Int-h (E174K) and its derivative Int-h/218 (E174K/E218K) have been described and were shown to catalyze intermolecular recombination reactions at least as efficiently as the corresponding intramolecular recombination reactions in human cells. Although the presence of arm-site sequences have been shown to increase the recombination of core-sites by Int-h/218 in vivo, given the absence of an attB site in the human genome, recombination reactions occur in non-cognate sites in an essentially random manner.

This makes it difficult to engineer cell lines in a controlled, reproducible fashion.

Therefore, there remains a need to provide mutant integrases having greater efficiency and specificity in catalyzing site specific recombination reactions.

Summary

In one aspect, there is provided a lambda integrase comprising at least one amino acid mutation selected from the group consisting of I43F, E319G and D336V.

In another aspect, there is provided a lambda integrase comprising an amino acid mutation at position 336 of the lambda integrase as set forth in SEQ ID NO: 1, wherein the amino acid residue aspartate at sequence position 336 is replaced by an aliphatic amino acid.

In another aspect, there is provided a nucleic acid molecule comprising a nucleotide sequence encoding the lambda integrase as disclosed herein.

In another aspect, there is provided a nucleic acid molecule. The nucleic acid molecule includes a nucleotide sequence encoding a mutant as described herein.

In a further aspect, there is provided a host cell. The host cell includes a nucleic acid molecule as described herein.

In another aspect, there is provided a method of recombining a nucleic acid of interest into a target nucleic acid, the method comprising contacting a targeting nucleic acid comprising the nucleic acid of interest with the target nucleic acid in the presence of a lambda integrase as disclosed herein.

In yet another aspect, there is provided a method of recombining a nucleic acid of interest into a target nucleic acid. The method includes contacting a targeting nucleic acid comprising the nucleic acid of interest with

Claims

1. A lambda integrase comprising an amino acid mutation at position 336 of the lambda integrase as set forth in SEQ ID NO: 1, wherein the amino acid residue aspartate at sequence position 336 is replaced by an aliphatic amino acid.
2. The lambda integrase according to claim 1, wherein the lambda integrase further comprises an amino acid mutation at position 319, 43 or both.
3. The lambda integrase according to claims 1 or 2, wherein the aliphatic amino acid at sequence position 336 is selected from the group consisting of isoleucine, leucine and valine.
4. The lambda integrase according to claim 3, wherein the lambda integrase comprises the amino acid mutation D336V in the lambda integrase as set forth in SEQ ID NO: 2.
5. The lambda integrase according to claim 4, wherein the amino acid residue glutamate at sequence position 319 is replaced by glycine; optionally wherein said lambda integrase comprises the amino acid mutations E319G and D336V in the lambda integrase as set forth in SEQ ID NO: 3.
6. The lambda integrase according to claims 1 to 5, wherein the lambda integrase comprises amino acid mutations at positions 43, 319 and 336 of the lambda integrase as set forth in SEQ ID NO: 1; optionally wherein the amino acid residue isoleucine at sequence position 43 is replaced by an aromatic amino acid; optionally wherein the aromatic amino acid is selected from the group consisting of phenylalanine, tyrosine and tryptophan.