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(54) Title of the Invention: **Use and method**
Abstract Title: **Use of rat and cat urinary proteins as mouse repellents**

(57) The present invention relates to uses of rat and cat urinary proteins and compositions thereof as rodent control agents, particularly mouse repellents. The proteins used are rat rMUP-13 and cat Cfeld4, or sequences with 75% identity thereto. Also described are peptide fragments of the proteins for use as repellents. The proteins or peptides may be applied alone, or as part of a composition, potentially in aqueous form, as a spray, or both. Also described is a method of repelling mice comprising applying the peptides or compositions to an area.

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Use and Method

Field of the Invention

The present invention relates to uses of peptides and compositions thereof comprising sequences related to fragments of ligands belonging to the major urinary protein (Mup) family from rat and cat as rodent control agents. The present invention also relates to methods for controlling rodents using said peptides and compositions.

Background to the Invention

Rodent infestation is a persistent problem for many households and businesses. Mice carry diseases such as salmonella and Lyme disease, cause damage to property and due to their small size, fast breeding and resourcefulness are difficult to control.

Despite it being an age-old problem, the current solutions for controlling, repelling or removing rodents are still relatively crude and ineffective. One of the most common solutions is the use of rodenticides but these are highly toxic chemicals that by design are tasteless and odourless. The result is that there are many cases of accidental poisoning: in the US alone in 2012 there were 12,231 cases of poisoning by rodenticides, of which 83% were children under the age of 5 (National Poison Data System 2012).

UK councils carried out 88,000 mouse house treatments in 2010/2011 at a reported cost of £133 per treatment, totalling £11.7m (Source: National Pest Control Association, Hackney Council). Recent cuts to council budgets have led to some councils reducing their pest control services. This will put extra burden on homeowners to take action to prevent mice infestation of their homes.

Studies have shown that 82% of US households show evidence of mice in at least one room (Cohn *et. al. J. Allergy Clin. Immunol.*, 2004, 1167). Of the 400,000 public housing residences in New York City, 48% reported mouse sightings within the preceding three months, a total of some 198,000 homes (Kass *et. al.*, *Environ Health Perspect*, 2009, 1219). Removing a mice infestation is costly - a private professional pest control treatment can cost over £400 and mice infestation is not covered as standard by home insurance policies. It has been reported that in the UK, houses containing mice infestations can expect to be sold for 9% less than equivalent un-infested properties (a burden that on

average equates to £22,000), indicating the high cost associated with the problem (The Guardian, 2012).

Existing rodent control agents are used in industrial food processing, storage, commercial kitchens and restaurants; professional pest controllers; and private residences.

The most popular current methods of resolving mice infestations are rodenticides and lethal traps. These options are both inhumane and unhygienic as they result in dead mice which are either hidden (rodenticides), or need disposing of. These methods are also ineffective given the rapid rate of reproduction in mice and the growing resistance to common rodenticides.

Current non-lethal solutions to mouse infestation take the form of either ultrasonic repellents (which emit an uncomfortable sound) or humane traps (which require manual removal of the mouse from the property by the user). Ultrasonic repellents are ineffective (mice quickly become accustomed to the noise) and leading pest control company Rentokil does not recommend their use. Humane traps are only as effective as their bait, plus if the mouse is released insufficiently far from the property it may return. In addition to this many people consider the process of handling mice, dead or alive, very undesirable.

There is therefore a need in the art for an improved method of controlling rodents that avoids the disadvantages of the currently known and used methods.

Papes *et al* (2010), Cell 141:692-703 describes the mediation of interspecies defensive behaviours by sensory neurons of the vomeronasal organ of mice. The effects of ligands belonging to the Mup family and the nature of the neural responses to these ligands were discussed in the context of evolutionary biology.

Summary of the Invention

The present invention solves the problems listed above by providing a peptide that is used to control rodents. The present invention does not require human contact with rodents to prevent them from entering premises. Unwilling to risk the dangers of searching for food where there is a feared risk of predation, rodents are impelled to move away to find new, safer, sources. In some embodiments, periodic reapplication of the product is effective in preventing re-entry.

Accordingly, in a first aspect, the present invention provides use of a peptide comprising a sequence having at least 75% identity to SEQ ID NO: 1 and/or SEQ ID NO: 2 or to a fragment of at least four amino acid residues of either thereof as a rodent control agent.

Detailed Description of the Invention

The present inventors have discovered that peptides and compositions thereof comprising sequences related to fragments of ligands belonging to the major urinary protein (Mup) family from rat and cat can be used as rodent control agents.

According to a first aspect of the invention, there is provided the use of a peptide as a rodent control agent. The peptide for use in the invention comprises a sequence having at least 75% identity to SEQ ID NO:1 and/or SEQ ID NO:2 or to a fragment of at least 4 amino acid residues thereof, wherein SEQ ID NO:1 and SEQ ID NO:2 have the following sequences:

MKLLLLLLCLGLTLVCGHAEEASSTRGNLDVAKLNGDWFSIVVASNKREKIEENGS
MRVFMQHIDVLENSLGFKFRIKENGECRELYLVAYKTPEDGEYFVEYDGGNTFTIL
KTDYDRYVMFHLINFKNGETFQLMVLYGRTKDLSSDIKEKFAKLCEAHGITRDNIID
LTKTDRCLQARG (SEQ ID NO: 1)

MKLLLLCLGLILVCAHEEENVVRSNIDISKISGEWYSILLASDVKEKIEENGSMRVFV
EHIKALDNSSLSFVFHTKENGKCTEIFLVADKTKDGVYTVVYDGYNVFSIVETVYDE
YILLHLLNFDKTRPFQLVEFYAREPDVSQKLKEKFVKYCQEHGIVNILDLTEVDRCL
QARGSEVAQDSSVE (SEQ ID NO: 2)

SEQ ID NO:1 is the amino acid sequence of the rat major urinary protein rMup13. SEQ ID NO:2 is the amino acid sequence of the cat major urinary cFeld4 protein.

In the above, and throughout this specification, amino acids may be referred to using the three letter and one letter codes as follows: glycine (G or Gly), alanine (A or Ala), valine (V or Val), leucine (L or Leu), isoleucine (I or Ile), proline (P or Pro), phenylalanine (F or Phe), tyrosine (Y or Tyr), tryptophan (W or Trp), lysine (K or Lys), arginine (R or Arg), histidine (H or His), aspartic acid (D or Asp), glutamic acid (E or Glu), asparagine (N or Asn), glutamine (Q or Gln), cysteine (C or Cys), methionine (M or Met), serine (S or Ser) and Threonine (T or Thr). Where a residue may be aspartic acid or asparagine, the symbols Asx or B may be used. Where a residue may be glutamic acid or glutamine, the

symbols Glx or Z may be used. References to aspartic acid include aspartate, and references to glutamic acid include glutamate, unless the context specifies otherwise.

As used herein, the term "peptide" includes oligopeptide and polypeptide and these terms may be used interchangeably. It is not intended to exclude proteins. To provide non-limiting examples, proteins of 50 amino acid residues or more, 100 amino acid residues or more, 150 amino acid residues or more, 200 amino acid residues or more, 250 amino acid residues or more, 300 amino acid residues or more, 350 amino acid residues or more, 400 amino acid residues or more, 450 amino acid residues or more, 500 amino acid residues or more, 600 amino acid residues or more, 700 amino acid residues or more, 800 amino acid residues or more, 900 amino acid residues or more, 1000 amino acid residues or more, are included within the scope of the invention. The peptide for use in the invention may contain other amino acids in addition to the sequence having at least 75% identity to SEQ ID NO:1 and/or SEQ ID NO:2 or to a fragment of at least four amino acid residues of either thereof.

As used herein, the term "fragment" includes sequences of at least 4 amino acid residues of SEQ ID NO:1 and/or SEQ ID NO:2. In some embodiments, fragments of SEQ ID NO: 1 and/or SEQ ID NO: 2 are at least 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178 or 179 amino acid residues in length. Fragments of SEQ ID NO: 1 are up to and including 180 amino acid residues in length. Fragments of SEQ ID NO: 2 are up to and including 185 amino acid residues in length, for example at least 180, 181, 182, 183 or 184 amino acid residues in length.

In some preferred embodiments, the fragment is selected from the group consisting of DRCLQARG, TKTDRCLQARG, TEVDRCLQARG, KENG, ENGSMRVFMQH, ENGSMRVFVEH, CRELYLVAYKEP, CTEIFLVADKTK, KENGECRELYLV, KENGKCTEIFLV, SIVVAS, SILLAS, and NCSMRVF. In some particularly preferred embodiments, the fragment is DRCLQARG, TKTDRCLQARG, TEVDRCLQARG, KENG,

ENGSMRVFMQH or ENGSMRVFVEH. In some most preferable embodiments, the fragment is DRCLQARG, TKTDRCLQARG or TEVDRCLQARG.

The effectiveness of a peptide comprising a sequence having at least a defined percentage identity to SEQ ID NO: 1 and/or SEQ ID NO: 2 or to a fragment of either thereof may be unexpectedly more effective as a rodent control agent when the sequence has a defined level of percentage identity in both SEQ ID NO: 1 and SEQ ID NO: 2. Accordingly, in some embodiments the sequence has at least 50% identity, at least 55% identity, at least 60% identity, at least 65% identity, at least 70% identity, at least 75% identity, at least 80% identity, at least 85% identity, at least 90% identity or at least 95% identity in both SEQ ID NO: 1 and SEQ ID NO: 2. In some embodiments the sequence has 100% identity in SEQ ID NO: 1 and SEQ ID NO: 2.

The effectiveness of a peptide comprising a sequence having at least a defined percentage identity to SEQ ID NO: 1 and/or SEQ ID NO: 2 or to a fragment of either thereof may also be unexpectedly more effective as a rodent control agent when the sequence does not have a defined percentage identity to the sequence of the mouse major urinary protein mMup13 or a fragment thereof. mMup13 has the following amino acid sequence:

MLLLLCLGLTLVCVHAEEASSTGRNFNVQKINGEWHTIILASDKREKIEDNGNFRLF
LEQIHVLENSLVLKFHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDY
DNFLMAHLINEKDGETFQLMGLYGREPDLSSDIKERFAQLCEKHGILRENIIDLSNA
NRCLQARE (SEQ ID NO: 3)

Accordingly, in some embodiments the sequence has less than 5% identity, less than 10% identity, less than 15% identity, less than 20% identity, less than 25% identity, less than 30% identity, less than 35% identity, less than 40% identity, less than 45% identity, less than 50% identity, less than 55% identity, less than 60% identity, less than 65% identity, less than 70% identity, less than 75% identity, less than 80% identity, less than 85% identity, less than 90% identity, less than 95% identity, less than 100% identity to SEQ ID NO: 3 or to a fragment thereof.

In some embodiments of the invention, the sequence does not have a defined percentage identity to a sequence of any mouse urinary protein, for example any member of the Mup family as found in mice. In some embodiments, the sequence has less than 100% identity to any or all other members of the Mup family as found in mice. In other embodiments, the

sequence has less than 99%, 97%, 95%, 90%, 85%, 80%, 75%, 70%, 60%, 50%, 40%, or 30% identity to any or all other members of the Mup family as found in mice.

In some embodiments of the invention, any of the sequences having at least a defined percentage identity to SEQ ID NO: 1 and/or SEQ ID NO: 2 or to a fragment of either thereof are predicted to have a disordered secondary structure. Typically, they will be disordered in structural simulations. In some embodiments they will not form part of an alpha helix in structural simulations. In some embodiments they will not form part of a beta sheet in structural simulations. In some embodiments they will not form part of an alpha helix or a beta sheet in structural simulations. In some embodiments they will not form part of an alpha helix and will be disordered in structural simulations.

While there exist a number of methods to predict secondary structure of a peptide, methods commonly employed to predict secondary structure are codified in computer programs, for example the Pyre program package (Kelley LA and Sternberg MJE. Nature Protocols 4, 363 - 371 (2009)).

A peptide for use in the invention may have a sequence with a defined level of percentage identity in SEQ ID NO: 1 and not SEQ ID NO: 2. Accordingly, in some embodiments the sequence occurring in SEQ ID NO: 1 or a fragment thereof has less than 5% identity, less than 10% identity, less than 15% identity, less than 20% identity, less than 25% identity, less than 30% identity, less than 35% identity, less than 40% identity, less than 45% identity, less than 50% identity, less than 55% identity, less than 60% identity, less than 65% identity, less than 70% identity, less than 75% identity, less than 80% identity, less than 85% identity, less than 90% identity, less than 95% identity, or less than 100% identity to SEQ ID NO: 2 or to a fragment thereof.

A peptide for use in the invention may have a sequence with a defined level of percentage identity in SEQ ID NO: 2 and not SEQ ID NO: 1. Accordingly, in some embodiments the sequence occurring in SEQ ID NO: 2 or a fragment thereof has less than 5% identity, less than 10% identity, less than 15% identity, less than 20% identity, less than 25% identity, less than 30% identity, less than 35% identity, less than 40% identity, less than 45% identity, less than 50% identity, less than 55% identity, less than 60% identity, less than 65% identity, less than 70% identity, less than 75% identity, less than 80% identity, less than 85% identity, less than 90% identity, less than 95% identity or less than 100% identity to SEQ ID NO: 1 or to a fragment thereof.

The present invention also extends to uses of peptides comprising variants of the sequences and/or fragments referred to above. As used herein the term "variant" relates to peptides which have a similar amino acid sequence and/or which retain the same function. For instance, the term "variant" encompasses proteins, polypeptides or peptides which include one or more amino acid additions, deletions, substitutions or the like. An example of a variant of the present invention is a peptide comprising a sequence as defined above, apart from the substitution of one or more amino acids with one or more other amino acids. The skilled person is aware that various amino acids have similar properties. One or more such amino acids of a protein, polypeptide or peptide can often be substituted by one or more other such amino acids without eliminating a desired activity of that protein, polypeptide or peptide.

Thus the amino acids glycine, alanine, valine, leucine and isoleucine can often be substituted for one another (amino acids having aliphatic side chains). Of these possible substitutions it is preferred that glycine and alanine are used to substitute for one another (since they have relatively short side chains) and that valine, leucine and isoleucine are used to substitute for one another (since they have larger aliphatic side chains which are hydrophobic). Other amino acids which can often be substituted for one another include: phenylalanine, tyrosine and tryptophan (amino acids having aromatic side chains); lysine, arginine and histidine (amino acids having basic side chains); aspartate and glutamate (amino acids having acidic side chains); asparagine and glutamine (amino acids having amide side chains); and cysteine and methionine (amino acids having sulphur containing side chains).

Substitutions of this nature are often referred to as "conservative" or "semi-conservative" amino acid substitutions. The present invention therefore extends to use of a peptide comprising an amino acid sequence described above but with one or more conservative substitutions in the sequence, such that the amino acid sequence has at least 75% identity to those described above.

For example, if the sequence has 75% identity to SEQ ID NO: 1, the sequence may have 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, or 45 conservative substitutions and if the sequence has 75% identity to SEQ ID NO: 2, the sequence may have 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45 or 46 conservative substitutions.

The number of conservative substitutions in a sequence having at least 75% identity to a fragment of SEQ ID NO: 1 or SEQ ID NO: 2 will depend on the length of the fragment. For example, there can be 1 or 2 conservative substitutions in the amino acid sequence of DRCLQARG, there can be 1, 2 or 3 conservative substitutions in the amino acid sequence of TKTDRCLQARG, there can be 1, 2 or 3 conservative substitutions in the amino acid sequence of TEVDRCLQARG, there can be 1 conservative substitution in the amino acid sequence of KENG, there can be 1, 2 or 3 conservative substitutions in the amino acid sequence of ENGSMRVFMQH, there can be 1, 2 or 3 conservative substitutions in the amino acid sequence of ENGSMRVFVEH, there can be 1, 2 or 3 conservative substitutions in the amino acid sequence of CRELYLVAYKEP, there can be 1, 2 or 3 conservative substitutions in the amino acid sequence of CTEIFLVADKTK, there can be 1, 2 or 3 conservative substitutions in the amino acid sequence of KENGECRELYLV, there can be 1, 2 or 3 conservative substitutions in the amino acid sequence of KENGKCTEIFLV, there can be 1 conservative substitution in the amino acid sequence of SIVVAS, there can be 1 conservative substitution in the amino acid sequence of SILLAS, and there can be 1 conservative substitution in the amino acid sequence of NCSMRVF and the sequence will still retain at least 75% identity to the amino acid sequence of each respective fragment.

Amino acid deletions or insertions can also be made relative to the amino acid sequence for the peptide, such as a fusion protein referred to below. Thus, for example, amino acids which do not have a substantial effect on the activity of the peptide, or at least which do not eliminate such activity, can be deleted. Such deletions can be advantageous since the overall length and the molecular weight of a peptide can be reduced whilst still retaining activity. This can enable the amount of peptide required for a particular purpose to be reduced, for example, dosage levels can be reduced.

Amino acid insertions relative to the sequence of the peptide, such as a fusion protein, referred to below, can also be made. This can be done to alter the properties of a substance of the present invention (e.g. to assist in identification, purification or expression, as explained above in relation to fusion proteins).

Amino acid changes relative to the sequences given above can be made using any suitable technique e.g. by using site-directed mutagenesis or solid state synthesis.

It should be appreciated that amino acid substitutions or insertions within the scope of the present invention can be made using naturally occurring or non-naturally occurring amino acids. For example, it is contemplated herein that the methyl group on an alanine (such as in DRCLQARG) may be replaced with an ethyl group, and/or that minor changes may be made to the peptide backbone. Whether or not natural or synthetic amino acids are used, it is preferred that only L- amino acids are present.

"Identity" as known in the art is the relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, identity also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. While there exist a number of methods to measure identity between two polypeptide or two polynucleotide sequences, methods commonly employed to determine identity are codified in computer programs. Preferred computer programs to determine identity between two sequences include, but are not limited to, GCG program package (Devereux, et al., Nucleic Acids Research, 12, 387 (1984), BLASTP, BLASTN, and FASTA (Atschul et al., J. Molec. Biol. 215, 403 (1990)).

One can use a program such as the CLUSTAL program to compare amino acid sequences. This program compares amino acid sequences and finds the optimal alignment by inserting spaces in either sequence as appropriate. It is possible to calculate amino acid identity or similarity (identity plus conservation of amino acid type) for an optimal alignment. A program like BLASTx will align the longest stretch of similar sequences and assign a value to the fit. It is thus possible to obtain a comparison where several regions of similarity are found, each having a different score. Both types of identity analysis are contemplated in the present invention.

The percent identity of two amino acid sequences or of two nucleic acid sequences is determined by aligning the sequences for optimal comparison purposes (e.g., gaps can be introduced in the first sequence for best alignment with the sequence) and comparing the amino acid residues or nucleotides at corresponding positions. The "best alignment" is an alignment of two sequences which results in the highest percent identity. The percent identity is determined by the number of identical amino acid residues or nucleotides in the sequences being compared (i.e., % identity = number of identical positions/total number of positions x 100).

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm known to those of skill in the art. An example of a mathematical algorithm for comparing two sequences is the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5877. The NBLAST and XBLAST programs of Altschul, et al. (1990) J. Mol. Biol. 215:403-410 have incorporated such an algorithm. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to nucleic acid molecules. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to protein molecules for use in the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilised as described in Altschul et al. (1997) Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules (Id.). When utilising BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See http://www.ncbi.nlm.nih.gov. Another example of a mathematical algorithm utilised for the comparison of sequences is the algorithm of Myers and Miller, CABIOS (1989). The ALIGN program (version 2.0) which is part of the CGC sequence alignment software package has incorporated such an algorithm. Other algorithms for sequence analysis known in the art include ADVANCE and ADAM as described in Torellis and Robotti (1994) Comput. Appl. Biosci., 10 :3-5; and FASTA described in Pearson and Lipman (1988) Proc. Natl. Acad. Sci. 85:2444-8. Within FASTA, ktup is a control option that sets the sensitivity and speed of the search.

Typically, the peptide for use in the invention comprises a sequence having at least 75% identity, using the default parameters of the BLAST computer program (Atschul et al., J. Mol. Biol. 215, 403-410 (1990)) provided by HGMP (Human Genome Mapping Project), at the amino acid level, to the amino acid sequence of SEQ ID NO: 1 and/or SEQ ID NO: 2 or to a fragment of either thereof as described above. For example, the sequence has at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or at least 99% identity, at the amino acid level, to the amino acid sequence of SEQ ID NO:1 and/or SEQ ID NO:2 or to a fragment of either thereof, using these parameters.

In some embodiments, a peptide for use in the invention includes more than one sequence having at least 75% identity to SEQ ID NO: 1 and/or SEQ ID NO: 2 or to a fragment of at least four amino acid residues of either thereof. Any sequence disclosed herein may be incorporated into a peptide for use in the invention along with any number of other

sequences disclosed herein. Typically in these embodiments, a number of sequences as disclosed herein are combined. For example the peptide may comprise more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, or 45 sequences as disclosed herein. In some embodiments a peptide for use in the invention may comprise sequences having a defined percentage identity to SEQ ID NO: 1, and/or SEQ ID NO: 2, and/or DRCLQARG, and/or TKTDRCLQARG, and/or TEVDRCLQARG, and/or KENG, and/or ENGSMRVFMQH, and/or ENGSMRVFVEH, and/or CRELYLVAYKEP, and/or CTEIFLVADKTK, and/or KENGECRELYLV, and/or KENGKCTEIFLV, and/or SIVVAS, and/or SILLAS, and/or NCSMRVF. In some preferred embodiments, the peptide comprises regions sharing a defined percentage identity to DRCLQARG and KENG. To provide a non-limiting example a peptide for use in the invention may comprise regions sharing a defined percentage identity to SEQ ID NO: 1, SEQ ID NO: 2, DRCLQARG, TKTDRCLQARG, TEVDRCLQARG, KENG, ENGSMRVFMQH, ENGSMRVFVEH, CRELYLVAYKEP, CTEIFLVADKTK, KENGECRELYLV, KENGKCTEIFLV, SIVVAS, SILLAS and NCSMRVF. It is contemplated herein that the sequences may be arranged in any order. It is also contemplated that any sequence may be found at least once within a peptide for use in the invention, i.e. multiple copies of a particular sequence may be present within the peptide. In some embodiments, any sequence may be found more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, or 45 times in a peptide for use in the invention.

In some embodiments the peptide for use in the invention is a fusion protein, wherein at least two sequences having at least 75% identity to SEQ ID NO: 1 and/or SEQ ID NO: 2 or to a fragment of at least four amino acid residues of either thereof are fused in any arrangement as described above. In some embodiments wherein the peptide is a fusion protein, it may further comprise linker regions of any sequence and any length between the sequences having at least 75% identity to SEQ ID NO: 1 and/or SEQ ID NO: 2 or to a fragment of at least four amino acid residues of either thereof. In some embodiments the linker regions are at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, or 45 amino acid residues in length.

In some embodiments a peptide for use in the invention or a fusion protein for use in the invention may comprise sequences having a defined percentage identity to both SEQ ID NO: 1 and SEQ ID NO: 2; and/or sequences having a defined percentage identity to both

SEQ ID NO: 1 and SEQ ID NO: 2 and not SEQ ID NO: 3; and/or sequences having a defined percentage identity to SEQ ID NO: 1 and not SEQ ID NO: 3; and/or sequences having a defined percentage identity to SEQ ID NO: 2 and not SEQ ID NO: 3. Without wishing to be bound by theory, it is thought that certain murine sensory neurons may respond selectively to peptides of the invention comprising sequences having a defined percentage identity to both SEQ ID NO: 1 and SEQ ID NO: 2; and/or sequences having a defined percentage identity to both SEQ ID NO: 1 and SEQ ID NO: 2 and not SEQ ID NO: 3; and/or sequences having a defined percentage identity to SEQ ID NO: 1 and not SEQ ID NO: 3; and/or sequences having a defined percentage identity to SEQ ID NO: 2 and not SEQ ID NO: 3. As such, the combination of multiple such sequences into a peptide or fusion protein may result in a more efficacious rodent control agent.

In some embodiments the peptide for use in the invention is recombinant. In preferred embodiments, it is effective as a rodent control agent in its recombinant form, with tag still attached, which allows for easy production and purification from *E. coli*. Recombinant peptides according to the invention can be produced, for example by fermentation of *E. coli* in a manner similar to other large scale enzyme production such as cellulase and amylase, but any other method of producing recombinant peptides can be used. Methods of purification of recombinant peptides are well known to the person skilled in the art and any may be employed in the purification of peptides for use in the invention. Accordingly, in one embodiment the peptide for use in the invention is purified.

The uptake of foreign DNA by *E. coli* for the production of recombinant peptides may be achieved by means known in the art. For example, competent *E. coli* may undergo transformation by being induced to take up foreign DNA encoding the recombinant peptide. Transformation of *E. coli* can be achieved by, for example, the calcium chloride method or electroporation. For the purposes of transformation DNA encoding the recombinant peptide is typically cloned into a plasmid. Following transformation, successfully transformed cells may be selected by methods including antibiotic resistance conferred by the exogenous DNA or expression of an exogenous reporter gene such as *lacZ,* luciferase or Green Fluorescent Protein (GFP).

DNA sequences encoding peptides for use in the invention include the following sequences:

Felix catus Feld d 4 allergen DNA sequence:

Source: http://www.uniprot.org/uniprot/Q5VFH6

Sequence ID: AY497902

Original sequencing reference: W. Smith *et. al.* Fel d 4, a cat lipocalin allergen, *Clin. Exp. Allergy*, **2004**, 34 (11), 1732-1738, Available online: http://goo.gl/mrUHTQ

CGGCACGAGGCTATTTTCCTGCCAAGATGAAGCTGCTGTTGCTGTGTCTAGGGCTGA
TTCTAGTCTGTGCCCATGAGGAAGAAAACGTTGTGAGAAGCAACATCGATATTTCAAA
GATTTCAGGAGAGTGGTATTCCATTCTCTTGGCCTCAGATGTTAAGGAAAAGATAGAA
GAAAATGGTAGCATGAGGGTTTTTGTCGAACACATCAAAGCCCTGGACAACTCTTCT
CTGTCCTTTGTATTTCATACAAAAGAGAACGGAAAGTGTACTGAAATATTTTTGGTTGC
TGACAAAACAAAGGATGGTGTATATACTGTTGTGTATGATGGATACAATGTATTTAGC
ATAGTTGAAACGGTCTATGATGAGTATATCCTGTTACATCTTCTGAATTTTGACAAGAC
GAGACCATTCCAGTTGGTAGAGTTCTATGCCCGAGAACCAGATGTGAGCCAAAAACT
CAAGGAAAAGTTTGTGAAATACTGCCAAGAACATGGGATTGTTAACATACTTGACCTG
ACTGAAGTTGATCGCTGTTTACAGGCCCGAGGAAGTGAAGTGGCCCAGGACTCCAG
TGTTGAGTGAATGCTTCCTTACCTGGGCTCCAGGATCTTCCCTTCTGTGGTCCCCAC
AACATCTAGTGGCAAGTGCTGTGACCTGATTTCCATCATAATCACATAGGAAAGCATT
ATCTCTGCATCTTCAGAATCTTGTCTAGGAAAACATCAACCAACCAAGATTTCAAGAT
TTTCTCCAAATTTTCCAGCTGTCTTTCCCATACCCAGGAGAACTCTATCATGAATAAGA
ACTTCCTATACCTGGTCAATAAATGATTAGCCTTGAAAAAAAAAAAAAAAAAAA (SEQ ID NO: 4)

Rattus norvegicus rMup13 DNA sequences. There are 8 different sequences available from five different references. All gene sequences code for the same amino acid sequence.

1.

Sequence ID: M26835

Source: http://www.ebi.ac.uk/ena/data/view/M26835

Original sequencing reference: Y. Ichiyoshi *et. al,* Length polymorphism in the 3' noncoding region of rat hepatic α2u-globulin mRNAs, *BBA-Gene Struct. Expr.* **1987,** 910 (1), 43-51, Available online: http://goo.gl/NxVAs5

ATTCTATTCCCTACCAACATGAAGCTGTTGCTGCTGCTGCTGTGTCTGGGCCTGACA
CTGGTCTGTGGCCATGCAGAAGAAGCTAGTTCCACAAGAGGGAACCTCGATGTGGC
TAAGCTCAATGGGGATTGGTTTTCTATTGTCGTGGCCTCTAACAAAAGAGAAAAGATA
GAAGAGAATGGCAGCATGAGAGTTTTTATGCAGCACATCGATGTCTTGGAGAATTCC

TTAGGCTTCAAGTTCCGTATTAAGGAAAATGGAGAGTGCAGGGAACTATATTTGGTTG
CCTACAAAACGCCAGAGGATGGCGAATATTTTGTTGAGTATGACGGAGGGAATACAT
TTACTATACTTAAGACAGACTATGACAGATATGTCATGTTTCATCTCATTAATTTCAAG
AACGGGGAAACCTTCCAGCTGATGGTGCTCTACGGCAGAACAAAGGATCTGAGTTCA
GACATCAAGGAAAAGTTTGCAAAACTATGTGAGGCGCATGGAATCACTAGGGACAAT
ATCATTGATCTAACCAAGACTGATCGCTGTCTCCAGGCCCGAGGATGAAGAAAGGCC
TGAGCCTCCAGGTGGGCAATCTCCAGTGAGAGCAAGTGCTGAGTGGAGACTTCTCA
CCAGGACTCTAGCATCACCATTTCCTGTCCATGGAGCATCCTGAGACAAATTCTGCG
ATCTGATTTCCATCCTCTGTCACAGAAAAGTGCAATCCTGGTCTCTCCAGCATCTTCC
CTAGTTACCCAGGACAACACATCGAGAATTAAAAGCTTTCTTAAATTTCTCTTGGCCC
CACCCATGATCATTCCGCACAAATATCTTGCTCTTGCAGTTCAATAAATGATTACCCTT
GCACTT (SEQ ID NO: 5)

2.

Sequence ID: M26837

Source: http://www.ebi.ac.uk/ena/data/view/M26837

Original sequencing reference: Y. Ichiyoshi *et. al,* Length polymorphism in the 3′ noncoding region of rat hepatic α2u-globulin mRNAs, *BBA-Gene Struct. Expr.* **1987,** 910 (1), 43-51, Available online: http://goo.gl/NxVAs5

TATTCCCTACCAACATGAAGCTGTTGCTGCTGCTGCTGTGTCTGGGCCTGACACTGG
TCTGTGGCCATGCAGAAGAAGCTAGTTCCACAAGAGGGAACCTCGATGTGGCTAAG
CTCAATGGGGATTGGTTTTCTATTGTCGTGGCCTCTAACAAAAGAGAAAAGATAGAAG
AGAATGGCAGCATGAGAGTTTTTATGCAGCACATCGATGTCTTGGAGAATTCCTTAG
GCTTCAAGTTCCGTATTAAGGAAAATGGAGAGTGCAGGGAACTATATTTGGTTGCCT
ACAAAACGCCAGAGGATGGCGAATATTTTGTTGAGTATGACGGAGGGAATACATTTA
CTATACTTAAGACAGACTATGACAGATATGTCATGTTTCATCTCATTAATTTCAAGAAC
GGGGAAACCTTCCAGCTGATGGTGCTCTACGGCAGAACAAAGGATCTGAGTTCAGA
CATCAAGGAAAAGTTTGCAAAACTATGTGAGGCGCATGGAATCACTAGGGACAATAT
CATTGATCTAACCAAGACTGATCGCTGTCTCCAGGCCCGAGGATGAAGAAAGGCCTG
AGCCTCCAGTGCTGAGTGGAGACTTCTCACCAGGACTCTAGCATCACCATTTCCTGT
CCATGGAGCATCCTGAGACAAATTCTGCGATCTGATTTCCATCCTCTGTCACAGAAAA
GTGCAATCCTGGTCTCTCCAGCATCTTCCCTAGTTACCCAGGACAACACATCGAGAA
TTAAAAGCTTTCTTAAATTTCTCTTGGCCCCACCCATGATCATTCCGCACAAATATCTT
GCTCTTGCAGTTCAATAAATGATTACCCTTGCACTT (SEQ ID NO: 6)

3.

Sequence ID: AB039822

Source: http://www.ebi.ac.uk/ena/data/view/AB039822

Original sequencing reference: K. Saito *et. al.* Molecular evidence of complex tissue- and sex-specific mRNA expression of the rat alpha(2u)-globulin multigene family, *Biochem. Biophys. Res. Commun.* **2000**, 272 (2), 337-344, Available online: http://goo.gl/yMXEl5

GATTGTCCCAACAGAGAGGCAATTCTATTCCCTACCAACATGAAGCTGTTGCTGCTG
CTGCTGTGTCTGGGCCTGACACTGGTCTGTGGCCATGCAGAAGAAGCTAGTTCCACA
AGAGGGAACCTCGATGTGGCTAAGCTCAATGGGGATTGGTTTTCTATTGTCGTGGCC
TCTAACAAAAGAGAAAAGATAGAAGAGAATGGCAGCATGAGAGTTTTTATGCAGCAC
ATCGATGTCTTGGAGAATTCCTTAGGCTTCAAGTTCCGTATTAAGGAAAATGGAGAGT
GCAGGGAACTATATTTGGTTGCCTACAAAACGCCAGAGGATGGCGAATATTTTGTTG
AGTATGACGGAGGGAATACATTTACTATACTTAAGACAGACTATGACAGATATGTCAT
GTTTCATCTCATTAATTTCAAGAACGGGGAAACCTTCCAGCTGATGGTGCTCTACGGC
AGAACAAAGGATCTGAGTTCAGACATCAAGGAAAAGTTTGCAAAACTATGTGAGGCG
CATGGAATCACTAGGGACAATATCATTGATCTAACCAAGACTGATCGCTGTCTCCAG
GCCCGAGGATGAAGAAAGGCCTGAGCCTCCAGTGCTGAGTGGAGACTTCTCACCAG
GACTCTAGCATCACCATTTCCTGTCCATGGAGCATCCTGAGACAAATTCTGCGATCTG
ATTTCCATCCTCTGTCACAGAAAAGTGCAATCCTGGTCTCTCCAGCATCTTCCCTAGT
TACCCAGGACAACACATCGAGAATTAAAAGCT (SEQ ID NO: 7)

4.

Sequence ID: BC088109

Source: http://www.ebi.ac.uk/ena/data/view/BC088109

Original sequencing reference: R. L. Strausberg *et. al,* Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences, *Proc. Natl. Acad. Sci. USA,* **2002,** 99 (26), 16899-16903, Available online: http://goo.gl/VU79zM

GAGATTGTCCCAACAGAGAGGCAATTCTATTCCCTACCAACATGAAGCTGTTGCTGC
TGCTGCTGTGTCTGGGCCTGACACTGGTCTGTGGCCATGCAGAAGAAGCTAGTTCCA
CAAGAGGGAACCTCGATGTGGCTAAGCTCAATGGGGATTGGTTTTCTATTGTCGTGG
CCTCTAACAAAAGAGAAAAGATAGAAGAGAATGGCAGCATGAGAGTTTTTATGCAGC
ACATCGATGTCTTGGAGAATTCCTTAGGCTTCAAGTTCCGTATTAAGGAAAATGGAGA
GTGCAGGGAACTATATTTGGTTGCCTACAAAACGCCAGAGGATGGCGAATATTTTGT
TGAGTATGACGGAGGGAATACATTTACTATACTTAAGACAGACTATGACAGATATGTC
ATGTTTCATCTCATTAATTTCAAGAACGGGGAAACCTTCCAGCTGATGGTGCTCTACG
GCAGAACAAAGGATCTGAGTTCAGACATCAAGGAAAAGTTTGCAAAACTATGTGAGG

CGCATGGAATCACTAGGGACAATATCATTGATCTAACCAAGACTGATCGCTGTCTCC
AGGCCCGAGGATGAAGAAAGGCCTGAGCCTCCAGTGCTGAGTGGAGACTTCTCACC
AGGACTCTAGCATCACCATTTCCTGTCCATGGAGCATCCTGAGACAAATTCTGCGAT
CTGATTTCCATCCTCTGTCACAGAAAAGTGCAATCCTGGTCTCTCCAGCATCTTCCCT
AGTTACCCAGGACAACACATCGAGAATTAAAAGCTTTCTTAAATTTCTCTTGGCCCCA
CCCATGATCATTCCGCACAAATATCTTGCTCTTGCAGTTCAATAAATGATTACCCTTG
CAAAAAAAAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO: 8)

5.

Sequence ID: BC098654

Source: http://www.ebi.ac.uk/ena/data/view/BC098654

Original sequencing reference: R. L. Strausberg *et. al,* Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences, *Proc. Natl. Acad. Sci. USA,* **2002,** 99 (26), 16899-16903, Available online: http://goo.gl/VU79zM

GCAGAGAGATTGTCCCAACAGAGAGGCAATTCTATTCCCTACCAACATGAAGCTGTT
GCTGCTGCTGCTGTGTCTGGGCCTGACACTGGTCTGTGGCCATGCAGAAGAAGCTA
GTTCCACAAGAGGGAACCTCGATGTGGCTAAGCTCAATGGGGATTGGTTTTCTATTG
TCGTGGCCTCTAACAAAAGAGAAAAGATAGAAGAGAATGGCAGCATGAGAGTTTTTA
TGCAGCACATCGATGTCTTGGAGAATTCCTTAGGCTTCAAGTTCCGTATTAAGGAAAA
TGGAGAGTGCAGGGAACTATATTTGGTTGCCTACAAAACGCCAGAGGATGGCGAATA
TTTTGTTGAGTATGACGGAGGGAATACATTTACTATACTTAAGACAGACTATGACAGA
TATGTCATGTTTCATCTCATTAATTTCAAGAACGGGGAAACCTTCCAGCTGATGGTGC
TCTACGGCAGAACAAAGGATCTGAGTTCAGACATCAAGGAAAAGTTTGCAAAACTAT
GTGAGGCGCATGGAATCACTAGGGACAATATCATTGATCTAACCAAGACTGATCGCT
GTCTCCAGGCCCGAGGATGAAGAAAGGCCTGAGCCTCCAGTGCTGAGTGGAGACTT
CTCACCAGGACTCTAGCATCACCATTTCCTGTCCATGGAGCATCCTGAGACAAATTCT
GCGATCTGATTTCCATCCTCTGTCACAGAAAAGTGCAATCCTGGTCTCTCCAGCATCT
TCCCTAGTTACCCAGGACAACACATCGAGAATTAAAAGCTTTCTTAAATTTCTCTTGG
CCCCACCCATGATCATTCCGCACAAATATCTTGCTCTTGCAGTTCAATAAATGATTAC
CCTTGCACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO: 9)

6.

Sequence ID: BC105816

Source: http://www.ebi.ac.uk/ena/data/view/BC105816

Original sequencing reference: R. L. Strausberg *et. al,* Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences, *Proc. Natl. Acad. Sci. USA,* **2002,** 99 (26), 16899-16903, Available online: http://goo.gl/VU79zM

GAGAGATTGTCCCAACAGAGAGGCAATTCTATTCCCTACCAACATGAAGCTGTTGCT
GCTGCTGCTGTGTCTGGGCCTGACACTGGTCTGTGGCCATGCAGAAGAAGCTAGTT
CCACAAGAGGGAACCTCGATGTGGCTAAGCTCAATGGGGATTGGTTTTCTATTGTCG
TGGCCTCTAACAAAAGAGAAAAGATAGAAGAGAATGGCAGCATGAGAGTTTTTATGC
AGCACATCGATGTCTTGGAGAATTCCTTAGGCTTCAAGTTCCGTATTAAGGAAAATGG
AGAGTGCAGGGAACTATATTTGGTTGCCTACAAAACGCCAGAGGATGGCGAATATTT
TGTTGAGTATGACGGAGGGAATACATTTACTATACTTAAGACAGACTATGACAGATAT
GTCATGTTTCATCTCATTAATTTCAAGAACGGGGAAACCTTCCAGCTGATGGTGCTCT
ACGGCAGAACAAAGGATCTGAGTTCAGACATCAAGGAAAAGTTTGCAAAACTATGTG
AGGCGCATGGAATCACTAGGGACAATATCATTGATCTAACCAAGACTGATCGCTGTC
TCCAGGCCCGAGGATGAAGAAAGGCCTGAGCCTCCAGTGCTGAGTGGAGACTTCTC
ACCAGGACTCTAGCATCACCATTTCCTGTCCATGGAGCATCCTGAGACAAATTCTGC
GATCTGATTTCCATCCTCTGTCACAGAAAAGTGCAATCCTGGTCTCTCCAGCATCTTC
CCTAGTTACCCAGGACAACACATCGAGAATTAAAAGCTTTCTTAAATTTCTCTTGGCC
CCACCCATGATCATTCCGCACAAATATCTTGCTCTTGCAGTTCAATAAATGATTACCC
TTGCACTTAAAAAAAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO: 10)

7.

Sequence ID: U31287

Source: http://www.ebi.ac.uk/ena/data/view/U31287

Original sequencing reference: Submitted to EMBL/GenBank/DDBJ Databases May 1995 by M. Dey and D. T. Kurtz

GGCACGAGCAGAGAGATTGTCCCAACAGAGAGGCAATTCTATTCCCTACCAACATGA
AGCTGTTGCTGCTGCTGCTGTGTCTGGGCCTGACACTGGTCTGTGGCCATGCAGAA
GAAGCTAGTTCCACAAGAGGGAACCTCGATGTGGCTAAGCTCAATGGGGATTGGTTT
TCTATTGTCGTGGCCTCTAACAAAAGAGAAAAGATAGAAGAGAATGGCAGCATGAGA
GTTTTTATGCAGCACATCGATGTCTTGGAGAATTCCTTAGGCTTCAAGTTCCGTATTA
AGGAAAATGGAGAGTGCAGGGAACTATATTTGGTTGCCTACAAAACGCCAGAGGATG
GCGAATATTTTGTTGAGTATGACGGAGGGAATACATTTACTATACTTAAGACAGACTA
TGACAGATATGTCATGTTTCATCTCATTAATTTCAAGAACGGGGAAACCTTCCAGCTG
ATGGTGCTCTACGGCAGAACAAAGGATCTGAGTTCAGACATCAAGGAAAAGTTTGCA
AAACTATGTGAGGCGCATGGAATCACTAGGGACAATATCATTGATCTAACCAAGACT

GATCGCTGTCTCCAGGCCCGAGGATGAAGAAAGGCCTGAGCCTCCAGTGCTGAGTG
GAGACTTCTCACCAGGACTCTAGCATCACCATTTCCTGTCCATGGAGCATCCTGAGA
CAAATTCTGCGATCTGATTTCCATCCTCTGTCACAGAAAAGTGCAATCCTGGTCTCTC
CAGCATCTTCCCTAGGTTACCCAGGACAACACATCGAGAATTAAAAGCTTTCTTAAAT
TTCTCTTGGCCCCACCCATGATCATTCCGCACAAATATCTTGCTCTTGCAGTTCAATA
AATGATTACCCTTGCACTT (SEQ ID NO: 11)

8.

Sequence ID: J00737

Source: http://www.ebi.ac.uk/ena/data/view/J00737

Original sequencing reference: R. D. Unterman *et. al.*, Cloning and sequence of several alpha 2u-globulin cDNAs, *Proc. Natl. Acad. Sci. USA*, **1981**, 78 (6), 3478-3482, Available online: http://goo.gl/KmqgxD

CTGCTGCTGCTGTGTCTGGGCCTGACACTGGTCTGTGGCCATGCAGAAGAAGCTAG
TTCCACAAGCGGGAACCTCGATGTGGCTAAGCTCAATGGGGATTGGTTTTCTATTGT
CGTGGCCTCTAACAAAAGAGAAAAGATAGAAGAGAATGGCAGCATGAGAGTTTTTAT
GCAGCACATCGATGTCTTGGAGAATTCCTTAGGCTTCAAGTTCCGTATTAAGGAAAAT
GGAGAGTGCAGGGAACTATATTTGGTTGCCTACAAAACGCCAGAGGATGGCGAATAT
TTTGTTGAGTATGACGGAGGGAATACATTTACTATACTTAAGACAGACTATGACAGAT
ATGTCATGTTTCATCTCATTAATTTCAAGAACGGGGAAACCTTCCAGCTGATGGTGCT
CTACGGCAGAACAAAGGATCTGAGTTCAGACATCAAGGAAAAGTTTGCAAAACTATG
TGAGGCGCATGGAATCACTAGGGACAATATCATTGATCTAACCAAGACTGATCGCTG
TCTCCAGGCCCGAGGATGAAGAAAGGCCTGAGCCTCCAGTGCTGAGTGGAGAACTT
CTCACCAGGACTCTAGCATCACCATTTCCTGTCCATGGAGCATCCTGAGACAAATTCT
GCGATCTGATTTCCATCCTCTGTCACAGAAAAGTGCAATCCTGGTCTCTCCAGCATCT
TCCCTAGTTACCCAGGACAACACATCGAGAATTAAAAGCTTTCTTAAATTTCTCTTGG
CCCCACCCATGATCATTCCGCACAAATATCTTGCTCTTGCAGTTCAATAAATGATTAC
CCTTGCACTT (SEQ ID NO: 12)

The *Mus musculus m*Mup13 DNA sequence is as follows:

Source: http://www.ncbi.nlm.nih.gov/nuccore/BK006661

Sequence ID: BK006661

Original sequencing reference: L. Stowers *et. al*, Identification of protein pheromones that promote aggressive behaviour, *Nature*, **2007**, 450 (7171), 899-902, Available online: http://goo.gl/tC6t6N

ATGCTGTTGCTGCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAAGAAGCT
AGTTCTACGGGAAGGAACTTTAATGTACAAAAGGTATGATCACTGAATAGTAGCTTCT
GACTCAGAATGTGCTTTGGGGAACTCTTGAAGCCAAGTAGGTCCTTTGAGGGGATGG
GTATAGTGCCCCAATCTCTTAGACAAATGAATGGATCCAGACCTTGAAGTAAGACCAG
CTCTTCATAACTGAAAATGTTGGGGGACCTCTAGTCTCACTGAGAGGCAGGGACAGT
ATGCTAAGTATTGTGACAACTGGCATGAGATCTACCCTTGTGTATGCTCAGGCCCTAA
CCCATAGGATGGAGTTCAAGTGGACACATGTGCATGTGGTATCCCTGCTTCTTCTCCC
TTAACCATTTGCTTATCTATTACAGATTAATGGGGAATGGCATACTATTATCCTGGCCT
CTGACAAAAGAGAAAAGATAGAAGATAATGGCAACTTTAGACTTTTTCTGGAGCAAAT
CCATGTCTTGGAGAATTCCTTAGTTCTTAAATTCCATACTGTGTAAGTGAGATGCTCTT
AGCTGAGAAAGAGGAAATGAAACCTGGTATGGTCTCACGCCTACAAACACTCGGGAC
TGGGGGGAAGAGATGCCTCTCAGTATGTACATTTGTACACACATACTAAGTCTGTATCC
TAAACCAGAACGCTCCATCTGACACTGAACCAAGATCTCATAACCAGGGATTTTTCAA
AAGTCAGAGACAAGAGTTGGTGACAGGAATTAATTCACTAGGAGTTCCTTAAGGAAAG
GTCAGAGACACTTCTGAAACCACATTATTGAGCCAGTTTATCACAAGTTAAGATTATGT
GATCATGAATCAAATTTTTCTTTCTAGTTGTTAGCCAAATAAATCCACCCCTTTGTACTT
CCGTTTTCCTGCAGTAAAGGCGATAATAATAATTCTCCTCTGTGGTACTGGGAACCAC
ATCAGGCAACATTACAGAGTGCTAATTTGAGGCAGATGGTGGAAATCTGGCTGATAAT
CTACACCGCTGGCTGAAGCCCGGCACTGGTGAAACTTGGAAGTAGTTGCAGTTGTAA
TAAGGATGAGAAGTGATTGTTGTTTTCTTTTTTTTTAAATACTAGGCAAATTTGTGATTG
CTAAAGCATGAAATATAAAGGAATTAATGTAAATAAACGCCTTTTGCTAATTTTACAAAA
ACAGTCAAAAGTTAAATGGAATCAGAAACTGGAGATAGGTACAGAGTACAGGGTCCA
GAATCCATCCAGATCAAAATCCCTTACGAACCAGCTCACTCTGTTTTACAGAAGAGAT
GAAGAGTGCTCGGAATTATCTATGGTTGCTGACAAAACAGAAAAGGCTGGTGAATATT
CTGTGACGTGTGAGTATATAAAATCTATATATCTATCCACAAGATGATTAGTAAACCTT
AATACCTTTAGTGTGTGTGTTTGTGTGTGTGTGTGTTGTTTTTGTTGTTGTTGTTGTTG
TTGTTGTTGTTGTTGTTGTTATTGTTGTGTGAGTTTTGCTGCAGTTTGAACTCAGGAAC
TTGCACCTACTAGTAAAATTGGTGCCATCTTATAACTAACACCCTGTGGCAGGAAAGT
AGGATAAGTAGGGAGAGATGGAATCTATCTGATACTGCCTGGAGGCTAGCACTGGTG
TTAATCGCTTAGGGTGTAGCAGTGGATGTTTGATACAACAAACTTATAAAAGATAGAAA
CATGTTGCTTGAAGCTGCTGAGGGAGGGAGGTAAGCCTAGGAGATGATCAGAGAGT
GGTGCTGCTGTGGCTGACTGTTTACTAGTGGTGTGGACCTCTCAGAGTCCCTTTTCTT
AGCATTTACTTCTTGAAGTTCAGAAAACTAAAGACAGAAAGGCTCAGACACTTCACCC
ATCTCTTCCACGATATGTATTTTACTGATTTTATGTTGGGGTAAAACAAGAAAAGGGTA
TCCAAAATTTCCTGCAGAACAAAAAATTTCTGAGCTGTGTTCCATTTCTTCCACAGATG
ATGGATTCAATACATTTACTATACCTAAGACAGACTATGATAACTTTCTTATGGCTCAT
CTCATTAACGAAAAGGATGGGGAAACCTTCCAGCTGATGGGGCTCTATGGTAAAGTA

TTTTCACACAGAAACTGATCCTCGGATGGGAAAAGAACGAAGAACCTCTAGCTTTAAT
ATGGTCTTCCCAGCTTGGGCTTACCTCTTTGTAACCTCCTGAAGATTGATGCTCTCCC
CATCAACCCTTGAGCATAGTAATGGAAGCATACTGAAATCTCTCAGTGTGACTGAAAG
ATATTCTATGGATGCCAAATCCAGGATAGATCATACCAATGCCTGTCAATTGTGTTGG
CAAAAAATATTCCCATCCTTATGGGGAAGTCCCTGTCCCCTCACTCAGGCTGTGGTCA
ATGCACACAATATAGCTGCTACACTCACTATTGCTCTTCTCACAGGCCGAGAACCAGA
TTTGAGTTCAGACATCAAGGAAAGGTTTGCACAACTATGTGAGAAGCATGGAATCCTT
AGAGAAAATATCATTGACCTATCCAATGCCAGTAAGTCAGGATTCAGTTATTTTTCTCA
TCCTGAATATTTTATCATAGAGGAAACAAACCTAGTTGGCTACCAGTCATTTTTGAATG
CTGGAGAGTCCTATCCTTATTCTTGGGGAAATAAAGTGGACCTGGTACCTGAACATGT
TCTTGTTCTCACACTACAGATCGCTGCCTCCAGGCCCGAGAATGA (SEQ ID NO: 13)

In alternative embodiments of the invention the peptide for use in the invention is isolated or derived from a wild type protein using techniques known in the art.

In some embodiments the peptide for use in the invention is produced by other methods of peptide synthesis known in the art, for example solid phase peptide synthesis.

The peptide as defined herein can be included as part of a composition. Typically the peptide is the active ingredient of the composition. In some embodiments, the composition may comprise one peptide as defined herein. In other embodiments, the composition may comprise more than 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40 or 50 peptides as defined herein in any combination. To provide a non-limiting example, the composition may comprise a 1:1 mixture of peptides comprising a sequence having at least 75% identity to SEQ ID NO: 1 and peptides comprising a sequence having at least 75% identity to SEQ ID NO: 2. Alternatively, the same peptides, or any other peptides as defined herein may be mixed in any ratio to form a composition comprising any number of peptides.

It is contemplated herein that in a composition comprising more than one of the peptides for use in the invention one of the peptides may provide a synergistic effect by increasing the efficacy of the composition more than the additive amount.

Typically, the composition may include one or more of the peptides for use in the invention along with an acceptable carrier, additive or adjuvant.

The compositions for use in the invention can take the form of a solid or a liquid or a gas or a gel. Solid compositions include agriculturally useful and/or commercially available powders; liquid compositions may be aqueous or non-aqueous, and take the form of emulsions, suspension or solutions. Non-limiting examples of compositions for use in the invention include powders, dusts, granulates, topical oils, encapsulations, concentrates capable of emulsification, suspension concentrates, directly sprayable or dilutable solutions, aerosolized solutions, coatable pastes, dilute emulsions, wettable powders, soluble powders, dispersible powders or fumigants.

The composition for use in the invention is typically an aqueous solution. In some embodiments the composition is suitable for application as a spray, optionally from a spray bottle. In some embodiments the composition for use in the invention consists of an aerosolized solution of the peptide that would be periodically applied by spraying to the corners of rooms and other places where rodents may enter a room or building. Spray bottle application allows home and business owners to easily and quickly rodent-proof their property.

In some embodiments of the invention, the composition for use in the invention is suitable for application by means of an automated dispenser. The automated dispenser typically allows for release of the composition into the air. The automated dispenser may be automated by means of a battery and/or coupling to mains electrical power and/or by a mechanical means. Automated dispenser application allows home and business owners to easily mouse-proof their property with minimal maintenance.

The peptide is typically soluble and stable in aqueous solutions for extended periods of time in the presence of reducing and/or peptide denaturing agents including but not limited to urea. In some embodiments, the stability of the peptides for use in the invention permits reapplication of the peptide or composition for use in the invention to be less frequent than once per hour, two hours, four hours, eight hours, 16 hours, day, two days, three days, four days, five days, six days, seven days, fortnight or month.

The peptides or compositions for use in the invention are typically substantially non-toxic to humans. The peptides or compositions for use in the invention are also typically substantially not detectable to human senses. For example, they may not be detectable by smell. In preferred embodiments, the peptides or compositions for use in the invention are suitable for use in food processing areas and/or residences and/or for application by professional pest controllers

The present invention provides use of a peptide and/or composition as a rodent control agent. As used herein a "rodent control agent" is an agent that has any adverse effect on a rodent population, which includes (but is not limited to) physiological damage to a rodent, inhibition or modulation of rodent growth, inhibition or modulation of rodent reproduction, repelling rodents, for example by inhibition or complete deterrence of rodent movement from a locus or initiation or promotion of rodent movement away from a locus or promoting an innate fear and/or avoidance response, inhibition or elimination of rodent feeding activity, or death of the rodent. In preferred embodiments the rodent control agent is a rodent repellent, for example a mouse repellent.

The peptides and compositions for use in the invention are thought to be effective as control agents when the rodent belongs to the superfamily *Muroidea*. This superfamily includes mice, hamsters, gerbils and rats. In some embodiments the rodent belongs to the family *Muridae*, the genus *Mus* and/or is *Mus musculus* (house mouse). In other embodiments the rodent belongs to the family *Cricetidae, Nesomyidae* or *Calomyscinae*. In some embodiments the rodent belongs to the superfamily *Muroidea* and is not a rat. In typical embodiments the rodent belongs to the family *Muridae* and is not a rat. In other embodiments the rodent belongs to the family *Cricetidae, Nesomyidae* or *Calomyscinae* and is not a rat. Typically, the rodent is a mouse. When the rodent is a rat, the peptide typically comprises a sequence having at least 75% identity to SEQ ID NO: 2 or to a fragment of at least four amino acid residues thereof.

The skilled person will understand that the effects of the peptides and/or compositions for use in the invention may be dependent upon the concentration and/or manner at which they are administered and/or their dosage and that concentration manner of delivery and dosage can be optimized according to standard procedures in the art.

The peptides and compositions as defined herein in relation to the first aspect of the invention can also be used in a method of controlling a rodent.

Accordingly, in a second aspect, the present invention provides a method of controlling a rodent belonging to the superfamily *Muroidea* comprising applying a peptide or composition as defined in relation to the first aspect of the invention to an area. In some embodiments the rodent belongs to the family *Muridae*, the genus *Mus* and/or is *Mus musculus.* In some embodiments, controlling a rodent comprises repelling a rodent as defined above.

The area is typically one in which it is suspected or known for rodents to be present, for example a room or part of a room in a building such as a home or business. The peptide or composition is applied or administered to the area as defined herein in relation to the first aspect of the invention. Any rodents coming into contact with the peptide or composition will then controlled and/or be repelled, as described herein.

Preferred features for the second aspect of the invention are as for the first aspect of the invention *mutatis mutandis*.

In some embodiments, the peptides for use in the invention are non-toxic and/or odourless for humans. Without wishing to be bound by theory, the peptides for use in the invention are thought to be undetectable by humans as humans lack the sensory olfactory receptors and/or systems necessary to detect these peptides.

In some embodiments, rodents exhibit an innate aversion to the peptides for use in the invention. Without wishing to be bound by theory, the peptides for use in the invention are thought to be salient for rodents as the fragments for use in the invention are secreted by predatory animals and evolutionary pressure has favoured rodents that could smell the presence of a predator. In some embodiments the peptides for use in the invention are detectable by rodents by smell. In other embodiments the peptides for use in the invention are detectable by rodents by taste. In other embodiments the peptides for use in the invention are detectable by rodents by taste and touch.

The present invention will now be further described by way of reference to the following Example which is present for the purposes of illustration only.

Example 1 – Active amino acid sequence analysis

The repellent action of excreted predator proteins rMUP-13 [rat] (SEQ ID NO: 1) and Cfeld4 [cat] (SEQ ID NO: 2) is due to the differences between these proteins and their homolog protein in mice, MUP13 [which actually has a non-repellent pheromonal, identification role between mice populations]. The cause of this differential response of mice to stimulation by these proteins must be due to differences in the amino acid sequence of the respective proteins, specifically there must be a fear-response inducing motif within the rat and cat proteins which is not present in the mouse protein. The criteria for this motif are as follows:

(1) the residues of the motif must be identical [or near-identical] in the rat and cat proteins

(2) non-identical residues in the motif between rat and cat proteins must conservatively substitute

(3) the residues of the motif also present in the mouse protein must be minimised

This can be visualised in the whole mouse [MUP-13] protein (SEQ ID NO: 3), showing the common and substituted residues in the rat and cat proteins:

m####llllclglt lvc*v*haeeasstGrnfNvqkingew*h*Ti*i*lasdkrekie|DngNFrLf*l*eQ|ihvlenslvLkfht|VR DE|ecse*l*sMvadktekAgeysvtydgfntfti*p*ktdydnF*/*mahlinEkdgetfglmglygrepdlssdikeRfaQlc ekhgi*/*reniidl|S*na*NrclqarE|

Key:

Single underline=identity between mouse and rat, or mouse and cat

Bold=differences between rat and cat

CAPITALISED=different between mouse and [either] rat or cat, AND are the same between rat and cat

italics=conservative substitutions between rat and cat

#=location of single-residue additions in either rat or cat

|=added to aid clarity, displaying potential location of active motifs

Protein sequences of rat (SEQ ID NO: 1) and cat (SEQ ID NO: 2) showing the regions identified as the likely active motifs according to the above analysis:

Rat

MKLLLLLLCLGLTLVCGHAEEASSTRGNLDVAKLNGDWFSIVVASNKREKIE|**ENGSMRVF MQH**|IDVLENSL#GFKFRI|**KENG**|ECRELYLVAYKTPEDGEYFVEYDGGNTFTILKTDYDR YVMFHLINFKNGETFQLMVLYGRTKDLSSDIKEKFAKLCEAHGITRDNIIDL|**TKTDRCLQA RG**

Cat

MK##LLLLCLGLILVCAHEEENVV#RSNIDISKISGEWYSILLASDVKEKIE|**ENGSMRVFVE H**|IKALDNSSLSFVFHT|**KENG**|KCTEIFLVADKT#KDGVYTVVYDGYNVFSIVETVYDEYILL HLLNFDKTRPFQLVEFYAREPDVSQKLKEKFVKYCQEHGIV##NILDL|**TEVDRCLQARG**| SEVAQDSSVE

Key:

Bold and underline = likely active motifs for inducing mouse fear-response

|=added to aid clarity, displaying potential location of active motifs

#=location of single-residue additions in either rat or cat

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CLAIMS

1. Use of a peptide comprising a sequence having at least 75% identity to SEQ ID NO: 1 and/or SEQ ID NO: 2 or to a fragment of at least four amino acid residues of either thereof as a rodent control agent wherein the rodent belongs to the superfamily *Muroidea*.
2. The use of claim 1 wherein the fragment is selected from the group consisting of:
    i. DRCLQARG,
    ii. TKTDRCLQARG,
    iii. TEVDRCLQARG,
    iv. KENG
    v. ENGSMRVFMQH,
    vi. ENGSMRVFVEH,
    vii. CRELYLVAYKEP,
    viii. CTEIFLVADKTK,
    ix. KENGECRELYLV,
    x. KENGKCTEIFLV,
    xi. SIVVAS,
    xii. SILLAS, and
    xiii. NCSMRVF.
3. The use of claim 1 wherein the peptide comprises a sequence having at least 95% identity to SEQ ID NO:1 and/or SEQ ID NO: 2.
4. The use of claim 1 wherein the peptide comprises SEQ ID NO:1 or SEQ ID NO: 2.
5. The use of any preceding claim wherein the peptide is a recombinant peptide.
6. The use of any preceding claim wherein the peptide is part of a composition.
7. The use of claim 6 wherein the composition is an aqueous solution.
8. The use of claim 6 or claim 7 wherein the composition is for application as a spray.
9. The use of any one of claims 6 to 8 wherein the composition is for application by an automated dispenser.
10. The use of any preceding claim wherein the rodent belongs to the family *Muridae.*
11. The use of any preceding claim wherein the rodent belongs to the genus *Mus.*
12. The use of any preceding claim wherein the rodent is *Mus musculus.*
13. The use of any preceding claim wherein the rodent control agent is a rodent repellent.
14. A method of controlling a rodent belonging to the superfamily *Muroidea* comprising applying a peptide or composition as defined in any preceding claim to an area.
15. The method of claim 14 wherein the rodent belongs to the family *Muridae.*

16. The method of claim 14 or claim 15 wherein the rodent belongs to the genus *Mus.*
17. The method of any of claims 14 to 16 wherein the rodent is *Mus musculus.*
18. The method of any of claims 14 to 17 wherein controlling a rodent comprises repelling a rodent.

Intellectual Property Office

Application No:	GB1422366.3	**Examiner:**	Dr Andrew Guy
Claims searched:	1 (in part) and 3-18 (in part)	**Date of search:**	9 September 2015

Patents Act 1977: Search Report under Section 17

Documents considered to be relevant:

Category	Relevant to claims	Identity of document and passage or figure of particular relevance
X	1, 3-18	Cell, vol. 141, May 2010, Papes et al, 'The vomeronasal organ mediates interspecies defensive behaviors...' pp. 692-703 See in particular: figures 4C and D; page 697 column 2 lines 8-10; page 698, 'Cat Mup functions as a kairomone' section; 'Behavioral assays' section, page 701
X	14-18	Proceedings of the National Academy of Sciences USA, vol. 107 issue 11, 2010, Ben-Shaul et al, 'In vivo vomeronasal stimulation reveals sensory encoding...' pp. 5172-5177 See in particular abstract and 'Responses to allospecific stimuli' section, page 5174
A	-	US2006/130391 A1 (LIVINGSTON) See whole document, paragraph 0023 in particular
A	-	US5252326 A (RES CORP TECHNOLOGIES) See abstract
A	-	Proceedings of the National Academy of Sciences USA, vol. 78, 1981, Unterman et al, 'Cloning and sequence of several alpha2u-globulin cDNAS' pp. 3478-3482 See figure 5
A	-	Journal of Chemical Ecology, vol. 28 issue 9, September 2002, Mucignat-Caretta, 'Modulation of exploratory behavior in female mice...' pp. 1853-1863 See abstract

Categories:

X	Document indicating lack of novelty or inventive step	A	Document indicating technological background and/or state of the art.
Y	Document indicating lack of inventive step if combined with one or more other documents of same category.	P	Document published on or after the declared priority date but before the filing date of this invention.
&	Member of the same patent family	E	Patent document published on or after, but with priority date earlier than, the filing date of this application.

Field of Search:

Search of GB, EP, WO & US patent documents classified in the following areas of the UKC^{X} :

Worldwide search of patent documents classified in the following areas of the IPC

The following online and other databases have been used in the preparation of this search report

WPI, EPODOC, CAPLUS, BIOSIS, MEDLINE, TXTE, XPESP, GENEP

International Classification:

Subclass	Subgroup	Valid From
A01N	0033/04	01/01/2006
A01N	0063/02	01/01/2006
A01P	0017/00	01/01/2006
C07K	0005/10	01/01/2006
C07K	0007/06	01/01/2006
C07K	0007/08	01/01/2006
C07K	0014/47	01/01/2006