after a self-binding stage, which presents a low in vitro efficiency, reducing its enzyme activity.

[0017] Studies on human-asparaginase (ASRGL1) have intensified in recent years due to the interest in its potential therapeutic use in some types of cancer, especially in ALL cases.

[0018] As a human protein, ASRGL1 can drastically reduce the immunogenicity of treatment; it meets the requirement of high thermal stability essential for drugs; it has a high affinity for asparagine and does not yet have glutaminase activity, ASRGL1 is unable to hydrolyze glutamine, its specificity being asparagine greater than other substrates (CANTOR *et al.* , 2009).

[0019] The great challenge regarding the use of ASRGL1 in the therapeutic protocol of ALL lies in its enzymatic activity. The clinical prerequisite for the KM of an asparaginase protein is a low value in the micromolar order, while bacterial asparaginases fulfill this requirement, *in vitro*, hASRGL1 has a KM in the order of millimolar. The bacterial asparaginases used to treat ALL are from a different subfamily than human protein; while ASRGL1 belongs to the subfamily of the plant-type L-asparaginases, the bacterial ones belong to the bacterial-type, which do not have the need to undergo self-processing to become active (CANTOR *et al.*, 2009).

[0020] As self-processing is a crucial event for enzyme activity and it

has been demonstrated that kinetic activity is proportional to the self-processing rate, the low enzyme activity of ASGRL1 is understood to be due to the autocatalysis mechanism. Advances in genetic engineering have allowed various modifications to be made in order to increase the efficiency of in vitro self-processing, but without yet achieving success.

[0021] The auto cleavage mechanism starts with a proton acceptor solution from the T168 hydroxyl group. After deprotonation, T168 (with increased nucleophilic character) attacks the carbonyl group of G167 forming a covalent bond that will be hydrolyzed. The complete cleavage between the two residues leaves the amino grouping of T168 free to catalyze the hydrolysis of asparagine (SU *et al.* , *2013).* It is observed that the essential residue T168 of ASRGL1 plays a double role: first, its lateral chain is necessary for the autocleavage reaction. Secondly, with the breakdown of the peptide bond between G167 and T168, the T168-free amino group participates in the catalysis of asparagine hydrolysis.

[0022] Understanding the exact mechanism of ASRGL1 self-processing is essential to achieve a solution for low in vitro activity on the substrate. However, biochemical, and structural studies of the human enzyme have proven challenging, since the recombinant proteins generated for study are a mixture of the unprocessed (inactive) states and processed (active). Thus, the low activation rate (only 50% self-processing is achieved with the wild enzyme) makes both structural and enzymatic characterization difficult (CANTOR *et al.* , 2009; LI *et al.* , 2012).

[0023] In inactive protein, the distance between T168 hydroxyl and G167 carbonyl is 4.0 Å, which does not favor the chemical events necessary for self-processing, showing the need for a conformational change to cleavage (NOMME *et al.* , 2012). The inactivation of self-processing through the T168A mutation has caused a large increase in the thermal stability of the mutant protein (• TM=10°C)...giving evidence of a steric voltage activation

mechanism. This tension is due to the orientation of T168 in inactive protein. The electrons in your methyl grouping are very close to the hydroxyl of this residue, creating repulsive forces and unfavorable interactions. The self-processing causes a relaxation in the T168 lateral chain, bringing the T168 hydroxyl closer to the active site, since the distance between this hydroxyl and the amino grouping of T168 is reasonable 2.7 Å (LI *et al.*, 2012).

[0024] The conformational change in the auto cleavage region can be facilitated by glycine 9 (G9) (NOMME *et al.* , *2012).* The comparison between ASRGL1 structures before and after processing indicates a 180º rotation of the G9 carboxyl group (Figure 1.10 B). This change in G9 conformation was also observed in the enzyme asparaginase type III of guinea pig 47 and can promote the repositioning of G167 (NOMME *et al.* , 2012) in order to bring it closer to T168 and encourage auto cleavage (NOMME *et al.* , 2012; LI *et al.* , 2012).

[0025] G9 is part of a glycine rich loop called the HGG loop (Histidine 8-Glycine 9-Glycine 10). This loop is strongly conserved (~100%) throughout the phylogeny of L-asparaginases plant-type (*LI),* 2012).

[0026] LI *et al.* , 2012 analyzed mutations in ASRGL1 HGG loop residues, particularly glycine 9 (G9) and glycine 10 (G10), to alanine, which resulted in reduced auto-processing rate (6 and 30 times, respectively) and kinetic activity (14 and 50 times, respectively).

[0027] LI *et al.* , 2016 also evaluated variants of ASRGL1 with mutations in asparagine residues (N62), threonine 186 (T186) and threonine 219 (T219) for the auto-processing rate and to catalytic activity compared to wild ASRGL1. In Nomme *et al.* , 2016, mutations in the ASRGL1 threonine 168 (T168) and threonine 219 (T219) waste were also studied with respect to the auto-processing rate and to catalytic activity compared to wild ASRGL1. Although some of these variants showed an increase in catalytic activity, none of the mutations performed resulted in an increase in the self-processing rate,

[0028] All the mutations generated in different waste so far have helped to understand the mechanistic bases of ASRGL1 operation, but all have failed to increase their auto-processing rate and its hydrolytic activity on asparagine.

[0029] In this context, the present invention describes polypeptides with asparaginase activity, variants of the human L-asparaginase enzyme, useful in the treatment of cancer, which have lower side effects due to their low toxicity and immunogenicity compared to bacterial enzymes used therapeutically. These and other advantages of invention, as well as the additional inventive features joined to the same inventive concept, will be evident in the description of the invention provided in this document.

SUMMARY OF THE INVENTION

[0030] This invention aims to provide a polypeptide with asparaginase activity that solves the main state of the art problems listed above.

[0031] In a first aspect, the present invention provides a polypeptide with asparaginase activity selected from the group consisting of:

(i) a polypeptide that has an increased rate of auto-processing compared to human L-asparaginase in the wild presented in SEQ ID NO: 1;

(ii) a polypeptide comprising the amino acid sequence having at least 90% identity with the sequences of any of the SEQ ID Nos: 3-5;

(iii) a polypeptide in which the amino acid glycine at position 10 of the SEQ ID NO: 1 is replaced by an amino acid selected from the group consisting of glutamic acid, aspartic acid and histidine;

(iv) a polypeptide comprising the amino acid sequence presented in SEQ ID NO: 3-5; e

(v) a polypeptide of (i) to (iv) comprising one or more conservative amino acid substitutions.

[0032] In a second aspect, this invention provides a polynucleotide

that encodes a polypeptide with asparaginase activity as above defined.

[0033] In a third aspect, this invention provides an expression cassette comprising a polynucleotide as defined above operationally linked to a promoter and to a transcription terminator.

[0034] In a fourth aspect, an expression vector comprising a polynucleotide, or an expression cassette as defined above is also provided.

[0035] In a fifth aspect, the present invention provides a host cell comprising an expression cassette or an expression vector as defined above.

[0036] In a sixth aspect, a pharmaceutical composition is provided which comprises a polypeptide of the invention and a pharmaceutically acceptable carrier or excipient.

[0037] In a seventh aspect, the use of the invention polypeptide is provided in the manufacture of a medicine for cancer prevention or treatment.

[0038] In an eighth aspect, this invention provides a method for producing a polypeptide with asparaginase activity, comprising the steps of: (a) providing a transformed host cell; (b) cultivating that cell under conditions conducive to polypeptide production; and (c) isolating that polypeptide from that cell or the surrounding culture medium.

[0039] In a ninth aspect, a method is provided to prevent or treat cancer, including administering a therapeutically effective amount of the polypeptide with asparaginase activity to an individual in need of such prevention, or treatment.

BRIEF DESCRIPTION OF THE FIGURES

[0040] Figure 1 shows a *Western Blot* assay of ASRGL1 and ASRGL1_G10E purified by affinity chromatography [M - Molecular weight marker (110, 48 and 25 kDa); 1 - *Flow through*; 2 - Elution with 50 mM imidazole; 3 - Elution with 100 mM imidazole; 4 - Elution with 500 mM imidazole; 5 - Nickel resin].

[0041] Figure 2 shows a structural analysis and electrophoretic profile

of ASRGL1 dimers in different cleavage states.

[0042] Figure 3 shows the molecular weight patterns used for the agarose gel electrophoresis test.

[0043] Figure 4 shows the electrophoretic profile of the PCR products of ASRGL1 and ASRGL1_G10E sequences.

[0044] Figure 5 shows the electrophoretic profile of the analytical digestion after cloning of ASRGL1 and ASRGL1_G10E PCR products in pGEM-T Easy.

[0045] Figure 6 shows the electrophoretic profile of the analytical digestion after subcloning in pET28a-TEV expression vector.

DEFINITIONS

[0046] To ensure a better understanding of the scope of the invention, without being a limiting factor, the technical terms of the related areas of technology as used in the present invention, are defined below.

[0047] "Comprising" or variations such as "comprise", "that comprises" or "comprised of" are used throughout the specification and claims in an inclusive sense, i.e., to specify the presence of the determined resources, but not to exclude the presence or addition of additional resources that may materially improve the operation or the usefulness of any of the terms of the invention unless the context requires otherwise due to the of the language of expression or implication required.

[0048] "consists essentially of" and variations such as "consist essentially of" or "consisting essentially of", as used throughout the specification, and claims, indicate the inclusion of any elements or group of elements referred and the optional inclusion of other elements, of a similar or different nature to the elements referred, that do not materially alter the basic or innovative properties of the material claimed.

[0049] The terms "nucleic acid" and "polynucleotide" are used interchangeably, and refer to RNA and DNA. Polynucleotides can be single

or double tape. Non-limiting examples of polynucleotides include genes, gene fragments, exons, introns, messenger RNA, siRNA, miRNA, complementary DNA, genomic DNA, synthetic DNA, recombinant DNA, cassettes, vectors, probes and initiators. The term "recombinant DNA" refers to any artificial nucleotide sequence that results from the combination of DNA sequences of different origins.

[0050] The term 'degenerated nucleotide sequence' denotes a nucleotide sequence comprising one or more degenerated codons when compared with a reference nucleic acid molecule encoding a given polypeptide. Degenerated codons contain different nucleotide triplets, but encode the same amino acid residue (e.g., GAU and GAC both encode Asp).

[0051] The term "therapeutically effective amount" refers to an amount of protein or polypeptide that provides activity against cancer, when given in accordance with the dose and via appropriate administration.

[0052] The term 'pharmaceutically acceptable carriers or excipients' refers to ingredients that are compatible with other ingredients contained in pharmaceutical preparations and which have no therapeutic effect and are not harmful to humans or animals.

[0053] "Chemotherapeutic agent" is a chemical compound useful in cancer treatment. The classes of chemotherapeutic agents include, but are not limited to: alkylating agents, antimetabolites, kinase inhibitors, antifuse poison plant alkaloids, cytoxic / antitumor antibiotics, topoisomerase inhibitors, photosensitizers, antiestrogens and selective estrogen receptor modulators (SERMs), antiprogesterones, estrogen receptor descending regulators (ERDs), estrogen receptor antagonists, luteinizing hormone release agonists, antiandrogens, aromatase inhibitors, EGFR inhibitors, inhibitors of VEGF, antisense oligonucleotides that inhibit the expression of genes involved in abnormal cell proliferation or tumor growth. Chemotherapeutic agents useful in the treatment methods of this invention include cytostatic

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and/or cytotoxic agents.

[0054] The term “individual” refers to human beings and animals. Preferably the individual is a human being.

[0055] The term ‘identity’ is defined as the degree of equality between DNA or amino acid sequences when nucleotide by nucleotide or amino acid by amino acid is compared with a reference sequence.

[0056] The term “percentage of sequence identity” refers to comparisons between polynucleotides or polypeptides and is determined by two ideally aligned sequences, under certain comparison parameters. This alignment can comprise *gaps* (spaces), generating intervals when compared to the reference sequence, that facilitate a proper comparison of them. In general, the calculation of the percentage of identity takes into account the number of positions where the same nucleotide or amino acid occurs in the sequences compared to the reference sequence and is performed through several algorithms for comparing sequences and programs known in the state of the art. Such algorithms and programs include, but are not limited to, TBLASTN, BLASTP, FASTA, TFASTA, CLUSTALW, FASTDB.

[0057] The term “Polymerase Chain Reaction” or PCR refers to a method in which a nucleic acid fragment is amplified as described in US Patent 4,683,195. Generally, the information contained at the 5’ and 3’ ends of the sequence of interest is used for the design of the initiating oligonucleotides or primers they cover, around 8 synthetic nucleotides. These primers have sequences complementary to the sequence to be amplified. PCR can be used to amplify RNA sequences, DNA or cDNA.

[0058] An “expression cassette” refers to a nucleic acid construction comprising a coding region and a regulatory region, operationally linked, when introduced into a host cell, results in the transcription and/or translation of an RNA or polypeptide, respectively. Generally, an expression cassette is made up or understood by a promoter that allows the transcription to begin, a

nucleic acid according to the invention, and transcription terminator. The expression "operationally linked" indicates that the elements are combined in such a way that the coding sequence expression is under the control of the transcriptional promoter and/or signal peptide. Typically, the promoter sequence is placed upstream of the gene of interest, at a distance from the gene of interest compatible with the control of the expression. Similarly, the signal peptide sequence is usually merged upstream of the gene sequence of interest, and in phase with this, and downstream of any promoter. Spacing sequences may be present between the regulatory elements and the gene as they do not prevent expression and/or sorting. In a performance mode, the said expression cassette comprises at least one activation sequence "enhancer" *linked* operationally to the promoter.

[0059] The term "vector" refers to nucleic acid molecules designed to transport, transfer and/or store genetic material, as well as express and/or integrate genetic material into the host cell's chromosomal DNA, such as plasmids, cosmids, artificial chromosomes, bacteriophages and other viruses. The vector usually consists of at least three basic units, the source of replication, a selection marker and the multiple cloning site.

[0060] The vectors used in this invention preferably have at least one "selection marker", which is a genetic element that allows the selection of genetically modified organisms/cells. These markers include antibiotic resistance genes such as, but not limited to ampicillin, chloramphenicol, tetracycline, kanamycin, hygromycin, bleomycin, phleomycin, puremycin and/or phenotype complementation genes, such as but not limited to methotrexate, dihydrofolate reductase, ampicillin, neomycin, mycophenolic acid, glutamine synthetase.

[0061] The term "expression vector" refers to any vector that is capable of transporting, transferring, and/or storing genetic material, and that once in the host cell, is used as a source of genetic information for the

production of one or more gene products (gene expression).

[0062] In addition, the expression vectors of this invention may include one or more regulatory nucleotide sequences to control gene replication, transfer, transport, storage and expression of genetic material, such as origin of replication, selection marker, multiple cloning site , promoter (for example, T7 pol, pL and pR lambda phage, SV40, CMV, HSV tk, pgk, T4 pol, or EF-1 alpha and its derivatives), ribosome binding site, RNA splice site, site polyadenylation, signal peptide for secretion and gene transcription termination sequence. However, the vectors of expression of this invention are not limited thereby. The technique of incorporating the control sequences into a vector is well characterized in the state of the art.

[0063] The vector of expression used in this invention may also have "enhancer" sequences, also *called* "cis" elements which can influence positively or negatively the promoter-dependent gene expression.

[0064] A "coding sequence" refers to a nucleotide sequence that is transcribed into mRNA (messenger RNA) and translated into a polypeptide when under the control of appropriate regulatory sequences. The limits of the encoding sequence are determined by a translation initiation codon at the 5'-end of the DNA sense tape and by a translation termination codon at the 3' end of the DNA sense tape. As a result of genetic code degeneration, different DNA sequences can encode the same polypeptide sequence. Therefore, such degenerated substitutions in the coding region are considered to be inserted in the sequences described in this invention.

[0065] The term "promoter" is a minimum sequence of DNA sufficient to direct the gene transcription, i.e., a sequence that directs the binding of the RNA polymerase enzyme thus promoting messenger RNA synthesis. Promoters can be specific to the cell type, type of tissue and species, and in certain cases are modulated by regulatory elements in response to some external physical or chemical agent called inductor.

[0066] The terms “transformation” and “transfection” refer to the act of inserting a vector or other carrier vehicle of exogenous genetic material into a host cell, prokaryotic or eukaryotic, for transport, transfer, storage and/or genetic expression of genetic material of interest.

[0067] The term “recombinant expression” refers to the expression of recombinant polypeptide in host cells.

[0068] The term “host cell” refers to the cell that will receive the genetic material through a vector and/or cells that have already received the genetic material through a vector (transformed cells or transfected). These host cells can be either of prokaryotic (prokaryotic microorganisms) or eukaryotic (eukaryotic cells or microorganisms) origin.

[0069] In this application, the terms ‘peptide’, ‘polypeptide’ or ‘protein’ may be used interchangeably, and refer to an amino acid polymer connected by peptidic bonds, regardless of the number of amino acid residues that make up this chain. Polypeptides, as used here, include “variants” or “derivatives” of them, which refer to a polypeptide that includes variations or modifications, e.g. substitution, deletion, addition, or chemical modification in its amino acid sequence in relation to the reference polypeptide, provided the derived polypeptide has immunosuppressive activity, stability, midlife, pharmacokinetic characteristics, and/or physico-chemical characteristics equal or higher than initially observed for the original polypeptide. Examples of chemical modifications are glycosylation, PEGlation, PEG alkylation, alkylation, phosphorylation, acetylation, amidation, etc. The amino acids in the polypeptides of the invention, depending on the orientation of the amino group of the carbon alpha atom may belong to the L series or D. Polypeptide may be artificially produced from cloned nucleotide sequences using the recombinant DNA technique (“recombinant polypeptide”) or can be prepared by a known chemical synthesis reaction (“synthetic polypeptide”).

[0070] The term “amino acid substitutions” refers to the substitution

of at least one polypeptide amino acid residue for the production of derivatives with asparaginase activity, stability, midlife, pharmacokinetic characteristics, and/or physico-chemical characteristics equal to or better than those initially observed for the original polypeptides. Replacement amino acids can be natural, modified, or unusual.

[0071] In this respect, the term ‘conservative replacement of amino acids’ refers to the replacement of amino acids in a polypeptide by those with similar side chains and, therefore, with remarkably close physical and chemical properties. For example, exchanging an alanine for a valine or leucine or isoleucine is considered conservative, since the amino acids involved have as a common characteristic an aliphatic lateral chain. The group containing as a characteristic a basic side chain is composed of lysine, arginine and histidine. The group containing sulfur in the lateral chain comprises the amino acids cysteine and methionine. The amino acids phenylalanine, tyrosine and tryptophan contain an aromatic side chain. Asparagine and glutamine are part of the side-chain amino acids containing amide, while serine and threonine contain a hydroxyl bound to their aliphatic sidechain. Other examples of conservative replacement include replacement of an apolar amino acid or hydrophobic like isoleucine, valine, leucine, or methionine for another, also apolar. Similarly, the invention described here contemplates the substitution of polar amino acids or hydrophilics such as arginine per lysine, glutamine per asparagine and threonine per serine. Additionally, substitution between basic amino acids such as lysine, arginine or histidine or the substitution between amino acids of acid character such as aspartic acid or glutamic acid is also contemplated. Examples of conservative replacement of amino acids are: valine by leucine or isoleucine, phenylalanine by tyrosine, lysine by arginine, alanine by valine and asparagine by glutamine.

[0072] In addition, illustrative examples of modified or unusual amino

acids include 2-Aminoadipic acid, 3-Aminoadipic acid, beta-alanine, 2-Aminobutyric acid, 4-aminobutyric acid, 6-aminocaproic acid, 2aminoheptanic acid, 2aminoisobutyric acid, 3aminoisobutyric acid, 2aminoheptanic acid, 2aminopimelic acid, 2,4-diaminobutyric, desmosin, 2,2'-diaminopimelic acid, 2,3-diaminopropionic acid, N-ethylglycine, N-ethylasparagine, hydroxylisin, alohydroxylisin, 3-hydroxyproline, 4-hydroxyproline, isodesmosin, aloisoleucine, N-methyl glycine, N-methyl isoleucine, 6-N-methyllysine, N-methyl valine, norvaline, norleucine, ornithine, etc.

[0073] The objects of this invention will be better understood from the detailed description of the invention and the attached claims.

DETAILED DESCRIPTION OF THE INVENTION

[0074] Unless they are defined differently, all the technical and scientific terms used here have the same meaning understood by a technician on the subject to which the invention belongs. The terminology used in the description of the invention is intended to describe particular achievements only, and has no intention of limiting the scope of the teachings. Unless otherwise stated, all figures expressing quantities, percentages and proportions, and other numerical values used in the specification and the claims should be understood as being modified in all cases by the term "approximately". Thus, unless otherwise stated, the numerical parameters shown in the specification and the claims are approximations that may vary, depending on the properties to be obtained.

[0075] The present inventors solved the problem of the state of the art by providing polypeptides with asparaginase activity by modifying human L-asparaginase (SEQ ID NO:1), having in its sequence a proton acceptor in the position occupied by free glycine in the wild protein and, consequently, with an improved self-processing mechanism.

[0076] The auto cleavage mechanism starts with a proton acceptor

solution from the T168 hydroxyl group. After deprotonation, T168 (with increased nucleophilic character) attacks the carbonyl group of G167 forming a covalent bond that will be hydrolyzed. The complete cleavage between the two residues leaves the amino grouping of T168 free to catalyze the hydrolysis of asparagine.

[0077] It is observed that the essential residue T168 of ASRGL1 plays a double role: first, its lateral chain is necessary for the autocleavage reaction and second, with the rupture of the peptide bond between G167 and T168, the T168-free amino group participates in the catalysis of asparagine hydrolysis.

[0078] In inactive protein, the distance between T168 hydroxyl and G167 carbonyl is 4.0 Å, which does not favor the chemical events necessary for self-processing, showing the need for a conformational shift to cleavage. The self-processing causes a relaxation in the T168 lateral chain, bringing the T168 hydroxyl closer to the active site, since the distance between this hydroxyl and the amino group of T168 is reasonable 2,7 Å.

[0079] The proximity of glycine to the T168 hydroxyl grouping provides its operation as an extrinsic self-processing primer. An intrinsic initiator would be advantageous for activating this process since the translation of the protein. In this context, the inventors of the present invention introduced a proton acceptor in the position occupied by free glycine and thus improved the in vitro self-processing mechanism.

[0080] Although free glycine acts satisfactorily as a proton acceptor, the same is not true for glycine included in a protein structure. In a protein, its amino and carboxyl groups form the peptide bond and are not free to act in the sense of protons. Moreover, its lateral chain formed only by hydrogen does not perform this function.

[0081] Since blood pH is 7.4, glutamic acid, aspartic acid and histidine could act as a proton acceptor in the blood. These amino acids have in common the pKa of the lateral chain lower than blood pH, so under these

conditions there is a predominance of COO- radicals over COOH.

[0082] The conformational change in the auto cleavage region can be facilitated by glycine 9 (G9). G9 is part of a glycine rich loop called the HGG loop (Histidine 8-Glycine 9-Glycine 10). This loop is strongly conserved (~100%) throughout the phylogeny of L-asparaginases plant-type.

[0083] In the inactive protein structure, the position of G10 carbonyl favors hydrogen binding between G11 and T219 and blocks the HGG loop in a closed conformation. In addition, the close proximity (1.6 Å) between G9 of the HGG and L166 loop contributes to the closed conformation. In contrast, in the active enzyme, the rotation of G9 modifies the position of the G10 carbonyl resulting in the position change of the HGG loop.

[0084] Given the flexibility of the HGG loop and its importance for activating self-processing, this region was considered for mutation purposes aimed at improvement of the self-processing mechanism.

[0085] Through in silico modifications *to* ASRGL1 structures the inventors observed that a mutation in G10 to an amino acid working as a proton acceptor could place the carboxyl of the lateral chain near the active site, in a position similar to free glycine which optimizes the self-processing reaction.

[0086] The studies showed that the mutated protein had a higher proportion of auto-processing compared to the wild protein. The proposed changes in the present invention have been able to raise the rates of self-processing and of human L-asparaginase enzyme activity, achieving the goal of improving autocleavage and hydrolysis reactions, as demonstrated by the examples presented here.

[0087] In a first aspect, the present invention provides a polypeptide with selected asparaginase activity from the group consisting of:

(i) a polypeptide that has an increased rate of auto-processing compared to human L-asparaginase in the wild presented in SEQ ID NO: 1;

(ii) a polypeptide comprising the amino acid sequence having at least 90% identity with the sequences of any of the SEQ ID NOs: 3-5;

(iii) a polypeptide in which the amino acid glycine at position 10 of the SEQ ID NO: 1 is replaced by an amino acid selected from the group consisting of glutamic acid, aspartic acid and histidine;

(iv) a polypeptide comprising the amino acid sequence presented in any of the SEQ ID NO: 3-5; e

(v) a polypeptide of (i) to (iv) comprising one or more conservative amino acid substitutions.

[0088] In one respect, the polypeptides of this invention are at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% identical to the SEQ ID NOs amino acid sequences: 3-5.

[0089] In an embodiment, the polypeptide of invention comprises the amino acid sequence of any of the SEQ ID NO:3-5, where the amino acid glycine at position 10 of SEQ ID NO: 1 is replaced by glutamic acid, aspartic acid and histidine respectively.

[0090] In a preferred embodiment, the polypeptide of invention comprises the amino acid sequence of SEQ ID NO:3, where the amino acid glycine in heading 10 of SEQ ID NO: 1 is replaced by glutamic acid (G10E mutation).

[0091] The induction of the recombinant expression of ASRGL1 (SEQ ID NO: 1) and ASRGL1_G10E (SEQ ID NO: 3) in *E. coli* allowed the production of a greater amount of protein for self-processing analysis. A band of ~38 kDa, indicated in Figure 1 corresponds to the unprocessed protein and the band of ~24 kDa corresponds to the chain •. The • chain is not visualized, as the histidine tail is in the N-terminal portion of the protein. Besides the 38 kDa and 24 kDa bands, a third band of ~45 kDa was observed.

[0092] The ~45 kDa band is believed to correspond to a chain dimer •

connected by a disulphide bridge (SS bridge). This is based on the state of the art reports (Li *et al.* (2016)), in its size corresponding to twice the size of the chain • and also based on the existence of three cysteines in this chain that could form disulphide bridges (Figure 2a). It is known that because it is a strong covalent bond, the reducing agents of the electrophoresis sample buffer are often not efficient enough in breaking this strong interaction and so you can see a band on the gel corresponding to dimers with disulphide bridge. If this dimerized fraction were not processed we would have a band of approximately 75 kDa, however, as only a migration of 45 kDa can be seen, it is concluded that this is the processed state with disulphide bridge (Figure 2b).

[0093] In Figure 2a, the cartoon representation *of* processed and unprocessed ASRGL1 *dimers*. Chain • in beige, chain • in green, cysteines in colored spheres according to the atom where C- gray, N- blue, O- red and S- yellow. The oval circle in red describes the most likely region of disulphide bridge formation between the monomers.

[0094] Figure 2b shows the theoretical electrophoretic profile of dimers in different processing situations, where: 1- dimers connected by a disulphide bond composed of two cleaved monomers (45 kDa band - chain • with SS bridge, 15 kDa band - chain •), 2-dimers not connected by disulphide link composed of two cleaved monomers (24 kDa band - chain •, 15 kDa band - • chain), 3-dimers connected by disulphide bond composed of two unbonded monomers (75 kDa band corresponding to 38 kDa continuous protein connected by disulphide bridge), 4- inactive dimerized sample without disulphide bridge (35 kDa band corresponding to continuous polypeptide chain), 5- dimer connected by partially cleaved disulphide bond (only one monomer is cleaved, 65 kDa band corresponding to two chains • and one • and 15 kDa band corresponding to chain •), 6- dimers not connected by a partially cleaved disulphide link (only one monomer is cleaved, 38 kDa band

corresponding to unglued protein, 24 kDa band corresponding to chain • and 15 kDa band corresponding to chain • of the cleaved monomer).

[0095] From the analysis of the content of each state, it was concluded that the mutated protein showed a higher proportion of auto-processing compared to the wild protein. In addition, the G10E mutation favored the formation of the 45 kDa intermediary.

[0096] The fractions of ASRGL1 (SEQ ID NO: 1) and ASRGL1_G10E (SEQ ID NO: 3) presented different *kcat* values, as it was already expected since different states of intramolecular self-processing were found.

[0097] Considering that *kcat* is the maximum number of mols of substrate that can be converted into a product per mole of enzyme in a given unit of time, it was observed that ASRGL1_active showed the highest enzymatic efficiency among the three states of wild asparaginase, aSRGL1_intiva_a and ASRGL1_intiva_b had similar *kcat* values (see Example 5).

[0098] The mutation proposed by this invention is the first modification of ASRGL1 capable of increasing the rates of both self-processing and enzymatic activity. The two fractions of ASRGL1_G10E had the highest kcat values. A replacement G9A presented *kcat* 0,0126 s-1 and G10A *kcat* 0,0053 s-1.

[0099] The G10E mutation achieved the objective of improving in vitro autocleavage and hydrolysis reactions on asparagine, but further studies are still necessary in order to completely clarify the mechanism by which this mutation promoted such an effect.

[00100] In one embodiment, the polypeptide of invention is for use in cancer prevention or treatment. In a preferred embodiment, cancer is selected from acute myeloid leukemia (ALL)chronic lymphoid leukemia, ovarian cancer, brain cancer, prostate cancer, pulmonary adenocarcinoma, non-

Hodgkin's lymphoma and sarcoma (lymphosarcoma, reticulosarcoma and melanosarcoma). In a more preferred embodiment, cancer is acute myeloid leukemia (AMI).

[00101] In a second aspect, the present invention provides polynucleotides that encode the polypeptides described here.

[00102] Polynucleotides according to the invention comprise the nucleic acid sequences of any of the SEQ ID NO: 6-8 and their degenerations.

[00103] A technician in the field would recognize that degenerations are fully supported on the basis of the information provided in the application and the common knowledge of the state of the art. For example, the degeneration of the genetic code (i.e. different codons can encode the same amino acids) is a common knowledge in the technique and the identity of the amino acid encoded by each codon is well established.

[00104] On the basis of the information well known and established in the state of the art, the technician in the subject is able to identify nucleotide substitutions that do not alter the resulting amino acid sequence. For example, if a nucleotide sequence contains the CTA codon that encodes for a leucine, a technician in the field would understand that replacing the "A" with any other nucleotide (i.e, T, C or G) would still result in a codon coding for leucine. Thus, when in possession of both the nucleotide sequence of a gene and the amino acid sequence of the encoded protein, the technician in the subject will easily identify the degenerations that encode the same protein, with the same sequence of amino acids.

[00105] The use of the preferred codons can be adapted according to the host cell in which the nucleic acid is to be transcribed. These steps can be carried out according to methods well known to the versed in the technique and of which some are described in the reference manual Sambrook *et al.* (Sambrook *et al*, 2001).

[00106] In this sense, different species can display a preferential

"codon usage". See Grantham *et al.*, *Nuc. Acids Res.* 8:1893 (1980), Haas *et al. Curr. Biol.* 6:315 (1996), Wain-Hobson *et al.*, *Gene* 13:355 (1981), Grosjean and Fiers, *Gene* 18:199 (1982), Holm, *Nuc. Acids Res.* 14:3075 (1986), Ikemura, *J. Mol. Biol.* 158:573 (1982), Sharp and Matassi, *Curr. Opinion. Genet. Dev.* 4:851 (1994), Kane, *Curr. Opinion. Biotechnol.* 6:494 (1995), and Makrides, *Microbiol. Rev.* 60:512 (1996). As used here, the term "códon usage preferencial", or "preferential codons" is a term used in the art referring to codons that are most often used in cells of certain species. For example, the amino acid threonine (Thr) can be encoded by ACA, ACC, ACG, or ACT, but in mammalian cells, ACC is the most commonly used codon. In other species, for example, different Thr codons may be preferred. Preferred codons for a particular species can be introduced into the polynucleotides of this invention by a variety of methods known in the art. The introduction of preferential codon sequences into a recombinant DNA can, for example, to increase polypeptide production by making translation more efficient in a given cell type. Thus, the polynucleotide sequences of the invention can be optimized for different species.

[00107] The polynucleotides of this invention are obtained by methods already known in the state of the art, such as those described by Sambrook *et al.* (2001). For example, additional sequences can be identified and functionally noted by comparing sequences. Therefore, a technician in the field can readily identify a sequence functionally equivalent to the polynucleotides of the present invention in a suitable database as, for example, GenBank, using publicly available sequence and parameter analysis programs.

[00108] In another example, polynucleotides from the invention can be obtained through a reverse transcription reaction followed by PCR amplification. Both oligo-dT and randomic initiators can be used in the reverse transcription reaction to prepare single tape cDNAs, from the isolated

RNA of the *L. muta* snake, which contain the sequences of interest. RNA can be isolated by methods known as the use of Trizol reagent (GIBCO-BRL/Life Technologies), Gaithersburg, Maryland).

[00109] Gobinda *et al.* (PCR Methods Applic. 2:318-22, 1993), describes "restriction-site PCR" as a direct method using universal primers to obtain unknown sequences adjacent to a known locus. First, the genomic DNA is amplified in the presence of an adaptor-initiator, *which is homologous* to an adaptor sequence attached to the ends of the genomic DNA fragments, and in the presence of a specific *initiator* for a known region. The amplified sequences undergo a second round of PCR with the same adapter-initiator *and* another specific initiator, internal to the first. Products from each PCR round are transcribed with a suitable RNA polymerase and sequenced using a reverse transcriptase.

[00110] Still in an illustrative way, the inverse PCR allows the obtaining of unknown sequences starting with primers based on a known region (Triglia, T. *et al.*, Nucleic Acids *Res* 16:8186, 1988). The method uses several restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular connection and used as a mold for PCR. Divergent initiators are drawn from the known region.

[00111] In addition, it is known that sequences with reduced degrees of identity can also be obtained with the aid of degenerate primers and PCR-based methodologies.

[00112] Typically, the nucleic acid sequence of a primer useful for amplifying nucleic acid molecules by PCR can be based on the amino acid sequences of the polypeptides of the invention represented, for example, by the SEQ ID NOs: 3 a 5. In this invention, the initiating oligonucleotides used for the amplifications of genes coding for human wild L-asparaginase (ASRGL1) and mutated human L-asparaginase (ASRGL1_G10E; SEQ ID

NO: 3) are represented by SEQ ID NOs: 9-11.

[00113] In a third aspect, the present invention provides an expression cassette comprising a polynucleotide according to the invention operationally linked to the sequences necessary for its expression. Typically, coding and regulatory regions are heterologous with each other.

[00114] In a fourth aspect of this invention, this invention provides an expression vector comprising a polynucleotide or an expression cassette according to the invention. This expression vector can be used to transform a host cell and allow the expression of nucleic acid according to the invention in the cell.

[00115] With advantage, the expression vector comprises regulatory elements that allow the expression of nucleic acid and elements that allow its selection in the host cell according to the invention. The methods for selecting these elements according to the host cell in which the expression is desired, are well known of the versed in the technique and widely described in literature.

[00116] Vectors can be constructed by classical molecular biology techniques, well known from the versed in the technique. Non-limiting examples of expression vectors suitable for expression in host cells are plasmids and viral or bacterial vectors.

[00117] In a fifth aspect of this invention, this invention provides a polynucleotide, expression cassette or expression vector according to the invention to transform or transfect a cell. The host cell may be transformed/transferred in a transient or stable manner and the nucleic acid, cassette or vector may be contained in the cell in the form of an episome or in chromosomal form.

[00118] The polynucleotide, expression cassette or vector is inserted into competent prokaryotic or eukaryotic host cells. The recombinant clones are selected and then submitted to analysis by restriction enzymes and DNA

sequencing, allowing the confirmation of the cloned sequence, using methods, kits and equipment widely known by a technician on the subject.

[00119] Thus, the polypeptides of invention can be prepared using recombinant DNA technology, in which a cassette or expression vector comprising a polynucleotide sequence of invention, for example, which encodes any of the SEQ ID Nos polypeptides: 3 to 5, is operationally linked to a promoter. The host cells are cultivated under appropriate conditions and the polypeptide is expressed. The host cell can be a cell of bacteria, fungus, plant or animal. The polypeptide is recovered from the culture, where the recovery may include a purification step of the polypeptide. The recombinant polypeptide obtained is analyzed and treated in order to solubilize it, when appropriate. The solubilized polypeptide is then purified and biochemically characterized using, for example, methods common to the field of biochemistry, such as HPLC, SDS-PAGE, *Western Blotting*, isoelectric focusing with pH gradient, circular dichroism. Using these methods, you can determine characteristics such as the yield of recombinant polypeptide expression; the determination of the characteristics of secondary structures, in addition to other characteristics whose determination is important for the development of a biotechnological drug.

[00120] Polypeptides can be expressed “fused” to a label. The term “tag” or the English term “tag” refers to embedded encoding sequences near the multiple cloning site of an expression vector, enabling its translation concomitant and adjacent to the sequence of the cloned recombinant polypeptide. Thus, the label is expressed fused to the recombinant polypeptide. Such labels are well known in the state of the art and include compounds and peptides such as polyhistidine, polyarginine, FLAG, glutathione S-transferase, maltose binding protein (MBP), cellulose binding domain (CBD), Beta-Gal, OMNI, thioredoxine, NusA, mistine, chitin-binding domain, cutinase, fluorescent compounds (such as GFP, YFP, FITC,

rhodamine, lanthanides), enzymes (such as peroxidase, luciferase, alkaline phosphatase), chemiluminescent compounds, biotinyl groups, epitopes recognised by antibodies such as leucine zipper, c-myc, metal-binding domains and binding sites for secondary antibodies.

[00121] Polypeptides can also be obtained synthetically using methods known in art. Direct synthesis of the polypeptides of the invention can be performed using solid phase synthesis, synthesis in solution or other conventional media, usually using • -amino group, • -carboxyl and/or amino acid side chain functional groups. For example, in solid phase synthesis, an adequately protected amino acid residue is bound through its carboxyl group to an insoluble polymeric carrier, such as a polystyrene or polyamide cross-linked resin. Solid phase synthesis methods include both BOC and FMOC methods, which use tert-butyl carbonyl, and 9-fluorenylmethyloxycarbonyl as protective groups • -amino, respectively, both well known by technicians on the subject (Sambrook *et al.,* Molecular Cloning: A Laboratory Manual, 2nd edition, Cold Spring Harbor Press, Cold Spring Harbor, N.Y; Ausubel *et al.*, Current Protocols in Molecular Biology, John Wiley and Sons, New York, 1995).

[00122] The following protective groups may be examples used for the synthesis of polypeptides of invention: 9-fluorenylmethyloxycarboyl (Fmoc), tert-butylloxycarbonyl (Boc), carbobenzyloxy (Cbz), 2-chloro-3-indenylmethoxycarbonyl (Climoc), benz(f)inden-3-yl-methoxycarbonyl (Bimoc), 1,1-dioxobenzo[b]thiophene-2-yl-methoxycarbonyl (Bsmoc), 2,2,2-Trichloroethoxycarbonyl (Troc), 2-(trimethylsilyl)ethoxycarbonyl (Teoc), homobenzyloxycarbonyl (hZ), 1,1-dimethyl-2,2,2-trichloroethoxycarbonyl (TCBoc), 1-methyl-1 (4-biphenyl)ethoxycarbonyl (Bpoc), 1-(3,5-di-t-butylphenyl)-1-methylethoxycarbonyl (t-Bumeoc), 2-(2'-or 4'-pyridyl)ethoxycarbonyl (Pyoc), vinyloxycarbonyl (Voc),1-isopropylaliloxycarbonyl (Ipaoc), 3-(pyridyl)allyl-oxycarbonyl (Paloc), p-

methoxybenzyloxycarbonyl (Moz), p-nitrocarbamate (PNZ), 4-azidobenzyloxycarbonyl (AZBZ), Benzil (Bn) MeO, BnO, Metoxymethyl (Mom), methylthiomethyl (MTM), phenyldimethylsillmethoxymethyl (SMOM), t-butyldimethylsilyl (TBDMS), benzyloxymethyl (BOM), p-methoxybenzyloxymethyl (PMBM), nitrobenzyloxymethyl (NBOM), p-anisyloxylmethyl (p-AOM), pBuOCH2O-, 4-pentenyloxymethyl (POM), 2-methoxyethoxymethyl (MEM), 2-(trimethylsilyl)ethoxymethyl (SEM), menthoxymethyl (MM), tetrahydropyranil (THP), -OCOCOph, Acetyl, ClCH2CO2-, -CO2CH2CCl3, 2-(trimethylsilyl)ethyl (TMSE), 2(p-toluenesulfonyl)ethyl (Tse). (Greene T.W. Wuts P.G.M., Protective groups in organic synthesis, 3rd ed., John Wiley & Sons, INC, New York, USA, 1999).

[00123] After the chemical reaction, the polypeptides can be separated and purified by a known purification method. An example of such purification methods may include a combination of solvent extraction, distillation, column chromatography, liquid chromatography, recrystallization and the like.

[00124] In a sixth aspect, a pharmaceutical composition is provided here comprising a polypeptide with asparaginase activity according to invention and at least one carrier or a pharmaceutically acceptable excipient.

[00125] Pharmaceutically acceptable carriers or excipients are selected according to the final presentation of the composition of the present invention, which can be in the form of capsules, tablets or solution for oral administration, solution for nasal administration, solution for injection for intramuscular, intravenous, cutaneous or subcutaneous.

[00126] Pharmaceutically acceptable excipients, carriers or stabilizers are not toxic to the recipient organism in the dosages and concentrations employed and include buffers such as phosphate, citrate and other organic acids; antioxidants such as ascorbic acid and methionine; preservatives such as octadecyl dimethyl benzyl ammonium chloride, hexamethonium chloride, benzalkonium chloride, benzethonium chloride, phenol, butyl alcohol, benzyl

alcohol, alkyl parabens such as methyl and propyl paraben, catechol, resorcinol, cyclohexanol, 3-pentanol and m-cresol; proteins such as albumin, gelatin or immunoglobulins; amino acids, monosaccharides, disaccharides and other carbohydrates such as glucose, mannose, sucrose, mannitol or sorbitol; polymeric excipients such as polyvinylpyrrolidones, Ficoll®, dextrins and polyethylene glycols; flavoring agents; sweeteners; anti-static agents; chelating agents such as EDTA or EGTA; ion releasing salts such as sodium; metal complexes; non-ionic surfactants such as polysorbates 20 and 80; lipids such as phospholipids, fatty acids and steroids such as cholesterol. Methods for preparing various pharmaceutical compositions are well known, or will be apparent in the light of this invention, by the art expert in pharmaceutical technology.

[00127] In addition, the compositions may include additives in order to increase ease of administration, storage capacity and resistance to degradation, bioavailability, half-life, providing isotonic preparations, etc. Additives used for the preparation of pharmaceutical compositions are well known in the art.

[00128] In an embodiment, the composition according to the present invention comprises at least one additional chemotherapeutic agent selected from among alkylating agents, antimetabolites, kinase inhibitors, anti-spindle poison plant alkaloids, cytotoxic/antitumor antibiotics, topoisomerase inhibitors, photosensitizers, antiestrogens and selective estrogen receptor modulators (SERMs), antiprogesterones, estrogen receptor descending regulators (ERDs), estrogen receptor antagonists, luteinizing hormone release agonists, antiandrogens, aromatase inhibitors, EGFR inhibitors, inhibitors of VEGF, antisense oligonucleotides that inhibit the expression of genes involved in abnormal cell proliferation or tumor growth. Chemotherapeutic agents useful in the treatment methods of this invention include cytostatic and/or cytotoxic agents.

[00129] The pharmaceutical compositions of this invention must comprise a therapeutically effective quantity of the polypeptide. For any compound, the therapeutically effective dose can be estimated initially, either in cell culture trials, e.g. of neoplastic cells, or in animal models, usually mice, rabbits, dogs or pigs. The animal model can also be used to determine the appropriate concentration range and the route of administration. Information of this kind can then be used to determine usable doses and routes of administration in humans.

[00130] The pharmaceutical composition according to the present invention comprises from 0.1% to 99% w/w, preferably 1% to 60% w/w, particularly 10% to 50% w/w of the polypeptides of the present invention.

[00131] According to the present invention, the administration of the said pharmaceutical compositions can be done by oral, sublingual, nasal, intravenous, intramuscular, intraperitoneal, intra-articular, subcutaneous, cutaneous, transdermal routes of administration and is not limited to these. In a preferred embodiment, the composition of the present invention is for intravenous administration.

[00132] In a seventh aspect, this invention provides the use of the invention's polypeptides in the manufacture of a medicine for cancer prevention or treatment. In a preferred embodiment, cancer is selected from acute myeloid leukemia (AMI), chronic lymphoid leukemia, ovarian cancer, brain cancer, prostate cancer, lung adenocarcinoma, non-Hodgkin's lymphoma and sarcoma. In an embodiment, sarcoma is selected from lymphosarcoma, reticulosarcoma and melanosarcoma. In a preferred embodiment, cancer is acute myeloid leukemia (ALL).

[00133] This invention also refers to a method for producing polypeptide according to the invention with asparaginase activity comprising the insertion of a polynucleotide, a cassette or an expression vector according to the invention in an in vivo expression system and the *collection of the*

polypeptide produced by that system. Numerous in *vivo* expression systems, including the use of appropriate host cells, are available in the trade and the use of these systems is well known for its technical expertise.

[00134] Particularly suitable expression systems include microorganisms, such as bacteria transformed with bacteriophage, plasmid or cosmid recombinant DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (eg, baculovirus); plant cell systems transformed with virus expression vectors (for example, cauliflower mosaic virus, CaMV \ ; tobacco mosaic virus, TMV \ ) or with vectors of bacterial expression (for example, Ti or pBR322 plasmids); or animal cell systems. It is also possible to employ cell-free translation systems to produce the polypeptides of invention.

[00135] The introduction of polynucleotides that encode a polypeptide of this invention into host cells can be performed using methods described in many standard laboratory manuals, as Davis *et al.*, Basic Methods in Molecular Biology (1986) and Sambrook *et al.* , Molecular Cloning: Laboratory Manual, Cold Spring Harbor, NY (1989).

[00136] The transformed or transfected host cell described above is then grown into a suitable nutrient medium under conditions conducive to the expression of the invention's immunosuppressive polypeptides. The medium used to grow the cells can be any conventional medium suitable for developing the host cells, as a minimum or complex medium containing appropriate supplements. The appropriate means are available from commercial suppliers or can be prepared according to published recipes (for example, in the American Type Culture Collection catalogues). The polypeptides of the invention produced by the cells can then be recovered from the cell or culture medium by conventional procedures including separating the host cells from the medium by centrifugation or filtration, precipitating the aqueous protein components of the supernatant or filtered by

means of a salt, e.g. ammonium sulphate, purification by a variety of chromatographic procedures, e.g. ion exchange chromatography, exclusion chromatography, hydrophobic interaction chromatography, gel-filtration chromatography, affinity chromatography or depending on the type of polypeptide in question.

[00137] According to an eighth aspect of the invention is provided a method to produce a polypeptide with asparaginase activity according to the invention comprising:

(a) transfer to a host cell a polynucleotide of the present invention to obtain a transformed or transfected host cell;

(b) grow the transformed or transfected host cell to obtain a cell culture;

(c) express the polynucleotide of the present invention in a host cell transformed or transfected to produce a polypeptide; and

(e) isolate the polypeptide from the present invention of the cell or cell culture.

[00138] In one particular aspect of the invention, the host cell is a prokaryotic microorganism or a eukaryotic cell or microorganism. In an additional aspect of the invention, said polypeptide is provided with a “tag”.

[00139] In a ninth aspect of the invention, a method of cancer prevention or treatment is provided, characterized by understanding the administration to an individual in need of such prevention or treatment of a therapeutically effective amount of a polypeptide according to the invention.

[00140] The actual amount needed for a human individual will depend on the severity of the individual’s disease state, general health, age, weight, and gender, and diet, the time and frequency of administration, drug combination/combinations, reaction sensitivities, and tolerance/response to therapy. Thus, doses to be provided depend on a number of factors that cannot be measured before clinical trials are conducted. The technician on the

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subject, however, knows how to arrive at suitable doses for different treatments.

[00141] The following examples are merely illustrative and should only be used for a better understanding of the developments in the present invention, should not, however, be used in order to limit the objects described.

EXAMPLES

EXAMPLE 1: Cloning

[00142] The synthetic gene for ASRGL1 was designed with restriction sites for the enzymes NdeI and XhoI using the sequence deposited on GenBank (GI:20799289). GenScript (New Jersey, United States) performed gene synthesis and cloning in the pUC57 vector (ASRGL1-pUC57).

1.1 Drawing of oligonucleotides

[00143] The G10E mutation was inserted in the amplification step of the ASRG1 gene, since *the* target region is at the beginning of the sequence. The initiating oligonucleotides used for the amplifications of genes coding for human wild L-asparaginase (ASRGL1) and mutated human L-asparaginase (ASRGL1_G10E) are described in Table 1.

Table 1. Sequence of oligonucleotides used for the amplification of human wild L-asparaginases (ASRGL1) and mutated (ASRGL1_G10E) with their respective restriction sites.

Oligonucleotide	Sequence (5' - 3')	Restriction Site	SEQ ID NO:
ASRGL1 *Forward*	CATATGAATCCCATCGTAGTGGTC	Ndel	SEQ ID NO: 9
ASRGL1_G10E *Forward*	CATATGAATCCCATCGTAGTGGTCCACGGCGAAGGAGCC	Ndel	SEQ ID NO: 10
ASRGL1 *Reverse*	CTCGAGTTAGGGAAGGTCGGTGATAGT	Xhol	SEQ ID NO: 11

Note: The ASRGL1 *Reverse* initiator was used for the amplification of both wild and mutated constructions. The underlined codon in ASRGL1_G10E Forward initiator corresponds to the G10E mutation.

1.2 PCR gene amplification

[00144] The ASRGL1 and ASRGL1_G10E constructs were amplified by polymerase chain reaction (PCR) (MULLIS *et al.*, 1986) from the

synthetic gene ASRGL1-pUC57 to a total volume of 20 • L, using 6.75 ng DNA, 2 • L 10X PCR Buffer (Invitrogen), 1.6 • L 10 mM dNTPs (Invitrogen), 5 • M each pair oligonucleotide, 0.8 • L 50 mM MgCl2, 1 • L of Taq DNA Polymerase. The program was started at 94ºC for 5 minutes, followed by 30 cycles of: 94ºC/30s, XºC/30s, 72ºC/60s and finished at 72ºC for 15 minutes. The ring temperatures (X) used in each reaction are shown in Table 2.

Table 2. Ring temperatures for PCR reaction.

Construction	Ring temperature (X °C)
ASRGL1	58,9
ASRGL1_G10E	86,7

1.3 Agarose gel electrophoresis

[00145] DNA electrophoresis was performed on 1% agarose gel. 1 Kb Plus DNA Ladder (Invitrogen), O'GeneRuler 1 kb Plus DNA Ladder (Thermo Scientific) were used as molecular weight standard and MassRuler DNA Ladder Mix (Thermo Scientific). The electrophoresis was performed at 90 V for 1 hour. Figure 3 shows these molecular weight standards, A) being the one shown, 1 Kb Plus DNA Ladder (Invitrogen); B) O'GeneRuler 1 kb Plus DNA Ladder (Thermo Scientific) and C) MassRuler DNA Ladder Mix (Thermo Scientific).

[00146] The amplification of the ASRGL1 and ASRGL1_G10E encoding sequence by PCR has amplified an approximate 950 bp size sequence that corresponds to the ASRGL1 gene size (944 bp). Figure 4 shows the electrophoretic profile of the PCR products of ASRGL1 and ASRGL1_G10E sequences. In A, ASRGL1 (944 bp) (MW: 1 Kb Plus DNA Ladder, Invitrogen) and in B, ASRGL1_G10E (944 pb) (M: O'GeneRuler 1 kb Plus DNA Ladder, Thermo Scientific).

1.4 DNA extraction from agarose gel

[00147] After agarose gel electrophoresis of the PCR products, the desired nucleotide sequence bands were excised and purified using low melt agarose electrophoresis. DNA was separated from agarose after incubation at 65°C for 15 minutes and subsequent addition of phenol at room temperature.

1.5 Connection in cloning vector

[00148] The pGEM®-T Easy (Promega) vector insert was connected using 3 • L purified sample of the gel, 5 • L 2X Binding Plug (Promega), 1 • L of pGEM®-T Easy (Promega) and 1 • L of T4 DNA Ligase (Promega). Incubation was at 4°C for 16 hours.

1.6 Preparation of calcium-competent bacteria

[00149] For the preparation of calcium-competent bacteria, the CaCl2 method described by Sambrook *et al*. (2001). A colony of E. *coli DH5• was* inoculated with 5 mL of Luria-Bertani *(LB)* culture medium; 10.0 g/L of Bacto-triptone; 5.0 g/L of NaCl and 5.0 g/L of yeast extract) containing appropriate antibiotic. The culture was incubated at 37ºC for 18 hours under constant agitation of 200 rpm. A volume of 1 mL of this crop was transferred to 250 mL of LB medium. The cells were incubated at 37ºC under the same stirring conditions until reaching the exponential growth phase (D.O.600 of 0.6).

[00150] The culture was centrifuged at 2,700 x g for 10 minutes at 4ºC and the cells were suspended in 30 mL of Transformation Buffer I and kept on ice for 15 minutes. The suspension was centrifuged at 580 x g for 15 minutes at 4°C, the cells were suspended in 10 mL of Processing Buffer II, kept in dry ice for 2 hours and then aliquoted and stored at -70ºC.

1.7 Transformation of calcium-competent bacteria

[00151] Recombination or binding reactions were incubated with 70 • L of the E. coli calcium-competent suspension *for 30* minutes on ice. After this period, the cells were submitted to thermal shock through incubation at 42ºC for 2 minutes, followed by incubation for 2 minutes on ice and then adding 1 mL of LB medium for incubation under constant stirring of 200 rpm at 37ºC for one hour. Aliquots of 100 • L were distributed in half LB-agar (half LB with the addition of 1,5% agar-agar) added of antibiotic (selective medium) according to the resistance conferred by the vector used in the

transformation of bacteria and incubated at 37°C for 16 hours.

[00152] Particularly in the case of pGEM-T Easy cloning, LB-agar medium was added of 100 • g/mL ampicillin, 0.04 mg/mL X-gal (5-bromo-4-chloro-3-indoxyl-• -D-galactopiranoside) and 0.4 mM isopropyl-• -D-tiogalactopyranoside (IPTG) inductor. In this case, the selection of the positive clones was made by color analysis of the colonies due to the presence or absence of expression of the enzyme • -galactosidase. This, whose expression is induced by IPTG, degrades the X-gal substrate producing a blue substrate. If the fragment is incorporated into the vector, the enzyme • -galactosidase is not expressed and the colonies remain white, facilitating the identification of positive clones, which were later sequenced.

1.8 Small-scale plasmid DNA extraction

[00153] The positive clones had their plasmid DNA extracted. For this purpose, a colony was selected and incubated in 5 mL of LB medium under stirring of 200 rpm at 37 °C for 16 hours. The bacterial cells were centrifuged and suspended at 250 • L of Buffer containing 50 mM glucose, 25 mM Tris HCl pH 8.0 and 10 mM EDTA pH 8.0. 250 • L of Buffer containing NaOH 0.2N, SDS 1% followed by agitation to rupture the cells has been added, and immediate addition of 3 M Potassium Acetate Buffer, 11.5%(v/v) Glacial Acetic Acid. After centrifugation to remove the cell remains, the fraction containing nucleic acid was separated by incubation with phenol:chloroform (1:1). Plasmids were precipitated by the addition of Ethanol and then suspended at 10 mM Tris-HCl pH 8.5.

1.9 Selection of plasmids

[00154] Primary selection was by analytical digestion assay, in which previously extracted vectors were incubated with restriction enzymes flanking the region of interest. The enzymes used for the ASRGL1 and ASRGL1_G10E genes were FastDigestTM *NdeI* and *XhoI* (Thermo Scientific) enzymes, with manufacturer's indicated buffer and reagent

concentration. For the selection of plasmids the reactions were evaluated by agarose gel electrophoresis.

[00155] The selected plasmids were sequenced by the sequencing service of the Carlos Chagas Institute - FIOCRUZ/PR. The sequence used is Single Extension. After preparation of the sample by Macrogen (Korea) the sample is precipitated with ethanol and sequenced using *Automatic Sequencer 3730xl*. The result proved the identity of the human L-asparaginases contained in these clones.

[00156] Figure 5 shows the electrophoretic profile of the analytical digestion after cloning of ASRGL1 and ASRGL1_G10E PCR products in pGEM-T Easy. In A, ASRGL1_pGEM-T Easy (insert with 944 pb) (M: 1 Kb Plus DNA Ladder, Invitrogen); and in B, ASRGL1_G10E_pGEM-T Easy (insert with 944 pb) (M: MassRuler DNA Ladder Mix, Thermo Scientific).

<u>1.10 Connecting inserts to the vector of expression and transformation</u>

[00157] After the identity of the plasmid constructs (recombinant cloning vector containing the insert) sent to sequencing was confirmed, the preparatory digestion was performed in which the pGEM-T Easy vectors were incubated with the enzymes FastDigestTM NdeI and *XhoI* (Thermo Scientific) according to the manufacturer's indications. After agarose gel electrophoresis the inserts were purified by the QIAquick Gel Extraction Kit Protocol (QIAgen).

[00158] The purified inserts were subcloned in the expression vector pET28a-TEV. 2 U of T4 DNA Ligase (Invitrogen), 2 • L of 5X DNA Ligase Buffer (Invitrogen) and insert:plasmid in the ratio 1:1.5. The final volume was 10 • L and the reaction incubated for 16 hours at 4 ºC. The pET28a-TEV vector had previously been digested with the same enzymes. After connecting the insert in the vector, the transformation was done in the strain DH5• ({F- • 80lacZ• M15 • (lacZYA-argF) U169 *recA1* endA1 hsdR17 *(rk-*, mk+*) supE44* •-thi-1 gyrA96 relA1 phoA}), *following* the thermal shock

transformation protocol described in item 1.7. The confirmation of the expression vectors containing the inserts was also performed by analytical digestion followed by submission to sequencing.

[00159] Figure 6 shows the electrophoretic profile of the analytical digestion after subcloning in pET28a-TEV expression vector. In A, ASRGL1_pET28a-TEV (944 bp insert) and B, ASRGL1_G10E_pET28a-TEV (944 bp insert).

EXAMPLE 2: Expression test

[00160] ASRGL1-pET28a-TEV and ASRGL1_G10E-pET28a-TEV expression vectors were used to transform E. *coli BL21* Star (DE3; {F-ompT *hsdSB (*rB-, mB-) galdcmrne131 (DE3)}) and/or E. *coli C43* (DE3; {F-ompT *hsdSB (*rB-, mB-) galdcm (*DE3*)}) strains and thus test the expression at temperatures of 37, 30 and 20°C.

[00161] The BL21 Star (DE3) strain, derived from the strain used for ASRGL1 expression by Cantor *et al (*2009), is indicated for high levels of expression based on vectors regulated by the T7 promoter (such as pET28a-TEV). This is because they have a mutation in the rne131 gene *that encodes* for the enzyme RNase E, an endonuclease that participates in the degradation of mRNA. The mutation in the gene of this endonuclease allows greater stability to the transcribed mRNA, thus, an increase in the expression of the protein of interest (GRUNBERG-MANAGO *et al*, *1999).*

[00162] The *E. coli* C43 (DE3) strain was also tested for compliance with the protocol described by Nomme *et al (*2012). This is a strain effective in expressing toxic proteins from all organisms, including mammals. The activity level of T7 RNAP is reduced through a mutation, thus reducing cell death associated with over-expression of many toxic proteins (DUMON-SEGNOVERT *et al*, 2004).

[00163] One isolated colony was grown for 16 hours at 37ºC under agitation of 200 rpm in 5 mL of LB medium containing kanamycin (25

• g/ml). After this period, a dilution (1:100) was performed and the culture was grown at 37ºC until the log growth phase was reached (D.O.600 0.8). At this point, an aliquot was separated, and the culture was induced with 0,5 mM isopropyl-• -D-tiogalactopyranoside (IPTG) inductor. The incubation was continued for 4 hours at 37ºC, 30ºC and 20ºC. For the test the temperature of 20°C the culture was induced with IPTG only when reaching D.O.600 1,2.

[00164] The cells were collected by centrifugation at 6,000 x g for 15 minutes at 4ºC and resuspended in 1 mL of Buffer A (TrisHCl 50 mM pH 7.4, NaCl 300 mM). After 30 minutes incubation with lysozyme (10 • g/mL)The lysis was done by sonication, giving 2 pulses of 15 seconds with an interval of 30 seconds (Ultrasonic Processor 500, Cole Parmer). After centrifugation for 30 minutes at 20,000 x g at 4ºC the pellet and supernatant were separated, referring to the insoluble and soluble fractions respectively. The pellet was resuspended in 1 mL of Buffer A with the addition of 8 M urea. For polyacrylamide gel electrophoresis (SDS-Page) 5 • L protein sample buffer 4X to 15 • L aliquot removed in each pass (total extract and, after centrifugation, pellet and supernatant, corresponding to the insoluble and soluble fractions respectively), incubating at 95ºC for 5 minutes for application in gels prepared by the traditional protocol (LAEMMLI, 1970). The prepared samples were applied in separator gels (13% bisacrylamide) and concentrator (5% bisacrylamide). The molecular weight marker used was Precision Plus ProteinTM Unstained Standards (BioRad).

EXAMPLE 3: Self-processing test

3.1 Expression and purification by nickel resin

[00165] For the evaluation of the auto cleavage efficiency of recombinant proteins the expression in E. coli BL21 Star (*DE3; {F-ompT* hsdSB (rB-, mB-*)* galdcmrne131 (DE3)} was performed*.)* An isolated colony was inoculated in 5 mL of LB medium containing 25 • g/mL of canaminicin. After growth for 16 hours at 37°C and 200 rpm, a 1:100 dilution of this

culture was performed in 500 mL of LB medium plus 25 •g/mL of canaminicin. The growth of the crop to the exponential growth phase (D.O.600 0.8) occurred under agitation of 200 rpm at 37°C. Then 0.5 mM of IPTG inductor was added and growth continued for another 4 hours under the same conditions.

[00166] The cultures were centrifuged at 6,000 x g for 15 minutes at 4°C and suspended in Buffer A with the addition of 10 mg/ml of lysozyme. After a 30-minute incubation on ice, lysis was performed through 8 sonication cycles with 30-second pulses and 60-second intervals. Pellet and supernatant were separated as insoluble and soluble fraction, respectively, by centrifugation at 20,000 x g for 30 minutes at 4°C.

[00167] The soluble fractions were purified in nickel resin (Ni-NTA Superflow, QIAgen) through the following steps: incubation of the soluble fraction with the nickel resin for 1 hour under stirring; centrifugation and removal of the supernatant (called Flow through, as it corresponds to the fraction that did not bind to the column); washing *by incubation* with Buffer A plus 50 mM imidazole; centrifugation and removal of the supernatant (elution with 50 mM imidazole); washing by incubation with Buffer A plus 100 mM imidazole; centrifugation and removal of the supernatant (elution with 100 mM imidazole)elution with Buffer B (TrisHCl 50 mM pH 7.4, NaCl 300 mM, Imidazole 500 mM); centrifugation and removal of supernatant (elution with 500 mM imidazole). *Flow through* and elution fractions were evaluated by SDS-Page 13% electrophoresis.

3.2 *Western blot*

[00168] The efficiency of the self-processing was verified by visualizing the bands corresponding to each state in the Western blot technique (TOWBIN *et al.* , 1979). Initially the samples were submitted to SDS-Page gel electrophoresis of 13%. After electrophoresis, the proteins were transferred for 50 minutes at 20 V to a PVDF membrane, previously

sensitized with 100% methanol, in Semidry system. Once the transfer was completed, the membrane was stained with Ponceau's solution to check the quality of the transfer and, then decorated with water for incubation for 30 minutes with blocking solution at room temperature. After this period, three 5-minute washes were performed with PBS - TWEEN 20 Buffer.

[00169] The membrane containing the proteins was then incubated in PBS - TWEEN 20 Buffer (PBS -Tween 20 0.1%) containing the primary antibody (anti-his) at dilution 1:3,000. This incubation was performed under agitation at 4°C for 2 hours. After the washing steps as described above, the membrane was incubated with the secondary antibody (peroxidase-conjugated anti-mouse, Sigma) at a dilution of 1:10,000 in PBS Buffer - TWEEN 20 for 1 hour under stirring at 4°C.

[00170] The membrane was then washed again for chemiluminescence disclosure. The luminol and peroxidase solution in the 1:1 portion (SuperSignal™ West Pico Chemiluminescent Substrate, Thermo Scientific) was distributed on the membrane according to the manufacturer's indications and revealed through exposures of 5 to 20 minutes on the L-Pix Chemi Express photodocumenter (Loccus) through the L-Pix Image Software.

EXAMPLE 4: Expression and purification of recombinant proteins

4.1 Expression

[00171] The large-scale expression of ASRGL1 and ASRGL1_G10E in E. *coli BL21* Star (DE3; {F-ompT *hsdSB (*rB-, mB-) galdcmrne131 (DE3)}) was performed as follows: One isolated colony was grown for 16 hours at 37ºC under agitation of 200 rpm in 5 mL of LB medium containing kanamycin (25 • g/ml). After this period, a dilution (1:100) was performed and the culture was grown at 37ºC until the log growth phase was reached (D.O.600 0.8). At this point, an aliquot was separated, and the culture was induced with 0.5 mM isopropyl-• -D-tiogalactopyranoside (IPTG) inductor. The incubation was continued for 4 hours at 37ºC. The cells were collected by

centrifugation at 6,000 x g for 15 minutes at 4°C.

4.2 Sample preparation

[00172] After resuspension of the pellets in C Buffer (TrisHCl 50 mM pH 7.4, NaCl 300 mM), lysis was performed through 8 to 12 passages under a pressure of 80 psi in a microfluidizer (M-110L Microfluidizer®), Microfluidics) followed by centrifugation at 20,000 x g for 30 minutes at 4°C. The soluble fractions were reserved for purification.

4.3 ASRGL1 Purification

4.3.1 Affinity chromatography

[00173] The expression vector pET28a-TEV allows the recombinant protein to be expressed fused to an N-terminal histidine tail, which makes it possible to use chromatography columns containing immobilized solid phase nickel for the purification process, since the histidine tail has an affinity for this metal. For this chromatographic method, the buffers C (TrisHCl 50 mM pH 7,4, NaCl 300 mM) and D (TrisHCl 50 mM pH 7.4, NaCl 300 mM, Imidazole 1M).

[00174] Nickel column affinity chromatography was performed in the Äkta system (Äkta Pure M25 or Äkta Purifier UPC 100, GE Healthcare) FPLC (Fast Performance Liquid Chromatography), Amersham Bioscience) in column HisTrap HP 1 mL (GE Healthcare). The column was first balanced in C buffer (TrisHCl 50 mM pH 7.4, NaCl 300 mM). The sample was then injected, and the column was rinsed with C buffer to remove the unbound proteins. During purification, a 0-100% gradient of D buffer (TrisHCl 50 mM pH 7,4 , NaCl 300 mM, Imidazole 1M) was used for the elution of proteins in 20 column volumes, since imidazole competes with histidine for the binding to Nickel immobilized in the column. Depending on the amplitude of the absorbance signal, the D-buffer gradient was retained to improve the separation efficiency in chromatography. The fractions from the chromatography were collected with a flow of 1 mL per minute and analyzed

through SDS-Page. The fractions containing the protein of interest in its purest form were joined and concentrated by centrifugation at 3,000 x g using Amicon Ultra 10 (10000 MWCO) filters, Millipore).

4.3.2 Ion exchange chromatography

[00175] To achieve a higher purity level of ASRGL1 samples, HiTrap Q FF (GE Healthcare) column ion exchange chromatography was required. For this purpose, the samples were diluted 10X in E buffer (TrisHCl 50 mM pH 7.4) to reduce the salt concentration. The pH 7.4 of buffer E was chosen considering the positive resin charge and noting that the theoretical pI of ASRGL1 is equal to 6.27 (ExPASy ProtParam software), when the protein will then find itself negatively charged (anionic exchange) enabling efficient interaction with the column.

[00176] In Äkta FPLC system the column was balanced in E-buffer and after injection the sample was washed with E-buffer. The elution occurred in 20 column volumes through a 0-100% F buffer gradient (TrisHCl 50 mM pH 7,4, NaCl 1 M), whose high salt concentration promotes the decoupling of proteins from the column. Again, retention was used in the gradient according to absorbance. The fractions containing the protein of interest in its purest form were united and concentrated by centrifugation at 3,000 x g using Amicon Ultra 10 filters (10000 MWCO, Millipore).

4.3.3 Filtration gel chromatography

[00177] For complete removal of contaminants, the ASRGL1 fractions concentrated in the previous chromatographic step were subjected to gel chromatography filtration using Superdex 75 10/300 GL (GE Healthcare) column in Äkta FPLC system. The sample volume applied varied between 320 and 450 • L and the elution of the wild protein was done in 1.5 volumes of G buffer column (TrisHCl 50 mM pH 7.4, NaCl 180 mM) or H (TrisHCl 50 mM pH 7.4, NaCl 470 mM) according to the salt concentration observed in ion exchange chromatography, with flow rate of 0.5 mL per minute.

Filtration gel chromatography is a method of macromolecule analysis and which consists of separating biomolecules according to their size and shape. The column in this process contains a polymer with defined pore size cross-links. The larger molecules will migrate faster than the smaller ones, because they are not able to penetrate the interior of the resin pores, eluted directly from the column. The smaller molecules, by entering through the pores of the column, and take longer to go through the pores, are eluted late from the larger molecules.

4.4 ASRGL1_G10E Purification

4.1 Affinity chromatography

[00178] ASRGL1_G10E affinity chromatography was performed in Äkta FPLC system in HisTrap HP 1 mL column (GE Healthcare). The column was first balanced in C buffer. The sample was then injected, and the column was washed with C buffer ((TrisHCl 50 mM pH 7.4, NaCl 300 mM) to remove the unbound proteins. Two elution steps were performed, the first in 10 column volumes with a 0-15% gradient of D buffer (TrisHCl 50 mM pH 7,4, NaCl 300 mM, Imidazol 1M), and the second step with 15-100% D buffer in 10 column volumes.

[00179] The fractions of interest were united and concentrated, but because they showed consistent presence of contaminants a second affinity chromatography was performed, using the same methodology. Only the first elution step was changed, in which there was an increase to 20 column volumes. The resulting fractions were analyzed by SDS-Page and *Western blot*, followed by concentration by centrifugation.

4.2 Ion exchange chromatography

[00180] The ion exchange chromatography of ASRGL1_G10E presented the same anionic character of the chromatography performed with ASRGL1, because at pH 7.4 of E ASRGL1_G10E buffer (pI 5.81) is negatively charged. The methodology used was the same as described in

section 3.8.3.2, including sample preparation for application in the HiTrap Q FF column (GE Healthcare). The fractions from this chromatography were individually concentrated for use in the tests described in Examples 5 and 6.

EXAMPLE 5: Enzymatic assays

[00181] The kinetic activity of enzymes was evaluated by the AHA assay (FRAER; BURREL, 1955; VERMA, 2005; LI *et al.* , 2012).

[00182] Reactions with the enzymes ASRGL1 and ASRGL1_G10E were performed with 0.004 mg of each fraction, 10 • L of AHA solution (AHA 10 mM) and sufficient amount of the reaction buffer for a total volume of 200 • L. The reactions were incubated at 37°C for 10 minutes followed by the addition of TCA solution to stop the reaction. After adding 1000 • L of Oxin solution the samples were heated to 95°C for 1 minute and then cooled for 10 minutes at 4°C for subsequent reading at 705 nm (Synergy H1 Hybrid Reader, BioTek).

[00183] The absorbance values obtained were converted into • mols of aspartate generated in the reaction through the equation:

$$\bullet\, mol\ of\ aspartate\ in\ reaction = \left(\frac{DO_{705}}{1{,}77.10^4}\right).0{,}26.10^6$$

[00184] The amount of aspartate generated in the reaction is then converted into experimental enzymatic activity (• mols of aspartate generated by mL of enzyme) by the equation:

$$Enzyme\ activity\ experiment = \frac{\bullet\, mol\ of\ aspartate\ in\ reaction}{Enzyme\ volume\ .\ reaction\ time\ .\ total\ volume\ of\ the\ reaction}$$

[00185] To calculate the kcat values *of* each fraction the reaction speed is divided by the total concentration of enzyme in the reaction, where the speed is calculated by dividing the quantity in • mols of aspartate generated in the reaction by the total reaction time in seconds.

[00186] The kinetic parameters for AHA hydrolysis of the ASRGL1 and ASRGL1_G10E fractions are as shown in Table 3 below.

Table 3: Kinetic parameters of AHA hydrolysis of ASRGL1 and

ASRGL1_G10E fractions. The values of experimental enzymatic activity can be found at • mols of aspartate generated by ml of enzyme.

Sample	*Kcat* (s-1)	Experimental enzyme activity
ASRGL1_inactive_a	0,1 ± 0,05	5,87 ± 2,94
ASRGL1_ inactive _b	0,13 ± 0,04	7,83 ± 2,61
ASRGL1_active	0,32 ± 0,12	9,55 ± 3,67
ASRGL1_G10E_active_a	4,73 ± 0,13	143,95 ± 3,92
ASRGL1_G10E_active_b	3,35 ± 0,07	101,85 ± 2,28

EXAMPLE 6: Differential scanning fluorimetry

[00187] Each fraction of the wild and mutant proteins was diluted at 2 • M in the elution buffer of the last chromatographic step and dispensed in a 96-well (Axygen) PCR microplate. 200X of SYPRO *Orange* (SYPRO® Orange protein gel stain, Life Technologies) have been added to each well for a final volume of 25 • L. Each fraction was tested in triplicate. The plates were sealed with an adhesive seal (Adhesive PCR Film, Thermo Scientific) to prevent any evaporation. The experiment was conducted on a Real-Time 7500 PCR machine (Applied Biosystems).

[00188] The determination of the TM of each fraction was performed through the OriginProB software. For this, the data were adjusted by Boltzmann's sigmoidal regression model, where the point of inflection represents the TM.

REFERENCES

1. DOLOWY, W.C., HEMNSON, D., CORNET, J., SELLIN, H. Toxic and antineoplastic effects of L-asparaginase. *Cancer* **19,** 1813–1819 (1966).

2. Hill, J. M. *et al.* L-asparaginase therapy for leukemia and other malignant neoplasms. *JAMA J. Am. Med. Assoc.* **202,** 882–8 (1967).

3. Pejovic, T. & Schwartz, P. E. Leukemias. *Clin. Obstet. Gynecol.* **45,** 866–878 (2002).

4. INCA. Insituto Nacional de Câncer José Alencar Gomes da Silva. Estimativa 2016: Incidência de Câncer no Brasil. *Ministério da Saúde* (2015). Available at: http://www.inca.gov.br. (Accessed: 1st July 2016)

5. Rose-Inman, H. & Kuehl, D. Acute leukemia. *Emerg. Med. Clin. North*

Am. **32,** 579–96 (2014).

6. Avramis, V. I. Asparaginases: Biochemical pharmacology and modes of drug resistance. *Anticancer Res.* **32,** 2423–2437 (2012).

7. Instituto Nacional de Cancer José Alencar Gomes da Silva. *INCA - Instituto Nacional de Câncer - Estimativa 2016. Ministério da Saúde Instituto Nacional de Cancer José Alencar Gomes da Silva* (2016). doi:978-85-7318-283-5

8. Moghrabi, A. *et al.* Results of the Dana-Farber Cancer Institute ALL Consortium Protocol 95-01 for children with acute lymphoblastic leukemia. *Blood J.* **109,** 896–905 (2007).

9. Carroll, W. L. *et al.* Pediatric acute lymphoblastic leukemia. *Hematol. Am Soc Hematol Educ Program* 102–131 (2003). doi:10.1182/asheducation-2010.1.363

10. Cooper, S. L. & Brown, P. A. Treatment of pediatric acute lymphoblastic leukemia. *Pediatr. Clin. North Am.* **62,** 61–73 (2015).

11. Hunger, S. P. *et al.* Improved survival for children and adolescents with acute lymphoblastic leukemia between 1990 and 2005: A report from the children's oncology group. *J. Clin. Oncol.* **30,** 1663–1669 (2012).

12. American Cancer Society. Cancer Facts & Figures 2014. *Cancer Facts Fig.* 1–72 (2014). doi:10.1177/0300985809357753

13. Richards, N. G. J. & Kilberg, M. S. Asparagine synthetase chemotherapy. *Annu. Rev. Biochem.* **75,** 629–54 (2006).

14. Li, B. S. *et al.* The downregulation of asparagine synthetase expression can increase the sensitivity of cells resistant to l-asparaginase. *Leukemia* **20,** 2199–201 (2006).

15. Song, P. *et al.* Asparaginase induces apoptosis and cytoprotective autophagy in chronic myeloid leukemia cells. *Oncotarget* **6,** 3861–73 (2015).

16. Li, B. S. *et al.* The downregulation of asparagine synthetase expression can increase the sensitivity of cells resistant to L-asparaginase. *Leukemia* **20,**

2199–2201 (2006).

17. Pieters, R., Hunger, S. P., Boos, J., Rizzari, C. & Pui, C. L-asparaginase treatment in acute lymphoblastic leukemia: a focus on Erwinia asparaginase. *Cancer* **117,** 238–249 (2011).

18. Ueno, T. *et al.* Cell cycle arrest and apoptosis of leukemia cells induced by L-asparaginase. *Leukemia* **11,** 1858–61 (1997).

19. Yu, M. *et al.* L-asparaginase inhibits invasive and angiogenic activity and induces autophagy in ovarian cancer. **16,** 2369–2378 (2012).

20. Willems, L. *et al.* Inhibiting glutamine uptake represents an attractive new strategy for treating acute myeloid leukemia Inhibiting glutamine uptake represents an attractive new strategy for treating acute myeloid leukemia. **122,** 3521–3532 (2013).

21. Zhang, B. *et al.* Targeting asparagine and autophagy for pulmonary adenocarcinoma therapy. *Appl. Microbiol. Biotechnol.* **100,** 9145–9161 (2016).

22. Lorenzi, P. L., Claerhout, S., Mills, G. B. & Weinstein, J. N. A curated census of autophagy-modulating proteins and small molecules. *Autophagy* **10,** 1316–1326 (2014).

23. Panosyan, E. H. *et al.* Asparaginase depletion potentiates the cytotoxic effect of chemotherapy against brain tumors. *Mol Cancer Res* **12,** 694–702 (2014).

24. Sircar, K. *et al.* Integrative molecular profiling reveals asparagine synthetase is a target in castration-resistant prostate cancer. *Am. J. Pathol.* **180,** 895–903 (2012).

25. Kobrinsky, N. L. *et al.* Outcomes of Treatment of Children and Adolescents With Recurrent Non-Hodgkin ' s Lymphoma and Hodgkin ' s Chemotherapy , and Transplantation : Children ' s Cancer Group Study CCG-5912. *J. Clin. Oncol.* **19,** 2390–2396 (2001).

26. Bansal, S. *et al.* Hyperthermophilic asparaginase mutants with enhanced

substrate affinity and antineoplastic activity: structural insights on their mechanism of action. *FASEB J.* **26,** 1161–1171 (2012).

27. Roth, G. *et al.* L-ASPARAGINASE II PRODUCTION IN Escherichia coli FED-BATCH CULTURES. *Braz. J. Chem. Eng.* **30,** 245–256 (2013).

28. Rytting, M. E. Role of L-asparaginase in acute lymphoblastic leukemia: focus on adult patients. *Blood Lymphat. Cancer Targets Ther.* **2,** 117–124 (2012).

29. Müller, H. J. & Boos, J. Use of L -asparaginase in childhood ALL. *Oncology/Hematology* **28,** 97–113 (1998).

30. Patel, N. *et al.* A dyad of lymphoblastic lysosomal cysteine proteases degrades the antileukemic drug L-asparaginase. *J. Clin. Invest.* **119,** 1964–1973 (2009).

31. Avramis, V. I. & Tiwari, P. N. Asparaginase (native ASNase or pegylated ASNase) in the treatment of acute lymphoblastic leukemia. *Int. J. Nanomedicine* **1,** 241–254 (2006).

32. Oinonen, C., Tikkanen, R., Rouvinen, J. & Peltonen, L. Three-dimensional structure of human lysosomal aspartylglucosaminidase. *Nat. Struct. Biol.* **2,** 1102–1108 (1995).

33. Sugimoto, H., Odani, S. & Yamashita, S. Cloning and expression of cDNA encoding rat liver 60-kDa lysophospholipase containing an asparaginase-like region and ankyrin repeat. *J. Biol. Chem.* **273,** 12536–12542 (1998).

34. Cantor, J. R., Stone, E. M., Chantranupong, L. & Georgiou, G. The Human Asparaginase-Like Protein 1 hASRGL1 is an Ntn-Hydrolase with • -aspartyl Peptidase Activity. *Biochemistry (Mosc.)* **48,** 11025–11031 (2009).

35. Böhme, L. *et al.* Isoaspartate residues dramatically influence substrate recognition and turnover by proteases. *Biol. Chem.* **389,** 1043–1053 (2008).

36. Michalska, K. & Jaskólski, M. Structural aspects of l -asparaginases , their friends and relations. *Acta Biochim. Pol.* **53,** 627–640 (2006).

37. Dieterich, D. C. *et al.* Gliap) a novel untypical L -asparaginase localized to rat brain astrocytes. 1117–1125 (2003). doi:10.1046/j.1471-4159.2003.01766.x

38. Evtimova, V., Zeillinger, R., Kaul, S. & Weidle, U. H. Identification of CRASH, a gene deregulated in gynecological tumors. *Int. J. Oncol.* **24,** 33–41 (2004).

39. Brannigan, J. A. *et al.* A protein catalytic framework with an N-terminal nucleophile is capable of self-activation. *Nature* **378,** 416–419 (1995).

40. Bush, L. A. N. N. *et al.* A Novel Asparaginase-Like Protein Is a Sperm Autoantigen in Rats. **247,** 233–247 (2002).

41. Nomme, J., Su, Y., Konrad, M. & Lavie, A. Structures of apo and product-bound human L-asparaginase: Insights into the mechanism of autoproteolysis and substrate hydrolysis. *Biochemistry (Mosc.)* **51,** 6816–6826 (2012).

42. Li, W. *et al.* Intramolecular Cleavage of the hASRGL1 Homodimer Occurs in Two Stages. *Biochemistry (Mosc.)* **55,** 960–969 (2016).

43. Nomme, J., Su, Y. & Lavie, A. Elucidation of the specific function of the conserved threonine triad responsible for human l-Asparaginase autocleavage and substrate hydrolysis. *J. Mol. Biol.* **426,** 2471–2485 (2014).

44. Su, Y. *et al.* Free glycine accelerates the autoproteolytic activation of human asparaginase. *Chem. Biol.* **20,** 533–540 (2013).

45. Li, W., Cantor, J. R., Yogesha, S. D., Yang, S. & Chantranupong, L. Uncoupling Intramolecular Processing and Substrate Hydrolysis in the N-terminal Nucleophile Hydrolase hASRGL1 by Circular Permutation. *ACS Chem. Biol.* **7,** 1840–1847 (2012).

46. Karamitros, C. S. & Konrad, M. Bacterial co-expression of the alpha and beta protomers of human l-asparaginase-3: Achieving essential N-terminal exposure of a catalytically critical threonine located in the beta-subunit. *Protein Expr. Purif.* **93,** 1–10 (2014).

47. Schalk, A. M. & Lavie, A. Structural and Kinetic Characterization of Guinea Pig. *Biochemistry (Mosc.)* **53,** 2318–2328 (2014).

CLAIMS

1. A polypeptide with asparaginase activity, characterized by the fact that it is selected from the group consisting of

(i) a polypeptide that has an increased rate of auto-processing compared to human L-asparaginase in the wild presented in SEQ ID NO: 1;

(ii) a polypeptide comprising the amino acid sequence having at least 90% identity with the sequences of any of the SEQ ID NOs: 3-5;

(iii) a polypeptide in which the amino acid glycine at position 10 of the SEQ ID NO: 1 is replaced by an amino acid selected from the group consisting of glutamic acid, aspartic acid and histidine;

(iv) a polypeptide comprising the amino acid sequence presented in any of the SEQ ID NO: 3-5; e

(v) a polypeptide of (i) to (iv) comprising one or more conservative amino acid substitutions.

2. Polypeptide according to claim 1, characterized by the fact that it comprises the SEQ ID NO:3 amino acid sequence.

3.Polypeptide according to claims 1 or 2, characterized by the fact that it is for use in cancer prevention or treatment.

4. Polypeptide according to claim 3, characterized by the fact that the cancer is acute myeloid leukemia (AMI), chronic lymphoid leukemia, ovarian cancer, brain cancer, prostate cancer, lung adenocarcinoma, non-Hodgkin's lymphoma or sarcoma.

5. Polypeptide according to claim 4, characterized by the fact that sarcoma is lymphosarcoma, reticulosarcoma or melanosarcoma.

6. Polypeptide according to claim 4, characterized by the fact that cancer is acute myeloid leukemia.

7. Polynucleotide, characterized by the fact that it encodes the polypeptide as defined in claim 1 or 2.

8. Polynucleotide according to claim 7, characterized by

comprising the nucleic acid sequence of any of the SEQ ID NO: 6-8 and their degenerations.

9. An expression cassette, characterized by the fact that it comprises a polynucleotide as defined in claim 7 or 8 operationally linked to a promoter and to a transcription terminator.

10. A vector of expression, characterized by the fact that it comprises a polynucleotide as defined in claim 7 or 8 or an expression cassette as defined in claim 9.

11. A host cell, characterized by the fact that it comprises an expression cassette as defined in claim 9, or an expression vector as defined in claim 10.

12. A pharmaceutical composition, characterized by the fact that it comprises a polypeptide as defined in claim 1 or 2 and a pharmaceutically acceptable carrier or excipient.

13. Composition according to claim 12, characterized by the fact that it is for intravenous administration.

14. Composition according to claim 12 and 13, characterized by the fact that it also includes an additional chemotherapeutic agent.

15. Use of a polypeptide as defined in claim 1 or 2, characterized by the fact that said use occurs in the manufacture of a drug for cancer prevention or treatment.

16. Use according to claim 15, characterized by the fact that the cancer is acute myeloid leukemia (AMI), chronic lymphoid leukemia, ovarian cancer, brain cancer, prostate cancer, pulmonary adenocarcinoma, non-Hodgkin's lymphoma or sarcoma.

17. Use according to claim 16, characterized by the fact that the sarcoma is lymphosarcoma, reticulosarcoma or melanosarcoma.

18. Use according to claim 16, characterized by the fact that the cancer is acute myeloid leukemia.

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19. A method to produce a polypeptide with asparaginase activity, characterized by the fact that it comprises:

(a) provide a host cell as defined in claim 11;

(b) cultivating such a cell under conditions conducive to the production of polypeptide; and

(c) isolate said polypeptide from the surrounding cell or culture medium.

20. Method according to claim 19, characterized by the fact that said polypeptide is provided with a label.

21. A method to prevent or treat cancer, characterized by comprising administering a therapeutically effective amount of the polypeptide as defined in Claim 1 and 2 to an individual in need of such prevention or treatment.

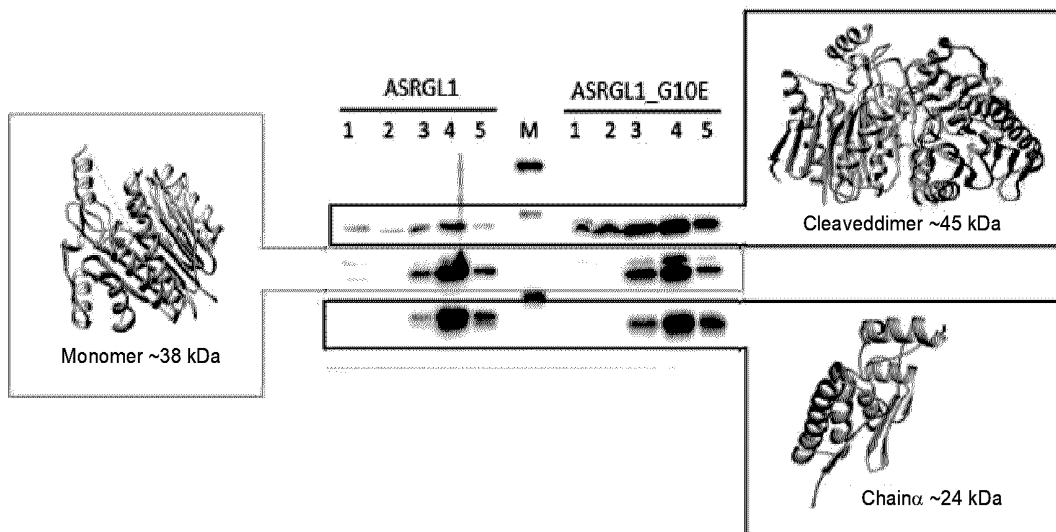
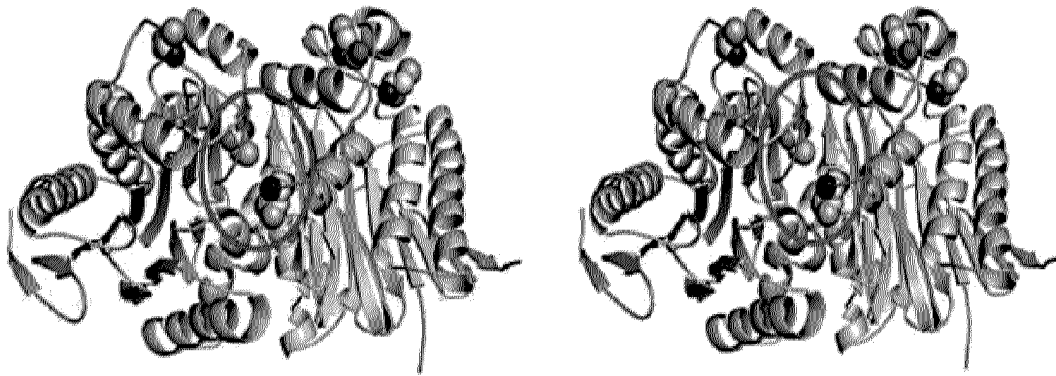


FIGURE 1



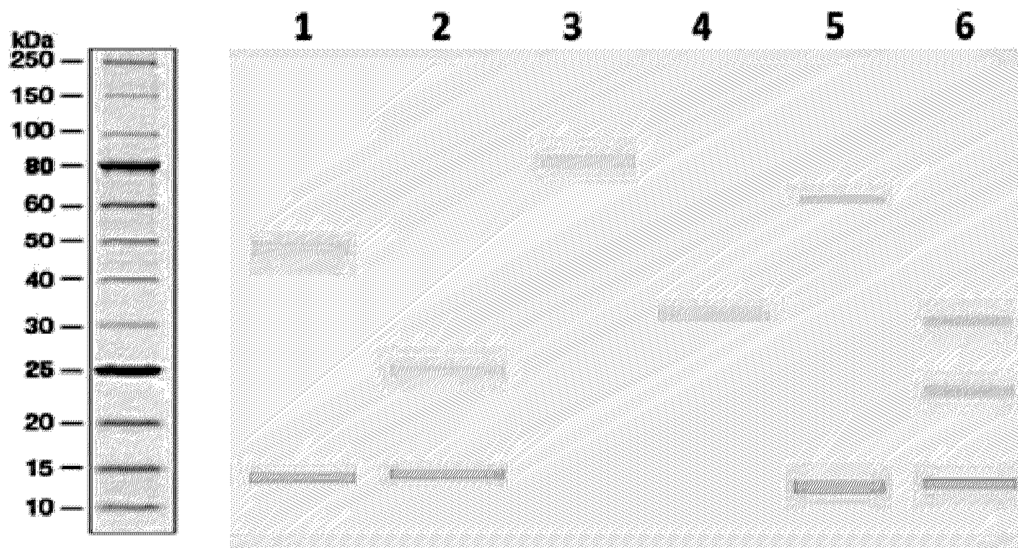


FIGURE 2

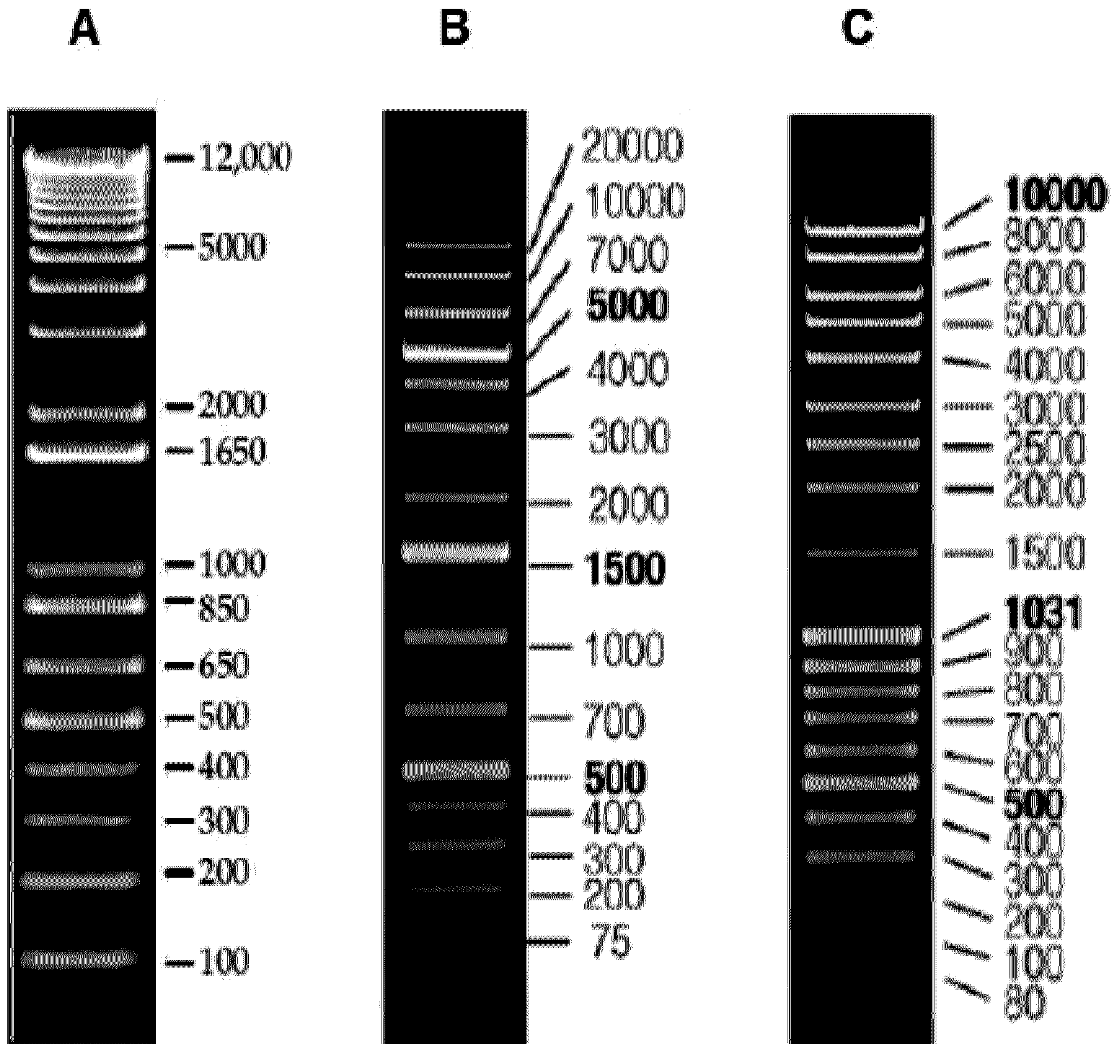


FIGURE 3

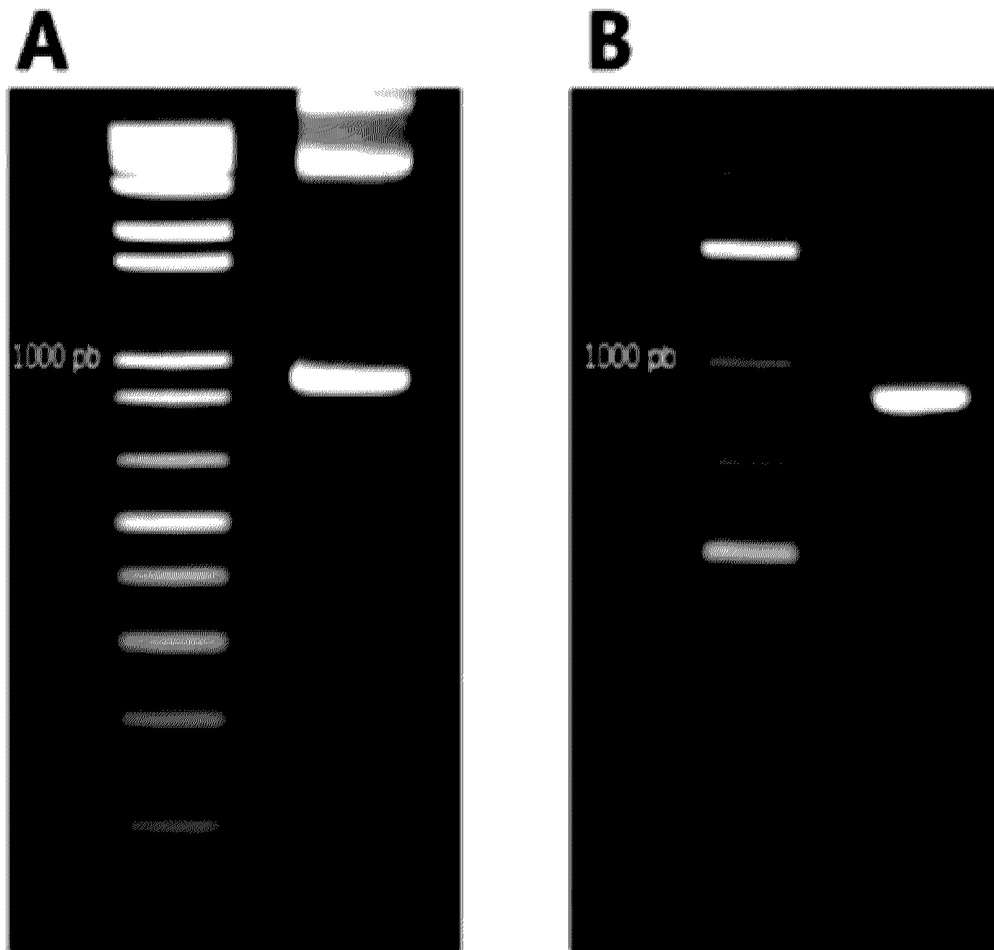


FIGURE 4

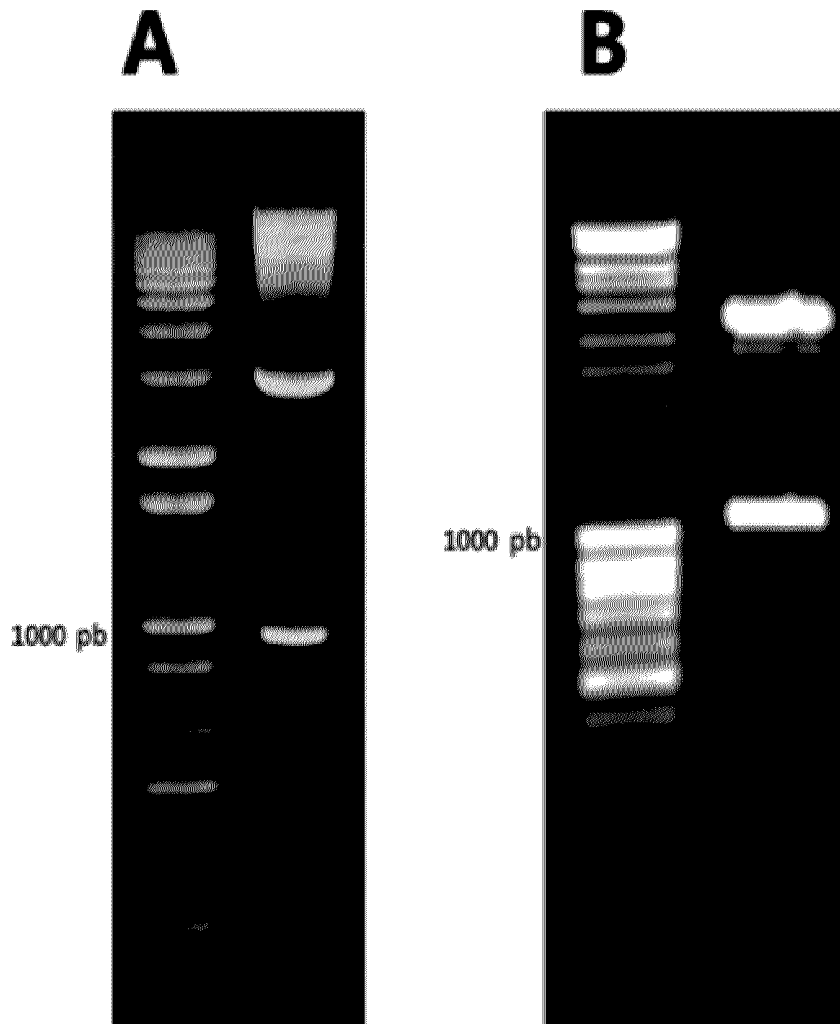


FIGURE 5

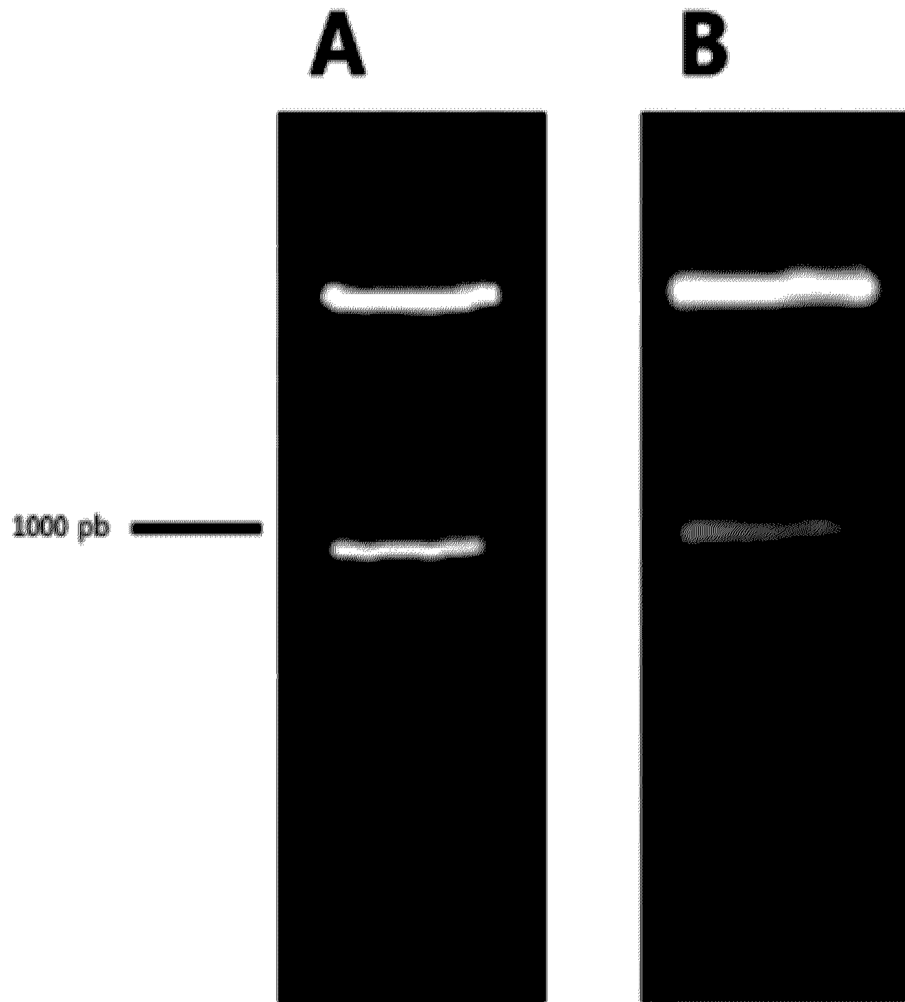


FIGURE 6

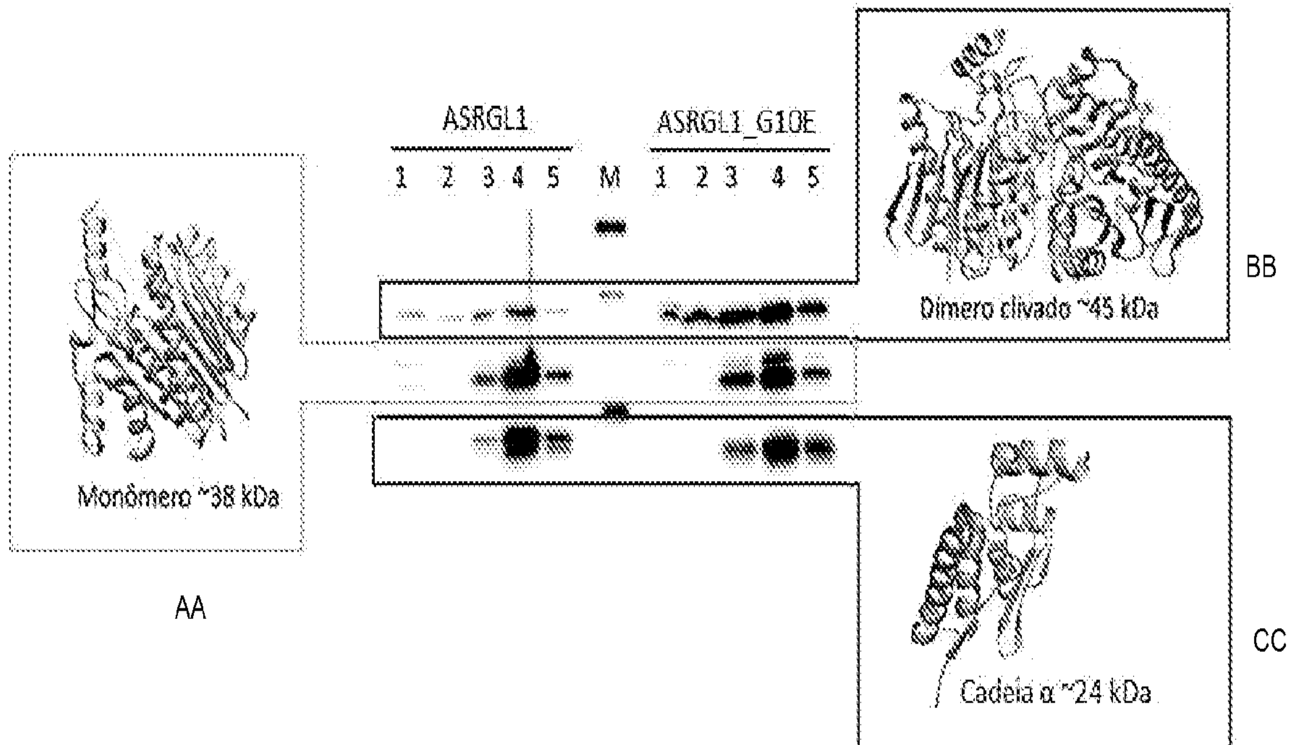


FIGURA 1

AA Monomer ~38 kDa
BB Cleaved dimer ~45 kDa
CC α chain ~24 kDa