2-MICRON FAMILY PLASMID AND USE THEREOF

FIELD OF THE INVENTION

The present application relates to modified plasmids and uses thereof.

BACKGROUND OF THE INVENTION

Certain closely related species of budding yeast have been shown to contain naturally occurring circular double stranded DNA plasmids. These plasmids, collectively termed 2μm-family plasmids, include pSR1, pSB3 and pSB4 from *Zygosaccharomyces rouxii* (formerly classified as *Zygosaccharomyces bisporus*), plasmids pSB1 and pSB2 from *Zygosaccharomyces bailii*, plasmid pSM1 from *Zygosaccharomyces fermentati*, plasmid pKD1 from *Kluyveromyces drosphilarum*, an un-named plasmid from *Pichia membranaefaciens* (hereinafter referred to as "pPM1") and the 2μm plasmid and variants (such as Scp1, Scp2 and Scp3) from *Saccharomyces cerevisiae* (Volkert, *et al.*, 1989, *Microbiological Reviews*, **53**, 299; Painting, *et al.*, 1984, *J. Applied Bacteriology*, **56**, 331) and other *Saccharomyces* species, such as S. *carlsbergensis*. As a family of plasmids these molecules share a series of common features in that they possess two inverted repeats on opposite sides of the plasmid, have a similar size around 6-kbp (range 4757 to 6615-bp), at least three open reading frames, one of which encodes for a site specific recombinase (such as *FLP* in 2μm) and an autonomously replicating sequence (*ARS*), also known as an origin of replication (*ori*), located close to the end of one of the inverted repeats. (Futcher, 1988, *Yeast,* **4**, 27; Murray *et al.*, 1988, *J. Mol. Biol.* **200**, 601 and Toh-e *et al.*, 1986, *Basic Life Sci.* **40**, 425). Despite their lack of discernible DNA sequence homology, their shared molecular architecture and the conservation of function of the open reading frames have demonstrated a common link between the family members.

The 2μm plasmid (Figure 1) is a 6,318-bp double-stranded DNA plasmid, endogenous in most *Saccharomyces cerevisiae* strains at 60-100 copies per haploid genome. The 2μm plasmid comprises a small-unique (US) region and a large unique (UL) region, separated

by two 599-bp inverted repeat sequences. Site-specific recombination of the inverted repeat sequences results in inter-conversion between the A-form and B-form of the plasmid *in vivo* (Volkert & Broach, 1986, *Cell,* **46**, 541). The two forms of 2μm differ only in the relative orientation of their unique regions.

While DNA sequencing of a cloned 2μm plasmid (also known as Scp1) from *Saccharomyces cerevisiae* gave a size of 6,318-bp (Hartley and Donelson, 1980, *Nature*, **286**, 860), other slightly smaller variants of 2μm, Scp2 and Scp3, are known to exist as a result of small deletions of 125-bp and 220-bp, respectively, in a region known as *STB* (Cameron *et al.*, 1977, *Nucl. Acids Res.*, **4**, 1429: Kikuchi, 1983, *Cell*, **35**, 487 and Livingston & Hahne, 1979, *Proc. Natl. Acad. Sci. USA*, **76**, 3727). In one study about 80% of natural *Saccharomyces* strains from around the world contained DNA homologous to 2μm (by Southern blot analysis) (Hollenberg, 1982, *Current Topics in Microbiology and Immunobiology*, **96**, 119). Furthermore, variation (genetic polymorphism) occurs within the natural population of 2μm plasmids found in *S. cerevisiae* and *S. carlsbergensis,* with the NCBI sequence (accession number NC_001398) being one example.

The 2μm plasmid has a nuclear localisation and displays a high level of mitotic stability (Mead *et al*, 1986, *Molecular & General Genetics*, **205**, 417). The inherent stability of the 2μm plasmid results from a plasmid-encoded copy number amplification and partitioning mechanism, which is easily compromised during the development of chimeric vectors (Futcher & Cox, 1984, *J. Bacteriol.*, **157**, 283; Bachmair & Ruis, 1984, *Monatshefte für Chemie*, **115**, 1229). A yeast strain, which contains a 2μm plasmid is known as [cir^+], while a yeast strain which does not contain a 2μm plasmid is known as [cir^0].

The US-region contains the *REP2* and *FLP* genes, and the UL-region contains the *REP1* and *D* (also known as *RAF*) genes, the *STB*-locus and the origin of replication (Broach & Hicks, 1980, *Cell*, **21**, 501; Sutton & Broach, 1985, *Mol. Cell. Biol.*, **5**, 2770). The Flp recombinase binds to FRT-sites (Flp Recognition Target) within the inverted repeats to mediate site-specific recombination, which is essential for natural plasmid amplification

and control of plasmid copy number *in vivo* (Senecoff *et al*, 1985, *Proc. Natl. Acad. Sci. U.S.A.*, **82**, 7270; Jayaram, 1985, *Proc. Natl. Acad. Sci. U.S.A.*, **82**, 5875). The copy number of 2μm-family plasmids can be significantly affected by changes in Flp recombinase activity (Sleep *et al*, 2001, *Yeast*, **18**, 403; Rose & Broach, 1990, *Methods Enzymol.*, **185**, 234). The Rep1 and Rep2 proteins mediate plasmid segregation, although their mode of action is unclear (Sengupta *et al*, 2001, *J. Bacteriol.*, **183**, 2306). They also repress transcription of the *FLP* gene (Reynolds *et al*, 1987, *Mol. Cell. Biol.*, **7**, 3566).

The *FLP* and *REP2* genes are transcribed from divergent promoters, with apparently no intervening sequence defined between them. The *FLP* and *REP2* transcripts both terminate at the same sequence motifs within the inverted repeat sequences, at 24-bp and 178-bp respectively after their translation termination codons (Sutton & Broach, 1985, *Mol. Cell. Biol.*, **5**, 2770).

In the case of *FLP*, the C-terminal coding sequence also lies within the inverted repeat sequence. Furthermore, the two inverted repeat sequences are highly conserved over 599-bp, a feature considered advantageous to efficient plasmid replication and amplification *in vivo*, although only the FRT-sites (less than 65-bp) are essential for site-specific recombination *in vitro* (Senecoff *et al*, 1985, *Proc. Natl. Acad. Sci. U.S.A.*, **82**, 7270; Jayaram, 1985, *Proc. Natl. Acad. Sci. U.S.A.*, **82**, 5875; Meyer-Leon *et al*, 1984, *Cold Spring Harbor Symposia On Quantitative Biology*, **49**, 797). The key catalytic residues of Flp are arginine-308 and tyrosine-343 (which is essential) with strand-cutting facilitated by histidine-309 and histidine 345 (Prasad *et al*, 1987, *Proc. Natl. Acad. Sci. U.S.A.*, **84**, 2189; Chen *et al*, 1992, *Cell*, **69**, 647; Grainge *et al*, 2001, *J. Mol. Biol.*, **314**, 717).

Two functional domains are described in Rep2. Residues 15-58 form a Rep1-binding domain, and residues 59-296 contain a self-association and STB-binding region (Sengupta *et al*, 2001, *J. Bacteriol.*, **183**, 2306).

Chimeric or large deletion mutant derivatives of 2μm which lack many of the essential functional regions of the 2μm plasmid but retain functional the *cis* element *ARS* and *STB*,

cannot effectively partition between mother and daughter cells at cell division. Such plasmids can do so if these functions are supplied in *trans*, by for instance the provision of a functional 2μm plasmid within the host, a so called [cir$^+$] host.

Genes of interest have previously been inserted into the UL-region of the 2μm plasmid. For example, see plasmid pSAC3U1 in EP 0 286 424. However, there is likely to be a limit to the amount of DNA that can usefully be inserted into the UL-region of the 2μm plasmid without generating excessive asymmetry between the US and UL-regions. Therefore, the US-region of the 2μm plasmid is particularly attractive for the insertion of additional DNA sequences, as this would tend to equalise the length of DNA fragments either side of the inverted repeats.

This is especially true for expression vectors, such as that shown in Figure 2, in which the plasmid is already crowded by the introduction of a yeast selectable marker and adjacent DNA sequences. For example, the plasmid shown in Figure 2 includes a β-lactamase gene (for ampicillin resistance), a *LEU2* selectable marker and an oligonucleotide linker, the latter two of which are inserted into a unique *Sna*BI-site within the UL-region of the 2μm-family disintegration vector, pSAC3 (see EP 0 286 424). The *E. coli* DNA between the *Xba*I-sites that contains the ampicillin resistance gene is lost from the plasmid shown in Figure 2 after transformation into yeast. This is described in Chinery & Hinchliffe, 1989, *Curr. Genet.*, **16**, 21 and EP 0 286 424, where these types of vectors are designated "disintegration vectors". In the crowded state shown in Figure 2, it is not readily apparent where further polynucleotide insertions can be made. A *Not*I-site within the linker has been used for the insertion of additional DNA fragments, but this contributes to further asymmetry between the UL and US regions (Sleep *et al*, 1991, *Biotechnology (N Y)*, **9**, 183).

We had previously attempted to insert additional DNA into the US-region of the 2μm plasmid and maintain its high inherent plasmid stability. In the 2μm-family disintegration plasmid pSAC300, a 1.1-kb DNA fragment containing the *URA3* gene was inserted into *Eag*I-site between *REP2* and *FLP* in US-region in such a way that transcription from the *URA3* gene was in same direction as *REP2* transcription (see EP 0

286 424). When S150-2B [cir^0] was transformed to uracil prototrophy by pSAC300, it was shown to be considerably less stable (50% plasmid loss in under 30 generations) than comparable vectors with *URA3* inserted into the UL-region of 2μm (0-10% plasmid loss in under 30 generations) (Chinery & Hinchliffe, 1989, *Curr. Genet.*, **16**, 21; EP 0 286 424). Thus, insertion at the *Eag*I site may have interfered with *FLP* expression and it was concluded that the insertion position could have a profound effect upon the stability of the resultant plasmid, a conclusion confirmed by Bijvoet *et al.*, 1991, *Yeast*, 7, 347.

It is desirable to insert further polynucleotide sequences into 2μm-family plasmids. For example, the insertion of polynucleotide sequences that encode host derived proteins, recombinant proteins, or non-coding antisense or RNA interference (RNAi) transcripts may be desirable. Moreover, it is desirable to introduce multiple further polynucleotide sequences into 2μm-family plasmids, thereby to provide a plasmid which encodes, for example, multiple separately encoded multi-subunit proteins, different members of the same metabolic pathway, additional selective markers or a recombinant protein (single or multi-subunit) and a chaperone to aid the expression of the recombinant protein.

However, the 6,318-bp 2μm plasmid, and other 2μm-family plasmids, are crowded with functional genetic elements (Sutton & Broach, 1985, *Mol. Cell. Biol.*, **5**, 2770; Broach *et al*, 1979, *Cell,* **16**, 827), with no obvious positions existing for the insertion of additional DNA sequences without a concomitant loss in plasmid stability. In fact, except for the region between the origin of replication and the *D* gene locus, the entire 2μm plasmid genome is transcribed into at least one poly(A)$^+$ species and often more (Sutton & Broach, 1985, *Mol. Cell. Biol.*, **5**, 2770). Consequently, most insertions might be expected to have a detrimental impact on plasmid function *in vivo*.

Indeed, persons skilled in the art have given up on inserting heterologous polynucleotide sequences into 2μm-family plasmids.

Robinson *et al*, 1994, *Bio/Technology*, **12**, 381-384 reported that a recombinant additional PDI gene copy in *Saccharomyces cerevisiae* could be used to increase the recombinant expression of human platelet derived growth factor (PDGF) B homodimer

by ten-fold and *Schizosacharomyces pombe* acid phosphatase by four-fold. Robinson obtained the observed increases in expression of PDGF and *S. pombe* acid phosphatase using an additional chromosomally integrated PDI gene copy. Robinson reported that attempts to use the multi-copy 2μm expression vector to increase PDI protein levels had had a detrimental effect on heterologous protein secretion.

Shusta *et al*, 1998, *Nature Biotechnology*, **16**, 773-777 described the recombinant expression of single-chain antibody fragments (scFv) in *Saccharomyces cerevisiae*. Shusta reported that in yeast systems, the choice between integration of a transgene into the host chromosome versus the use of episomal expression vectors can greatly affect secretion and, with reference to Parekh & Wittrup, 1997, *Biotechnol. Prog.*, **13**, 117-122, that stable integration of the scFv gene into the host chromosome using a δ integration vector was superior to the use of a 2μm-based expression plasmid. Parekh & Wittrup, *op. cit.*, had previously taught that the expression of bovine pancreatic trypsin inhibitor (BPTI) was increased by an order of magnitude using a δ integration vector rather than a 2μm-based expression plasmid. The 2μm-based expression plasmid was said to be counter-productive for the production of heterologous secreted protein.

Bao *et al*, 2000, *Yeast*, **16**, 329-341, reported that the *KlPDI1* gene had been introduced into *K. lactis* on a multi-copy plasmid, pKan707, and that the presence of the plasmid caused the strain to grow poorly. In the light of the earlier findings in Bao *et al*, 2000, Bao & Fukuhara, 2001, *Gene*, **272**, 103-110, chose to introduce a single duplication of *KlPDI1* on the host chromosome.

Accordingly, the art teaches the skilled person to integrate transgenes into the yeast chromosome, rather than into a multicopy vector. There is, therefore, a need for alternative ways of transforming yeast.

DESCRIPTION OF THE INVENTION

The present invention relates to recombinantly modified versions of 2μm-family plasmids.

A 2μm-family plasmid is a circular, double stranded, DNA plasmid. It is typically small, such as between 3,000 to 10,000 bp, preferably between 4,500 to 7000 bp, excluding recombinantly inserted sequences. Preferred 2μm-family plasmids for use in the present invention comprise sequences derived from one or more of plasmids pSR1, pSB3, or pSB4 as obtained from *Zygosaccharomyces rouxii*, pSB1 or pSB2 both as obtained from *Zygosaccharomyces bailli*, pSM1 as obtained from *Zygosaccharomyces fermentati*, pKD1 as obtained from *Kluyveromyces drosophilarum*, pPM1 as obtained from *Pichia membranaefaciens* and the 2μm plasmid and variants (such as Scp1, Scp2 and Scp3) as obtained from *Saccharomyces cerevisiae*, for example as described in Volkert *et al*, 1989, *Microbiological Reviews*, **53**(3), 299-317, Murray *et al*, 1988, *Mol. Biol.*, **200**, 601-607 and Painting, *et al.*, 1984, *J. Applied Bacteriology*, **56**, 331.

A 2μm-family plasmid is capable of stable multicopy maintenance within a yeast population, although not necessarily all 2μm-family plasmids will be capable of stable multicopy maintenance within all types of yeast population. For example, the 2μm plasmid is capable of stable multicopy maintenance, *inter alia*, within *Saccharomyces cerevisiae* and *Saccharomyces carlsbergensis*.

By "multicopy maintenance" we mean that the plasmid is present in multiple copies within each yeast cell. A yeast cell comprising 2μm-family plasmid is designated [cir^+], whereas a yeast cell that does not comprise 2μm-family plasmid is designated [cir^0]. A [cir^+] yeast cell typically comprises 10-100 copies of 2μm-family plasmid per haploid genome, such as 20-90, more typically 30-80, preferably 40-70, more preferably 50-60 copies per haploid genome. Moreover, the plasmid copy number can be affected by the genetic background of the host which can increase the plasmid copy number of 2μm-like plasmid to above 100 per haploid genome (Gerbaud and Guerineau, 1980, *Curr. Genetics*, **1**, 219, Holm, 1982, *Cell*, **29**, 585, Sleep *et al.*, 2001, *Yeast*, **18**, 403 and WO99/00504). Multicopy stability is defined below.

A 2μm-family plasmid typically comprises at least three open reading frames ("ORFs") that each encode a protein that functions in the stable maintenance of the 2μm-family

plasmid as a multicopy plasmid. The proteins encoded by the three ORFs can be designated FLP, REP1 and REP2. Where a 2μm-family plasmid comprises not all three of the ORFs encoding FLP, REP1 and REP2 then ORFs encoding the missing protein(s) should be supplied in *trans*, either on another plasmid or by chromosomal integration.

A "FLP" protein is a protein capable of catalysing the site-specific recombination between inverted repeat sequences recognised by FLP. The inverted repeat sequences are termed FLP recombination target (FRT) sites and each is typically present as part of a larger inverted repeat (see below). Preferred FLP proteins comprise the sequence of the FLP proteins encoded by one of plasmids pSR1, pSB1, pSB2, pSB3, pSB4, pSM1, pKD1, pPM1 and the 2μm plasmid, for example as described in Volkert *et al*, *op. cit.*, Murray *et al*, *op. cit* and Painting *et al, op. cit.* Variants and fragments of these FLP proteins are also included in the present invention. "Fragments" and "variants" are those which retain the ability of the native protein to catalyse the site-specific recombination between the same FRT sequences. Such variants and fragments will usually have at least 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or more, homology with an FLP protein encoded by one of plasmids pSR1, pSB1, pSB2, pSB3, pSM1, pKD1 and the 2μm plasmid. Different FLP proteins can have different FRT sequence specificities. A typical FRT site may comprise a core nucleotide sequence flanked by inverted repeat sequences. In the 2μm plasmid, the FRT core sequence is 8 nucleotides in length and the flanking inverted repeat sequences are 13 nucleotides in length (Volkert *et al*, *op. cit.*). However the FRT site recognised by any given FLP protein may be different to the 2μm plasmid FRT site.

REP1 and REP2 are proteins involved in the partitioning of plasmid copies during cell division, and may also have a role in the regulation of FLP expression. Considerable sequence divergence has been observed between REP1 proteins from different 2μm-family plasmids, whereas no sequence alignment is currently possible between REP2 proteins derived from different 2μm-family plasmids. Preferred REP1 and REP2 proteins comprise the sequence of the REP1 and REP2 proteins encoded by one of plasmids pSR1, pSB1, pSB2, pSB3, pSB4, pSM1, pKD1, pPM1 and the 2μm plasmid, for example as described in Volkert *et al*, *op. cit.*, Murray *et al*, *op. cit.* and Painting *et al,*

op. cit. Variants and fragments of these REP1 and REP2 proteins are also included in the present invention. "Fragments" and "variants" of REP1 and REP2 are those which, when encoded by the plasmid in place of the native ORF, do not disrupt the stable multicopy maintenance of the plasmid within a suitable yeast population. Such variants and fragments of REP1 and REP2 will usually have at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or more, homology with a REP1 and REP2 protein, respectively, as encoded by one of plasmids pSR1, pSB1, pSB2, pSB3, pSB4, pSM1, pKD1, pPM1 and the 2μm plasmid.

The REP1 and REP2 proteins encoded by the ORFs on the plasmid must be compatible. REP1 and REP2 are compatible if they contribute, in combination with the other functional elements of the plasmid, towards the stable multicopy maintenance of the plasmid which encodes them. Whether or not a REP1 and REP2 ORF contributes towards the stable multicopy maintenance of the plasmid which encodes them can be determined by preparing mutants of the plasmid in which each of the REP1 and REP2 ORFs are specifically disrupted. If the disruption of an ORF impairs the stable multicopy maintenance of the plasmid then the ORF can be concluded to contribute towards the stable multicopy maintenance of the plasmid in the non-mutated version. It is preferred that the REP1 and REP2 proteins have the sequences of REP1 and REP2 proteins encoded by the same naturally occurring 2μm-family plasmid, such as pSR1, pSB1, pSB2, pSB3, pSB4, pSM1, pKD1, pPM1 and the 2μm plasmid, or variant or fragments thereof.

A 2μm-family plasmid comprises two inverted repeat sequences. The inverted repeats may be any size, so long as they each contain an FRT site (see above). The inverted repeats are typically highly homologous. They may share greater than 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5% or more sequence identity. In a preferred embodiment they are identical. Typically the inverted repeats are each between 200 to 1000 bp in length. Preferred inverted repeat sequences may each have a length of from 200 to 300 bp, 300 to 400 bp, 400 to 500 bp, 500 to 600 bp, 600 to 700 bp, 700 to 800 bp, 800 to 900 bp, or 900 to 1000 bp. Particularly preferred inverted repeats are those of the

plasmids pSR1 (959 bp), pSB1 (675 bp), pSB2 (477 bp), pSB3 (391 bp), pSM1 (352 bp), pKD1 (346 bp), the 2μm plasmid (599 bp), pSB4 and pPM1.

The sequences of the inverted repeats may be varied. However, the sequences of the FRT site in each inverted repeat should be compatible with the specificity of the FLP protein encoded by the plasmid, thereby to enable the encoded FLP protein to act to catalyse the site-specific recombination between the inverted repeat sequences of the plasmid. Recombination between inverted repeat sequences (and thus the ability of the FLP protein to recognise the FRT sites with the plasmid) can be determined by methods known in the art. For example, a plasmid in a yeast cell under conditions that favour FLP expression can be assayed for changes in the restriction profile of the plasmid which would result from a change in the orientation of a region of the plasmid relative to another region of the plasmid. The detection of changes in restriction profile indicate that the FLP protein is able to recognise the FRT sites in the plasmid and therefore that the FRT site in each inverted repeat are compatible with the specificity of the FLP protein encoded by the plasmid.

In a particularly preferred embodiment, the sequences of inverted repeats, including the FRT sites, are derived from the same 2μm-family plasmid as the ORF encoding the FLP protein, such as pSR1, pSB1, pSB2, pSB3, pSB4, pSM1, pKD1, pPM1 or the 2μm plasmid.

The inverted repeats are typically positioned within the 2μm-family plasmid such that the two regions defined between the inverted repeats (e.g. such as defined as UL and US in the 2μm plasmid) are of approximately similar size, excluding exogenously introduced sequences such as transgenes. For example, one of the two regions may have a length equivalent to at least 40%, 50%, 60%, 70%, 80%, 90%, 95% or more, up to 100%, of the length of the other region.

A 2μm-family plasmid comprises the ORF that encodes FLP and one inverted repeat (arbitrarily termed "IR1" to distinguish it from the other inverted repeat mentioned in the next paragraph) juxtaposed in such a manner that IR1 occurs at the distal end of the FLP

ORF, without any intervening coding sequence, for example as seen in the 2μm plasmid. By "distal end" in this context we mean the end of the FLP ORF opposite to the end from which the promoter initiates its transcription. In a preferred embodiment, the distal end of the FLP ORF overlaps with IR1.

A 2μm-family plasmid comprises the ORF that encodes REP2 and the other inverted repeat (arbitrarily termed "IR2" to distinguish it from IR1 mentioned in the previous paragraph) juxtaposed in such a manner that IR2 occurs at the distal end of the REP2 ORF, without any intervening coding sequence, for example as seen in the 2μm plasmid. By "distal end" in this context we mean the end of the REP2 ORF opposite to the end from which the promoter initiates its transcription.

In one embodiment, the ORFs encoding REP2 and FLP may be present on the same region of the two regions defined between the inverted repeats of the 2μm-family plasmid, which region may be the bigger or smaller of the regions (if there is any inequality in size between the two regions).

In one embodiment, the ORFs encoding REP2 and FLP may be transcribed from divergent promoters.

Typically, the regions defined between the inverted repeats (e.g. such as defined as UL and US in the 2μm plasmid) of a 2μm-family plasmid may comprise not more than two endogenous genes that encode a protein that functions in the stable maintenance of the 2μm-family plasmid as a multicopy plasmid. Thus in a preferred embodiment, one region of the plasmid defined between the inverted repeats may comprise not more than the ORFs encoding FLP and REP2; FLP and REP1; or REP1 and REP2, as endogenous coding sequence.

A 2μm-family plasmid comprises an origin of replication (also known as an autonomously replicating sequence - "ARS"), which is typically bidirectional. Any appropriate ARS sequence can be present. Consensus sequences typical of yeast chromosomal origins of replication may be appropriate (Broach *et al*, 1982, *Cold Spring*

Harbor Symp. Quant. Biol., **47**, 1165-1174; Williamson, *Yeast*, 1985, **1**, 1-14). Preferred ARSs include those isolated from pSR1, pSB1, pSB2, pSB3, pSB4, pSM1, pKD1, pPM1 and the 2μm plasmid.

Thus, a 2μm-family plasmid typically comprises at least ORFs encoding FLP and REP2, two inverted repeat sequences each inverted repeat comprising an FRT site compatible with FLP protein, and an ARS sequence. Preferably the plasmid also comprises an ORF encoding REP1, although it may be supplied in *trans*, as discussed above. Preferably the FRT sites are derived from the same 2μm-family plasmid as the sequence of the encoded FLP protein. Preferably the sequences of the encoded REP1 and REP2 proteins are derived from the same 2μm-family plasmid as each other. More preferably, the FRT sites are derived from the same 2μm-family plasmid as the sequence of the encoded FLP, REP1 and REP2 proteins. Even more preferably, the sequences of the ORFs encoding FLP, REP1 and REP2, and the sequence of the inverted repeats (including the FRT sites) are derived from the same 2μm-family plasmid. Yet more preferably, the ARS site is obtained from the same 2μm-family plasmid as one or more of the ORFs of FLP, REP1 and REP2, and the sequence of the inverted repeats (including the FRT sites). Preferred plasmids include plasmids pSR1, pSB3 and pSB4 as obtained from *Zygosaccharomyces rouxii*, pSB1 or pSB2 both as obtained from *Zygosaccharomyces bailli*, pSM1 as obtained from *Zygosaccharomyces fermentati*, pKD1 as obtained from *Kluyveromyces drosophilarum*, pPM1 as obtained from *Pichia membranaefaciens*, and the 2μm plasmid as obtained from *Saccharomyces cerevisiae*, for example as described in Volkert *et al*, 1989, *op. cit.*, Murray *et al*, *op. cit.* and Painting *et al, op. cit.*

Optionally, a 2μm-family plasmid may comprise a region equivalent to the *STB* region (also known as REP3) of the 2μm plasmid, as defined in Volkert *et al*, *op. cit.* The *STB* region in a 2μm-family plasmid of the invention may comprise two or more tandem repeat sequences, such as three, four, five or more. Alternatively, no tandem repeat sequences may be present. The tandem repeats may be any size, such as 10, 20, 30, 40, 50, 60 70, 80, 90, 100 bp or more in length. The tandem repeats in the *STB* region of the 2μm plasmid are 62 bp in length. It is not essential for the sequences of the tandem repeats to be identical. Slight sequence variation can be tolerated. It may be preferable

to select an *STB* region from the same plasmid as either or both of the REP1 and REP2 ORFs. The *STB* region is thought to be a *cis*-acting element and preferably is not transcribed.

Optionally, a 2μm-family plasmid may comprise an additional ORF that encodes a protein that functions in the stable maintenance of the 2μm-family plasmid as a multicopy plasmid. The additional protein can be designated RAF or D. ORFs encoding the RAF or D gene can be seen on, for example, the 2μm plasmid and pSM1. Thus a RAF or D ORF can comprise a sequence suitable to encode the protein product of the RAF or D gene ORFs encoded by the 2μm plasmid or pSM1, or variants and fragments thereof. Thus variants and fragments of the protein products of the RAF or D genes of the 2μm plasmid or pSM1 are also included in the present invention. "Fragments" and "variants" of the protein products of the RAF or D genes of the 2μm plasmid or pSM1 are those which, when encoded by the 2μm plasmid or pSM1 in place of the native ORF, do not disrupt the stable multicopy maintenance of the plasmid within a suitable yeast population. Such variants and fragments will usually have at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99%, or more, homology with the protein product of the RAF or D gene ORFs encoded by the 2μm plasmid or pSM1.

The present invention provides a 2μm-family plasmid comprising a polynucleotide sequence insertion, deletion and/or substitution between the first base after the last functional codon of at least one of either a *REP2* gene or an *FLP* gene and the last base before the FRT site in an inverted repeat adjacent to said gene.

A polynucleotide sequence insertion is any additional polynucleotide sequence inserted into the plasmid. Preferred polynucleotide sequence insertions are described below. A deletion is removal of one or more base pairs, such as the removal of up to 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more base pairs, which may be as a single contiguous sequence or from spaced apart regions within a DNA sequence. A substitution is the replacement of one or more base pairs, such as the replacement of up to 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more base pairs, which may be

as a single contiguous sequence or from spaced apart regions within a DNA sequence. It is possible for a region to be modified by any two of insertion, deletion or substitution, or even all three.

The last functional codon of either a *REP2* gene or a *FLP* gene is the codon in the open reading frame of the gene that is furthest downstream from the promoter of the gene whose replacement by a stop codon will lead to an unacceptable loss of multicopy stability of the plasmid, when determined by a test such as defined in Chinery & Hinchliffe (1989, *Curr. Genet.*, **16**, 21-25). It may be appropriate to modify the test defined by Chinery & Hinchcliffe, for example to maintain exponential logarithmic growth over the desired number of generations, by introducing modifications to the inocula or sub-culturing regime. This can help to account for differences between the host strain under analysis and *S. cerevisiae* S150-2B used by Chinery & Hinchcliffe, and/or to optimise the test for the individual characteristics of the plasmid(s) under assay, which can be determined by the identity of the insertion site within the small US-region of the 2μm-like plasmid, and/or other differences in the 2μm-like plasmid, such as the size and nature of the inserted sequences within the 2μm-like plasmid and/or insertions elsewhere in the 2μm-like plasmid. For yeast that do not grow in the non-selective medium (YPD, also designated YEPD) defined in Chinery & Hinchliffe (1989, *Curr. Genet.*, **16**, 21-25) other appropriate non-selective media might be used. A suitable alternative non-selective medium typically permits exponential logarithmic growth over the desired number of generations. For example, sucrose or glucose might be used as alternative carbon sources. Plasmid stability may be defined as the percentage cells remaining prototrophic for the selectable marker after a defined number of generations. The number of generations will preferably be sufficient to show a difference between a control plasmid, such as pSAC35 or pSAC310, or to show comparable stability to such a control plasmid. The number of generations may be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100 or more. Higher numbers are preferred. The acceptable plasmid stability might be 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9% or substantially 100%. Higher percentages are preferred. The skilled person will appreciate that, even though a plasmid may have a stability less than

100% when grown on non-selective media, that plasmid can still be of use when cultured in selective media. For example plasmid pDB2711 as described in the examples is only 10% stable when the stability is determined accordingly to Example 1, but provides a 15-fold increase in recombinant transferrin productivity in shake flask culture under selective growth conditions.

Thus, disruption of the *REP2* or *FLP* genes at any point downstream of the last functional codon in either gene, by insertion of a polynucleotide sequence insertion, deletion or substitution will not lead to an unacceptable loss of multicopy stability of the plasmid. We have surprisingly found that the *REP2* gene of the 2μm plasmid can be disrupted after codon 59 and that the *FLP* gene of the 2μm plasmid can be disrupted after codon 344, each without leading to an unacceptable loss of multicopy stability of the plasmid. The last functional codon in equivalent genes in other 2μm-family plasmids can be determined routinely by modifying the relevant genes and determining stability as described above. Typically, therefore, modified plasmids of the present invention are stable, in the sense that the modifications made thereto do not lead to an unacceptable loss of multicopy stability of the plasmid.

The *REP2* and *FLP* genes in a 2μm plasmid of the invention each have an inverted repeat adjacent to them. The inverted repeat can be identified because (when reversed) it matches the sequence of another inverted repeat within the same plasmid. By "adjacent" is meant that the *FLP* or *REP2* gene and its inverted repeat are juxtaposed in such a manner that the inverted repeat occurs at the distal end of the gene, without any intervening coding sequence, for example as seen in the 2μm plasmid. By "distal end" in this context we mean the end of the gene opposite to the end from which the promoter initiates its transcription. In a preferred embodiment, the distal end of the gene overlaps with the inverted repeat.

In a first preferred aspect of the invention, the polynucleotide sequence insertion, deletion and/or substitution occurs between the first base after the last functional codon of the *REP2* gene and the last base before the FRT site in an inverted repeat adjacent to said gene, preferably between the first base of the inverted repeat and the last base before the

FRT site, even more preferably at a position after the translation termination codon of the *REP2* gene and before the last base before the FRT site.

The term "between", in this context, includes the defined outer limits and so, for example, an insertion, deletion and/or substitution "between the first base after the last functional codon of the *REP2* gene and the last base before the FRT site" includes insertions, deletions and/or substitutions at the first base after the last functional codon of the *REP2* gene and insertions, deletions and/or substitutions at the last base before the FRT site.

In a second preferred aspect of the invention, the polynucleotide sequence insertion, deletion and/or substitution occurs between the first base after the last functional codon of the *FLP* gene and the last base before the FRT site in an inverted repeat adjacent to said gene, preferably between the first base of the inverted repeat and the last base before the FRT site, more preferably between the first base after the end of the FLP coding sequence and the last base before the FRT site, such as at the first base after the end of the FLP coding sequence. The polynucleotide sequence insertion, deletion and/or substitution may occur between the last base after the end of *FLP* and the *Fsp*I-site in the inverted repeat, but optionally not within the *Fsp*I-site.

In one embodiment, other than the polynucleotide sequence insertion, deletion and/or substitution, the *FLP* gene and/or the *REP2* gene has the sequence of a *FLP* gene and/or a *REP2* gene, respectively, derived from a naturally occurring 2μm-family plasmid.

The term "derived from" includes sequences having an identical sequence to the sequence from which they are derived. However, variants and fragments thereof, as defined above, are also included. For example, an *FLP* gene having a sequence derived from the *FLP* gene of the 2μm plasmid may have a modified promoter or other regulatory sequence compared to that of the naturally occurring gene. Alternatively, an *FLP* gene having a sequence derived from the *FLP* gene of the 2μm plasmid may have a modified nucleotide sequence in the open reading frame which may encode the same protein as the

naturally occurring gene, or may encode a modified FLP protein. The same considerations apply to *REP2* genes having a sequence derived from a particular source.

A naturally occurring 2μm-family plasmid is any plasmid having the features defined above as being essential features for a 2μm-family plasmid, which plasmid is found to naturally exist in yeast, i.e. has not been recombinantly modified to include heterologous sequence. Preferably the naturally occurring 2μm-family plasmid is selected from pSR1 (Accession No. X02398), pSB3 (Accession No. X02608) or pSB4 as obtained from *Zygosaccharomyces rouxii*, pSB1 or pSB2 (Accession No. NC_002055 or M18274) both as obtained from *Zygosaccharomyces bailli*, pSM1 (Accession No. NC_002054) as obtained from *Zygosaccharomyces fermentati*, pKD1 (Accession No. X03961) as obtained from *Kluyveromyces drosophilarum*, pPM1 as obtained from *Pichia membranaefaciens*, or, most preferably, the 2μm plasmid (Accession No. NC_001398 or J01347) as obtained from *Saccharomyces cerevisiae*. Accession numbers refer to deposits at the NCBI.

Preferably, other than the polynucleotide sequence insertion, deletion and/or substitution, the sequence of the inverted repeat adjacent to said *FLP* and/or *REP2* gene is derived from the sequence of the corresponding inverted repeat in the same naturally occurring 2μm-family plasmid as the sequence from which the gene is derived. Thus, for example, if the *FLP* gene is derived from the 2μm plasmid as obtained from *S. cerevisiae*, then it is preferred that the inverted repeat adjacent to the *FLP* gene has a sequence derived from the inverted repeat that is adjacent to the *FLP* gene in the 2μm plasmid as obtained from *S. cerevisiae*. If the *REP2* gene is derived from the 2μm plasmid as obtained from *S. cerevisiae*, then it is preferred that the inverted repeat adjacent to the *REP2* gene has a sequence derived from the inverted repeat that is adjacent to the *REP2* gene in the 2μm plasmid as obtained from *S. cerevisiae*.

Where, in the first preferred aspect of the invention, other than the polynucleotide sequence insertion, deletion and/or substitution, the *REP2* gene and the inverted repeat sequence have sequences derived from the corresponding regions of the 2μm plasmid as obtained from *S. cerevisiae*, then it is preferred that the polynucleotide sequence

insertion, deletion and/or substitution occurs at a position between the first base of codon 59 of the *REP* gene and the last base before the FRT site in the adjacent inverted repeat, more preferably at a position between the first base of the inverted repeat and the last base before the FRT site, even more preferably at a position after the translation termination codon of the *REP2* gene and before the last base before the FRT site, such as at the first base after the end of the *REP2* coding sequence.

Where, other than the polynucleotide sequence insertion, deletion and/or substitution, the *REP2* gene and the inverted repeat sequence have sequences derived from the corresponding regions of the 2μm plasmid as obtained from *S. cerevisiae*, then in one embodiment, other than the polynucleotide sequence insertion, deletion and/or substitution, the sequence of the *REP2* gene and the adjacent inverted repeat is as defined by SEQ ID NO:1 or variant thereof. In SEQ ID NO:1, the first base of codon 59 of the REP2 gene is represented by base number 175 and the last base before the FRT site is represented by base number 1216. The FRT sequence given here is the 55-base-pair sequence from Sadowski *et al*, 1986, pp7-10, *Mechanisms of Yeast Recombination* (Current Communications in Molecular Biology) CSHL. Ed. Klar, A. Strathern, J. N. In SEQ ID NO:1, the first base of the inverted repeat is represented by base number 887 and the first base after the translation termination codon of the *REP2* gene is represented by base number 892.

In an even more preferred embodiment of the first aspect of the invention, other than the polynucleotide sequence insertion, deletion and/or substitution, the *REP2* gene and the inverted repeat sequence have sequences derived from the corresponding regions of the 2μm plasmid as obtained from *S. cerevisiae* and, in the absence of the interruption the polynucleotide sequence insertion, deletion and/or substitution, comprise an *XcmI* site or an *FspI* site within the inverted repeat and the polynucleotide sequence insertion, deletion and/or substitution occurs at the *XcmI* site, or at the *FspI* site. In SEQ ID NO:1, the *XcmI* site is represented by base numbers 935-949 and the *FspI* site is represented by base numbers 1172-1177.

Where, in the second preferred aspect of the invention, other than the polynucleotide sequence insertion, deletion and/or substitution, the *FLP* gene and the adjacent inverted repeat sequence have sequences derived from the corresponding regions of the 2μm plasmid as obtained from *S. cerevisiae*, then it is preferred that the polynucleotide sequence insertion, deletion and/or substitution occurs at a position between the first base of codon 344 of the *FLP* gene and the last base before the FRT site, more preferably between the first base of the inverted repeat and the last base before the FRT site, yet more preferably between the first base after the end of the FLP coding sequence and the last base before the FRT site, such as at the first base after the end of the FLP coding sequence. The *Fsp*I site between the FLP gene and the FRT site can be avoided as an insertion site.

Where, other than the polynucleotide sequence insertion, deletion and/or substitution, the *FLP* gene and the adjacent inverted repeat sequence have sequences derived from the corresponding regions of the 2μm plasmid as obtained from *S. cerevisiae*, then in one embodiment, other than the polynucleotide sequence insertion, deletion and/or substitution, the sequence of the *FLP* gene and the inverted repeat that follows the *FLP* gene is as defined by SEQ ID NO:2 or variant thereof. In SEQ ID NO:2, the first base of codon 344 of the *FLP* gene is represented by base number 1030 and the last base before the FRT site is represented by base number 1419, the first base of the inverted repeat is represented by base number 1090, and the first base after the end of the FLP coding sequence is represented by base number 1273.

In an even more preferred embodiment of the second preferred aspect of the invention, other than the polynucleotide sequence insertion, deletion and/or substitution, the *FLP* gene and the adjacent inverted repeat sequence have sequences derived from the corresponding regions of the 2μm plasmid as obtained from *S. cerevisiae* and, in the absence of the polynucleotide sequence insertion, deletion and/or substitution, comprise an *HgaI* site or an *FspI* site within the inverted repeat and the polynucleotide sequence insertion, deletion and/or substitution occurs at the cut formed by the action of *HgaI* on the *HgaI* site (*HgaI* cuts outside the 5bp sequence that it recognises), or at the *FspI*. In

SEQ ID NO:2, the *HgaI* site is represented by base numbers 1262-1266 and the *FspI* site is represented by base numbers 1375-1380.

The skilled person will appreciate that the features of the plasmid defined by the first and second preferred aspects of the present invention are not mutually exclusive. Thus, a plasmid according to a third preferred aspect of the present invention may comprise polynucleotide sequence insertions, deletions and/or substitutions between the first bases after the last functional codons of both of the *REP2* gene and the *FLP* gene and the last bases before the FRT sites in the inverted repeats adjacent to each of said genes, which polynucleotide sequence insertions, deletions and/or substitutions can be the same or different. For example, a plasmid according to a third aspect of the present invention may, other than the polynucleotide sequence insertions, deletions and/or substitutions, comprise the sequence of SEQ ID NO:1 or variant thereof and the sequence of SEQ ID NO:2 or variant thereof, each comprising a polynucleotide sequence insertion, deletion and/or substitution at a position as defined above for the first and second preferred aspects of the invention, respectively.

The skilled person will appreciate that the features of the plasmid defined by the first, second and third preferred aspects of the present invention do not exclude the possibility of the plasmid also having other sequence modifications. Thus, for example, a 2μm-family plasmid of the first, second and third preferred aspects of the present invention may additionally comprise a polynucleotide sequence insertion, deletion and/or substitution which is not at a position as defined above. Accordingly, the plasmid may additionally carry transgenes at a site other than the insertion sites of the invention.

Alternative insertion sites in 2μm plasmids are known in the art, but do not provide the advantages of using the insertion sites defined by the present invention. Nevertheless, plasmids which already include a polynucleotide sequence insertion, deletion and/or substitution at a site known in the art can be further modified by making one or more further modifications at one or more of the sites defined by the first, second and third preferred aspects of the present invention. The skilled person will appreciate that, as discussed in the introduction to this application, there are considerable technical

limitations placed on the insertion of transgenes at sites of 2μm-family plasmids other than as defined by the first and second aspects of the invention.

Typical modified 2μm plasmids known in the art include those described in Rose & Broach (1990, *Methods Enzymol.*, **185**, 234-279), such as plasmids pCV19, pCV20, CV_{neo}, which utilise an insertion at *Eco*RI in *FLP*, plasmids pCV21, pGT41 and pYE which utilise *Eco*RI in *D* as the insertion site, plasmid pHKB52 which utilises *Pst*I in *D* as the insertion site, plasmid pJDB248 which utilises an insertion at *Pst*I in *D* and *Eco*RI in *D*, plasmid pJDB219 in which *Pst*I in *D* and *Eco*RI in *FLP* are used as insertion sites, plasmid G18, plasmid pAB18 which utilises an insertion at *Cla*I in *FLP*, plasmids pGT39 and pA3, plasmids pYT11, pYT14 and pYT11-LEU which use *Pst*I in *D* as the insertion site, and plasmid PTY39 which uses *Eco*RI in *FLP* as the insertion site. Other 2μm plasmids include pSAC3, pSAC3U1, pSAC3U2, pSAC300, pSAC310, pSAC3C1, pSAC3PL1, pSAC3SL4, and pSAC3SC1 are described in EP 0 286 424 and Chinery & Hinchliffe (1989, *Curr. Genet.*, **16**, 21-25) which also described *Pst*I, *Eag*I or *Sna*BI as appropriate 2μm insertion sites. Further 2μm plasmids include pAYE255, pAYE316, pAYE443, pAYE522 (Kerry-Williams *et al*, 1998, *Yeast*, **14**, 161-169), pDB2244 (WO 00/44772) and pAYE329 (Sleep *et al*, 2001, *Yeast*, **18**, 403-421).

In one preferred embodiment, a 2μm-like plasmid as defined by the first, second and third preferred aspects of the present invention additionally comprises a polynucleotide sequence insertion, deletion and/or substitution which occurs within an untranscribed region around the ARS sequence. For example, in the 2μm plasmid obtained from *S. cerevisiae*, the untranscribed region around the ARS sequence extends from end of the D gene to the beginning of ARS sequence. Insertion into *Sna*BI (near the origin of replication sequence ARS) is described in Chinery & Hinchliffe, 1989, *Curr. Genet.*, **16**, 21-25. The skilled person will appreciate that an additional polynucleotide sequence insertion, deletion and/or substitution can also occur within the untranscribed region at neighbouring positions to the *Sna*BI site described by Chinery & Hinchliffe.

A plasmid according to any of the first, second or third aspects of the present invention may be a plasmid capable of autonomous replication in yeast, such as a member of the

Saccharomyces, *Kluyveromyces*, *Zygosaccharomyces*, or *Pichia* genus, such *Saccharomyces cerevisiae*, *Saccharomyces carlsbergensis*, *Kluyveromyces lactis*, *Pichia pastoris and Pichia membranaefaciens*, *Zygosaccharomyces rouxii*, *Zygosaccharomyces bailii*, *Zygosaccharomyces fermentati*, or *Kluyveromyces drosphilarum*. *S. cerevisiae* and *S. carlsbergensis* are thought to provide a suitable host cell for the autonomous replication of all known 2μm plasmids.

In a preferred embodiment, the, or at least one, polynucleotide sequence insertion, deletion and/or substitution included in a 2μm-family plasmid of the invention is a polynucleotide sequence insertion. Any polynucleotide sequence insertion may be used, so long as it is not unacceptably detrimental to the stability of the plasmid, by which we mean that the plasmid is at least 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 40% 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9% or substantially 100% stable on non-selective media such as YEPD media compared to the unmodified plasmid, the latter of which is assigned a stability of 100%. Preferably, the above mentioned level of stability is seen after separately culturing yeast cells comprising the modified and unmodified plasmids in a culture medium for one, two, three, four, five, six, seven, eight, nine ten, 11, 12, 13, 14, 15, 16, 17, 18, 19 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100 or more generations.

Where the plasmid comprises a selectable marker, higher levels of stability can be obtained when transformants are grown under selective conditions (e.g. in minimal medium), since the medium can place a selective pressure on the host to retain the plasmid.

Stability in non-selective and selective (e.g. minimal) media can be determined using the methods set forth above. Stability in selective media can be demonstrated by the observation that the plasmids can be used to transform yeast to prototrophy.

Typically, the polynucleotide sequence insertion will be at least 4, 6, 8, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500 or more base pairs in length. Usually, the polynucleotide sequence insertion will be up to 1kb, 2kb, 3kb, 4kb, 5kb, 6kb,

7kb, 8kb, 9kb, 10kb or more in length. The skilled person will appreciate that the 2μm plasmid of the present invention may comprise multiple polynucleotide sequence insertions at different sites within the plasmid. Typically, the total length of polynucleotide sequence insertions is no more than 5kb, 10kb, 15kb, 20kb, 25kb or 30kb although greater total length insertion may be possible.

The polynucleotide sequence may or may not be a linker sequence used to introduce new restriction sites. For example a synthetic linker may or may not be introduced at the *Fsp*I site after the FLP gene, such as to introduce a further restriction site (e.g. *Bam*HI).

The polynucleotide sequence insertion may contain a transcribed region or may contain no transcribed region. A transcribed region may encode an open reading frame, or may be non-coding. The polynucleotide sequence insertion may contain both transcribed and non-transcribed regions.

A transcribed region is a region of DNA that can be transcribed by RNA polymerase, typically yeast RNA polymerase. A transcribed region can encode a functional RNA molecule, such as ribosomal or transfer RNA or an RNA molecule that can function as an antisense or RNA interference ("RNAi") molecule. Alternatively a transcribed region can encode a messenger RNA molecule (mRNA), which mRNA can contain an open reading frame (ORF) which can be translated *in vivo* to produce a protein. The term "protein" as used herein includes all natural and non-natural proteins, polypeptides and peptides. Preferably, the ORF encodes a heterologous protein. By "heterologous protein" we mean a protein that is not naturally encoded by a 2μm-family plasmid (i.e. a "non- 2μm-family plasmid protein"). For convenience the terms "heterologous protein" and "non- 2μm-family plasmid protein" are used synonymously throughout this application. Preferably, therefore, the heterologous protein is not a FLP, REP1, REP2, or a RAF/D protein as encoded by any one of pSR1, pSB3 or pSB4 as obtained from *Z. rouxii*, pSB1 or pSB2 both as obtained from *Z. bailli*, pSM1 as obtained from *Z. fermentati*, pKD1 as obtained from *K. drosophilarum*, pPM1 as obtained from *P. membranaefaciens* and the 2μm plasmid as obtained from *S. cerevisiae*.

Where the polynucleotide sequence insertion encodes an open reading frame, then it may additionally comprise some polynucleotide sequence that does not encode an open reading frame (termed "non-coding region").

Non-coding region in the polynucleotide sequence insertion may contain one or more regulatory sequences, operatively linked to the open reading frame, which allow for the transcription of the open reading frame and/or translation of the resultant transcript.

The term "regulatory sequence" refers to a sequence that modulates (i.e., promotes or reduces) the expression (i.e., the transcription and/or translation) of an open reading frame to which it is operably linked. Regulatory regions typically include promoters, terminators, ribosome binding sites and the like. The skilled person will appreciate that the choice of regulatory region will depend upon the intended expression system. For example, promoters may be constitutive or inducible and may be cell- or tissue-type specific or non-specific.

Where the expression system is yeast, such as *Saccharomyces cerevisiae*, suitable promoters for *S. cerevisiae* include those associated with the *PGK1* gene, *GAL1* or *GAL10* genes, *TEF1*, *TEF2*, *PYK1*, *PMA1*, *CYC1*, *PHO5*, *TRP1*, *ADH1*, *ADH2*, the genes for glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, triose phosphate isomerase, phosphoglucose isomerase, glucokinase, α-mating factor pheromone, a-mating factor pheromone, the *PRB1* promoter, the *PRA1* promoter, the *GPD1* promoter, and hybrid promoters involving hybrids of parts of 5' regulatory regions with parts of 5' regulatory regions of other promoters or with upstream activation sites (e.g. the promoter of EP-A-258 067).

Suitable transcription termination signals are well known in the art. Where the host cell is eukaryotic, the transcription termination signal is preferably derived from the 3' flanking sequence of a eukaryotic gene, which contains proper signals for transcription termination and polyadenylation. Suitable 3' flanking sequences may, for example, be those of the gene naturally linked to the expression control sequence used, i.e. may correspond to the promoter. Alternatively, they may be different. In that case, and where

the host is a yeast, preferably *S. cerevisiae*, then the termination signal of the *S. cerevisiae ADH1*, *ADH2*, *CYC1*, or *PGK1* genes are preferred.

It may be beneficial for the promoter and open reading frame of the heterologous gene, such as the those of the chaperone *PDI1*, to be flanked by transcription termination sequences so that the transcription termination sequences are located both upstream and downstream of the promoter and open reading frame, in order to prevent transcriptional read-through into neighbouring genes, such as 2μm genes, and vice versa.

In one embodiment, the favoured regulatory sequences in yeast, such as *Saccharomyces cerevisiae*, include: a yeast promoter (e.g. the *Saccharomyces cerevisiae PRB1* promoter), as taught in EP 431 880; and a transcription terminator, preferably the terminator from *Saccharomyces ADH1*, as taught in EP 60 057.

It may be beneficial for the non-coding region to incorporate more than one DNA sequence encoding a translational stop codon, such as UAA, UAG or UGA, in order to minimise translational read-through and thus avoid the production of elongated, non-natural fusion proteins. The translation stop codon UAA is preferred. Preferably, at least two translation stop codons are incorporated.

The term "operably linked" includes within its meaning that a regulatory sequence is positioned within any non-coding region such that it forms a relationship with an open reading frame that permits the regulatory region to exert an effect on the open reading frame in its intended manner. Thus a regulatory region "operably linked" to an open reading frame is positioned in such a way that the regulatory region is able to influence transcription and/or translation of the open reading frame in the intended manner, under conditions compatible with the regulatory sequence.

Where the polynucleotide sequence insertion as defined by the first, second or third aspects of the present invention includes an open reading frame that encodes a protein, then it may be advantageous for the encoded protein to be secreted. In that case, a

sequence encoding a secretion leader sequence may be included in the open reading frame.

For production of proteins in eukaryotic species such as the yeasts *Saccharomyces cerevisiae*, *Zygosaccharomyces* species, *Kluyveromyces lactis* and *Pichia pastoris*, known leader sequences include those from the *S. cerevisiae* acid phosphatase protein (Pho5p) (see EP 366 400), the invertase protein (Suc2p) (see Smith *et al.* (1985) *Science*, **229**, 1219-1224) and heat-shock protein-150 (Hsp150p) (see WO 95/33833). Additionally, leader sequences from the *S. cerevisiae* mating factor alpha-1 protein (MFα-1) and from the human lysozyme and human serum albumin (HSA) protein have been used, the latter having been used especially, although not exclusively, for secreting human albumin. WO 90/01063 discloses a fusion of the MFα-1 and HSA leader sequences, which advantageously reduces the production of a contaminating fragment of human albumin relative to the use of the MFα-1 leader sequence. In addition, the natural transferrin leader sequence may be used to direct secretion of transferrin and other heterologous proteins.

Alternatively, the encoded protein may be intracellular.

In one preferred embodiment, at least one polynucleotide sequence insertion as defined by the first, second or third aspects of the present invention includes an open reading frame comprising a sequence that encodes a yeast protein. In another preferred embodiment, at least one polynucleotide sequence insertion as defined by the first, second or third aspects of the present invention includes an open reading frame comprising a sequence that encodes a yeast protein from the same host from which the 2μm-like plasmid is derived.

In another preferred embodiment, at least one polynucleotide sequence insertion as defined by the first, second or third aspects of the present invention includes an open reading frame comprising a sequence that encodes a protein involved in protein folding, or which has chaperone activity or is involved in the unfolded protein response (Stanford Genome Database (SGD), http:://db.yeastgenome.org). Preferred proteins may be

selected from protein encoded by *AHA1*, *CCT2*, *CCT3*, *CCT4*, *CCT5*, *CCT6*, *CCT7*, *CCT8*, *CNS1*, *CPR3*, *CPR6*, *ERO1*, *EUG1*, *FMO1*, *HCH1*, *HSP10*, *HSP12*, *HSP104*, *HSP26*, *HSP30*, *HSP42*, *HSP60*, *HSP78*, *HSP82*, *JEM1*, *MDJ1*, *MDJ2*, *MPD1*, *MPD2*, *PDI1*, *PFD1*, *ABC1*, *APJ1*, *ATP11*, *ATP12*, *BTT1*, *CDC37*, *CNS1*, *CPR6*, *CPR7*, *HSC82*, *KAR2*, *LHS1*, *MGE1*, *MRS11*, *NOB1*, *ECM10*, *SSA1*, *SSA2*, *SSA3*, *SSA4*, *SSC1*, *SSE2*, *SIL1*, *SLS1*, *ORM1*, *UBI4*, *ORM2*, *PER1*, *PTC2*, *PSE1* and HAC1 or a truncated intronless *HAC1* (Valkonen *et al.* 2003, *Applied Environ. Micro.* **69**, 2065).

A preferred protein involved in protein folding, or protein with chaperone activity or a protein involved in the unfolded protein response may be:

- a heat shock protein, such as a protein that is a member of the hsp70 family of proteins (including Kar2p, SSA and SSB proteins, for example proteins encoded by *SSA1, SSA2, SSA3, SSA4, SSB1* and *SSB2*), a protein that is a member of the HSP90-family, or a protein that is a member of the HSP40-family or proteins involved in their modulation (e.g. Sil1p), including DNA-J and DNA-J-like proteins (e.g. Jem1p, Mdj2p);

- a protein that is a member of the karyopherin/importin family of proteins, such as the alpha or beta families of karyopherin/importin proteins, for example the karyopherin beta protein encoded by *PSE1*;

- a protein that is a member of the ORMDL family described by Hjelmqvist *et al*, 2002, *Genome Biology*, **3**(6), research0027.1-0027.16, such as Orm2p.

- a protein that is naturally located in the endoplasmic reticulum or elsewhere in the secretory pathway, such as the golgi. For example, a protein that naturally acts in the lumen of the endoplasmic reticulum (ER), particularly in secretory cells, such as PDI

- a protein that is a transmembrane protein anchored in the ER, such as a member of the ORMDL family described by Hjelmqvist *et al*, 2002, *supra*, (for example, Orm2p);

- a protein that acts in the cytosol, such as the hsp70 proteins, including SSA and SSB proteins, for example proteins encoded by *SSA1, SSA2, SSA3, SSA4, SSB1* and *SSB2*;

- a protein that acts in the nucleus, the nuclear envelope and/or the cytoplasm, such as Pse1p;

- a protein that is essential to the viability of the cell, such as PDI or an essential karyopherin protein, such as Pse1p;

- a protein that is involved in sulphydryl oxidation or disulphide bond formation, breakage or isomerization, or a protein that catalyses thiol:disulphide interchange reactions in proteins, particularly during the biosynthesis of secretory and cell surface proteins, such as protein disulphide isomerases (e.g. Pdi1p, Mpd1p), homologues (e.g. Eug1p) and/or related proteins (e.g. Mpd2p, Fmo1p, Ero1p);

- a protein that is involved in protein synthesis, assembly or folding, such as PDI and Ssa1p;

- a protein that binds preferentially or exclusively to unfolded, rather than mature protein, such as the hsp70 proteins, including SSA and SSB proteins, for example proteins encoded by *SSA1, SSA2, SSA3, SSA4, SSB1* and *SSB2*;

- a protein that prevents aggregation of precursor proteins in the cytosol, such as the hsp70 proteins, including SSA and SSB proteins, for example proteins encoded by *SSA1, SSA2, SSA3, SSA4, SSB1* and *SSB2*;

- a protein that binds to and stabilises damaged proteins, for example Ssa1p;

- a protein that is involved in the unfolded protein response or provides for increased resistance to agents (such as tunicamycin and dithiothreitol) that induce the unfolded protein response, such as a member of the ORMDL family described by Hjelmqvist *et al*, 2002, *supra* (for example, Orm2p) or a protein involved in the response to stress (e.g. Ubi4p);

- a protein that is a co-chaperone and/or a protein indirectly involved in protein folding and/or the unfolded protein response (e.g. hsp104p, Mdj1p);

- a protein that is involved in the nucleocytoplasmic transport of macromolecules, such as Pse1p;

- a protein that mediates the transport of macromolecules across the nuclear membrane by recognising nuclear location sequences and nuclear export sequences and interacting with the nuclear pore complex, such as Pse1p;

- a protein that is able to reactivate ribonuclease activity against RNA of scrambled ribonuclease as described in as described in EP 0 746 611 and Hillson *et al*, 1984, *Methods Enzymol.*, **107**, 281-292, such as PDI;

- a protein that has an acidic pI (for example, 4.0-4.5), such as PDI;

- a protein that is a member of the Hsp70 family, and preferably possesses an N-terminal ATP-binding domain and a C-terminal peptide-binding domain, such as Ssa1p.

- a protein that is a peptidyl-prolyl cis-trans isomerases (e.g. Cpr3p, Cpr6p);

- a protein that is a homologues of known chaperones (e.g. Hsp10p);

- a protein that is a mitochondrial chaperone (e.g Cpr3p);

- a protein that is a cytoplasmic or nuclear chaperone (e.g Cns1p);

- a protein that is a membrane-bound chaperone (e.g. Orm2p, Fmo1p);

- a protein that has chaperone activator activity or chaperone regulatory activity (e.g. Aha1p, Hac1p, Hch1p);

- a protein that transiently binds to polypeptides in their immature form to cause proper folding transportation and/or secretion, including proteins required for efficient translocation into the endoplasmic reticulum (e.g. Lhs1p) or their site of action within the cell (e.g. PseIp);

- a protein that is a involved in protein complex assembly and/or ribosome assembly (e.g. Atp11p, PseIp, Nob1p);

- a protein of the chaperonin T-complex (e.g. Cct2p); or

- a protein of the prefoldin complex (e.g. Pfd1p).

One preferred chaperone is protein disulphide isomerase (PDI) or a fragment or variant thereof having an equivalent ability to catalyse the formation of disulphide bonds within the lumen of the endoplasmic reticulum (ER). By "PDI" we include any protein having the ability to reactivate the ribonuclease activity against RNA of scrambled ribonuclease as described in EP 0 746 611 and Hillson *et al*, 1984, *Methods Enzymol.*. **107**, 281-292.

Protein disulphide isomerase is an enzyme which typically catalyzes thiol:disulphide interchange reactions, and is a major resident protein component of the E.R. lumen in secretory cells. A body of evidence suggests that it plays a role in secretory protein biosynthesis (Freedman, 1984, *Trends Biochem. Sci.*, **9**, 438-41) and this is supported by direct cross-linking studies *in situ* (Roth and Pierce, 1987, *Biochemistry*, **26**, 4179-82). The finding that microsomal membranes deficient in PDI show a specific defect in

cotranslational protein disulphide formation (Bulleid and Freedman, 1988, *Nature*, **335**, 649-51) implies that the enzyme functions as a catalyst of native disulphide bond formation during the biosynthesis of secretory and cell surface proteins. This role is consistent with what is known of the enzyme's catalytic properties *in vitro*; it catalyzes thiol: disulphide interchange reactions leading to net protein disulphide formation, breakage or isomerization, and can typically catalyze protein folding and the formation of native disulphide bonds in a wide variety of reduced, unfolded protein substrates (Freedman *et al.*, 1989, *Biochem. Soc. Symp.*, **55**, 167-192). PDI also functions as a chaperone since mutant PDI lacking isomerase activity accelerates protein folding (Hayano *et al*, 1995, *FEBS Letters*, **377**, 505-511). Recently, sulphydryl oxidation, not disulphide isomerisation was reported to be the principal function of Protein Disulphide Isomerase in *S. cerevisiae* (Solovyov *et al.*, 2004, J. Biol. Chem., 279 (33) 34095-34100). The DNA and amino acid sequence of the enzyme is known for several species (Scherens *et al*, 1991, *Yeast*, **7**, 185-193; Farquhar *et al*, 1991, *Gene*, **108**, 81-89; EP074661; EP0293793; EP0509841) and there is increasing information on the mechanism of action of the enzyme purified to homogeneity from mammalian liver (Creighton *et al*, 1980, *J. Mol. Biol.*, **142**, 43-62; Freedman *et al*, 1988, *Biochem. Soc. Trans.*, **16**, 96-9; Gilbert, 1989, *Biochemistry*, **28**, 7298-7305; Lundstrom and Holmgren, 1990, *J. Biol. Chem.*, **265**, 9114-9120; Hawkins and Freedman, 1990, *Biochem. J.*, **275**, 335-339). Of the many protein factors currently implicated as mediators of protein folding, assembly and translocation in the cell (Rothman, 1989, *Cell*, **59**, 591-601), PDI has a well-defined catalytic activity.

The deletion or inactivation of the endogenous PDI gene in a host results in the production of an inviable host. In other words, the endogenous PDI gene is an "essential" gene.

PDI is readily isolated from mammalian tissues and the homogeneous enzyme is a homodimer (2×57 kD) with characteristically acidic pI (4.0-4.5) (Hillson *et al*, 1984, *Methods Enzymol.*, **107**, 281-292). The enzyme has also been purified from wheat and from the alga *Chlamydomonas reinhardii* (Kaska *et al*, 1990, *Biochem. J.*, **268**, 63-68), rat (Edman *et al*, 1985, *Nature*, **317**, 267-270), bovine (Yamauchi *et al*, 1987, *Biochem. Biophys. Res. Comm.*, **146**, 1485-1492), human (Pihlajaniemi *et al*, 1987, *EMBO J.*, **6**,

643-9), yeast (Scherens *et al*, *supra*; Farquhar *et al*, *supra*) and chick (Parkkonen *et al*, 1988, *Biochem. J.*, **256**, 1005-1011). The proteins from these vertebrate species show a high degree of sequence conservation throughout and all show several overall features first noted in the rat PDI sequence (Edman *et al.*, 1985, *op. cit.*).

A yeast protein disulphide isomerase precursor, PDI1, can be found as Genbank accession no. CAA42373 or BAA00723. It has the following sequence of 522 amino acids:

```
1   mkfsagavls wsslllassv faqqeavape dsavvklatd sfneyiqshd lvlaeffapw
61  cghcknmape yvkaaetlve knitlaqidc tenqdlcmeh nipgfpslki fknsdvnnsi
121 dyegprtaea ivqfmikqsq pavavvadlp aylanetfvt pvivqsgkid adfnatfysm
181 ankhfndydf vsaenadddf klsiylpsam depvvyngkk adiadadvfe kwlqvealpy
241 fgeidgsvfa qyvesglplg ylfyndeeel eeykplftel akknrglmnf vsidarkfgr
301 hagnlnmkeq fplfaihdmt edlkyglpql seeafdelsd kivleskaie slvkdflkgd
361 aspivksqei fenqdssvfq lvgknhdeiv ndpkkdvlvl yyapwcghck rlaptyqela
421 dtyanatsdv liakldhten dvrgvviegy ptivlypggk ksesvvyqgs rsldslfdfi
481 kenghfdvdg kalyeeaqek aaeeadadae ladeedaihd el
```

An alternative PDI sequence can be found as Genbank accession no. CAA38402. It has the following sequence of 530 amino acids

```
1   mkfsagavls wsslllassv faqqeavape dsavvklatd sfneyiqshd lvlaeffapw
61  cghcknmape yvkaaetlve knitlaqidc tenqdlcmeh nipgfpslki fknrdvnnsi
121 dyegprtaea ivqfmikqsq pavavvadlp aylanetfvt pvivqsgkid adfnatfysm
181 ankhfndydf vsaenadddf klsiylpsam depvvyngkk adiadadvfe kwlqvealpy
241 fgeidgsvfa qyvesglplg ylfyndeeel eeykplftel akknrglmnf vsidarkfgr
301 hagnlnmkeq fplfaihdmt edlkyglpql seeafdelsd kivleskaie slvkdflkgd
361 aspivksqei fenqdssvfq lvgknhdeiv ndpkkdvlvl yyapwcghck rlaptyqela
421 dtyanatsdv liakldhten dvrgvviegy ptivlypggk ksesvvyqgs rsldslfdfi
481 kenghfdvdg kalyeeaqek aaeeaeadae aeadadaela deedaihdel
```

Variants and fragments of the above PDI sequences, and variants of other naturally occurring PDI sequences are also included in the present invention. A "variant", in the context of PDI, refers to a protein wherein at one or more positions there have been amino acid insertions, deletions, or substitutions, either conservative or non-conservative, provided

that such changes result in a protein whose basic properties, for example enzymatic activity (type of and specific activity), thermostability, activity in a certain pH-range (pH-stability) have not significantly been changed. "Significantly" in this context means that one skilled in the art would say that the properties of the variant may still be different but would not be unobvious over the ones of the original protein.

By "conservative substitutions" is intended combinations such as Val, Ile, Leu, Ala, Met; Asp, Glu; Asn, Gln; Ser, Thr, Gly, Ala; Lys, Arg, His; and Phe, Tyr, Trp. Preferred conservative substitutions include Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr.

A "variant" typically has at least 25%, at least 50%, at least 60% or at least 70%, preferably at least 80%, more preferably at least 90%, even more preferably at least 95%, yet more preferably at least 99%, most preferably at least 99.5% sequence identity to the polypeptide from which it is derived.

The percent sequence identity between two polypeptides may be determined using suitable computer programs, as discussed below. Such variants may be natural or made using the methods of protein engineering and site-directed mutagenesis as are well known in the art.

A "fragment", in the context of PDI, refers to a protein wherein at one or more positions there have been deletions. Thus the fragment may comprise at most 5, 10, 20, 30, 40 or 50%, typically up to 60%, more typically up to 70%, preferably up to 80%, more preferably up to 90%, even more preferably up to 95%, yet more preferably up to 99% of the complete sequence of the full mature PDI protein. Particularly preferred fragments of PDI protein comprise one or more whole domains of the desired protein.

A fragment or variant of PDI may be a protein that, when expressed recombinantly in a host cell, such as *S. cerevisiae*, can complement the deletion of the endogenously encoded PDI gene in the host cell and may, for example, be a naturally occurring homolog of PDI, such as a homolog encoded by another organism, such as another yeast

or other fungi, or another eukaryote such as a human or other vertebrate, or animal or by a plant.

Another preferred chaperone is SSA1 or a fragment or variant thereof having an equivalent chaperone-like activity. *SSA1*, also known as YG100, is located on chromosome I of the *S. cerevisiae* genome and is 1.93-kbp in size.

One published protein sequence of SSA1 is as follows:

MSKAVGIDLGTTYSCVAHFANDRVDIIANDQGNRTTPSFVAFTDTERLIGDAAKNQAAMN
PSNTVFDAKRLIGRNFNDPEVQADMKHFPFKLIDVDGKPQIQVEFKGETKNFTPEQISSM
VLGKMKETAESYLGAKVNDAVVTVPAYFNDSQRQATKDAGTIAGLNVLRIINEPTAAAIA
YGLDKKGKEEHVLIFDLGGGTFDVSLLFIEDGIFEVKATAGDTHLGGEDFDNRLVNHFIQ
EFKRKNKKDLSTNQRALRRLRTACERAKRTLSSSAQTSVEIDSLFEGIDFYTSITRARFE
ELCADLFRSTLDPVEKVLRDAKLDKSQVDEIVLVGGSTRIPKVQKLVTDYFNGKEPNRSI
NPDEAVAYGAAVQAAILTGDESSKTQDLLLLDVAPLSLGIETAGGVMTKLIPRNSTISTK
KFEIFSTYADNQPGVLIQVFEGERAKTKDNNLLGKFELSGIPPAPRGVPQIEVTFDVDSN
GILNVSAVEKGTGKSNKITITNDKGRLSKEDIEKMVAEAEKFKEEDEKESQRIASKNQLE
SIAYSLKNTISEAGDKLEQADKDTVTKKAEETISWLDSNTTASKEEFDDKLKELQDIANP
IMSKLYQAGGAPGGAAGGAPGGFPGGAPPAPEAEGPTVEEVD

A published coding sequence for SSA1 is as follows, although it will be appreciated that the sequence can be modified by degenerate substitutions to obtain alternative nucleotide sequences which encode an identical protein product:

ATGTCAAAAGCTGTCGGTATTGATTTAGGTACAACATACTCGTGTGTTGCTCACTTTGCT
AATGATCGTGTGGACATTATTGCCAACGATCAAGGTAACAGAACCACTCCATCTTTTGTC
GCTTTCACTGACACTGAAAGATTGATTGGTGATGCTGCTAAGAATCAAGCTGCTATGAAT
CCTTCGAATACCGTTTTCGACGCTAAGCGTTTGATCGGTAGAAACTTCAACGACCCAGAA
GTGCAGGCTGACATGAAGCACTTCCCATTCAAGTTGATCGATGTTGACGGTAAGCCTCAA
ATTCAAGTTGAATTTAAGGGTGAAACCAAGAACTTTACCCCAGAACAAATCTCCTCCATG
GTCTTGGGTAAGATGAAGGAAACTGCCGAATCTTACTTGGGAGCCAAGGTCAATGACGCT
GTCGTCACTGTCCCAGCTTACTTCAACGATTCTCAAAGACAAGCTACCAAGGATGCTGGT
ACCATTGCTGGTTTGAATGTCTTGCGTATTATTAACGAACCTACCGCCGCTGCCATTGCT
TACGGTTTGGACAAGAAGGGTAAGGAAGAACACGTCTTGATTTTCGACTTGGGTGGTGGT
ACTTTCGATGTCTCTTTGTTGTTCATTGAAGACGGTATCTTTGAAGTTAAGGCCACCGCT
GGTGACACCCATTTGGGTGGTGAAGATTTTGACAACAGATTGGTCAACCACTTCATCCAA

GAATTCAAGAGAAAGAACAAGAAGGACTTGTCTACCAACCAAAGAGCTTTGAGAAGATTA
AGAACCGCTTGTGAAAGAGCCAAGAGAACTTTGTCTTCCTCCGCTCAAACTTCCGTTGAA
ATTGACTCTTTGTTCGAAGGTATCGATTTCTACACTTCCATCACCAGAGCCAGATTCGAA
GAATTGTGTGCTGACTTGTTCAGATCTACTTTGGACCCAGTTGAAAAGGTCTTGAGAGAT
GCTAAATTGGACAAATCTCAAGTCGATGAAATTGTCTTGGTCGGTGGTTCTACCAGAATT
CCAAAGGTCCAAAAATTGGTCACTGACTACTTCAACGGTAAGGAACCAAACAGATCTATC
AACCCAGATGAAGCTGTTGCTTACGGTGCTGCTGTTCAAGCTGCTATTTTGACTGGTGAC
GAATCTTCCAAGACTCAAGATCTATTGTTGTTGGATGTCGCTCCATTATCCTTGGGTATT
GAAACTGCTGGTGGTGTCATGACCAAGTTGATTCCAAGAAACTCTACCATTTCAACAAAG
AAGTTCGAGATCTTTTCCACTTATGCTGATAACCAACCAGGTGTCTTGATTCAAGTCTTT
GAAGGTGAAAGAGCCAAGACTAAGGACAACAACTTGTTGGGTAAGTTCGAATTGAGTGGT
ATTCCACCAGCTCCAAGAGGTGTCCCACAAATTGAAGTCACTTTCGATGTCGACTCTAAC
GGTATTTTGAATGTTTCCGCCGTCGAAAAGGGTACTGGTAAGTCTAACAAGATCACTATT
ACCAACGACAAGGGTAGATTGTCCAAGGAAGATATCGAAAAGATGGTTGCTGAAGCCGAA
AAATTCAAGGAAGAAGATGAAAAGGAATCTCAAAGAATTGCTTCCAAGAACCAATTGGAA
TCCATTGCTTACTCTTTGAAGAACACCATTTCTGAAGCTGGTGACAAATTGGAACAAGCT
GACAAGGACACCGTCACCAAGAAGGCTGAAGAGACTATTTCTTGGTTAGACAGCAACACC
ACTGCCAGCAAGGAAGAATTCGATGACAAGTTGAAGGAGTTGCAAGACATTGCCAACCCA
ATCATGTCTAAGTTGTACCAAGCTGGTGGTGCTCCAGGTGGCGCTGCAGGTGGTGCTCCA
GGCGGTTTCCCAGGTGGTGCTCCTCCAGCTCCAGAGGCTGAAGGTCCAACCGTTGAAGAA
GTTGATTAA

The protein Ssa1p belongs to the Hsp70 family of proteins and is resident in the cytosol. Hsp70s possess the ability to perform a number of chaperone activities; aiding protein synthesis, assembly and folding; mediating translocation of polypeptides to various intracellular locations, and resolution of protein aggregates (Becker & Craig, 1994, *Eur. J. Biochem.* **219**, 11-23). Hsp70 genes are highly conserved, possessing an N-terminal ATP-binding domain and a C-terminal peptide-binding domain. Hsp70 proteins interact with the peptide backbone of, mainly unfolded, proteins. The binding and release of peptides by hsp70 proteins is an ATP-dependent process and accompanied by a conformational change in the hsp70 (Becker & Craig, 1994, *supra*).

Cytosolic hsp70 proteins are particularly involved in the synthesis, folding and secretion of proteins (Becker & Craig, 1994, *supra*). In *S. cerevisiae* cytosolic hsp70 proteins have been divided into two groups; SSA (SSA 1-4) and SSB (SSB 1 and 2) proteins, which are functionally distinct from each other. The SSA family is essential in that at least one

protein from the group must be active to maintain cell viability (Becker & Craig, 1994, *supra*). Cytosolic hsp70 proteins bind preferentially to unfolded and not mature proteins. This suggests that they prevent the aggregation of precursor proteins, by maintaining them in an unfolded state prior to being assembled into multimolecular complexes in the cytosol and/or facilitating their translocation to various organelles (Becker & Craig, 1994, *supra*). SSA proteins are particularly involved in post-translational biogenesis and maintenance of precursors for translocation into the endoplasmic reticulum and mitochondria (Kim *et al.*, 1998, *Proc. Natl. Acad. Sci. USA.* **95**, 12860-12865; Ngosuwan *et al.*, 2003, *J. Biol. Chem.* **278** (9), 7034-7042). Ssa1p has been shown to bind damaged proteins, stabilising them in a partially unfolded form and allowing refolding or degradation to occur (Becker & Craig, 1994, *supra*; Glover & Lindquist, 1998, *Cell.* **94**, 73-82).

Variants and fragments of SSA1 are also included in the present invention. A "variant", in the context of SSA1, refers to a protein having the sequence of native SSA1 other than for at one or more positions where there have been amino acid insertions, deletions, or substitutions, either conservative or non-conservative, provided that such changes result in a protein whose basic properties, for example enzymatic activity (type of and specific activity), thermostability, activity in a certain pH-range (pH-stability) have not significantly been changed. "Significantly" in this context means that one skilled in the art would say that the properties of the variant may still be different but would not be unobvious over the ones of the original protein.

By "conservative substitutions" is intended combinations such as Val, Ile, Leu, Ala, Met; Asp, Glu; Asn, Gln; Ser, Thr, Gly, Ala; Lys, Arg, His; and Phe, Tyr, Trp. Preferred conservative substitutions include Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr.

A "variant" of SSA1 typically has at least 25%, at least 50%, at least 60% or at least 70%, preferably at least 80%, more preferably at least 90%, even more preferably at least 95%, yet more preferably at least 99%, most preferably at least 99.5% sequence identity to the sequence of native SSA1.

The percent sequence identity between two polypeptides may be determined using suitable computer programs, as discussed below. Such variants may be natural or made using the methods of protein engineering and site-directed mutagenesis as are well known in the art.

A "fragment", in the context of SSA1, refers to a protein having the sequence of native SSA1 other than for at one or more positions where there have been deletions. Thus the fragment may comprise at most 5, 10, 20, 30, 40 or 50%, typically up to 60%, more typically up to 70%, preferably up to 80%, more preferably up to 90%, even more preferably up to 95%, yet more preferably up to 99% of the complete sequence of the full mature SSA1 protein. Particularly preferred fragments of SSA1 protein comprise one or more whole domains of the desired protein.

A fragment or variant of SSA1 may be a protein that, when expressed recombinantly in a host cell, such as *S. cerevisiae*, can complement the deletion of the endogenously encoded SSA1 gene in the host cell and may, for example, be a naturally occurring homolog of SSA1, such as a homolog encoded by another organism, such as another yeast or other fungi, or another eukaryote such as a human or other vertebrate, or animal or by a plant.

Another preferred chaperone is PSE1 or a fragment or variant thereof having equivalent chaperone-like activity.

PSE1, also known as *KAP121*, is an essential gene, located on chromosome XIII.

A published protein sequence for the protein pse1p is as follows:

MSALPEEVNRTLLQIVQAFASPDNQIRSVAEKALSEEWITENNIEYLLTFLAEQAAFSQD
TTVAALSAVLFRKLALKAPPSSKLMIMSKNITHIRKEVLAQIRSSLLKGFLSERADSIRH
KLSDAIAECVQDDLPAWPELLQALIESLKSGNPNFRESSFRILTTVPYLITAVDINSILP
IFQSGFTDASDNVKIAAVTAFVGYFKQLPKSEWSKLGILLPSLLNSLPRFLDDGKDDALA
SVFESLIELVELAPKLFKDMFDQIIQFTDMVIKNKDLEPPARTTALELLTVFSENAPQMC
KSNQNYGQTLVMVTLIMMTEVSIDDDDAAEWIESDDTDDEEEVTYDHARQALDRVALKLG
GEYLAAPLFQYLQQMITSTEWRERFAAMMALSSAAEGCADVLIGEIPKILDMVIPLINDP

HPRVQYGCCNVLGQISTDFSPFIQRTAHDRILPALISKLTSECTSRVQTHAAAALVNFSE
FASKDILEPYLDSLLTNLLVLLQSNKLYVQEQALTTIAFIAEAAKNKFIKYYDTLMPLLL
NVLKVNNKDNSVLKGKCMECATLIGFAVGKEKFHEHSQELISILVALQNSDIDEDDALRS
YLEQSWSRICRILGDDFVPLLPIVIPPLLITAKATQDVGLIEEEEAANFQQYPDWDVVQV
QGKHIAIHTSVLDDKVSAMELLQSYATLLRGQFAVYVKEVMEEIALPSLDFYLHDGVRAA
GATLIPILLSCLLAATGTQNEELVLLWHKASSKLIGGLMSEPMPEITQVYHNSLVNGIKV
MGDNCLSEDQLAAFTKGVSANLTDTYERMQDRHGDGDEYNENIDEEEDFTDEDLLDEINK
SIAAVLKTTNGHYLKNLENIWPMINTFLLDNEPILVIFALVVIGDLIQYGGEQTASMKNA
FIPKVTECLISPDARIRQAASYIIGVCAQYAPSTYADVCIPTLDTLVQIVDFPGSKLEEN
RSSTENASAAIAKILYAYNSNIPNVDTYTANWFKTLPTITDKEAASFNYQFLSQLIENNS
PIVCAQSNISAVVDSVIQALNERSLTEREGQTVISSVKKLLGFLPSSDAMAIFNRYPADI
MEKVHKWFA*

A published nucleotide coding sequence of PSE1 is as follows, although it will be appreciated that the sequence can be modified by degenerate substitutions to obtain alternative nucleotide sequences which encode an identical protein product:

ATGTCTGCTTTACCGGAAGAAGTTAATAGAACATTACTTCAGATTGTCCAGGCGTTTGCT
TCCCCTGACAATCAAATACGTTCTGTAGCTGAGAAGGCTCTTAGTGAAGAATGGATTACC
GAAAACAATATTGAGTATCTTTTAACTTTTTTGGCTGAACAAGCCGCTTTCTCCCAAGAT
ACAACAGTTGCAGCATTATCTGCTGTTCTGTTTAGAAAATTAGCATTAAAAGCTCCCCCT
TCTTCGAAGCTTATGATTATGTCCAAAAATATCACACATATTAGGAAAGAAGTTCTTGCA
CAAATTCGTTCTTCATTGTTAAAAGGGTTTTTGTCGGAAAGAGCTGATTCAATTAGGCAC
AAACTATCTGATGCTATTGCTGAGTGTGTTCAAGACGACTTACCAGCATGGCCAGAATTA
CTACAAGCTTTAATAGAGTCTTTAAAAAGCGGTAACCCAAATTTTAGAGAATCCAGTTTT
AGAATTTTGACGACTGTACCTTATTTAATTACCGCTGTTGACATCAACAGTATCTTACCA
ATTTTTCAATCAGGCTTTACTGATGCAAGTGATAATGTCAAAATTGCTGCAGTTACGGCT
TTCGTGGGTTATTTTAAGCAACTACCAAAATCTGAGTGGTCCAAGTTAGGTATTTTATTA
CCAAGTCTTTTGAATAGTTTACCAAGATTTTTAGATGATGGTAAGGACGATGCCCTTGCA
TCAGTTTTTGAATCGTTAATTGAGTTGGTGGAATTGGCACCAAAACTATTCAAGGATATG
TTTGACCAAATAATACAATTCACTGATATGGTTATAAAAAATAAGGATTTAGAACCTCCA
GCAAGAACCACAGCACTCGAACTGCTAACCGTTTTCAGCGAGAACGCTCCCCAAATGTGT
AAATCGAACCAGAATTACGGGCAAACTTTAGTGATGGTTACTTTAATCATGATGACGGAG
GTATCCATAGATGATGATGATGCAGCAGAATGGATAGAATCTGACGATACCGATGATGAA
GAGGAAGTTACATATGACCACGCTCGTCAAGCTCTTGATCGTGTTGCTTTAAAGCTGGGT
GGTGAATATTTGGCTGCACCATTGTTCCAATATTTACAGCAAATGATCACATCAACCGAA
TGGAGAGAAAGATTCGCGGCCATGATGGCACTTTCCTCTGCAGCTGAGGGTTGTGCTGAT
GTTCTGATCGGCGAGATCCCAAAAATCCTGGATATGGTAATTCCCCTCATCAACGATCCT
CATCCAAGAGTACAGTATGGATGTTGTAATGTTTTGGGTCAAATATCTACTGATTTTTCA

CCATTCATTCAAAGAACTGCACACGATAGAATTTTGCCGGCTTTAATATCTAAACTAACG
TCAGAATGCACCTCAAGAGTTCAAACGCACGCCGCAGCGGCTCTGGTTAACTTTTCTGAA
TTCGCTTCGAAGGATATTCTTGAGCCTTACTTGGATAGTCTATTGACAAATTTATTAGTT
TTATTACAAAGCAACAAACTTTACGTACAGGAACAGGCCCTAACAACCATTGCATTTATT
GCTGAAGCTGCAAAGAATAAATTTATCAAGTATTACGATACTCTAATGCCATTATTATTA
AATGTTTTGAAGGTTAACAATAAAGATAATAGTGTTTTGAAAGGTAAATGTATGGAATGT
GCAACTCTGATTGGTTTTGCCGTTGGTAAGGAAAAATTTCATGAGCACTCTCAAGAGCTG
ATTTCTATATTGGTCGCTTTACAAAACTCAGATATCGATGAAGATGATGCGCTCAGATCA
TACTTAGAACAAAGTTGGAGCAGGATTTGCCGAATTCTGGGTGATGATTTTGTTCCGTTG
TTACCGATTGTTATACCACCCCTGCTAATTACTGCCAAAGCAACGCAAGACGTCGGTTTA
ATTGAAGAAGAAGAAGCAGCAAATTTCCAACAATATCCAGATTGGGATGTTGTTCAAGTT
CAGGGAAAACACATTGCTATTCACACATCCGTCCTTGACGATAAAGTATCAGCAATGGAG
CTATTACAAAGCTATGCGACACTTTTAAGAGGCCAATTTGCTGTATATGTTAAAGAAGTA
ATGGAAGAAATAGCTCTACCATCGCTTGACTTTTACCTACATGACGGTGTTCGTGCTGCA
GGAGCAACTTTAATTCCTATTCTATTATCTTGTTTACTTGCAGCCACCGGTACTCAAAAC
GAGGAATTGGTATTGTTGTGGCATAAAGCTTCGTCTAAACTAATCGGAGGCTTAATGTCA
GAACCAATGCCAGAAATCACGCAAGTTTATCACAACTCGTTAGTGAATGGTATTAAAGTC
ATGGGTGACAATTGCTTAAGCGAAGACCAATTAGCGGCATTTACTAAGGGTGTCTCCGCC
AACTTAACTGACACTTACGAAAGGATGCAGGATCGCCATGGTGATGGTGATGAATATAAT
GAAAATATTGATGAAGAGGAAGACTTTACTGACGAAGATCTTCTCGATGAAATCAACAAG
TCTATCGCGGCCGTTTTGAAAACCACAAATGGTCATTATCTAAAGAATTTGGAGAATATA
TGGCCTATGATAAACACATTCCTTTTAGATAATGAACCAATTTTAGTCATTTTTGCATTA
GTAGTGATTGGTGACTTGATTCAATATGGTGGCGAACAAACTGCTAGCATGAAGAACGCA
TTTATTCCAAAGGTTACCGAGTGCTTGATTTCTCCTGACGCTCGTATTCGCCAAGCTGCT
TCTTATATAATCGGTGTTTGTGCCCAATACGCTCCATCTACATATGCTGACGTTTGCATA
CCGACTTTAGATACACTTGTTCAGATTGTCGATTTTCCAGGCTCCAAACTGGAAGAAAAT
CGTTCTTCAACAGAGAATGCCAGTGCAGCCATCGCCAAAATTCTTTATGCATACAATTCC
AACATTCCTAACGTAGACACGTACACGGCTAATTGGTTCAAAACGTTACCAACAATAACT
GACAAAGAAGCTGCCTCATTCAACTATCAATTTTTGAGTCAATTGATTGAAAATAATTCG
CCAATTGTGTGTGCTCAATCTAATATCTCCGCTGTAGTTGATTCAGTCATACAAGCCTTG
AATGAGAGAAGTTTGACCGAAAGGGAAGGCCAAACGGTGATAAGTTCAGTTAAAAAGTTG
TTGGGATTTTTGCCTTCTAGTGATGCTATGGCAATTTTCAATAGATATCCAGCTGATATT
ATGGAGAAAGTACATAAATGGTTTGCATAA

The PSE1 gene is 3.25-kbp in size. Pse1p is involved in the nucleocytoplasmic transport of macromolecules (Seedorf & Silver, 1997, *Proc. Natl. Acad. Sci. USA.* **94**, 8590-8595). This process occurs via the nuclear pore complex (NPC) embedded in the nuclear envelope and made up of nucleoporins (Ryan & Wente, 2000, *Curr. Opin. Cell Biol.* **12**,

361-371). Proteins possess specific sequences that contain the information required for nuclear import, nuclear localisation sequence (NLS) and export, nuclear export sequence (NES) (Pemberton *et al.*, 1998, *Curr. Opin. Cell Biol.* **10**, 392-399). Pse1p is a karyopherin/importin, a group of proteins, which have been divided up into α and β families. Karyopherins are soluble transport factors that mediate the transport of macromolecules across the nuclear membrane by recognising NLS and NES, and interact with and the NPC (Seedorf & Silver, 1997, *supra*; Pemberton *et al.*, 1998, *supra*; Ryan & Wente, 2000, *supra*). Translocation through the nuclear pore is driven by GTP hydrolysis, catalysed by the small GTP-binding protein, Ran (Seedorf & Silver, 1997, *supra*). Pse1p has been identified as a karyopherin β. 14 karyopherin β proteins have been identified in *S. cerevisiae*, of which only 4 are essential. This is perhaps because multiple karyopherins may mediate the transport of a single macromolecule (Isoyama *et al.*, 2001, *J. Biol. Chem.* **276** (24), 21863-21869). Pse1p is localised to the nucleus, at the nuclear envelope, and to a certain extent to the cytoplasm. This suggests the protein moves in and out of the nucleus as part of its transport function (Seedorf & Silver, 1997, *supra*). Pse1p is involved in the nuclear import of transcription factors (Isoyama *et* al., 2001, *supra*; Ueta *et al.*, 2003, *J. Biol. Chem.* **278** (50), 50120-50127), histones (Mosammaparast *et* al., 2002, *J. Biol. Chem.* **277** (1), 862-868), and ribosomal proteins prior to their assembly into ribosomes (Pemberton *et al.*, 1998, *supra*). It also mediates the export of mRNA from the nucleus. Karyopherins recognise and bind distinct NES found on RNA-binding proteins, which coat the RNA before it is exported from the nucleus (Seedorf & Silver, 1997, Pemberton *et al.*, 1998, *supra*).

As nucleocytoplasmic transport of macromolecules is essential for proper progression through the cell cycle, nuclear transport factors, such as pse1p are novel candidate targets for growth control (Seedorf & Silver, 1997, *supra*).\

Overexpression of Pse1p (protein secretion enhancer) on a multicopy plasmid in *S. cerevisiae* has also been shown to increase protein secretion levels of a repertoire of biologically active proteins (Chow *et al.*, 1992; *J. Cell. Sci.* **101** (3), 709-719).

Variants and fragments of PSE1 are also included in the present invention. A "variant", in the context of PSE1, refers to a protein having the sequence of native PSE1 other than for at one or more positions where there have been amino acid insertions, deletions, or substitutions, either conservative or non-conservative, provided that such changes result in a protein whose basic properties, for example enzymatic activity (type of and specific activity), thermostability, activity in a certain pH-range (pH-stability) have not significantly been changed. "Significantly" in this context means that one skilled in the art would say that the properties of the variant may still be different but would not be unobvious over the ones of the original protein.

By "conservative substitutions" is intended combinations such as Val, Ile, Leu, Ala, Met; Asp, Glu; Asn, Gln; Ser, Thr, Gly, Ala; Lys, Arg, His; and Phe, Tyr, Trp. Preferred conservative substitutions include Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr.

A "variant" of PSE1 typically has at least 25%, at least 50%, at least 60% or at least 70%, preferably at least 80%, more preferably at least 90%, even more preferably at least 95%, yet more preferably at least 99%, most preferably at least 99.5% sequence identity to the sequence of native PSE1.

The percent sequence identity between two polypeptides may be determined using suitable computer programs, as discussed below. Such variants may be natural or made using the methods of protein engineering and site-directed mutagenesis as are well known in the art.

A "fragment", in the context of PSE1, refers to a protein having the sequence of native PSE1 other than for at one or more positions where there have been deletions. Thus the fragment may comprise at most 5, 10, 20, 30, 40 or 50%, typically up to 60%, more typically up to 70%, preferably up to 80%, more preferably up to 90%, even more preferably up to 95%, yet more preferably up to 99% of the complete sequence of the full mature PSE1 protein. Particularly preferred fragments of PSE1 protein comprise one or more whole domains of the desired protein.

A fragment or variant of PSE1 may be a protein that, when expressed recombinantly in a host cell, such as *S. cerevisiae*, can complement the deletion of the endogenous PSE1 gene in the host cell and may, for example, be a naturally occurring homolog of PSE1, such as a homolog encoded by another organism, such as another yeast or other fungi, or another eukaryote such as a human or other vertebrate, or animal or by a plant.

Another preferred chaperone is ORM2 or a fragment or variant thereof having equivalent chaperone-like activity.

ORM2, also known as YLR350W, is located on chromosome XII (positions 828729 to 829379) of the *S. cerevisiae* genome and encodes an evolutionarily conserved protein with similarity to the yeast protein Orm1p. Hjelmqvist *et al*, 2002, *Genome Biology*, 3(6), research0027.1-0027.16 reports that *ORM2* belongs to gene family comprising three human genes (ORMDL1, ORMDL2 and ORMDL3) as well as homologs in microsporidia, plants, *Drosophila*, urochordates and vertebrates. The ORMDL genes are reported to encode transmembrane proteins anchored in the proteins endoplasmic reticulum (ER).

The protein Orm2p is required for resistance to agents that induce the unfolded protein response. Hjelmqvist et al, 2002 (*supra*) reported that a double knockout of the two *S. cerevisiae* ORMDL homologs (*ORM1* and *ORM2*) leads to a decreased growth rate and greater sensitivity to tunicamycin and dithiothreitol.

One published sequence of Orm2p is as follows:

```
MIDRTKNESPAFEESPLTPNVSNLKPFPSQSNKISTPVTDHRRRRSSSVISHVEQETFED
ENDQQMLPNMNATWVDQRGAWLIHIVVIVLLRLFYSLFGSTPKWTWTLTNMTYIIGFYIM
FHLVKGTPFDFNGGAYDNLTMWEQINDETLYTPTRKFLLIVPIVLFLISNQYYRNDMTLF
LSNLAVTVLIGVVPKLGITHRLRISIPGITGRAQIS*
```

The above protein is encoded in *S. cerevisiae* by the following coding nucleotide sequence, although it will be appreciated that the sequence can be modified by

degenerate substitutions to obtain alternative nucleotide sequences which encode an identical protein product:

ATGATTGACCGCACTAAAAACGAATCTCCAGCTTTTGAAGAGTCTCCGCTTACCCCCAAT
GTGTCTAACCTGAAACCATTCCCTTCTCAAAGCAACAAAATATCCACTCCAGTGACCGAC
CATAGGAGAAGACGGTCATCCAGCGTAATATCACATGTGGAACAGGAAACCTTCGAAGAC
GAAAATGACCAGCAGATGCTTCCCAACATGAACGCTACGTGGGTCGACCAGCGAGGCGCG
TGGTTGATTCATATCGTCGTAATAGTACTCTTGAGGCTCTTCTACTCCTTGTTCGGGTCG
ACGCCCAAATGGACGTGGACTTTAACAAACATGACCTACATCATCGGATTCTATATCATG
TTCCACCTTGTCAAAGGTACGCCCTTCGACTTTAACGGTGGTGCGTACGACAACCTGACC
ATGTGGGAGCAGATTAACGATGAGACTTTGTACACACCCACTAGAAAATTTCTGCTGATT
GTACCCATTGTGTTGTTCCTGATTAGCAACCAGTACTACCGCAACGACATGACACTATTC
CTCTCCAACCTCGCCGTGACGGTGCTTATTGGTGTCGTTCCTAAGCTGGGAATTACGCAT
AGACTAAGAATATCCATCCCTGGTATTACGGGCCGTGCTCAAATTAGTTAG

Variants and fragments of ORM2 are also included in the present invention. A "variant", in the context of ORM2, refers to a protein having the sequence of native ORM2 other than for at one or more positions where there have been amino acid insertions, deletions, or substitutions, either conservative or non-conservative, provided that such changes result in a protein whose basic properties, for example enzymatic activity (type of and specific activity), thermostability, activity in a certain pH-range (pH-stability) have not significantly been changed. "Significantly" in this context means that one skilled in the art would say that the properties of the variant may still be different but would not be unobvious over the ones of the original protein.

By "conservative substitutions" is intended combinations such as Val, Ile, Leu, Ala, Met; Asp, Glu; Asn, Gln; Ser, Thr, Gly, Ala; Lys, Arg, His; and Phe, Tyr, Trp. Preferred conservative substitutions include Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr.

A "variant" of ORM2 typically has at least 25%, at least 50%, at least 60% or at least 70%, preferably at least 80%, more preferably at least 90%, even more preferably at least 95%, yet more preferably at least 99%, most preferably at least 99.5% sequence identity to the sequence of native ORM2.

The percent sequence identity between two polypeptides may be determined using suitable computer programs, as discussed below. Such variants may be natural or made using the methods of protein engineering and site-directed mutagenesis as are well known in the art.

A "fragment", in the context of ORM2, refers to a protein having the sequence of native ORM2 other than for at one or more positions where there have been deletions. Thus the fragment may comprise at most 5, 10, 20, 30, 40 or 50%, typically up to 60%, more typically up to 70%, preferably up to 80%, more preferably up to 90%, even more preferably up to 95%, yet more preferably up to 99% of the complete sequence of the full mature ORM2 protein. Particularly preferred fragments of ORM2 protein comprise one or more whole domains of the desired protein.

A fragment or variant of ORM2 may be a protein that, when expressed recombinantly in a host cell, such as *S. cerevisiae*, can complement the deletion of the endogenous ORM2 gene in the host cell and may, for example, be a naturally occurring homolog of ORM2, such as a homolog encoded by another organism, such as another yeast or other fungi, or another eukaryote such as a human or other vertebrate, or animal or by a plant.

It is particularly preferred that a plasmid according to a first, second or third aspects of the invention includes, either within a polynucleotide sequence insertion, or elsewhere on the plasmid, an open reading frame encoding a protein comprising the sequence of albumin or a fragment or variant thereof. Alternatively, the host cell into which the plasmid is transformed may include within its genome a polynucleotide sequence encoding a protein comprising the sequence of albumin or a fragment or variant thereof, either as an endogenous or heterologous sequence.

By "albumin" we include a protein having the sequence of an albumin protein obtained from any source. Typically the source is mammalian. In one preferred embodiment the serum albumin is human serum albumin ("HSA"). The term "human serum albumin" includes the meaning of a serum albumin having an amino acid sequence naturally occurring in humans, and variants thereof. Preferably the albumin has the amino acid

sequence disclosed in WO 90/13653 or a variant thereof. The HSA coding sequence is obtainable by known methods for isolating cDNA corresponding to human genes, and is also disclosed in, for example, EP 73 646 and EP 286 424.

In another preferred embodiment the "albumin" has the sequence of bovine serum albumin. The term "bovine serum albumin" includes the meaning of a serum albumin having an amino acid sequence naturally occurring in cows, for example as taken from Swissprot accession number P02769, and variants thereof as defined below. The term "bovine serum albumin" also includes the meaning of fragments of full-length bovine serum albumin or variants thereof, as defined below.

In another preferred embodiment the albumin is an albumin derived from (i.e. has the sequence of) one of serum albumin from dog (e.g. see Swissprot accession number P49822), pig (e.g. see Swissprot accession number P08835), goat (e.g. as available from Sigma as product no. A2514 or A4164), turkey (e.g. see Swissprot accession number O73860), baboon (e.g. as available from Sigma as product no. A1516), cat (e.g. see Swissprot accession number P49064), chicken (e.g. see Swissprot accession number P19121), ovalbumin (e.g. chicken ovalbumin) (e.g. see Swissprot accession number P01012), donkey (e.g. see Swissprot accession number P39090), guinea pig (e.g. as available from Sigma as product no. A3060, A2639, O5483 or A6539), hamster (e.g. as available from Sigma as product no. A5409), horse (e.g. see Swissprot accession number P35747), rhesus monkey (e.g. see Swissprot accession number Q28522), mouse (e.g. see Swissprot accession number O89020), pigeon (e.g. as defined by Khan *et al*, 2002, *Int. J. Biol. Macromol.*, **30**(3-4),171-8), rabbit (e.g. see Swissprot accession number P49065), rat (e.g. see Swissprot accession number P36953) and sheep (e.g. see Swissprot accession number P14639) and includes variants and fragments thereof as defined below.

Many naturally occurring mutant forms of albumin are known. Many are described in Peters, (1996, *All About Albumin: Biochemistry, Genetics and Medical Applications*, Academic Press, Inc., San Diego, California, p.170-181). A variant as defined above may be one of these naturally occurring mutants.

A "variant albumin" refers to an albumin protein wherein at one or more positions there have been amino acid insertions, deletions, or substitutions, either conservative or non-conservative, provided that such changes result in an albumin protein for which at least one basic property, for example binding activity (type of and specific activity e.g. binding to bilirubin), osmolarity (oncotic pressure, colloid osmotic pressure), behaviour in a certain pH-range (pH-stability) has not significantly been changed. "Significantly" in this context means that one skilled in the art would say that the properties of the variant may still be different but would not be unobvious over the ones of the original protein.

By "conservative substitutions" is intended combinations such as Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr. Such variants may be made by techniques well known in the art, such as by site-directed mutagenesis as disclosed in US Patent No 4,302,386 issued 24 November 1981 to Stevens, incorporated herein by reference.

Typically an albumin variant will have more than 40%, usually at least 50%, more typically at least 60%, preferably at least 70%, more preferably at least 80%, yet more preferably at least 90%, even more preferably at least 95%, most preferably at least 98% or more sequence identity with naturally occurring albumin. The percent sequence identity between two polypeptides may be determined using suitable computer programs, for example the GAP program of the University of Wisconsin Genetic Computing Group and it will be appreciated that percent identity is calculated in relation to polypeptides whose sequence has been aligned optimally. The alignment may alternatively be carried out using the Clustal W program (Thompson *et al.*, 1994). The parameters used may be as follows:

Fast pairwise alignment parameters: K-tuple(word) size; 1, window size; 5, gap penalty; 3, number of top diagonals; 5. Scoring method: x percent. Multiple alignment parameters: gap open penalty; 10, gap extension penalty; 0.05. Scoring matrix: BLOSUM.

The term "fragment" as used above includes any fragment of full-length albumin or a variant thereof, so long as at least one basic property, for example binding activity (type of and specific activity e.g. binding to bilirubin), osmolarity (oncotic pressure, colloid osmotic pressure), behaviour in a certain pH-range (pH-stability) has not significantly been changed.

"Significantly" in this context means that one skilled in the art would say that the properties of the variant may still be different but would not be unobvious over the ones of the original protein. A fragment will typically be at least 50 amino acids long. A fragment may comprise at least one whole sub-domain of albumin. Domains of HSA have been expressed as recombinant proteins (Dockal, M. *et al.*, 1999, *J. Biol. Chem.*, **274**, 29303-29310), where domain I was defined as consisting of amino acids 1-197, domain II was defined as consisting of amino acids 189-385 and domain III was defined as consisting of amino acids 381-585. Partial overlap of the domains occurs because of the extended α-helix structure (h10-h1) which exists between domains I and II, and between domains II and III (Peters, 1996, *op. cit.*, Table 2-4). HSA also comprises six sub-domains (sub-domains IA, IB, IIA, IIB, IIIA and IIIB). Sub-domain IA comprises amino acids 6-105, sub-domain IB comprises amino acids 120-177, sub-domain IIA comprises amino acids 200-291, sub-domain IIB comprises amino acids 316-369, sub-domain IIIA comprises amino acids 392-491 and sub-domain IIIB comprises amino acids 512-583. A fragment may comprise a whole or part of one or more domains or sub-domains as defined above, or any combination of those domains and/or sub-domains.

Thus the polynucleotide insertion may comprise an open reading frame that encodes albumin or a variant or fragment thereof.

Alternatively, it is preferred that a plasmid according to a first, second or third aspects of the invention includes, either within a polynucleotide sequence insertion, or elsewhere on the plasmid, an open reading frame encoding a protein comprising the sequence of transferrin or a variant or fragment thereof. Alternatively, the host cell into which the plasmid is transformed may include within its genome a polynucleotide sequence encoding a protein comprising the sequence of transferrin or a variant or fragment thereof, either as an endogenous or heterologous sequence.

The term "transferrin" as used herein includes all members of the transferrin family (Testa, *Proteins of iron metabolism*, CRC Press, 2002; Harris & Aisen, *Iron carriers and iron proteins*, Vol. 5, Physical Bioinorganic Chemistry, VCH, 1991) and their derivatives, such as transferrin, mutant transferrins (Mason *et al*, 1993, *Biochemistry*, **32**,

5472; Mason *et al*, 1998, *Biochem. J.*, **330**(1), 35), truncated transferrins, transferrin lobes (Mason *et al*, 1996, *Protein Expr. Purif.*, **8**, 119; Mason *et al*, 1991, *Protein Expr. Purif.*, **2**, 214), lactoferrin, mutant lactoferrins, truncated lactoferrins, lactoferrin lobes or fusions of any of the above to other peptides, polypeptides or proteins (Shin *et al*, 1995, *Proc. Natl. Acad. Sci. USA*, **92**, 2820; Ali *et al*, 1999, *J. Biol. Chem.*, **274**, 24066; Mason *et al*, 2002, *Biochemistry*, **41**, 9448).

The transferrin may be human transferrin. The term "human transferrin" is used herein to denote material which is indistinguishable from transferrin derived from a human or which is a variant or fragment thereof. A "variant" includes insertions, deletions and substitutions, either conservative or non-conservative, where such changes do not substantially alter the useful ligand-binding or immunogenic properties of transferrin.

Mutants of transferrin are included in the invention. Such mutants may have altered immunogenicity. For example, transferrin mutants may display modified (e.g. reduced) glycosylation. The N-linked glycosylation pattern of a transferrin molecule can be modified by adding/removing amino acid glycosylation consensus sequences such as N-X-S/T, at any or all of the N, X, or S/T position. Transferrin mutants may be altered in their natural binding to metal ions and/or other proteins, such as transferrin receptor. An example of a transferrin mutant modified in this manner is exemplified below.

We also include naturally-occurring polymorphic variants of human transferrin or human transferrin analogues. Generally, variants or fragments of human transferrin will have at least 50% (preferably at least 80%, 90% or 95%) of human transferrin's ligand binding activity (for example iron-binding), weight for weight. The iron binding activity of transferrin or a test sample can be determined spectrophotometrically by 470nm:280nm absorbance ratios for the proteins in their iron-free and fully iron-loaded states. Reagents should be iron-free unless stated otherwise. Iron can be removed from transferrin or the test sample by dialysis against 0.1M citrate, 0.1M acetate, 10mM EDTA pH4.5. Protein should be at approximately 20mg/mL in 100mM HEPES, 10mM $NaHCO_3$ pH8.0. Measure the 470nm:280nm absorbance ratio of apo-transferrin (Calbiochem, CN Biosciences, Nottingham, UK) diluted in water so that absorbance at 280nm can be accurately determined spectrophotometrically (0% iron binding). Prepare 20mM iron-

nitrilotriacetate (FeNTA) solution by dissolving 191mg nitrotriacetic acid in 2mL 1M NaOH, then add 2mL 0.5M ferric chloride. Dilute to 50mL with deionised water. Fully load apo-transferrin with iron (100% iron binding) by adding a sufficient excess of freshly prepared 20mM FeNTA, then dialyse the holo-transferrin preparation completely against 100mM HEPES, 10mM $NaHCO_3$ pH8.0 to remove remaining FeNTA before measuring the absorbance ratio at 470nm:280nm. Repeat the procedure using test sample, which should initially be free from iron, and compare final ratios to the control.

Additionally, single or multiple heterologous fusions comprising any of the above; or single or multiple heterologous fusions to albumin, transferrin or immunoglobins or a variant or fragment of any of these may be used. Such fusions include albumin N-terminal fusions, albumin C-terminal fusions and co-N-terminal and C–terminal albumin fusions as exemplified by WO 01/79271, and transferrin N-terminal fusions, transferrin C-terminal fusions, and co-N-terminal and C-terminal transferrin fusions.

The skilled person will also appreciate that the open reading frame of any other gene or variant, or part or either, can be utilised to form a whole or part of an open reading frame in forming a polynucleotide sequence insertion for use with the present invention. For example, the open reading frame may encode a protein comprising any sequence, be it a natural protein (including a zymogen), or a variant, or a fragment (which may, for example, be a domain) of a natural protein; or a totally synthetic protein; or a single or multiple fusion of different proteins (natural or synthetic). Such proteins can be taken, but not exclusively, from the lists provided in WO 01/79258, WO 01/79271, WO 01/79442, WO 01/79443, WO 01/79444 and WO 01/79480, or a variant or fragment thereof; the disclosures of which are incorporated herein by reference. Although these patent applications present the list of proteins in the context of fusion partners for albumin, the present invention is not so limited and, for the purposes of the present invention, any of the proteins listed therein may be presented alone or as fusion partners for albumin, the Fc region of immunoglobulin, transferrin, lactoferrin or any other protein or fragment or variant of any of the above, including fusion proteins comprising any of the above, as a desired polypeptide. Further examples of transferrin fusions are given in US patent applications US2003/0221201 and US2003/0226155.

Preferred other examples of desirable proteins for expression by the present invention includes sequences comprising the sequence of a monoclonal antibody, an etoposide, a serum protein (such as a blood clotting factor), antistasin, a tick anticoagulant peptide, transferrin, lactoferrin, endostatin, angiostatin, collagens, immunoglobulins or immunoglobulin-based molecules or fragment of either (e.g. a Small Modular ImmunoPharmaceutical™ ("SMIP") or dAb, Fab' fragments, F(ab')2, scAb, scFv or scFv fragment), a Kunitz domain protein (such as those described in WO 03/066824, with or without albumin fusions) interferons, interleukins, IL10, IL11, IL2, interferon α species and sub-species, interferon β species and sub-species, interferon γ species and sub-species, leptin, CNTF, $CNTF_{Ax15}$, IL1-receptor antagonist, erythropoetin (EPO) and EPO mimics, thrombopoetin (TPO) and TPO mimics, prosaptide, cyanovirin-N, 5-helix, T20 peptide, T1249 peptide, HIV gp41, HIV gp120, urokinase, prourokinase, tPA (tissue plasminogen activator), hirudin, platelet derived growth factor, parathyroid hormone, proinsulin, insulin, glucagon, glucagon-like peptides, insulin-like growth factor, calcitonin, growth hormone, transforming growth factor β, tumour necrosis factor, G-CSF, GM-CSF, M-CSF, FGF, coagulation factors in both pre and active forms, including but not limited to plasminogen, fibrinogen, thrombin, pre-thrombin, pro-thrombin, von Willebrand's factor, α_1-antitrypsin, plasminogen activators, Factor VII, Factor VIII, Factor IX, Factor X and Factor XIII, nerve growth factor, LACI (lipoprotein associated coagulation inhibitor, also known as tissue factor pathway inhibitor or extrinsic pathway inhibitor), platelet-derived endothelial cell growth factor (PD-ECGF), glucose oxidase, serum cholinesterase, aprotinin, amyloid precursor, inter-alpha trypsin inhibitor, antithrombin III, apo-lipoprotein species, Protein C, Protein S, a variant or fragment or fusion protein of any of the above. The protein may or may not be hirudin.

A "variant", in the context of the above-listed proteins, refers to a protein wherein at one or more positions there have been amino acid insertions, deletions, or substitutions, either conservative or non-conservative, provided that such changes result in a protein whose basic properties, for example enzymatic activity or receptor binding (type of and specific activity), thermostability, activity in a certain pH-range (pH-stability) have not significantly been changed. "Significantly" in this context means that one skilled in the art would say that the

properties of the variant may still be different but would not be unobvious over the ones of the original protein.

By "conservative substitutions" is intended combinations such as Val, Ile, Leu, Ala, Met; Asp, Glu; Asn, Gln; Ser, Thr, Gly, Ala; Lys, Arg, His; and Phe, Tyr, Trp. Preferred conservative substitutions include Gly, Ala; Val, Ile, Leu; Asp, Glu; Asn, Gln; Ser, Thr; Lys, Arg; and Phe, Tyr.

A "variant" typically has at least 25%, at least 50%, at least 60% or at least 70%, preferably at least 80%, more preferably at least 90%, even more preferably at least 95%, yet more preferably at least 99%, most preferably at least 99.5% sequence identity to the polypeptide from which it is derived.

The percent sequence identity between two polypeptides may be determined using suitable computer programs, for example the GAP program of the University of Wisconsin Genetic Computing Group and it will be appreciated that percent identity is calculated in relation to polypeptides whose sequence has been aligned optimally.

The alignment may alternatively be carried out using the Clustal W program (Thompson *et al.*, (1994) *Nucleic Acids Res.*, **22**(22), 4673-80). The parameters used may be as follows:

- Fast pairwise alignment parameters: K-tuple(word) size; 1, window size; 5, gap penalty; 3, number of top diagonals; 5. Scoring method: x percent.
- Multiple alignment parameters: gap open penalty; 10, gap extension penalty; 0.05.
- Scoring matrix: BLOSUM.

Such variants may be natural or made using the methods of protein engineering and site-directed mutagenesis as are well known in the art.

A "fragment", in the context of the above-listed proteins, refers to a protein wherein at one or more positions there have been deletions. Thus the fragment may comprise at most 5, 10, 20, 30, 40 or 50% of the complete sequence of the full mature polypeptide. Typically a

fragment comprises up to 60%, more typically up to 70%, preferably up to 80%, more preferably up to 90%, even more preferably up to 95%, yet more preferably up to 99% of the complete sequence of the full desired protein. Particularly preferred fragments of a desired protein comprise one or more whole domains of the desired protein.

It is particularly preferred that a plasmid according to a first, second or third aspects of the invention includes, either within a polynucleotide sequence insertion, or elsewhere on the plasmid, an open reading frame encoding a protein comprising the sequence of albumin or a fragment or variant thereof, or any other protein take from the examples above (fused or unfused to a fusion partner) and at least one other heterologous sequence, wherein the at least one other heterologous sequence may contain a transcribed region, such as an open reading frame. In one embodiment, the open reading frame may encode a protein comprising the sequence of a yeast protein. In another embodiment the open reading frame may encode a protein comprising the sequence of a protein involved in protein folding, or which has chaperone activity or is involved in the unfolded protein response, preferably protein disulphide isomerase.

The resulting plasmids may or may not have symmetry between the US and UL regions. For example, a size ratio of 1:1, 5:4, 5:3, 5:2, 5:1 or 5:<1 can be achieved between US and UL or between UL and US regions. The benefits of the present invention do not rely on symmetry being maintained.

The present invention also provides a method of preparing a plasmid of the invention, which method comprises –

(a) providing a 2μm-family plasmid comprising a *REP2* gene or an *FLP* gene and an inverted repeat adjacent to said gene;

(b) providing a polynucleotide sequence and inserting the polynucleotide sequence into the plasmid at a position according to the first, second or third preferred aspects of the invention; and/or

(c) additionally or as an alternative to step (b), deleting some or all of the nucleotide bases at the positions according to the first, second or third preferred aspects of the invention; and/or

(d) additionally or as an alternative to either of steps (b) and (c), substituting some or all of the nucleotide bases at the positions according to the first, second or third preferred aspects of the invention with alternative nucleotide bases.

Steps (b), (c) and (d) can be achieved using techniques well known in the art, including cloning techniques, site-directed mutagenesis and the like, such as are described in by Sambrook *et al.,* Molecular Cloning: A Laboratory Manual, 2001, 3rd edition, the contents of which are incorporated herein by reference. For example, one such method involves ligation via cohesive ends. Compatible cohesive ends can be generated on a DNA fragment for insertion and plasmid by the action of suitable restriction enzymes. These ends will rapidly anneal through complementary base pairing and remaining nicks can be closed by the action of DNA ligase.

A further method uses synthetic double stranded oligonucleotide linkers and adaptors. DNA fragments with blunt ends are generated by bacteriophage T4 DNA polymerase or *E.coli* DNA polymerase I which remove protruding 3' termini and fill in recessed 3' ends. Synthetic linkers and pieces of blunt-ended double-stranded DNA, which contain recognition sequences for defined restriction enzymes, can be ligated to blunt-ended DNA fragments by T4 DNA ligase. They are subsequently digested with appropriate restriction enzymes to create cohesive ends and ligated to an expression vector with compatible termini. Adaptors are also chemically synthesised DNA fragments which contain one blunt end used for ligation but which also possess one preformed cohesive end. Alternatively a DNA fragment or DNA fragments can be ligated together by the action of DNA ligase in the presence or absence of one or more synthetic double stranded oligonucleotides optionally containing cohesive ends.

Synthetic linkers containing a variety of restriction endonuclease sites are commercially available from a number of sources including Sigma-Genosys Ltd, London Road, Pampisford, Cambridge, United Kingdom.

Accordingly, the present invention also provides a plasmid obtainable by the above method.

The present invention also provides a host cell comprising a plasmid as defined above. The host cell may be any type of cell. Bacterial and yeast host cells are preferred. Bacterial host cells may be useful for cloning purposes. Yeast host cells may be useful for expression of genes present in the plasmid.

In one embodiment the host cell is a cell in which the plasmid is stable as a multicopy plasmid. Plasmids obtained from one yeast type can be maintained in other yeast types (Irie *et al*, 1991, *Gene*, **108**(1), 139-144; Irie *et al*, 1991, *Mol. Gen. Genet.*, **225**(2), 257-265). For example, pSR1 from *Zygosaccharomyces rouxii* can be maintained in *Saccharomyces cerevisiae*. Where the plasmid is based on pSR1, pSB3 or pSB4 the host cell may be *Zygosaccharomyces rouxii*, where the plasmid is based on pSB1 or pSB2 the host cell may be *Zygosaccharomyces bailli*, where the plasmid is based on pPM1 the host cell may be *Pichia membranaefaciens*, where the plasmid is based on pSM1 the host cell may be *Zygosaccharomyces fermentati*, where the plasmid is based on pKD1 the host cell may be *Kluyveromyces drosophilarum* and where the plasmid is based on the 2μm plasmid the host cell may be *Saccharomyces cerevisiae* or *Saccharomyces carlsbergensis*. A 2μm-family plasmid of the invention can be said to be "based on" a naturally occurring plasmid if it comprises one, two or preferably three of the genes *FLP*, *REP1* and *REP2* having sequences derived from that naturally occurring plasmid.

A plasmid as defined above, may be introduced into a host through standard techniques. With regard to transformation of prokaryotic host cells, see, for example, Cohen *et al* (1972) *Proc. Natl. Acad. Sci. USA* **69**, 2110 and Sambrook *et al* (2001) *Molecular Cloning, A Laboratory Manual*, 3rd Ed. Cold Spring Harbor Laboratory, Cold Spring Harbor, NY. Transformation of yeast cells is described in Sherman *et al* (1986) *Methods In Yeast Genetics, A Laboratory Manual*, Cold Spring Harbor, NY. The method of Beggs (1978) *Nature* **275**, 104-109 is also useful. Methods for the transformation of *S. cerevisiae* are taught generally in EP 251 744, EP 258 067 and WO 90/01063, all of which are

incorporated herein by reference. With regard to vertebrate cells, reagents useful in transfecting such cells, for example calcium phosphate and DEAE-dextran or liposome formulations, are available from Stratagene Cloning Systems, or Life Technologies Inc., Gaithersburg, MD 20877, USA.

Electroporation is also useful for transforming cells and is well known in the art for transforming yeast cell, bacterial cells and vertebrate cells. Methods for transformation of yeast by electroporation are disclosed in Becker & Guarente (1990) *Methods Enzymol.* **194**, 182.

Generally, the plasmid will transform not all of the hosts and it will therefore be necessary to select for transformed host cells. Thus, a plasmid according to any one of the first, second or third aspects of the present invention may comprise a selectable marker, either within a polynucleotide sequence insertion, or elsewhere on the plasmid, including but not limited to bacterial selectable marker and/or a yeast selectable marker. A typical bacterial selectable marker is the β-lactamase gene although many others are known in the art. Suitable yeast selectable marker include *LEU2* (or an equivalent gene encoding a protein with the activity of β-lactamase malate dehydrogenase), *TRP1, HIS3, HIS4, URA3, URA5, SFA1, ADE2, MET15, LYS5, LYS2, ILV2, FBA1, PSE1, PDI1* and *PGK1*. In light of the different options available, the most suitable selectable markers can be chosen. If it is desirable to do so, *URA3* and/or *LEU2* can be avoided. Those skilled in the art will appreciate that any gene whose chromosomal deletion or inactivation results in an inviable host, so called essential genes, can be used as a selective marker if a functional gene is provided on the plasmid, as demonstrated for *PGK1* in a *pgk1* yeast strain (Piper and Curran, 1990, *Curr. Genet.* **17**, 119). Suitable essential genes can be found within the Stanford Genome Database (SGD), http:://db.yeastgenome.org).

Additionally, a plasmid according to any one of the first, second or third aspects of the present invention may comprise more than one selectable marker, either within a polynucleotide sequence insertion, or elsewhere on the plasmid.

One selection technique involves incorporating into the expression vector a DNA sequence marker, with any necessary control elements, that codes for a selectable trait in the transformed cell. These markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture, and tetracyclin, kanamycin or ampicillin (i.e. β-lactamase) resistance genes for culturing in *E.coli* and other bacteria. Alternatively, the gene for such selectable trait can be on another vector, which is used to co-transform the desired host cell.

Another method of identifying successfully transformed cells involves growing the cells resulting from the introduction of a plasmid of the invention, optionally to allow the expression of a recombinant polypeptide (i.e. a polypeptide which is encoded by a polynucleotide sequence on the plasmid and is heterologous to the host cell, in the sense that that polypeptide is not naturally produced by the host). Cells can be harvested and lysed and their DNA or RNA content examined for the presence of the recombinant sequence using a method such as that described by Southern (1975) *J. Mol. Biol.* **98**, 503 or Berent *et al* (1985) *Biotech.* **3**, 208, or other methods of DNA and RNA analysis common in the art. Alternatively, the presence of a polypeptide in the supernatant of a culture of a transformed cell can be detected using antibodies.

In addition to directly assaying for the presence of recombinant DNA, successful transformation can be confirmed by well known immunological methods when the recombinant DNA is capable of directing the expression of the protein. For example, cells successfully transformed with an expression vector produce proteins displaying appropriate antigenicity. Samples of cells suspected of being transformed are harvested and assayed for the protein using suitable antibodies.

Thus, in addition to the transformed host cells themselves, the present invention also contemplates a culture of those cells, preferably a monoclonal (clonally homogeneous) culture, or a culture derived from a monoclonal culture, in a nutrient medium. Alternatively, transformed cells may themselves represent an industrially/commercially or pharmaceutically useful product and can be purified from a culture medium and optionally formulated with a carrier or diluent in a manner appropriate to their intended

industrial/commercial or pharmaceutical use, and optionally packaged and presented in a manner suitable for that use. For example, whole cells could be immobilised; or used to spray a cell culture directly on to/into a process, crop or other desired target. Similarly, whole cell, such as yeast cells can be used as capsules for a huge variety of applications, such as fragrances, flavours and pharmaceuticals.

Transformed host cells may then be cultured for a sufficient time and under appropriate conditions known to those skilled in the art, and in view of the teachings disclosed herein, to permit the expression of any ORF(s) in the one or more polynucleotide sequence insertions within the plasmid.

The present invention thus also provides a method for producing a protein comprising the steps of (a) providing a plasmid according to the first, second or third aspects of the invention as defined above; (b) providing a suitable host cell; (c) transforming the host cell with the plasmid; and (d) culturing the transformed host cell in a culture medium, thereby to produce the protein.

Many expression systems are known, including bacteria (for example *E. coli* and *Bacillus subtilis*), yeasts, filamentous fungi (for example *Aspergillus*), plant cells, whole plants, animal cells and insect cells.

In one embodiment the preferred host cells are the yeasts in which the plasmid is capable of being maintained as a stable multicopy plasmid. Such yeasts include *Saccharomyces cerevisiae, Kluyveromyces lactis, Pichia pastoris, Zygosaccharomyces rouxii, Zygosaccharomyces bailli, Zygos-accharomyces fermentati,* and *Kluyveromyces drosophilarum.*

A plasmid is capable of being maintained as a stable multicopy plasmid in a host, if the plasmid contains, or is modified to contain, a selectable (e.g. *LEU2*) marker, and stability, as measured by the loss of the marker, is at least 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9% or substantially 100% after one, two, three, four, five, six, seven, eight, nine ten, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100 or more

generations. Loss of a marker can be assessed as described above, with reference to Chinery & Hinchliffe (1989, *Curr. Genet.*, **16**, 21-25).

It is particularly advantageous to use a yeast deficient in one or more protein mannosyl transferases involved in O-glycosylation of proteins, for instance by disruption of the gene coding sequence.

Recombinantly expressed proteins can be subject to undesirable post-translational modifications by the producing host cell. For example, the albumin protein sequence does not contain any sites for N-linked glycosylation and has not been reported to be modified, in nature, by O-linked glycosylation. However, it has been found that recombinant human albumin ("rHA") produced in a number of yeast species can be modified by O-linked glycosylation, generally involving mannose. The mannosylated albumin is able to bind to the lectin Concanavalin A. The amount of mannosylated albumin produced by the yeast can be reduced by using a yeast strain deficient in one or more of the *PMT* genes (WO 94/04687). The most convenient way of achieving this is to create a yeast which has a defect in its genome such that a reduced level of one of the Pmt proteins is produced. For example, there may be a deletion, insertion or transposition in the coding sequence or the regulatory regions (or in another gene regulating the expression of one of the *PMT* genes) such that little or no Pmt protein is produced. Alternatively, the yeast could be transformed to produce an anti-Pmt agent, such as an anti-Pmt antibody.

If a yeast other than *S. cerevisiae* is used, disruption of one or more of the genes equivalent to the *PMT* genes of *S. cerevisiae* is also beneficial, e.g. in *Pichia pastoris* or *Kluyveromyces lactis*. The sequence of *PMT1* (or any other *PMT* gene) isolated from *S. cerevisiae* may be used for the identification or disruption of genes encoding similar enzymatic activities in other fungal species. The cloning of the *PMT1* homologue of *Kluyveromyces lactis* is described in WO 94/04687.

The yeast will advantageously have a deletion of the *HSP150* and/or *YAP3* genes as taught respectively in WO 95/33833 and WO 95/23857.

The present application also provides a method of producing a protein comprising the steps of providing a host cell as defined above, which host cell comprises a plasmid of the present invention and culturing the host cell in a culture medium thereby to produce the protein. The culture medium may be non-selective or place a selective pressure on the stable multicopy maintenance of the plasmid.

A method of producing a protein expressed from a plasmid of the invention preferably further comprise the step of isolating the thus produced protein from the cultured host cell or the culture medium.

The thus produced protein may be present intracellularly or, if secreted, in the culture medium and/or periplasmic space of the host cell. The protein may be isolated from the cell and/or culture medium by many methods known in the art. For example purification techniques for the recovery of recombinantly expressed albumin have been disclosed in: WO 92/04367, removal of matrix-derived dye; EP 464 590, removal of yeast-derived colorants; EP 319 067, alkaline precipitation and subsequent application of the albumin to a lipophilic phase; and WO 96/37515, US 5 728 553 and WO 00/44772, which describe complete purification processes; all of which are incorporated herein by reference. Proteins other than albumin may be purified from the culture medium by any technique that has been found to be useful for purifying such proteins.

Such well-known methods include ammonium sulphate or ethanol precipitation, acid or solvent extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography, lectin chromatography, concentration, dilution, pH adjustment, diafiltration, ultrafiltration, high performance liquid chromatography ("HPLC"), reverse phase HPLC, conductivity adjustment and the like.

In one embodiment, any one or more of the above mentioned techniques may be used to further purifying the thus isolated protein to a commercially acceptable level of purity. By commercially acceptable level of purity, we include the provision of the protein at a concentration of at least 0.01 $g.L^{-1}$, 0.02 $g.L^{-1}$, 0.03 $g.L^{-1}$, 0.04 $g.L^{-1}$, 0.05 $g.L^{-1}$,0.06 $g.L^{-1}$,0.07 $g.L^{-1}$, 0.08 $g.L^{-1}$, 0.09 $g.L^{-1}$, 0.1 $g.L^{-1}$, 0.2 $g.L^{-1}$, 0.3 $g.L^{-1}$, 0.4 $g.L^{-1}$, 0.5 $g.L^{-1}$, 0.6 $g.L^{-1}$,

0.7 g.L^{-1}, 0.8 g.L^{-1}, 0.9 g.L^{-1}, 1 g.L^{-1}, 2 g.L^{-1}, 3 g.L^{-1}, 4 g.L^{-1}, 5 g.L^{-1}, 6 g.L^{-1}, 7 g.L^{-1}, 8 g.L^{-1}, 9 g.L^{-1}, 10 g.L^{-1}, 15 g.L^{-1}, 20 g.L^{-1}, 25 g.L^{-1}, 30 g.L^{-1}, 40 g.L^{-1},50 g.L^{-1}, 60 g.L^{-1}, 70 g.L^{-1}, 70 g.L^{-1}, 90 g.L^{-1}, 100 g.L^{-1}, 150 g.L^{-1}, 200 g.L^{-1},250 g.L^{-1}, 300 g.L^{-1}, 350 g.L^{-1}, 400 g.L^{-1}, 500 g.L^{-1}, 600 g.L^{-1}, 700 g.L^{-1}, 800 g.L^{-1}, 900 g.L^{-1}, 1000 g.L^{-1}, or more.

The thus purified protein may be lyophilised. Alternatively it may be formulated with a carrier or diluent, and optionally presented in a unit form.

It is preferred that the protein is isolated to achieve a pharmaceutically acceptable level of purity. A protein has a pharmaceutically acceptable level of purity if it is essentially pyrogen free and can be administered in a pharmaceutically efficacious amount without causing medical effects not associated with the activity of the protein.

The resulting protein may be used for any of its known utilities, which, in the case of albumin, include i.v. administration to patients to treat severe burns, shock and blood loss, supplementing culture media, and as an excipient in formulations of other proteins.

Although it is possible for a therapeutically useful desired protein obtained by a process of the invention to be administered alone, it is preferable to present it as a pharmaceutical formulation, together with one or more acceptable carriers or diluents. The carrier(s) or diluent(s) must be "acceptable" in the sense of being compatible with the desired protein and not deleterious to the recipients thereof. Typically, the carriers or diluents will be water or saline which will be sterile and pyrogen free.

Optionally the thus formulated protein will be presented in a unit dosage form, such as in the form of a tablet, capsule, injectable solution or the like.

We have also demonstrated that a plasmid-borne gene encoding a protein comprising the sequence of an "essential" protein can be used to stably maintain the plasmid in a host cell that, in the absence of the plasmid, does not produce the essential protein. A preferred essential protein is an essential chaperone, which can provide the further advantage that, as well as acting as a selectable marker to increase plasmid stability, its expression simultaneously increases the expression of a heterologous protein encoded by

a recombinant gene within the host cell. This system is advantageous because it allows the user to minimise the number of recombinant genes that need to be carried by a plasmid. For example, typical prior art plasmids carry marker genes (such as those as described above) that enable the plasmid to be stably maintained during host cell culturing process. Such marker genes need to be retained on the plasmid in addition to any further genes that are required to achieve a desired effect. However, the ability of plasmids to incorporate exogenous DNA sequences is limited and it is therefore advantageous to minimise the number of sequence insertions required to achieve a desired effect. Moreover, some marker genes (such as auxotrophic marker genes) require the culturing process to be conducted under specific conditions in order to obtain the effect of the marker gene. Such specific conditions may not be optimal for cell growth or protein production, or may require inefficient or unduly expensive growth systems to be used.

Thus, it is possible to use a gene that recombinantly encodes a protein comprising the sequence of an "essential protein" as a plasmid-borne gene to increase plasmid stability, where the plasmid is present within a cell that, in the absence of the plasmid, is unable to produce the "essential protein".

It is preferred that the "essential protein" is one that, when its encoding gene(s) in a host cell are deleted or inactivated, does not result in the host cell developing an auxotrophic (biosynthetic) requirement. By "auxotrophic (biosynthetic) requirement" we include a deficiency that can be complemented by additions or modifications to the growth medium. Therefore, an "essential marker gene" which encodes an "essential protein", in the context of the present invention is one that, when deleted or inactivated in a host cell, results in a deficiency which cannot be complemented by additions or modifications to the growth medium. The advantage of this system is that the "essential marker gene" can be used as a selectable marker on a plasmid in host cell that, in the absence of the plasmid, is unable to produce that gene product, to achieve increased plasmid stability without the disadvantage of requiring the cell to be cultured under specific selective (e.g. selective nutrient) conditions. Therefore, the host cell can be cultured under conditions that do not have to be adapted for any particular marker gene, without losing plasmid stability. For example, host cells produced using this system can be cultured in non-

selective media such as complex or rich media, which may be more economical than the minimal media that are commonly used to give auxotrophic marker genes their effect.

The cell may, for example, have its endogenous gene or genes deleted or otherwise inactivated.

It is particularly preferred if the "essential protein" is an "essential" chaperone, as this can provide the dual advantage of improving plasmid stability without the need for selective growth conditions and increasing the production of proteins, such as endogenously encoded or a heterologous proteins, in the host cell. This system also has the advantage that it minimises the number of recombinant genes that need to be carried by the plasmid if one chooses to use over-expression of an essential chaperone to increase protein production by the host cell.

Preferred "essential proteins" for use in this aspect of the invention include the "essential" chaperones PDI1 and PSE1, and other "essential" gene products such as PGK1 or FBA1 which, when the endogenous gene(s) encoding these proteins are deleted or inactivated in a host cell, do not result in the host cell developing an auxotrophic (biosynthetic) requirement.

Accordingly, in a fourth aspect, the present invention also provides a host cell comprising a plasmid (such as a plasmid according to any of the first, second or third aspects of the invention), the plasmid comprising a gene that encodes an essential chaperone wherein, in the absence of the plasmid, the host cell is unable to produce the chaperone. Preferably, in the absence of the plasmid, the host cell is inviable. The host cell may further comprise a recombinant gene encoding a heterologous (or homologous, in the sense that the recombinant gene encodes a protein identical in sequence to a protein encoded by the host cell) protein, such as those described above in respect of earlier aspects of the invention.

The present invention also provides, in a fifth aspect, a plasmid comprising, as the sole selectable marker, a gene encoding an essential chaperone. The plasmid may further

comprise a gene encoding a heterologous protein. The plasmid may be a 2μm-family plasmid and is preferably a plasmid according to any of the first, second or third aspects of the invention.

The present invention also provides, in a sixth aspect, a method for producing a heterologous protein comprising the steps of: providing a host cell comprising a plasmid, the plasmid comprising a gene that encodes an essential chaperone wherein, in the absence of the plasmid, the host cell is unable to produce the chaperone and wherein the host cell further comprises a recombinant gene encoding a heterologous protein; culturing the host cell in a culture medium under conditions that allow the expression of the essential chaperone and the heterologous protein; and optionally purifying the thus expressed heterologous protein from the cultured host cell or the culture medium; and further optionally, lyophilising the thus purified protein.

The method may further comprise the step of formulating the purified heterologous protein with a carrier or diluent and optionally presenting the thus formulated protein in a unit dosage form, in the manner discussed above. In one preferred embodiment, the method involves culturing the host cell in non-selective media, such as a rich media.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1 shows a plasmid map of the 2μm plasmid.

Figure 2 shows a plasmid map of pSAC35.

Figure 3 shows some exemplified FLP insertion sites.

Figures 4 to 8, 10, 11, 13 to 32, 36 to 42, 44 to 46, 48 to 54 and 57 to 76 show maps of various plasmids.

Figure 9 shows the DNA fragment from pDB2429 containing the *PDI1* gene.

Figure 12 shows some exemplified REP2 insertion sites.

Figure 33 shows table 3 as referred to in the Examples.

Figure 34 shows the sequence of SEQ ID NO: 1.

Figure 35 shows the sequence of SEQ ID NO: 2.

Figure 43 shows the sequence of PCR primers DS248 and DS250.

Figure 47 shows plasmid stabilities with increasing number of generation growth in non-selective liquid culture for *S. cerevisiae* containing various pSAC35-derived plasmids.

Figure 55 shows the results of RIE. 10mL YEPD shake flasks were inoculated with DXY1 *trp1Δ* [pDB2976], DXY1 *trp1Δ* [pDB2977], DXY1 *trp1Δ* [pDB2978], DXY1 *trp1Δ* [pDB2979], DXY1 *trp1Δ* [pDB2980] or DXY1 *trp1Δ* [pDB2981] transformed to tryptophan prototrophy with a 1.41kb *Not*I/*Pst*I *pdi1::TRP1* disrupting DNA fragment was isolated from pDB3078. Transformants were grown for 4-days at 30^{0}C, 200rpm. 4μL culture supernatant loaded per well of a rocket immunoelectrophoresis gel (Weeke, B. 1976. Rocket immunoelectrophoresis. *In* N. H. Azelsen, J. Kroll, and B. Weeke [eds.], A manual of quantitative immunoelectrophoresis. Methods and applications. Universitetsforlaget, Oslo, Norway). rHA standards concentrations are in μg/mL. 700μL goat anti-HA (Sigma product A-1151 resuspended in 5mL water) /50mL agarose. Precipin was stained with Coomassie blue. Isolates selected for further analysis are indicated (*).

Figure 56 shows the results of RIE. 10mL YEPD shake flasks were inoculated with DXY1 [pDB2244], DXY1 [pDB2976], DXY1 *trp1Δ pdi1::TRP1* [pDB2976], DXY1 [pDB2978], DXY1 *trp1Δ pdi1::TRP1* [pDB2978], DXY1 [pDB2980], DXY1 *trp1Δ pdi1::TRP1* [pDB2980], DXY1 [pDB2977], DXY1 *trp1Δ pdi1::TRP1* [pDB2977], DXY1 [pDB2979] DXY1 *trp1Δ pdi1::TRP1* [pDB2979], DXY1 [pDB2981] and DXY1 *trp1Δ pdi1::TRP1* [pDB2981], and were grown for 4-days at 30^{0}C, 200rpm. 4μL culture

supernatant loaded per well of a rocket immunoelectrophoresis gel. rHA standards concentrations are in μg/mL. 800μL goat anti-HA (Sigma product A-1151 resuspended in 5mL water) /50mL agarose. Precipin was stained with Coomassie blue. Isolates selected for further analysis are indicated (*)

EXAMPLES

These example describes the insertion of additional DNA sequences into a number of positions, defined by restriction endonuclease sites, within the US-region of a 2μm-family plasmid, of the type shown in Figure 2 and generally designated pSAC35, which includes a β-lactamase gene (for ampicillin resistance, which is lost from the plasmid following transformation into yeast), a *LEU2* selectable marker and an oligonucleotide linker, the latter two of which are inserted into a unique *Sna*BI-site within the UL-region of the 2μm-family disintegration vector, pSAC3 (see EP 0 286 424). The sites chosen were towards the 3'-ends of the *REP2* and *FLP* coding regions or in the downstream inverted repeat sequences. Short synthetic DNA linkers were inserted into each site, and the relative stabilities of the modified plasmids were compared during growth on non-selective media. Preferred sites for DNA insertions were identified. Insertion of larger DNA fragments containing "a gene of interest" was demonstrated by inserting a DNA fragment containing the *PDI1* gene into the *Xcm*I-site after *REP2*.

EXAMPLE 1

Insertion of Synthetic DNA Linker into XcmI-Sites in the Small Unique Region of pSAC35

Sites assessed initially for insertion of additional DNA into the US-region of pSAC35, were the *Xcm*I-sites in the 599-bp inverted repeats. One *Xcm*I-site cuts 51-bp after the *REP2* translation termination codon, whereas the other *Xcm*I-site cuts 127-bp before the end of the *FLP* coding sequence, due to overlap with the inverted repeat (see Figure 3).

The sequence inserted was a 52-bp linker made by annealing 0.5mM solutions of oligonucleotides CF86 and CF87. This DNA linker contained a core region "*Sna*BI-*Pac*I-*Fse*I/*Sfi*I-*Sma*I-*Sna*BI", which encoded restriction sites absent from pSAC35.

*Xcm*I Linker (CF86+CF87)

```
                                SfiI
                        --------------
                PacI                            SnaBI
          ---------                             -------
SnaBI                   FseI            SmaI
-------                 --------        ------
CF86  GGAGTGGTA CGTATTAATT AAGGCCGGCC AGGCCCGGGT ACGTACCAAT TGA
CF87 TCCTCACCAT GCATAATTAA TTCCGGCCGG TCCGGGCCCA TGCATGGTTA AC
```

Plasmid pSAC35 was partially digested with *Xcm*I, the linear 11-kb fragment was isolated from a 0.7%(w/v) agarose gel, ligated with the CF86/CF87 *Xcm*I linker (neat, 10^{-1} and 10^{-2} dilutions) and transformed into *E. coli* DH5α. Ampicillin resistant transformants were selected and screened for the presence of plasmids that could be linearised by *Sma*I digestion. Restriction enzyme analysis identified pDB2688 (Figure 4) with the linker cloned into the *Xcm*I-site after *REP2*. DNA sequencing using oligonucleotides primers CF88, CF98 and CF99 (Table 1) confirmed the insertion contained the correct linker sequence.

Table 1: Oligonucleotide sequencing primers:

Primer	Description	Sequence
CF88	*REP2* primer, 20mer	5'-ATCACGTAATACTTCTAGGG-3'
CF98	*REP2* primer, 20mer	5'-AGAGTGAGTTGGAAGGAAGG-3'
CF99	*REP2* primer, 20mer	5'-AGCTCGTAAGCGTCGTTACC-3'
CF90	*FLP* primer, 20mer	5'-CTAGTTTCTCGGTACTATGC-3'
CF91	*FLP* primer, 20mer	5'-GAGTTGACTAATGTTGTGGG-3'

Primer	Description	Sequence
CF100	*FLP* primer, 20mer	5'-AAAGCTTTGAAGAAAAATGC-3'
CF101	*FLP* primer, 20mer	5'-GCAAGGGGTAGGATCGATCC-3'
CF123	pDB2783 MCS, 24mer	5'-ATTCGAGCTCGGTACCTACGTACT-3'
CF126	pDB2783 MCS, 24mer	5'-CCCGGGCACGTGGGATCCTCTAGA-3'
M13-Forward	pDB2783 MCS, 17mer	5'-GTAAAACGACGGCCAGT-3'
M13-Reverse	pDB2783 MCS, 16mer	5'-AACAGCTATGACCATG-3'
CF129	Inverted repeat primer, 19mer	5'-GTGTTTATGCTTAAATGCG-3'
CF130	*REP2* primer, 20mer	5'-TCCTCTTGCATTTGTGTCTC-3'
CF131	*REP2* primer, 19mer	5'-ATCTTCCTATTATTATAGC-3'

Restriction enzyme analysis also identified pDB2689 (Figure 5), with the linker cloned into the *Xcm*I-site in the *FLP* gene. However, the linker in pDB2689 was shown by DNA sequencing using primers CF90 and CF91 to have a missing G:C base-pair within the *Fse*I/*Sfi*I site (marked above in bold in the CF86+CF87 linker). This generated a coding sequence for a mutant Flp-protein, with 39 C-terminal amino acid residues replaced by 56 different amino acids before the translation termination codon.

The missing base-pair in the pDB2689 linker sequence was corrected to produce pDB2786 (Figure 6). To achieve this, a 31-bp 5'-phosphorylated *Sna*BI-linker was made

from oligonucleotides CF104 and CF105. This was ligated into the *Sna*BI site of pDB2689, which had previously been treated with calf intestinal alkaline phosphatase. DNA sequencing with primers CF90, CF91, CF100 and CF101 confirmed the correct DNA linker sequence in pDB2786. This generated a coding sequence for a mutant Flp-protein, with 39 C-terminal residues replaced by 14 different residues before translation termination.

*Sna*BI Linker (CF104+CF105)

```
                        SfiI
                  ---------------
                    FseI
                  --------
             PacI                SmaI
          ---------             ------
CF104 Pi-GTATTAATTA AGGCCGGCCA GGCCCGGGTA C
CF105    CATAATTAAT TCCGGCCGGT CCGGGCCCAT G-Pi
```

An additional plasmid, pDB2798 (Figure 7), was also produced by ligation of the *Sna*BI linker in the opposite direction to pDB2786. The linker sequence in pDB2798 was confirmed by DNA sequencing. Plasmid pDB2798 contained a coding sequence for a mutant Flp-protein, with 39 C-terminal residues replaced by 8 different residues before translation termination.

A linker was also cloned into the *Xcm*I-site in the *FLP* gene to truncate the Flp protein at the site of insertion. The linker used was a 45-bp 5'-phosphorylated *Xcm*I-linker made from oligonucleotides CF120 and CF121.

*Xcm*I Linker (CF120+CF121)

```
                                    SfiI
                              ---------------
                        PacI                      SnaBI
                     ---------                   -------
                  SnaBI          FseI        SmaI
                 -------        --------    ------
CF120     Pi-GTAATAATA CGTATTAATT AAGGCCGGCC AGGCCCGGGT ACGTAA
CF121       TCATTATTAT GCATAATTAA TTCCGGCCGG TCCGGGCCCA TGCAT-Pi
```

This CF120/CF121 *Xcm*I linker was ligated with 11-kb pSAC35 fragments produced by partial digestion with *Xcm*I, followed by treatment with calf intestinal alkaline phosphatase. Analysis of ampicillin resistant *E. coli* DH5α transformants identified

clones containing pDB2823 (Figure 8). DNA sequencing with primers CF90, CF91, CF100 and CF101 confirmed the linker sequence in pDB2823. Translation termination within the linker inserted would result in the production of Flp (1-382), which lacked 41 C-terminal residues.

The impact on plasmid stability from insertion of linker sequences into the *Xcm*I-sites within the US-region of pSAC35 was assessed for pDB2688 and pDB2689. Plasmid stability was determined in a *S. cerevisiae* strain by loss of the *LEU2* marker during non-selective grown on YEPS. The same yeast strain, transformed with pSAC35, which is structurally similar to pSAC3, but contains additional DNA inserted at the *Sna*BI site that contained a *LEU2* selectable marker (Chinery & Hinchliffe, 1989, *Curr. Genet.*, **16**, 21), was used as the control.

The yeast strain was transformed to leucine prototrophy using a modified lithium acetate method (Sigma yeast transformation kit, YEAST-1, protocol 2; (Ito *et al*, 1983, *J. Bacteriol.*, **153**, 163; Elble, 1992, *Biotechniques*, **13**, 18)). Transformants were selected on BMMD-agar plates, and were subsequently patched out on BMMD-agar plates. Cryopreserved trehalose stocks were prepared from 10mL BMMD shake flask cultures (24 hrs, 30^0C, 200rpm).

The composition of YEPD and BMMD is described by Sleep *et al.*, 2002, *Yeast* **18**, 403. YEPS and BMMS are similar in composition to YEPD and BMMD accept that 2% (w/v) sucrose was substituted for the 2% (w/v) glucose as the sole initial carbon source.

For the determination of plasmid stability a 1mL cryopreserved stock was thawed and inoculated into 100mL YEPS (initial $OD_{600} \approx 0.04$-0.09) in a 250mL conical flask and grow for approximately 72 hours (70-74 hrs) at 30°C in an orbital shaker (200 rpm, Innova 4300 incubator shaker, New Brunswick Scientific).

Samples were removed from each flask, diluted in YEPS-broth (10^{-2} to 10^{-5} dilution), and 100µL aliquots plated in duplicate onto YEPS-agar plates. Cells were grown at 30°C for 3-4 days to allow single colonies to develop. For each yeast stock analysed, 100 random

colonies were patched in replica onto BMMS-agar plates followed by YEPS-agar plates. After growth at 30°C for 3-4 days the percentage of colonies growing on both BMMS-agar plates and YEPS-agar plates was determined as the measure of plasmid stability.

In the above analysis to measure the loss of the *LEU2* marker from transformants, pSAC35 and pDB2688 appeared to be 100% stable, whereas pDB2689 was 72% stable. Hence, insertion of the linker into the *Xcm*I-site after *REP2* had no apparent effect on plasmid stability, despite altering the transcribed sequence and disrupting the homology between the 599-bp inverted repeats. Insertion of the linker at the *Xcm*I-site in *FLP* also resulted in a surprisingly stable plasmid, despite both disruption of the inverted repeat and mutation of the Flp protein.

EXAMPLE 2

Insertion of the PDI1 Gene into the XcmI Linker of pDB2688

The insertion of a large DNA fragment into the US-region of 2μm-like vectors was demonstrated by cloning the *S. cerevisiae PDI1* gene into the *Xcm*I-linker of pDB2688. The *PDI1* gene (Figure 9) was cloned on a 1.9-kb *Sac*I-*Spe*I fragment from a larger *S. cerevisiae* SKQ2n genomic DNA fragment containing the *PDI1* gene (as provided in the plasmid pMA3a:C7 that is described in US 6,291,205 and also described as Clone C7 in Crouzet & Tuite, 1987, *Mol. Gen. Genet.*, **210**, 581-583 and Farquhar *et al*, 1991, *supra*), which had been cloned into YIplac211 (Gietz & Sugino, 1988, *Gene*, **74**, 527-534) and had a synthetic DNA linker containing a *Sac*I restriction site inserted at a unique *Bsu*36I-site in the 3' untranslated region of the *PDI1* gene. The 1.9-kb *Sac*I-*Spe*I fragment was treated with T4 DNA polymerase to fill the *Spe*I 5'-overhang and remove the *Sac*I 3'-overhang. This *PDI1* fragment included 212-bp of the *PDI1* promoter upstream of the translation initiation codon, and 148-bp downstream of the translation termination codon. This was ligated with *Sma*I linearised/calf intestinal alkaline phosphatase treated pDB2688, to create plasmid pDB2690 (Figure 10), with the *PDI1* gene transcribed in the same direction as *REP2*. A *S. cerevisiae* strain was transformed to leucine prototrophy with pDB2690.

An expression cassette for a human transferrin mutant (N413Q, N611Q) was subsequently cloned into the *Not*I-site of pDB2690 to create pDB2711 (Figure 11). The expression cassette in pDB271 1 contains the *S. cerevisiae PRB1* promoter, an HSA/MFα fusion leader sequence (EP 387319; Sleep *et al*, 1990, *Biotechnology (N.Y.)*, **8**, 42) followed by a coding sequence for the human transferrin mutant (N413Q, N611Q) and the *S. cerevisiae ADH1* terminator. Plasmid pDB2536 (Figure 36) was constructed similarly by insertion of the same expression cassette into the *Not*I-site of pSAC35.

The advantage of inserting "genes of interest" into the US-region of 2μm-vectors was demonstrated by the approximate 7-fold increase in recombinant transferrin N413Q, N611Q secretion during fermentation of yeast transformed with pDB2711, compared to the same yeast transformed with pDB2536. An approximate 15-fold increase in recombinant transferrin N413Q, N611Q secretion was observed in shake flask culture (data not shown).

The relative stabilities of plasmids pDB2688, pDB2690, pDB2711, pDB2536 and pSAC35 were determined in the same yeast strain grown in YEPS media, using the method described above (Table 2).

In this analysis, pDB2690 was 32% stable, compared to 100% stability for pDB2688 without the *PDI1* insert. This decrease in plasmid stability was less than the decrease in plasmid stability observed with pDB2536, due to insertion of the rTF (N413Q, N611Q) expression cassette into the *Not*I-site within the large unique region of pSAC35 (Table 2).

Furthermore, selective growth in minimal media during high cell density fermentations could overcome the increased plasmid instability due to the *PDI1* insertion observed in YEPS medium, as the rTF (N413Q, N611Q) yield from the same yeast transformed with pDB2711 did not decrease compared to that achieved from the same yeast transformed with pDB2536.

Table 2: Summary of plasmid stability data for *PDI1* insertion into the small unique region of pSAC35. Data from 3 days growth in non-selective shake flask culture before plating on YEPS-agar.

Plasmid	Insertion Site(s)	Additional Details	Relative Stability
pSAC35	-	-	100%
pDB2688	*Xcm*I	Linker in Inverted Repeat	100%
pDB2690	*Xcm*I	*PDI1* in *Xcm*I Linker	32%
pDB2711	*Xcm*I, *Not*I	*PDI1* in *Xcm*I Linker, rTf Cassette at *Not*I	10%
pDB2536	*Not*I	rTf Cassette at *Not*I	17%

EXAMPLE 3

Insertion of DNA Linkers into the REP2 Gene and Downstream Sequences in the Inverted Repeat of pSAC35

To define the useful limits for insertion of additional DNA into the *REP2* gene and sequences in the inverted repeat downstream of it, further linkers were inserted into pSAC35. Figure 12 indicates the restriction sites used for these insertions and the effects on the Rep2 protein of translation termination at these sites.

The linker inserted at the *Xmn*I-site in *REP2* was a 44-bp sequence made from oligonucleotides CF108 and CF109.

*Xmn*I Linker (CF108+CF109)

```
                                        SfiI
                                    --------------
                          PacI                          SnaBI
                      ---------                         -------
            SnaBI                   FseI          SmaI
           -------                 --------      ------
CF108      ATAATAATAC GTATTAATTA AGGCCGGCCA GGCCCGGGTA CGTA
CF109      TATTATTATG CATAATTAAT TCCGGCCGGT CCGGGCCCAT GCAT
```

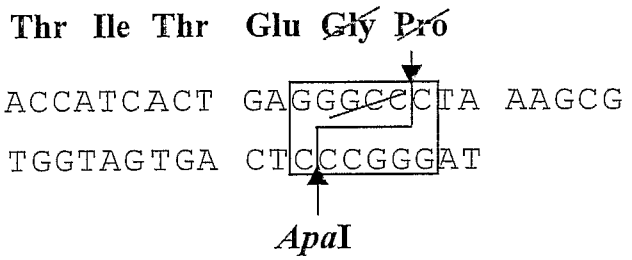
To avoid insertion into other *Xmn*I-sites in pSAC35, the 3,076-bp *Xba*I fragment from pSAC35 that contained the *REP2* and *FLP* genes was first sub-cloned into the *E. coli* cloning vector pDB2685 (Figure 13) to produce pDB2783 (Figure 14).

Plasmid pDB2685 is a pUC18-like cloning vector derived from pCF17 containing apramycin resistance gene aac(3)IV from *Klebsiella pneumoniae* (Rao *et al*, 1983, *Antimicrob. Agents Chemother.*, **24**, 689) and multiple cloning site from pMCS5 (Hoheisel, 1994, *Biotechniques*, **17**, 456). pCF17 was made from pIJ8600 (Sun *et al.*, 1999, *Microbiology*, **145**(9), 2221-7) by digestion with *Eco*RI, *Nhe*I and the Klenow fragment of DNA polymerase I, and self-ligation, followed by isolation from the reaction products by transformation of competent *E. coli* DH5α cells and selection with apramycin sulphate. Plasmid pDB2685 was constructed by cloning a 439bp *Ssp*I-*Swa*I fragment from pMCS5 into pCF17, which had been cut with *Msc*I and treated with calf intestinal alkaline phosphatase. Blue/white selection is not dependant on IPTG induction.

Plasmid pDB2783 was linearised with *Xmn*I and ligated with the CF108/CF109 *Xmn*I-linker to produce pDB2799 (Figure 15) and pDB2780 (not shown). Plasmid pDB2799 contained the CF108/CF109 *Xmn*I linker in the correct orientation for translation termination at the insertion site to produce Rep2 (1-244), whereas pDB2780 contained the linker cloned in the opposite orientation. DNA sequencing with primers CF98 and CF99 confirmed the correct linker sequences.

The 3,120bp *Xba*I fragment from pDB2799 was subsequently ligated with a 7,961-bp pSAC35 fragment which had been produced by partial *Xba*I digestion and treatment with calf intestinal alkaline phosphatase, to create plasmid pDB2817 (B-form) and pDB2818 (A-form) disintegration vectors (Figures 16 and 17 respectively).

Insertion of linkers at the *Apa*I-site in pSAC35 was performed with and without 3'-5' exonuclease digestion by T4 DNA polymerase. This produced coding sequences for either Rep2 (1-271) or Rep2 (1-269) before translation termination. In the following figure, the sequence GGCC marked with diagonal lines was deleted from the 3'-overhang produced after ApaI digestion resulting in removal of nucleotides from the codons for Glycine-170 (GGC) and Proline-171.



The linker inserted at the *Apa*I-site without exonuclease digestion was a 50-bp 5'-phosphorylated linker made from oligonucleotides CF116 and CF117.

*Apa*I-Linker (CF116+CF117)

```
                                        SfiI
                                    --------------
                              PacI                        SnaBI
                          ---------                       ------
                    SnaBI             FseI         SmaI
                    ------          ---------    -------
CF116      Pi-CTTAAT AATACGTATT AATTAAGGCC GGCCAGGCCC GGGTACGTAG GGCC
CF117     CCGGGAATTA TTATGCATAA TTAATTCCGG CCGGTCCGGG CCCATGCATC-Pi
```

This was ligated with pSAC35, which had been linearised with *Apa*I and treated with calf intestinal alkaline phosphatase, to produce pDB2788 (Figure 18) and pDB2789 (not shown). Within pDB2788, the linker was in the correct orientation for translation termination after proline-271, whereas in pDB2789 the linker was in the opposite orientation.

The linker inserted at the *Apa*I-site with exonuclease digestion by T4 DNA polymerase was a 43-bp 5'-phosphorylated linker made from oligonucleotides CF106 and CF107, which was called the core termination linker.

Core Termination-Linker (CF106+CF107)

```
                                        SfiI
                                    --------------
                          PacI                          SnaBI
                      --------                        -------
                 SnaBI            FseI         SmaI
                -------          --------     ------
CF106    Pi-TAATAATACG TATTAATTAA GGCCGGCCAG GCCCGGGTAC GTA
CF107       ATTATTATGC ATAATTAATT CCGGCCGGTC CGGGCCCATG CAT-Pi
```

The core termination linker was ligated with pSAC35, which had been linearised with *Apa*I, digested with T4 DNA polymerase and treated with calf intestinal alkaline phosphatase. This ligation produced pDB2787 (Figure 19) with the linker cloned in the correct orientation for translation termination after glutamate-269.

The correct DNA sequences were confirmed in all clones containing the *Apa*I-linkers, using oligonucleotide primers CF98 and CF99.

The core termination linker (CF106+CF107) was also used for insertion into the *Fsp*I-sites of pDB2783 (Figure 14). The core termination linker (CF106+CF107) was ligated into pDB2783 linearised by partial *Fsp*I digestion, which had been treated with calf intestinal alkaline phosphatase. Plasmids isolated from apramycin resistant *E. coli* DH5α transformants were screened by digestion with *Fsp*I, and selected clones were sequenced with M13 forward and reverse primers.

Plasmid pDB2801 (not shown) was identified containing two copies of the linker cloned in the correct orientation (with the *Pac*I-site nearest the *REP2* gene). The extra copy of the linker was subsequently removed by first deleting a 116-bp *Nru*I-*Hpa*I fragment containing an *Fse*I-site from the multiple cloning site region, followed by digestion with *Fse*I and re-ligation to produce pDB2802 (Figure 20). DNA sequencing using oligonucleotide CF126 confirmed the correct linker sequence.

The 3,119-bp pDB2802 *Xba*I fragment was subsequently ligated with a 7,961-bp pSAC35 fragment produced by partial *Xba*I digestion and treatment with calf intestinal alkaline phosphatase to create pDB2805 (B-form) and pDB2806 (A-form) disintegration vectors (Figures 21 and 22, respectively).

EXAMPLE 4

Insertion of DNA Linkers into the FLP Gene and Downstream Sequences in the Inverted Repeat of pSAC35

DNA linkers were inserted into pSAC35 to define the useful limits for insertion of additional DNA into the *FLP* gene and sequences downstream in the inverted repeat. Figure 3 indicates the restriction sites used for these insertions and the affects on the Flp protein of translation termination at these sites.

The linker inserted at the *Bcl*I-site was a 49-bp 5'-phosphorylated linker made from oligonucleotides CF118 and CF119.

*Bcl*I Linker (CF118+CF119)

```
                                        SfiI
                                    -------------
                              PacI                      SnaBI
                          ---------                     ------
                    SnaBI           FseI         SmaI
                    ------          --------     ------
CF118 Pi-GATCACTAATAATACGTATTAATTAAGGCCGGCCAGGCCCGGGTACGTA
CF119       TGATTATTATGCATAATTAATTCCGGCCGGTCCGGGCCCATGCATCTAG-Pi
```

Due to Dam-methylation of the *Bcl*I-site in pSAC35, the *Bcl*I-linker was cloned into non-methylated pSAC35 DNA, which had been isolated from the *E. coli* strain ET12567 pUZ8002 (MacNeil *et al*, 1992, *Gene*, **111**, 61; Kieser *et al*, 2000, *Practical Streptomyces Genetics*, The John Innes Foundation, Norwich). Plasmid pSAC35 was linearised with *Bcl*I, treated with calf intestinal alkaline phosphatase, and ligated with the *Bcl*I-linker to create pDB2816 (Figure 23). DNA sequencing with oligonucleotide primers CF91 and CF100 showed that three copies of the *Bcl*I-linker were present in pDB2816, which were all in the correct orientation for translational termination of Flp after histidine-353.

Digestion of pDB2816 with *Pac*I followed by self-ligation, was performed to produce pDB2814 and pDB2815, containing one and two copies of the *Bcl*I-linker respectively (Figures 24 and 25). The DNA sequences of the linkers were confirmed using primers

CF91 and CF100. In *S. cerevisiae* a truncated Flp (1-353) protein will be produced by yeast transformed with pDB2814, pDB2815 or pDB2816.

An additional plasmid pDB2846 (data not shown) was also produced by ligation of a single copy of the *Bcl*I-linker in the opposite orientation to pDB2814. This has the coding sequence for the first 352-residues from Flp followed by 14 different residues before translation termination.

The linker inserted at the *Hga*I-site was a 47-bp 5'-phosphorylated linker made from oligonucleotides CF114 and CF115.

*Hga*I Linker (CF114+CF115)

```
                                        SfiI
                                    -------------
                                PacI                    SnaBI
                            ---------                   -----
                    SnaBI               FseI        SmaI
                   ------             --------    ------
CF114  Pi-AGTACTATAATACGTATTAATTAAGGCCGGCCAGGCCCGGGTACGTA
CF115           ATATTATGCATAATTAATTCCGGCCGGTCCGGGCCCATGCATTCATG-Pi
```

The *Hga*I-linker was ligated with pDB2783, which had been linearised by partial *Hga*I digestion and treated with calf intestinal alkaline phosphatase to create pDB2811 (Figure 26). DNA sequencing with oligonucleotides CF90, CF91 and CF100 confirmed the correct linker insertion.

The 3,123-bp *Xba*I fragment from pDB2811 was subsequently ligated with the 7,961-bp pSAC35 fragment, produced by partial *Xba*I digestion and treatment with calf intestinal alkaline phosphatase to produce pDB2812 (B-form) and pDB2813 (A-form) disintegration vectors containing DNA inserted at the *Hga*I-site (Figures 27 and 28, respectively).

Plasmids pDB2803 and pDB2804 (Figures 29 and 30, respectively) with the core termination linker (CF106+CF107) inserted at the *Fsp*I after *FLP*, were isolated by the same method used to construct pDB2801. The correct linker insertions were confirmed by DNA sequencing. Plasmid pDB2804 contained the linker inserted in the correct

orientation (with the *Pac*I-site closest to the *FLP* gene), whereas pDB2803 contained the linker in the opposite orientation.

The pDB2804 3,119-bp *Xba*I fragment was ligated with the 7,961-bp pSAC35 fragment produced by partial *Xba*I digestion and treatment with calf intestinal alkaline phosphatase to create pDB2807 (B-form) and pDB2808 (A-form) disintegration vectors containing DNA inserted at the *Fsp*I-site after *FLP* (Figures 31 and 32 respectively).

EXAMPLE 5

Relative Stabilities of the LEU2 Marker in Yeast Transformed with pSAC35-Like Plasmids Containing DNA Linkers Inserted into the Small Unique Region and Inverted Repeats

A *S. cerevisiae* strain was transformed with the pSAC35-like plasmids containing DNA linkers inserted into the US-region and inverted repeats. Cryopreserved trehalose stocks were prepared for testing plasmid stabilities (Table 3). Plasmid stabilities were analysed as described above for linkers inserted at the *Xcm*I-sites in pSAC35. Duplicate flasks were set up for each insertion site analysed. In addition, to the analysis of colonies derived from cells after 3-days in shake flake culture, colonies were grown and analysed from cells with a further 4-days shake flask culture. For this, 100µL samples were removed from each 3-day old flask and sub-cultured in 100mL YEPS broth for a further period of approximately 96 hours (94-98 hrs) at 30.0°C in an orbital shaker, after which single colonies were obtained and analysed for loss of the *LEU2* marker. In this case analysis was restricted to a single flask from selected strains, for which 50 colonies were picked. The overall results are summarised in Table 4.

Table 4: Summary of plasmid stability data for DNA insertions into pSAC35

Set 1 represents data from 3 days in non-selective shake flask culture.

Set 2 represents data from 7 days in non-selective shake flask culture.

A) ***REP2*** **Insertion Sites**

Plasmid(s)	Insertion Site	Additional Details	Relative Stability	
			Set 1	Set 2
pSAC35	-	Control	99%	100%
pDB2817 & pDB2818	*Xmn*I	REP2 (1-244)	39%	16%
pDB2787	*Apa*I/T4 pol.	REP2 (1-269)	45%	0%
pDB2788	*Apa*I	REP2 (1-271)	33%	0%
pDB2688	*Xcm*I	Inverted Repeat	100%	100%
pDB2805 & pDB2806	*Fsp*I	Inverted Repeat	100%	100%

B) ***FLP*** **Insertion Sites**

Plasmid(s)	Insertion Site	Additional Details	Relative Stability	
			Set 1	Set 2
pDB2814	*Bcl*I	FLP (1-353)	67%	64%
pDB2823	*Xcm*I	FLP (1-382)	64%	53%
pDB2812 & pDB2813	*Hga*I	Inverted Repeat	100%	100%
pDB2808	*Fsp*I	Inverted Repeat	100%	100%

All of the modified pSAC35 plasmids were able to transform yeast to leucine prototrophy, indicating that despite the additional DNA inserted within the functionally crowded regions of 2μm DNA, all could replicate and partition in *S. cerevisiae.* This applied to plasmids with 43-52 base-pair linkers inserted at all the sites in the 2μm US-region, as well as the larger DNA insertion containing the *PDI1* gene.

For the linker insertion sites, data was reproducible between both experiments and duplicates. All sites outside *REP2* or *FLP* open reading frames, but within inverted repeats appeared to be 100% stable under the test conditions used. Plasmid instability (i.e. plasmid loss) was observed for linkers inserted into sites within the *REP2* or *FLP* open reading frames. The observed plasmid instability of *REP2* insertions was greater than for *FLP* insertions. For the *REP2* insertions, loss of the *LEU2* marker continued with the extended growth period in non-selective media, whereas there was little difference for the *FLP* insertions.

Insertions into the *REP2* gene produced Rep2 polypeptides truncated within a region known to function in self-association and binding to the STB-locus of 2μm (Sengupta *et al*, 2001, *J. Bacteriol.*, **183**, 2306).

Insertions into the *FLP* gene resulted in truncated Flp proteins. All the insertion sites were after tyrosine-343 in the C-terminal domain, which is essential for correct functioning of the Flp protein (Prasad *et al*, 1987, *Proc. Natl. Acad. Sci. U.S.A.*, **84**, 2189; Chen *et al*, 1992, *Cell*, **69**, 647; Grainge *et al*, 2001, *J. Mol. Biol.*, **314**, 717).

None of the insertions into the inverted repeat regions resulted in plasmid instability being detected, except for the insertion into the *FLP Xcm*I-site, which also truncated the Flp protein product. The insertions at the *FspI*-sites in the inverted repeat regions were the closest to the FRT (Flp recognition target) regions, important for plasmid replication.

pSAC35-like plasmids have been constructed with 43-52 base-pair DNA linkers inserted into the *REP2* open reading frame, or the *FLP* open reading frame or the inverted repeat sequences. In addition, a 1.9-kb DNA fragment containing the *PDI1* gene was inserted into a DNA linker at the *Xcm*I-site after *REP2*.

All of the pSAC35-like vectors with additional DNA inserted were able to transform yeast to leucine prototrophy. Therefore, despite inserting DNA into functionally crowded regions of 2μm plasmid DNA, the plasmid replication and partitioning mechanisms had not been abolished.

Determination of plasmid stability by measuring loss of the *LEU2* selectable marker during growth in non-selective medium indicated that inserting DNA linkers into the inverted repeats had not destabilised the plasmid, whereas plasmid stability had been reduced by insertions into the *REP2* and *FLP* open reading frames. However, despite a reduction in plasmid stability under non-selective media growth conditions when insertions were made into the *REP2* and *FLP* open reading frames at some positions defined by the first and second aspects of the invention, the resulting plasmid nevertheless has a sufficiently high stability for use in yeast when grown on selective media.

EXAMPLE 6

Insertion of DNA Sequences Immediately after the REP2 Gene in the Small Unique Region of pSAC35

To further define the useful limits for insertion of additional DNA into the *REP2* gene and sequences in the inverted repeat downstream of it, a synthetic DNA linker was inserted into pSAC35 immediately after the *REP2* translation termination codon (TGA). As there were no naturally occurring restriction endonuclease sites conveniently located immediately after the *REP2* coding sequence in 2μm (or pSAC35), a *Sna*BI-site was introduced at this position by oligonucleotide directed mutagenesis. The pSAC35 derivative with a unique *Sna*BI-site immediately downstream of *REP2* was named pDB2938 (Figure 37). In pDB2938, the end of the inverted repeat was displaced from the rest of the inverted repeat by insertion of the *Sna*BI-site. pDB2954 (Figure 38) was subsequently constructed with a 31-bp sequence identical to the *SnaB*I-linker made from oligonucleotides CF104 and CF105 (*supra*) inserted into the unique *Sna*BI site of pDB2938, such that the order of restriction endonuclease sites located immediately after the TGA translation termination codon of *REP2* was *Sna*BI-*Pac*I-*Fse*I/*Sfi*I-*Sma*I-*Sna*BI.

To construct pDB2938, the 1,085-bp *Nco*I-*Bam*HI fragment from pDB2783 (Figure 14) was first sub-cloned into pMCS5 (Hoheisel, 1994, *Biotechniques*, **17**, 456), which had

been digested with *Nco*I, *Bam*HI and calf intestinal alkaline phosphatase. This produced pDB2809 (Figure 39), which was subsequently mutated using oligonucleotides CF127 and CF128, to generate pDB2920 (Figure 40).

The 51-bp mutagenic oligonucleotides CF127 and CF128

The *Sna*BI recognition sequence is underlined

CF127 5′-CGTAATACTTCTAGGGTATGATACGTATCCAATATCAAAGGAAATGATAGC-3′

CF128 5′-GCTATCATTTCCTTTGATATTGGATACGTATCATACCCTAGAAGTATTACG-3′

Oligonucleotide directed mutagenesis was performed according to the instruction manual of the Statagene's QuickChange™ Site-Directed Mutagenesis Kit. *Sna*BI and *Hin*dIII restriction digestion of plasmid DNA was used to identify the ampicillin resistant *E. coli* transformants that contained pDB2920. The inserted 6-bp sequence of the *Sna*BI restriction site and the correct DNA sequence for the entire 1,091-bp *Nco*I-*Bam*HI fragment was confirmed in pDB2920 by DNA sequencing using oligonucleotide primers CF98, CF99, CF129, CF130, CF131 and M13 forward and reverse primers (Table 1).

The 1,091-bp *Nco*I-*Bam*HI fragment from pDB2920 was isolated by agarose gel purification and ligated with the approximately 4.7-kb *Nco*I-*Bam*HI fragment from pDB2783 to produce pDB2936 (Figure 41). The pDB2783 4.7-kb *Nco*I-*Bam*HI fragment was isolated by complete *Bam*HI digestion of pDB2783 DNA that had first been linearised by partial digestion with *Nco*I and purified by agarose gel electrophoresis. *E. coli* DH5α cells were transformed to apramycin resistance by the ligation products. pDB2936 was identified by *Sna*BI digestion of plasmid DNA isolated from the apramycin resistant clones.

The 3,082-bp *Xba*I fragment from pDB2936 was subsequently ligated with a 7,961-bp pSAC35 fragment, which had been produced by partial *Xba*I digestion and treatment with calf intestinal alkaline phosphatase, to create the disintegration vector pDB2938 (2μm B-form, Figure 37)

pDB2938 was digested with *Sna*BI and calf intestinal phosphatase and ligated with an approximately 2-kb *Sna*BI fragment from pDB2939 (Figure 42). pDB2939 was produced

by PCR amplifying the *PDI1* gene from *S. cerevisiae* S288c genomic DNA with oligonucleotide primers DS248 and DS250 (Figure 43), followed by digesting the PCR products with *Eco*RI and *Bam*HI and cloning the approximately 1.98-kb fragment into YIplac211 (Gietz & Sugino, 1988, *Gene*, **74**, 527-534), that had been cut with *Eco*RI and *Bam*HI. DNA sequencing of pDB2939 identified a missing 'G' from within the DS248 sequence, which is marked in bold in Figure 43. The approximately 2-kb *Sna*BI fragment from pDB2939 was subsequently cloned into the unique *Sna*BI-site of pDB2938 to produce plasmid pDB2950 (Figure 44). The *PDI1* gene in pDB2950 is transcribed in the same direction as the *REP2* gene.

pDB2950 was subsequently digested with *Sma*I and the approximately 11.1-kb DNA fragment was circularised to delete the S288c *PDI1* sequence. This produced plasmid pDB2954 (Figure 38) with the *Sna*BI-*Pac*I-*Fse*I/*Sfi*I-*Sma*I-*Sna*BI linker located immediately after the TGA translation termination codon of *REP2*.

In addition to cloning the *S. cerevisiae* S288c *PDI1* gene into the unique *Sna*BI-site of pDB2938, the *S. cerevisiae* SKQ2n *PDI1* gene was similarly inserted at this site. The *S. cerevisiae* SKQ2n *PDI1* gene sequence was PCR amplified from plasmid DNA containing the *PDI1* gene from pMA3a:C7 (US 6,291,205), also known as Clone C7 (Crouzet & Tuite, 1987, *supra*; Farquhar *et al*, 1991, *supra*). The SKQ2n *PDI1* gene was amplified using oligonucleotide primers DS248 and DS250 (Figure 43). The approximately 2-kb PCR product was digested with *Eco*RI and *Bam*HI and ligated into YIplac211 (Gietz & Sugino, 1988, *Gene*, **74**, 527-534) that has been cut with *Eco*RI and *Bam*HI, to produce plasmid pDB2943 (Figure 45). The 5' end of the SKQ2n PDI1 sequence is analogous to a blunt-ended *Spe*I-site extended to include the *Eco*RI, *Sac*I, *Sna*BI, *Pac*I, *Fse*I, *Sfi*I and *Sma*I sites, the 3' end extends up to a site analogous to a blunt-ended *Bsu*36I site, extended to include a *Sma*I, *Sna*BI and *Bam*HI sites. The *PDI1* promoter length is approximately 210bp. The entire DNA sequence was determined for the *PDI1* fragment and shown to code for the PDI protein of *S. cerevisiae* strain SKQ2n sequence (NCBI accession number CAA38402), but with a serine residue at position 114 (not an arginine residue). Similarly to the *S. cerevisiae* S288c sequence in pDB2939, pDB2943 had a missing 'G' from within the DS248 sequence, which is marked in bold in Figure 43. The approximately 1,989-bp *Sna*BI fragment from pDB2943 was

subsequently cloned into the unique *Sna*BI-site in pDB2938. This produced plasmid pDB2952 (Figure 46), in which the SKQ2n *PDI1* gene is transcribed in the same direction as *REP2*.

EXAMPLE 7

Relative Stabilities of the LEU2 Marker in Yeast Transformed with pSAC35-Like Plasmids Containing DNA Inserted Immediately after the REP2 gene

The impact on plasmid stability from insertion of the linker sequence at the *Sna*BI-site introduced after the *REP2* gene in pSAC35 was assessed for pDB2954. This was determined in the same *S. cerevisiae* strain as used in the earlier examples by loss of the *LEU2* marker during non-selective growth on YEPS. The stability of pDB2954 was compared to the stabilities of pSAC35 (control plasmid), pDB2688 (*Xcm*I-linker) and pDB2817 (*Xmn*I-linker) by the method described in Example 1.

The yeast strain was transformed to leucine prototrophy using a modified lithium acetate method (Sigma yeast transformation kit, YEAST-1, protocol 2; (Ito *et al*, 1983, *J. Bacteriol.*, **153**, 163; Elble, 1992, *Biotechniques*, **13**, 18)). Transformants were selected on BMMD-agar plates, and were subsequently patched out on BMMD-agar plates. Cryopreserved trehalose stocks were prepared from 10mL BMMD shake flask cultures (24 hrs, 30°C, 200rpm) by mixing with an equal volume of sterile 40% (w/v) trehalose and freezing aliquots at –80°C (i.e. minus 80°C).

For the determination of plasmid stability, a 1mL cryopreserved stock was thawed and inoculated into 100mL YEPS (initial $OD_{600} \approx 0.04$-0.09) in a 250mL conical flask and grown for approximately 72 hours (typically 70-74 hrs) at 30°C in an orbital shaker (200 rpm, Innova 4300 incubator shaker, New Brunswick Scientific). Each strain was analysed in duplicate.

Samples were removed from each flask, diluted in YEPS-broth (10^{-2} to 10^{-5} dilution), and 100µL aliquots plated in duplicate onto YEPS-agar plates. Cells were grown at 30°C for

3-4 days to allow single colonies to develop. For each yeast stock analysed, 100 random colonies were patched in replica onto BMMS-agar plates followed by YEPS-agar plates. After growth at 30°C for 3-4 days the percentage of colonies growing on both BMMS-agar plates and YEPS-agar plates was determined as the measure of plasmid stability.

The results of the above analysis are shown below in Table 5A. These results indicate that pDB2954 is essentially as stable as the pSAC35 control and pDB2688. In this type of assay a low level of instability can occasionally be detected even with the pSAC35 control (see Table 4). Hence, the *Sna*BI-site artificially introduced into the inverted repeat sequence immediately after the translation termination codon of *REP2* appeared to be equivalent to the *Xcm*I-site in the inverted repeat for insertion of synthetic linker sequences. However, the *Xcm*I-site appeared to be preferable to the *Sna*BI-site for insertion of the approximately 2-kb DNA fragment containing the *PDI1* gene.

Table 5A: Relative stabilities of pSAC35-based vectors containing various DNA insertions

Plasmid	Insertion site in US-Region	Gene inserted in US-Region	Gene(s) inserted at *Sna*BI/*Not*I-site in UL-Region	Relative Stability (%)
pSAC35	-	-	*LEU2*	100
pDB2688	*Xcm*I	-	*LEU2*	99.5
pDB2954	*Sna*BI	-	*LEU2*	99
pDB2817	*Xmn*I	-	*LEU2*	27
pDB2690	*Xcm*I	*PDI1* (SKQ2n)	*LEU2*	39.5
pDB2952	*Sna*BI	*PDI1* (SKQ2n)	*LEU2*	0
pDB2950	*Sna*BI	*PDI1* (S288c)	*LEU2*	0

A "zero percent stability" result of this assay for plasmids pDB2952 and pDB2950 was obtained *in non-selective media*, which gives an indication of the relative plasmid stabilities. This assay was optimised to compare the relative stabilities of the different linker inserts. In selective media, plasmids with *PDI1* at the *Sna*BI-site (even when comprising an *additional* transferrin gene at the Not*I* site, which is known to *further destabilise* the plasmid (such as pDB2959 and pDB2960 as described below)) produced "precipitin halos" of secreted transferrin on both non-selective YEPD-agar and selective BMMD-agar plates containing anti-transferrin antibodies. Precipitin halos of secreted transferrin were not observed from pDB2961, without the *PDI1* gene inserted at the *Sna*BI-site. These results demonstrate that the *Sna*BI-site is useful for the insertion of large genes such as *PDI1*, which can increase the secretion of heterologous proteins. These results were all generated in the control strain. An increase was also seen for Strain A containing pDB2959 and pDB2960, but in this case there was also a lower level of secretion observed with pDB2961 (because of the extra *PDI1* gene in the genome of Strain A). Results from the control strain are summarised in Table 5B below. Antibody plates were used contained 100µL of goat polyclonal anti-transferrin antiserum (Calbiochem) per 25mL BMMD-agar or YEPD-agar. Strains were patched onto antibody plates and grown for 48-72 hours at 30°C, after which the precipitin "halos" were observed within the agar around colonies secreting high levels of recombinant transferrin. Very low levels of transferrin secretion are not observed in this assay.

Plasmids pDB2959, pDB2960 and pDB2961 were constructed from pDB2950 (Figure 44), pDB2952 (Figure 46) and pDB2954 (Figure 38) respectively, by inserting the same 3.27-kb Not*I* cassette for rTf (N413Q, N611Q) as found in pDB2711 (Figure 11), into the unique *Not*I-site, in the same orientation as pDB2711.

Table 5B: Increased transferrin secretion from the Control Strain transformed with pSAC35-based vectors containing various *PDI1* gene insertions immediately-site after *REP2*

Plasmid	Insertion site in US-Region	Gene inserted in US-Region	Gene(s) inserted at *Sna*BI/*Not*I-site in UL-Region	Transferrin secretion Detected on Anti-Transferrin Ab-plates	
				BMMD- Anti Tf	YEPD-Anti Tf
pDB2960	*Sna*BI	*PDI1* (SKQ2n)	*LEU2* + *rTf*	Yes	Yes
pDB2959	*Sna*BI	*PDI1* (S288c)	*LEU2* + *rTf*	Yes	Yes
pDB2961	*Sna*BI	-	*LEU2* + *rTf*	No	No

EXAMPLE 8

Stabilities of the LEU2 Marker in Yeast Transformed with pSAC35-Like Plasmids Determined Over Thirty Generations of Growth in Non-Selective Conditions

The stabilities of pSAC35-like plasmids with DNA inserted in the US-region were determined using a method analogous to that defined by Chinery & Hinchcliffe (1989, *Curr. Genet.*, **16**, 21-25) This was determined in the same *S. cerevisiae* strain as used in previous examples by loss of the *LEU2* marker during logarithmic growth on non-selective YEPS medium over a defined number of generations. Thirty generations was suitable to show a difference between a control plasmid, pSAC35, or to shown comparable stability to the control plasmid. Plasmids selected for analysis by this assay were; pSAC35 (control), pDB2688 (*Xcm*I-linker), pDB2812 (*Hga*I-linker), pDB2817 (*Xmn*I-linker), pDB2960 (*PDI1* gene inserted at *Xcm*I site after *REP2*) and pDB2711 (*PDI1* gene inserted at *Xcm*I site after *REP2* and a transferrin expression cassette inserted at the *Not*I-site in the UL-region).

Strains were grown to logarithmic phase in selective (BMMS) media at 30°C and used to inoculate 100mL non-selective (YEPS) media pre-warmed to 30°C in 250mL conical flasks, to give between $1.25x10^5$ and $5x10^5$ cells/ml. The number of cells inoculated into each flask was determined accurately by using a haemocytometer to count the number of cells in culture samples. Aliquots were also plated on non-selective (YEPS) agar and incubated at 30°C for 3-4 days, after which for each stock analysed, 100 random colonies were replica plated on selective (BMMS) agar and non-selective (YEPS) agar to assess the proportion of cells retaining the plasmid. After growth at 30°C for 3-4 days the percentage of colonies growing on both BMMS agar and YEPS agar plates was determined as a measure of plasmid stability.

Non-selective liquid cultures were incubated at 30°C with shaking at 200rpm for 24 hours to achieve approximately $1x10^7$ cells/ml, as determined by haemocytometer counts. The culture was then re-inoculated into fresh pre-warmed non-selective media to give between $1.25x10^5$ and $5x10^5$ cells/ml. Aliquots were again plated on non-selective agar, and subsequently replicated plated on selective agar and non-selective agar to assess retention of the plasmid. Hence, it was possible to calculate the number of cell generations in non-selective liquid media. Exponential logarithmic growth was maintained for thirty generations in liquid culture, which was sufficient to show comparable stability to a control plasmid, such as pSAC35. Plasmid stability was defined as the percentage cells maintaining the selectable *LEU2* marker.

Results of the above analysis to measure the retention of the plasmid-encoded phenotype through growth in non-selective media are shown in Table 6 and Figure 47.

Table 6: The Relative Stabilities of Selected pSAC35-Like Plasmids in a *S. cerevisiae* Strain grown for Thirty Generations in Non-Selective Media

Plasmid	Linker Insertion site in US-region	Gene inserted in US-region	Gene(s) inserted at *Sna*BI/*Not*I-site in UL-region	Percentage Stability after 30 generations
pSAC35	-	-	*LEU2*	100
pDB2688	*Xcm*I after *REP2*	-	*LEU2*	100
pDB2812	*HgaI* after *FLP*	-	*LEU2*	100
pDB2817	*Xmn*I in *REP2*	-	*LEU2*	1
pDB2690	*Xcm*I after *REP2*	*PDI1* (SKQ2n)	*LEU2*	33
pDB2711	*Xcm*I after *REP2*	*PDI1* (SKQ2n)	*LEU2* + *rTf*	2

Figure 47 shows the loss of the *LEU2* marker with increasing number generation in non-selective liquid culture for each strain analysed.

The control plasmid pSAC35 remained 100% stable over the entire 30-generations of this assay. Plasmids pBD2688 and pDB2812 both appeared to be as stable as pSAC35. Therefore, insertion of the linker into the *Xcm*I-site after *REP2* or the *Hga*I-site after *FLP* respectively had no apparent effect on plasmid stability. In contrast, insertion of the *Xmn*I-linker within the *REP2* gene appeared to have reduced plasmid stability.

Plasmid pDB2690, which contains a *S. cerevisiae PDI*1 gene in the *Xcm*I-linker after *REP*2, was approximately 33% stable after thirty generations growth, indicating that insertion of this large DNA fragment into the US-region of the 2μm-based vector caused a decrease in plasmid stability. However, this decrease in stability was less than that observed with pDB2711, where insertion of the recombinant transferrin (N413Q, N611Q) expression cassette into the *Not*I-site within the large unique region of pSAC35 acted to

further destabilise the plasmid. These observations are consistent with the results of Example 2 (see Table 2).

The stability of plasmid pDB2711 was assessed by the above method in an alternative strain of *S. cerevisiae*, and similar results were obtained (data not shown). This indicates that the stability of the plasmid is not strain dependent.

EXAMPLE 9

PDI1 gene disruption, combined with a PDI1 gene on the 2μm-based plasmid enhanced plasmid stability

Single stranded oligonucleotide DNA primers listed in Table 7 were designed to amplify a region upstream of the yeast *PDI1* coding region and another a region downstream of the yeast *PDI1* coding region.

Table 7: Oligonucleotide primers

Primer	Description	Sequence
DS299	5' *PDI1* primer, 38mer	5'- CGTAGCGGCCGCCTGAAAGGGGTTGACCGTCCGT CGGC -3'
DS300	5' *PDI1* primer, 40mer	5'-CGTAAAGCTTCGCCGCCCGACAGGGTAACATATTAT CAC -3'
DS301	3' *PDI1* primer, 38mer	5'-CGTAAAGCTTGACCACGTAGTAATAATAAGTGCAT GGC-3'
DS302	3' *PDI1* primer, 41mer	5'-CGTACTGCAGATTGGATAGTGATTAGAGTGTATAGTCC CGG-3'
DS303	18mer	5'-GGAGCGACAAACCTTTCG-3'
DS304	20mer	5'-ACCGTAATAAAAGATGGCTG-3'
DS305	24mer	5'-CATCTTGTGTGTGAGTATGGTCGG-3'
DS306	14mer	5'-CCCAGGATAATTTTCAGG-3'

Primers DS299 and DS300 amplified the 5' region of *PDI1* by PCR, while primers DS301 and DS302 amplified a region 3' of *PDI1*, using genomic DNA derived S288c as a template. The PCR conditions were as follows: 1μL S288c template DNA (at 0.01ng/μL, 0.1ng/μL, 1ng/μL, 10ng/μL and 100ng/μL), 5μL 10XBuffer (Fast Start Taq+Mg, (Roche)), 1μL 10mM dNTP's, 5μL each primer (2μM), 0.4μL Fast Start Taq, made up to 50μL with H_2O. PCRs were performed using a Perkin-Elmer Thermal Cycler 9700. The conditions were: denature at 95°C for 4min [HOLD], then [CYCLE] denature at 95°C for 30 seconds, anneal at 45°C for 30 seconds, extend at 72°C for 45 seconds for 20 cycles, then [HOLD] 72°C for 10min and then [HOLD] 4°C. The 0.22kbp *PDI1* 5' PCR product was cut with *Not*I and *Hin*dIII, while the 0.34kbp *PDI1* 3' PCR product was cut with *Hin*dIII and *Pst*I.

Plasmid pMCS5 (Hoheisel, 1994, *Biotechniques* **17**, 456-460) (Figure 48) was digested to completion with *Hin*dIII, blunt ended with T4 DNA polymerase plus dNTPs and religated to create pDB2964 (Figure 49).

Plasmid pDB2964 was *Hin*dIII digested, treated with calf intestinal phosphatase, and ligated with the 0.22kbp *PDI1* 5' PCR product digested with *Not*I and *Hin*dIII and the 0.34kbp *PDI1* 3' PCR product digested with *Hin*dIII and *Pst*I to create pDB3069 (Figure 50) which was sequenced with forward and reverse universal primers and the DNA sequencing primers DS303, DS304, DS305 and DS306 (Table 7).

Primers DS234 and DS235 (Table 8) were used to amplify the modified *TRP1* marker gene from YIplac204 (Gietz & Sugino, 1988, *Gene*, **74**, 527-534), incorporating *Hin*dIII restriction sites at either end of the PCR product. The PCR conditions were as follows: 1μL template YIplac204 (at 0.01ng/μL, 0.1ng/μL, 1ng/μL, 10ng/μL and 100ng/μL), 5μL 10XBuffer (Fast Start Taq+Mg, (Roche)), 1μL 10mM dNTP's, 5μL each primer (2μM), 0.4μL Fast Start Taq, made up to 50μL with H_2O. PCRs were performed using a Perkin-Elmer Thermal Cycler 9600. The conditions were: denature at 95°C for 4min [HOLD], then [CYCLE] denature at 95°C for 30 seconds, anneal for 45 seconds at 45°C, extend at 72°C for 90sec for 20 cycles, then [HOLD] 72°C for 10min and then [HOLD] 4°C. The 0.86kbp PCR product was digested with *Hin*dIII and cloned into the *Hin*dIII site of

pMCS5 to create pDB2778 (Figure 51). Restriction enzyme digestions and sequencing with universal forward and reverse primers as well as DS236, DS237, DS238 and DS239 (Table 8) confirmed that the sequence of the modified *TRP1* gene was correct.

Table 8: Oligonucleotide primers

Primer	Description	Sequence
DS230	*TRP1* 5' UTR	5'-TAGCGAATTC AATCAGTAAAAATCAACGG-3'
DS231	*TRP1* 5' UTR	5'-GTCAAAGCTTCAAAAAAAGA AAAGCTCCGG-3'
DS232	*TRP1* 3' UTR	5'-TAGCGGATCCGAATTCGGCGGTTGTTTGCAAGACC GAG-3'
DS233	*TRP1* 3' UTR	5'-GTCAAAGCTTTAAAGATAATGCTAAATCATTTGG-3'
DS234	*TRP1*	5'-TGACAAGCTTTCGGTCGAAAAAAGAAAAGG AG AGG-3'
DS235	*TRP1*	5'-TGACAAGCTTGATCTTTTATGCTTGCTTTTC-3'
DS236	*TRP1*	5'-AATAGTTCAGGCACTCCG-3'
DS237	*TRP1*	5'-TGGAAGGCAAGAGAGCC-3'
DS238	*TRP1*	5'-TAAAATGTAAGCTCTCGG-3'
DS239	*TRP1*	5'-CCAACCAAGTATTTCGG-3'
CED005	*ΔTRP1*	5'-GAGCTGACAGGGAAATGGTC-3'
CED006	*ΔTRP1*	5'-TACGAGGATACGGAGAGAGG-3'

The 0.86kbp *TRP1* gene was isolated from pDB2778 by digestion with *Hin*dIII and cloned into the *Hin*dIII site of pDB3069 to create pDB3078 (Figure 52) and pDB3079 (Figure 53). A 1.41kb *pdi1::TRP1* disrupting DNA fragment was isolated from pDB3078 or pDB3079 by digestion with *Not*I/*Pst*I.

Yeast strains incorporating a *TRP1* deletion (*trp1Δ*) were to be constructed in such a way that no homology to the *TRP1* marker gene (pDB2778) should left in the genome once the *trp1Δ* had been created, so preventing homologous recombination between future *TRP1* containing constructs and the *TRP1* locus. In order to achieve the total removal of the native *TRP1* sequence from the genome of the chosen host strains, oligonucleotides were designed to amplify areas of the 5' UTR and 3' UTR of the *TRP1* gene outside of

TRP1 marker gene present on integrating vector YIplac204 (Gietz & Sugino, 1988, *Gene*, **74**, 527-534). The YIplac204 *TRP1* marker gene differs from the native/chromosomal *TRP1* gene in that internal *Hin*dIII, *Pst*I and *Xba*I sites were removed by site directed mutagenesis (Gietz & Sugino, 1988, *Gene*, **74**, 527-534). The YIplac204 modified *TRP1* marker gene was constructed from a 1.453kbp blunt-ended genomic fragment *Eco*RI fragment, which contained the *TRP1* gene and only 102bp of the *TRP1* promoter (Gietz & Sugino, 1988, *Gene*, **74**, 527-534). Although this was a relatively short promoter sequence it was clearly sufficient to complement *trp1* auxotrophic mutations (Gietz & Sugino, 1988, *Gene*, **74**, 527-534). Only DNA sequences upstream of the *Eco*RI site, positioned 102bp 5' to the start of the *TRP1* ORF were used to create the 5' *TRP1* UTR. The selection of the 3' UTR was less critical as long as it was outside the 3' end of the functional modified *TRP1* marker, which was chosen to be 85bp downstream of the translation stop codon.

Single stranded oligonucleotide DNA primers were designed and constructed to amplify the 5' UTR and 3' UTR regions of the *TRP1* gene so that during the PCR amplification restriction enzyme sites would be added to the ends of the PCR products to be used in later cloning steps. Primers DS230 and DS231 (Table 8) amplified the 5' region of *TRP1* by PCR, while primers DS232 and DS233 (Table 8) amplified a region 3' of *TRP1*, using S288c genomic DNA as a template. The PCR conditions were as follows: 1μL template S288c genomic DNA (at 0.01ng/μL, 0.1ng/μL, 1ng/μL, 10ng/μL and 100ng/μL), 5μL 10XBuffer (Fast Start Taq+Mg, (Roche)), 1μL 10mM dNTP's, 5μL each primer (2μM), 0.4μL Fast Start Taq, made up to 50μL with H_2O. PCRs were performed using a Perkin-Elmer Thermal Cycler 9600. The conditions were: denature at 95°C for 4min [HOLD], then [CYCLE] denature at 95°C for 30 seconds, anneal for 45 seconds at 45°C, extend at 72°C for 90sec for 20 cycles, then [HOLD] 72°C for 10min and then [HOLD] 4°C.

The 0.19kbp *TRP1* 5' UTR PCR product was cut with *Eco*RI and *Hin*dIII, while the 0.2kbp *TRP1* 3' UTR PCR product was cut with *Bam*HI and *Hin*dIII and ligated into pAYE505 linearised with *Bam*HI/*Eco*RI to create plasmid pDB2777 (Figure 54). The construction of pAYE505 is described in WO 95/33833. DNA sequencing using forward and reverse primers, designed to prime from the plasmid backbone and sequence the cloned inserts, confirmed that in both cases the cloned 5' and 3' UTR sequences of the

TRP1 gene had the expected DNA sequence. Plasmid pDB2777 contained a *TRP1* disrupting fragment that comprised a fusion of sequences derived from the 5' and 3' UTRs of *TRP1*. This 0.383kbp *TRP1* disrupting fragment was excised from pDB2777 by complete digestion with *Eco*RI.

Yeast strain DXY1 (Kerry-Williams *et al.*, 1998, *Yeast*, **14**, 161-169) was transformed to leucine prototrophy with the albumin expression plasmid pDB2244 using a modified lithium acetate method (Sigma yeast transformation kit, YEAST-1, protocol 2; (Ito *et al*, 1983, *J. Bacteriol.*, **153**, 163; Elble, 1992, *Biotechniques*, **13**, 18)) to create yeast strain DXY1 [pDB2244]. The construction of the albumin expression plasmid pDB2244 is described in WO 00/44772. Transformants were selected on BMMD-agar plates, and were subsequently patched out on BMMD-agar plates. Cryopreserved trehalose stocks were prepared from 10mL BMMD shake flask cultures (24 hrs, 30°C, 200rpm).

DXY1 [pDB2244] was transformed to tryptophan autotrophy with the 0.383kbp *Eco*RI *TRP1* disrupting DNA fragment from pDB2777 using a nutrient agar incorporating the counter selective tryptophan analogue, 5-fluoroanthranilic acid (5-FAA), as described by Toyn *et al.*, (2000 *Yeast* **16,** 553-560). Colonies resistant to the toxic effects of 5-FAA were picked and streaked onto a second round of 5-FAA plates to confirm that they really were resistant to 5-FAA and to select away from any background growth. Those colonies which grew were then were re-patched onto BMMD and BMMD plus tryptophan to identify which were tryptophan auxotrophs.

Subsequently colonies that had been shown to be tryptophan auxotrophs were selected for further analysis by transformation with YCplac22 (Gietz & Sugino, 1988, *Gene*, **74**, 527-534) to ascertain which isolates were *trp1*.

PCR amplification across the *TRP1* locus was used to confirm that the trp$^-$ phenotype was due to a deletion in this region. Genomic DNA was prepared from isolates identified as resistant to 5-FAA and unable to grow on minimal media without the addition of tryptophan. PCR amplification of the genomic *TRP1* locus with primers CED005 and CED006 (Table 8) was achieved as follows: 1μL template genomic DNA, 5μL 10XBuffer (Fast Start Taq+Mg, (Roche)), 1μL 10mM dNTP's, 5μL each primer (2μM), 0.4μL Fast Start Taq, made up to 50μL with H_2O. PCRs were performed using a Perkin-

Elmer Thermal Cycler 9600. The conditions were: denature at 94°C for 10min [HOLD], then [CYCLE] denature at 94°C for 30 seconds, anneal for 30 seconds at 55°C, extend at 72°C for 120sec for 40 cycles, then [HOLD] 72°C for 10min and then [HOLD] 4°C. PCR amplification of the wild type *TRP1* locus resulted in a PCR product of 1.34kbp in size, whereas amplification across the deleted *TRP1* region resulted in a PCR product 0.84kbp smaller at 0.50kbp. PCR analysis identified a DXY1 derived trp⁻ strain (DXY1 *trp1Δ* [pDB2244]) as having the expected deletion event.

The yeast strain DXY1 *trp1Δ* [pDB2244] was cured of the expression plasmid pDB2244 as described by Sleep *et al.*, 1991, *Bio/Technology*, **9**, 183-187. DXY1 *trp1Δ* cir^0 was re-transformed the leucine prototrophy with either pDB2244, pDB2976, pDB2977, pDB2978, pDB2979, pDB2980 or pDB2981 (the production of pDB2976, pDB2977 and pDB2980 or pDB2981 is discussed further in Example 10) using a modified lithium acetate method (Sigma yeast transformation kit, YEAST-1, protocol 2; (Ito *et al*, 1983, *J. Bacteriol.*, **153**, 163; Elble, 1992, *Biotechniques*, **13**, 18)). Transformants were selected on BMMD-agar plates supplemented with tryptophan, and were subsequently patched out on BMMD-agar plates supplemented with tryptophan. Cryopreserved trehalose stocks were prepared from 10mL BMMD shake flask cultures supplemented with tryptophan (24 hrs, 30°C, 200rpm).

The yeast strains DXY1 *trp1Δ* [pDB2976], DXY1 *trp1Δ* [pDB2977], DXY1 *trp1Δ* [pDB3078], DXY1 *trp1Δ* [pDB3079], DXY1 *trp1Δ* [pDB2980] or DXY1 *trp1Δ* [pDB2981] was transformed to tryptophan prototrophy using the modified lithium acetate method (Sigma yeast transformation kit, YEAST-1, protocol 2; (Ito *et al*, 1983, *J. Bacteriol.*, **153**, 163; Elble, 1992, *Biotechniques*, **13**, 18)) with a 1.41kb *pdi1::TRP1* disrupting DNA fragment was isolated from pDB3078 by digestion with *Not*I/*Pst*I. Transformants were selected on BMMD-agar plates and were subsequently patched out on BMMD-agar plates.

Six transformants of each strain were inoculated into 10mL YEPD in 50mL shake flasks and incubated in an orbital shaker at 30°C, 200rpm for 4-days. Culture supernatants and cell biomass were harvested. Genomic DNA was prepared (Lee, 1992, *Biotechniques*, **12**, 677) from the tryptophan prototrophs and DXY1 [pDB2244]. The genomic *PDI1*

locus amplified by PCR of with primers DS236 and DS303 (Table 7 and 8) was achieved as follows: 1μL template genomic DNA, 5μL 10XBuffer (Fast Start Taq+Mg, (Roche)), 1μL 10mM dNTP's, 5μL each primer (2μM), 0.4μL Fast Start Taq, made up to 50μL with H_2O. PCRs were performed using a Perkin-Elmer Thermal Cycler 9700. The conditions were: denature at 94°C for 4min [HOLD], then [CYCLE] denature at 94°C for 30 seconds, anneal for 30 seconds at 50°C, extend at 72°C for 60sec for 30 cycles, then [HOLD] 72°C for 10min and then [HOLD] 4°C. PCR amplification of the wild type *PDI1* locus resulted in no PCR product, whereas amplification across the deleted *PDI1* region resulted in a PCR product 0.65kbp. PCR analysis identified that all 36 potential *pdi1::TRP1* strains tested had the expected *pdi1::TRP1* deletion.

The recombinant albumin titres were compared by rocket immunoelectrophoresis (Figure 55). Within each group, all six *pdi1::TRP1* disruptants of DXY1 *trp1Δ* [pDB2976], DXY1 *trp1Δ* [pDB2978], DXY1 *trp1Δ* [pDB2980], DXY1 *trp1Δ* [pDB2977] and DXY1 *trp1Δ* [pDB2979] had very similar rHA productivities. Only the six *pdi1::TRP1* disruptants of DXY1 *trp1Δ* [pDB2981] showed variation in rHA expression titre. The six *pdi1::TRP1* disruptants indicated in Figure 55 were spread onto YEPD agar to isolate single colonies and then re-patched onto BMMD agar.

Three single celled isolates of DXY1 *trp1Δ pdi1::TRP1* [pDB2976], DXY1 *trp1Δ pdi1::TRP1* [pDB2978], DXY1 *trp1Δ pdi1::TRP1* [pDB2980], DXY1 *trp1Δ pdi1::TRP1* [pDB2977], DXY1 *trp1Δ pdi1::TRP1* [pDB2979] and DXY1 *trp1Δ pdi1::TRP1* [pDB2981] along with DXY1 [pDB2244], DXY1 [pDB2976], DXY1 [pDB2978], DXY1 [pDB2980], DXY1 [pDB2977], DXY1 [pDB2979] and DXY1 [pDB2981] were inoculated into 10mL YEPD in 50mL shake flasks and incubated in an orbital shaker at 30°C, 200rpm for 4-days. Culture supernatants were harvested and the recombinant albumin titres were compared by rocket immunoelectrophoresis (Figure 56). The thirteen wild type *PDI1* and *pdi1::TRP1* disruptants indicated in Figure 56 were spread onto YEPD agar to isolate single colonies. One hundred single celled colonies from each strain were then re-patched onto BMMD agar or YEPD agar containing a goat anti-HSA antibody to detect expression of recombinant albumin (Sleep *et al.*, 1991,

Bio/Technology, **9**, 183-187) and the Leu+/rHA+, Leu+/rHA-, Leu-/rHA+ or Leu-/rHA- phenotype of each colony scored (Table 9).

Table 9:

	PDI1				*pdi1::TRP1*			
	Leu+ rHA+	Leu- rHA+	Leu+ rHA-	Leu- rHA-	Leu+ rHA+	Leu- rHA+	Leu+ rHA-	Leu- rHA-
pDB2244	100	0	0	0				
PDB2976	7	0	47	46	97	0	3	0
pDB2978	86	0	0	14	100	0	0	0
pDB2980	98	0	0	2	100	0	0	0
pDB2977	0	0	4	96	100	0	0	0
pDB2979	69	0	6	25	100	0	0	0
pDB2981	85	0	0	15	92	0	0	8

These data indicate plasmid retention is increased when the *PDI1* gene is used as a selectable marker on a plasmid in a host strain having no chromosomally encoded PDI, even in non-selective media such as this rich medium. These show that an "essential" chaperone (e.g PDI1 or PSE1), or any other any "essential" gene product (e.g. PGK1 or FBA1) which, when deleted or inactivated, does not result in an auxotrophic (biosynthetic) requirement, can be used as a selectable marker on a plasmid in a host cell that, in the absence of the plasmid, is unable to produce that gene product, to achieve increased plasmid stability without the disadvantage of requiring the cell to be cultured under specific selective conditions. By "auxotrophic (biosynthetic) requirement" we include a deficiency, which can be complemented by additions or modifications to the growth medium. Therefore, "essential marker genes" in the context of the present

invention are those that, when deleted or inactivated in a host cell, result in a deficiency which can not be complemented by additions or modifications to the growth medium.

EXAMPLE 10

The construction of expression vectors containing various PDI1 genes and the expression cassettes for various heterologous proteins on the same 2μm-like plasmid

PCR amplification and cloning of *PDI1* genes into YIplac211

The *PDI1* genes from *S. cerevisiae* S288c and *S. cerevisiae* SKQ2n were amplified by PCR to produce DNA fragments with different lengths of the 5'-untranslated region containing the promoter sequence. PCR primers were designed to permit cloning of the PCR products into the *Eco*RI and *Bam*HI sites of YIplac211 (Gietz & Sugino, 1988, *Gene*, **74**, 527-534). Additional restriction endonuclease sites were also incorporated into PCR primers to facilitate subsequent cloning. Table 10 describes the plasmids constructed and Table 11 gives the PCR primer sequences used to amplify the *PDI1* genes. Differences in the *PDI1* promoter length within these YIplac211-based plasmids are described in Table 10.

pDB2939 (Figure 57) was produced by PCR amplification of the *PDI1* gene from *S. cerevisiae* S288c genomic DNA with oligonucleotide primers DS248 and DS250 (Table 11), followed by digesting the PCR product with *Eco*RI and *Bam*HI and cloning the approximately 1.98-kb fragment into YIplac211 (Gietz & Sugino, 1988, *Gene*, **74**, 527-534), that had been cut with *Eco*RI and *Bam*HI. DNA sequencing of pDB2939 identified a missing 'G' from within the DS248 sequence, which is marked in bold in Table 5. Oligonucleotide primers used for sequencing the *PDI1* gene are listed in Table 6, and were designed from the published S288c *PDI1* gene sequence (PDI1/YCL043C on chromosome III from coordinates 50221 to 48653 plus 1000 basepairs of upstream sequence and 1000 basepairs of downstream sequence. (http://www.yeastgenome.org/ Genebank Accession number NC001135).

Table 10: YIplac211-based Plasmids Containing PDI1 Genes

Plasmid	*Plasmid Base*	PDI1 *Gene*			*PCR Primers*
		Source	*Promoter*	*Terminator*	
pDB2939	***YIplac211***	***S288c***	***Long (~210-bp)***	**→ Bsu*36I***	***DS248 + DS250***
pDB2941	***YIplac211***	***S288c***	***Medium (~140-bp)***	**→ Bsu*36I***	***DS251 + DS250***
pDB2942	***YIplac211***	***S288c***	***Short (~80-bp)***	**→ Bsu*36I***	***DS252 + DS250***
pDB2943	***YIplac211***	***SKQ2n***	***Long (~210-bp)***	**→ Bsu*36I***	***DS248 + DS250***
pDB2963	***YIplac211***	***SKQ2n***	***Medium (~140-bp)***	**→ Bsu*36I***	***DS267 + DS250***
pDB2945	***YIplac211***	***SKQ2n***	***Short (~80-bp)***	**→ Bsu*36I***	***DS252 + DS250***

Table 11: Oligonucleotide Primers for PCR Amplification of *S. cerevisiae PDI1* Genes

5

Primer	**Sequence**
DS248	5′-GTCAGAATTCGAGCTCTACGTATTAATTAAGGCCGGCCAGGCCCGGGCTAGT CTCTTTTTCCAATTTGCCACCGTGTAGCATTTTGTTGT-3′
DS249	5′-GTCAGGATCCTACGTACCCGGGGATATCATTATCATCTTTGTCGTGGTCATCT TGTGTG-3′
DS250	5′-GTCAGGATCCTACGTACCCGGGTAAGGCGTTCGTGCAGTGTGACGAATAT AGCG-3′
DS251	5′-GTCAGAATTCGAGCTCTACGTATTAATTAAGGCCGGCCAGGCCCGGGCCCGT ATGGACATACATATATATATATATATATATATATATTTTGTTACGCG-3′
DS252	5′-GTCAGAATTCGAGCTCTACGTATTAATTAAGGCCGGCCAGGCCCGGGCTTGTTG CAAGCAGCATGTCTAATTGGTAATTTTAAAGCTGCC-3′
DS267	5′-GTCAGAATTCGAGCTCTACGTATTAATTAAGGCCGGCCAGGCCCGGGCCCGTA TGGACATACATATATATATATATATATATATATATATTTTGTTACGCG-3′

Table 12: Oligonucleotide Primers for DNA Sequencing *S. cerevisiae PDI1* Genes

Primer	Sequence
DS253	5′-CCTCCCTGCTGCTCGCC-3′
DS254	5′-CTGTAAGAACATGGCTCC-3′
DS255	5′-CTCGATCGATTACGAGGG-3′
DS256	5′-AAGAAAGCCGATATCGC-3′
DS257	5′-CAACTCTCTGAAGAGGCG-3′
DS258	5′-CAACGCCACATCCGACG-3′
DS259	5′-GTAATTCTGATCACTTTGG-3′
DS260	5′-GCACTTATTATTACTACGTGG-3′
DS261	5′-GTTTTCCTTGATGAAGTCG-3′
DS262	5′-GTGACCACACCATGGGGC-3′
DS263	5′-GTTGCCGGCGTGTCTGCC-3′
DS264	5′-TTGAAATCATCGTCTGCG-3′
DS265	5′-CGGCAGTTCTAGGTCCC-3′
DS266	5′-CCACAGCCTCTTGTTGGG-3′
M13/pUC Primer (-40)	5′-GTTTTCCCAGTCACGAC-3′

Plasmids pDB2941 (Figure 58) and pDB2942 (Figure 59) were constructed similarly using the PCR primers described in Tables 10 and 11, and by cloning the approximately 1.90-kb and 1.85-kb *Eco*RI-*Bam*HI fragments, respectively, into YIplac211. The correct DNA sequences were confirmed for the *PDI1* genes in pDB2941 and pDB2942.

The *S. cerevisiae* SKQ2n *PDI1* gene sequence was PCR amplified from plasmid DNA containing the *PDI1* gene from pMA3a:C7 (US 6,291,205), also known as Clone C7 (Crouzet & Tuite, 1987, *supra*; Farquhar *et al.*, 1991, *supra*). The SKQ2n *PDI1* gene

was amplified using oligonucleotide primers DS248 and DS250 (Tables 10 and 11). The approximately 2.01-kb PCR product was digested with *Eco*RI and *Bam*HI and ligated into YIplac211 (Gietz & Sugino, 1988, *Gene*, **74**, 527-534) that has been cut with *Eco*RI and *Bam*HI, to produce plasmid pDB2943 (Figure 60). The 5' end of the SKQ2n PDI1 sequence is analogous to a blunt-ended *Spe*I-site extended to include the *Eco*RI, *Sac*I, *Sna*BI, *Pac*I, *Fse*I, *Sfi*I and *Sma*I sites, the 3' end extends up to a site analogous to a blunt-ended *Bsu*36I site, extended to include a *Sma*I, *Sna*BI and *Bam*HI sites. The *PDI1* promoter length is approximately 210bp. The entire DNA sequence was determined for the *PDI1* fragment using oligonucleotide primers given in Table 12. This confirmed the presence of a coding sequence for the PDI protein of *S. cerevisiae* strain SKQ2n (NCBI accession number CAA38402), but with a serine residue at position 114 (not an arginine residue as previously published). Similarly, in the same way as in the *S. cerevisiae* S288c sequence in pDB2939, pDB2943 also had a missing 'G' from within the DS248 sequence, which is marked in bold in Table 5.

Plasmids pDB2963 (Figure 61) and pDB2945 (Figure 62) were constructed similarly using the PCR primers described in Tables 10 and 11, and by cloning the approximately 1.94-kb and 1.87-kb *Eco*RI-*Bam*HI fragments, respectively, into YIplac211. The expected DNA sequences were confirmed for the *PDI1* genes in pDB2963 and pDB2945, with a serine codon at the position of amino acid 114.

The construction of pSAC35-based rHA expression plasmids with different *PDI1* genes inserted at the *Xcm*I-site after *REP2*:

pSAC35-based plasmids were constructed for the co-expression of rHA with different *PDI1* genes (Table 13).

Table 13: pSAC35-based plasmids for co-expression of rHA with different *PDI1* genes

Plasmid	*Plasmid Base*	PDI1 *Gene at* XcmI*-site after* REP2				*Heterologous Protein Expression Cassette (at* NotI*-site)*
		Source	*Promoter*	*Terminator*	*Orientation*	
pDB2982	*pSAC35*	*SKQ2n*	*Long*	→ Bsu36I	*A*	*rHA*
pDB2983	*pSAC35*	*SKQ2n*	*Long*	→ Bsu36I	*B*	*rHA*
pDB2984	*pSAC35*	*SKQ2n*	*Medium*	→ Bsu36I	*A*	*rHA*
pDB2985	*pSAC35*	*SKQ2n*	*Medium*	→ Bsu36I	*B*	*rHA*
pDB2986	*pSAC35*	*SKQ2n*	*Short*	→ Bsu36I	*A*	*rHA*
pDB2987	*pSAC35*	*SKQ2n*	*Short*	→ Bsu36I	*B*	*rHA*
pDB2976	*pSAC35*	*S288c*	*Long*	→ Bsu36I	*A*	*rHA*
pDB2977	*pSAC35*	*S288c*	*Long*	→ Bsu36I	*B*	*rHA*
pDB2978	*pSAC35*	*S288c*	*Medium*	→ Bsu36I	*A*	*rHA*
pDB2979	*pSAC35*	*S288c*	*Medium*	→ Bsu36I	*B*	*rHA*
pDB2980	*pSAC35*	*S288c*	*Short*	→ Bsu36I	*A*	*rHA*
pDB2981	*pSAC35*	*S288c*	*Short*	→ Bsu36I	*B*	*rHA*

.The rHA expression cassette from pDB2243 (Figure 63, as described in WO 00/44772) was first isolated on a 2,992-bp *Not*I fragment, which subsequently was cloned into the *Not*I-site of pDB2688 (Figure 4) to produce pDB2693 (Figure 64). pDB2693 was digested with *Sna*BI, treated with calf intestinal alkaline phosphatase, and ligated with *Sna*BI fragments containing the *PDI1* genes from pDB2943, pDB2963, pDB2945, pDB2939, pDB2941 and pDB2942. This produced plasmids pDB2976 to pDB2987 (Figures 65 to 76). *PDI1* transcribed in the same orientation as *REP2* was designated "orientation A", whereas *PDI1* transcribed in opposite orientation to *REP2* was designated "orientation B" (Table 13).

CLAIMS

1. A 2μm-family plasmid comprising a polynucleotide sequence insertion, deletion and/or substitution between the first base after the last functional codon of at least one of either a *REP2* gene or an *FLP* gene and the last base before the FRT site in an inverted repeat adjacent to said gene.

2. The 2μm-family plasmid of Claim 1 wherein, other than the polynucleotide sequence insertion, deletion and/or substitution, the *FLP* gene and/or the *REP2* gene has the sequence of a *FLP* gene and/or a *REP2* gene, respectively, derived from a naturally occurring 2μm-family plasmid.

3. The 2μm-family plasmid of Claim 1 wherein the naturally occurring 2μm-family plasmid is selected from pSR1, pSB3 or pSB4 as obtained from *Zygosaccharomyces rouxii*, pSB1 or pSB2 both as obtained from *Zygosaccharomyces bailli*, pSM1 as obtained from *Zygosaccharomyces fermentati*, pKD1 as obtained from *Kluyveromyces drosophilarum*, pPM1 as obtained from *Pichia membranaefaciens*, and the 2μm plasmid as obtained from *Saccharomyces cerevisiae*.

4. The 2μm-family plasmid of Claim 2 or 3 wherein the sequence of the inverted repeat adjacent to said *FLP* and/or *REP2* gene is derived from the sequence of the corresponding inverted repeat in the same naturally occurring 2μm-family plasmid as the sequence from which the gene is derived.

5. The 2μm-family plasmid of any one of Claims 2 to 4 wherein the naturally occurring 2μm-family plasmid is the 2μm plasmid as obtained from *Saccharomyces cerevisiae*.

6. The 2μm-family plasmid of Claim 5 wherein the polynucleotide sequence insertion, deletion and/or substitution occurs at a position between the first base of

codon 59 of the *REP2* gene and the last base before the FRT site in the adjacent inverted repeat.

7. The 2μm-family plasmid of Claim 5 or 6 wherein, other than the polynucleotide sequence insertion, deletion and/or substitution, the sequence of the *REP2* gene and the adjacent inverted repeat is as defined by SEQ ID NO:1 or variant thereof.

8. The 2μm-family plasmid of any one of Claims 1 to 7 wherein polynucleotide sequence insertion, deletion and/or substitution occurs at a position between the first base of the inverted repeat and the last base before the FRT site.

9. The 2μm-family plasmid of any one of Claims 1 to 7 wherein the polynucleotide sequence insertion, deletion and/or substitution occurs between the first base after the end of the *REP2* coding sequence and the last base before the FRT site, such as at the first base after the end of the *REP2* coding sequence.

10. The 2μm-family plasmid of any one of Claims 1 to 7 wherein, other than the polynucleotide sequence insertion, deletion and/or substitution, the inverted repeat that follows the *REP2* coding sequence has a sequence derived from the corresponding region of the 2μm plasmid as obtained from *Saccharomyces cerevisiae* and preferably the polynucleotide sequence insertion, deletion and/or substitution occurs at an *XcmI* site or an *FspI* site within the inverted repeat.

11. The 2μm-family plasmid of Claim 5 wherein the polynucleotide sequence insertion, deletion and/or substitution occurs at a position between the first base of codon 344 of the *FLP* gene and the last base before the FRT site in the adjacent inverted repeat.

12. The 2μm-family plasmid of Claim 5 or 11 wherein, other than the polynucleotide sequence insertion, deletion and/or substitution, the sequence of the *FLP* coding sequence and the adjacent inverted repeat is as defined by SEQ ID NO:2 or variant thereof.

13. The 2μm-family plasmid of Claim 11 or 12 wherein the polynucleotide sequence insertion, deletion and/or substitution occurs at a position between the first base of the inverted repeat and the last base before the FRT site.

14. The 2μm-family plasmid of Claim 13 wherein the polynucleotide sequence insertion, deletion and/or substitution occurs at a position between the first base after the end of the *FLP* coding sequence and the last base before the FRT site.

15. The 2μm-family plasmid of Claim 14 wherein the polynucleotide sequence insertion, deletion and/or substitution occurs at the first base after the end of the *FLP* coding sequence.

16. The 2μm-family plasmid of any one of Claims 11 to 15 wherein, other than the polynucleotide sequence insertion, deletion and/or substitution, the inverted repeat that follows the *FLP* gene has a sequence derived from the corresponding region of the 2μm plasmid as obtained from *Saccharomyces cerevisiae*, and preferably the polynucleotide sequence insertion, deletion and/or substitution occurs at an *HgaI* site or an *FspI* site within the inverted repeat.

17. The 2μm-family plasmid of any one of the preceding claims comprising polynucleotide sequence insertions, deletions and/or substitutions between the first bases after the last functional codons of both of the *REP2* gene and the *FLP* gene and the last bases before the FRT sites in the inverted repeats adjacent to each of said genes, which polynucleotide sequence insertions, deletions and/or substitutions can be the same or different.

18. The 2μm-family plasmid of any preceding claim additionally comprising a polynucleotide sequence insertion, deletion and/or substitution which is not at a position as defined in any one of the preceding claims.

19. The 2μm-family plasmid of Claim 18 wherein the polynucleotide sequence insertion, deletion and/or substitution occurs within an untranscribed region around an ARS sequence.

20. The 2μm-family plasmid of any one of the preceding claims wherein the, or at least one, polynucleotide sequence insertion, deletion and/or substitution is a polynucleotide sequence insertion.

21. The 2μm-family plasmid of Claim 20 in which the polynucleotide sequence insertion encodes an open reading frame.

22. The 2μm-family plasmid of Claim 21 in which the open reading frame encodes a non- 2μm-family plasmid protein.

23. The 2μm-family plasmid of Claim 22 in which the non- 2μm-family plasmid protein comprises the sequence of a protein involved in protein folding, or which has chaperone activity or is involved in the unfolded protein response, albumin, a monoclonal antibody, an etoposide, a serum protein (such as a blood clotting factor), antistasin, a tick anticoagulant peptide, transferrin, lactoferrin, endostatin, angiostatin, collagens, immunoglobulins or immunoglobulin-based molecules or fragments of either (e.g. a dAb, Fab' fragments, F(ab')2, scAb, scFv or scFv fragment), a Kunitz domain protein, interferons, interleukins, IL10, IL11, IL2, interferon α species and sub-species, interferon β species and sub-species, interferon γ species and sub-species, leptin, CNTF, $CNTF_{Ax15}$, IL1-receptor antagonist, erythropoietin (EPO) and EPO mimics, thrombopoietin (TPO) and TPO mimics, prosaptide, cyanovirin-N, 5-helix, T20 peptide, T1249 peptide, HIV gp41, HIV gp120, urokinase, prourokinase, tPA, hirudin, platelet derived growth factor, parathyroid hormone, proinsulin, insulin, glucagon, glucagon-like peptides, insulin-like growth factor, calcitonin, growth hormone, transforming growth factor β, tumour necrosis factor, G-CSF, GM-CSF, M-CSF, FGF, coagulation factors in both pre and active forms, including but not limited to plasminogen, fibrinogen, thrombin, pre-thrombin, pro-thrombin, von

Willebrand's factor, α_1-antitrypsin, plasminogen activators, Factor VII, Factor VIII, Factor IX, Factor X and Factor XIII, nerve growth factor, LACI, platelet-derived endothelial cell growth factor (PD-ECGF), glucose oxidase, serum cholinesterase, aprotinin, amyloid precursor protein, inter-alpha trypsin inhibitor, antithrombin III, apo-lipoprotein species, Protein C, Protein S, or a variant or fragment of any of the above.

24. The 2μm-family plasmid of Claim 23 in which the non- 2μm-family plasmid protein comprises the sequence of albumin, a variant or fragment thereof, or a fusion protein comprising the sequence of any of these.

25. The 2μm-family plasmid of Claim 23 in which the non- 2μm-family plasmid protein comprises the sequence of transferrin, a variant or fragment thereof, or a fusion protein comprising the sequence of any of these.

26. The 2μm-family plasmid of Claim 23 in which the non- 2μm-family plasmid protein comprises the sequence of lactoferrin, a variant or fragment thereof, or a fusion protein comprising the sequence of any of these.

27. The 2μm-family plasmid of Claim 23 in which the non- 2μm-family plasmid protein comprises the sequence of Fc, a variant or fragment thereof, or a fusion protein comprising the sequence of any of these.

28. The 2μm-family plasmid of Claim 23 in which the non- 2μm-family plasmid protein comprises the sequence of a protein involved in protein folding, or which has chaperone activity or is involved in the unfolded protein response as encoded by any one of *AHA1*, *CCT2*, *CCT3*, *CCT4*, *CCT5*, *CCT6*, *CCT7*, *CCT8*, *CNS1*, *CPR3*, *CPR6*, *EPS1*, *ERO1*, *EUG1*, *FMO1*, *HCH1*, *HSP10*, *HSP12*, *HSP104*, *HSP26*, *HSP30*, *HSP42*, *HSP60*, *HSP78*, *HSP82*, *JEM1*, *MDJ1*, *MDJ2*, *MPD1*, *MPD2*, *PDI1*, *PFD1*, *ABC1*, *APJ1*, *ATP11*, *ATP12*, *BTT1*, *CDC37*, *CPR7*, *HSC82*, *KAR2*, *LHS1*, *MGE1*, *MRS11*, *NOB1*, *ECM10*, *SSA1*, *SSA2*, *SSA3*, *SSA4*,

SSC1, *SSE2*, *SIL1*, *SLS1*, *UBI4*, *ORM1*, *ORM2*, *PER1*, *PTC2*, *PSE1* and *HAC1* or a truncated intronless *HAC1*.

29. The 2μm-family plasmid of Claim 23 or 28 in which the chaperone is protein disulphide isomerase (PDI), or is a protein encoded by *ORM2*, *SSA1* or *PSE1*.

30. The 2μm-family plasmid of any one of Claims 22 to 29 in which the non- 2μm-family plasmid protein comprises a secretion leader sequence.

31. The 2μm-family plasmid of Claim 22 in which the non- 2μm-family plasmid protein comprises the sequence of a bacterial selectable marker and/or a yeast selectable marker.

32. The 2μm-family plasmid of Claim 31 in which the bacterial selectable marker is a β-lactamase gene and/or the yeast selectable marker is a *LEU2* selectable marker.

33. The 2μm-family plasmid according to any one of the preceding claims which plasmid comprises (i) a heterologous sequence encoding a non- 2μm-family plasmid protein; (ii) a heterologous sequence encoding a protein comprising the sequence of a protein involved in protein folding, a chaperone or a protein involved in the unfolded protein response, preferably protein disulphide isomerase; and (iii) a heterologous sequence encoding a protein comprising the sequence of a selectable marker; wherein at least one of the heterologous sequences occurs at a position as defined by any one of Claims 1 to 16.

34. A method of preparing a plasmid as defined by any one of the preceding claims comprising –

(a) providing a plasmid comprising the sequence of a *REP2* gene and the inverted repeat that follows the *REP2* gene, or a *FLP* gene and the inverted repeat that follows the *FLP* gene, in each case the inverted repeat comprising an FRT site;

(b) providing a polynucleotide sequence and inserting the polynucleotide sequence into the plasmid at a position as defined in any one of Claims 1 to 16; and/or

(c) deleting some or all of the nucleotide bases at the positions defined in any one of Claims 1 to 16; and/or

(d) substituting some or all of the nucleotide bases at the positions defined in any one of Claims 1 to 16 with alternative nucleotide bases.

35. A plasmid obtainable by the method of Claim 34.

36. A host cell comprising a plasmid as defined by any one of Claims 1 to 33 and 35.

37. A host cell according to Claim 36 which is a yeast cell.

38. A host cell according to Claim 36 or 37 in which the plasmid is stable as a multicopy plasmid.

39. A host cell according to Claim 38 in which the plasmid is based on pSR1, pSB3 or pSB4 and the yeast cell is *Zygosaccharomyces rouxii*, the plasmid is based on pSB1 or pSB2 and the yeast cell is *Zygosaccharomyces bailli*, the plasmid is based on pSM1 and the yeast cell is *Zygosaccharomyces fermentati*, the plasmid is based on pKD1 and the yeast cell is *Kluyveromyces drosophilarum*, the plasmid is based on pPM1 and the yeast cell is *Pichia membranaefaciens* or the plasmid is based on the 2μm plasmid and the yeast cell is *Saccharomyces cerevisiae* or *Saccharomyces carlsbergensis*.

40. A host cell according to Claim 38 or 39 in which, if the plasmid contains, or is modified to contain, a selectable marker then stability, as measured by the loss of the marker, is at least 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9% or substantially 100% after 5 generations.

41. A method of producing a protein comprising the steps of –

(a) providing a plasmid as defined by any one of Claims 1 to 33 or 35

(b) providing a suitable host cell;

(c) transforming the host cell with the plasmid; and

(d) culturing the transformed host cell in a culture medium;

(e) thereby to produce the protein.

42. A method of producing a protein comprising the steps of providing a host cell as defined by any one of Claims 36 to 40 which host cell comprises a plasmid as defined by any one of Claims 1 to 33 or 35 and culturing the host cell in a culture medium thereby to produce the protein.

43. A method according to Claim 41 or 42 further comprising the step of isolating the thus produced protein from the cultured host cell or the culture medium.

44. A method according to Claim 43 further comprising the step of purifying the thus isolated protein to a commercially acceptable level of purity.

45. A method according to Claim 44 further comprising the step of formulating the thus purified protein with a carrier or diluent, and optionally presenting the thus formulated protein in a unit form.

46. A method according to Claim 43 further comprising the step of purifying the thus isolated protein to a pharmaceutically acceptable level of purity.

47. A method according to Claim 44 further comprising the step of formulating the thus purified protein with a pharmaceutically acceptable carrier or diluent and optionally presenting the thus formulated protein in a unit dosage form.

48. A plasmid comprising, as the sole yeast selectable marker, a gene encoding a protein that is essential to the viability of a host yeast cell, in the sense that when the gene or genes encoding the essential protein are deleted or inactivated in a host yeast cell, then the host cell is inviable in culture and the deficiency cannot be complemented by additions or modifications to the culture medium.

49. The plasmid of Claim 48 wherein the gene encoding the essential protein is the sole selectable marker encoded by the plasmid.

50. The plasmid of Claim 48 or 49 wherein the essential protein is a chaperone.

51. The plasmid of 51, wherein the chaperone is protein disulphide isomerase or Pselp.

52. The plasmid of any one of Claims 48 to 51 further comprising a gene encoding a non- 2μm-family plasmid protein, such as a protein defined by any one of Claims 23 to 27.

53. The plasmid of any one of Claims 48 to 52 which is a 2μm-family plasmid.

54. The plasmid of Claim 53 which is a plasmid as defined by any one of Claims 1 to 33.

55. A host cell comprising a plasmid, the plasmid comprising a gene that encodes protein that is essential to the viability of the host cell and wherein, in the absence of the plasmid, the host cell is unable to produce the essential protein and cannot be made viable by additions or modifications to the culture medium.

56. A host cell according to Claim 55 in which the plasmid is a plasmid according to any one of Claims 1 to 33 or 48 to 54.

57. A host cell according to Claim 55 or 56 wherein, in the absence of the plasmid, the host cell is inviable.

58. The host cell of any one of Claims 55 to 57 wherein the host cell further comprises a recombinant gene encoding a desired protein, such as a protein defined by any one of Claims 23 to 27.

59. The host cell of Claim 58 wherein the desired protein is a non- 2μm-family plasmid protein defined by any one of Claims 23 to 27.

60. The host cell of Claim 59 wherein the essential protein is a chaperone, such as protein disulphide isomerase or PSE1.

61. The host cell of Claim 59 or 60 wherein the recombinant gene is located on the same plasmid as the gene encoding the essential protein.

62. A method for producing a desired recombinant protein comprising the steps of: providing a host cell as defined by any one of Claims 59 to 61; culturing the host cell in a culture medium under conditions that allow the expression of the essential protein and the desired protein; and optionally isolating the thus expressed desired protein from the cultured host cell or the culture medium; and optionally purifying the thus isolated desired protein to a commercially acceptable level of purity; and further optionally, lyophilising the thus purified protein or formulating the purified desired protein with a carrier or diluent (such as a pharmaceutically acceptable carrier or diluent); and optionally presenting the thus formulated desired protein in a unit dosage form.

63. The method of Claim 62 wherein the step of culturing the host cell involves culturing the host cell in a non-selective media, such as a complex or rich media.