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Aequorin and Obelin Mutants with Differing Wavelengths and Bioluminescence

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**ABSTRACT**

The invention relates to aequorin and obelin mutants whose emission is shifted with respect to wild type. The shift in emission is accomplished using a combination of mutations of amino acids within aequorin or obelin that affect bioluminescence; use of different types of chromophores, i.e. coelenterazines with variable emission characteristics; and modifications of the photoprotein with fluorophores that will allow for emission of light at longer wavelengths as a result of energy transfer. Additionally, an assay employing aequorin mutants to test for HIV-1 protease inhibitors is disclosed.

2 Claims, 18 Drawing Sheets
OTHER PUBLICATIONS


* cited by examiner
Fig. 1

Fig. 1 is a table showing the emission wavelength maximum (nm) of aequorin mutants with coelenterazine analogues.

<table>
<thead>
<tr>
<th>Coelenterazine Analogue</th>
<th>Wild Type Aequorin</th>
<th>Aequorin Mutant S (Aeq3)</th>
<th>Aequorin Mutant S Ser5Cys (Aeq5)</th>
<th>Aequorin Mutant S Tyr132Ile</th>
</tr>
</thead>
<tbody>
<tr>
<td>CTZ i</td>
<td>472</td>
<td>491</td>
<td>491</td>
<td>487</td>
</tr>
<tr>
<td>CTZ ip</td>
<td>472</td>
<td>470</td>
<td>454</td>
<td>453</td>
</tr>
<tr>
<td>CTZ h</td>
<td>472</td>
<td>476</td>
<td>471</td>
<td>471</td>
</tr>
<tr>
<td>CTZ hcp</td>
<td>472</td>
<td>476</td>
<td>448</td>
<td>465</td>
</tr>
<tr>
<td>CTZ cp</td>
<td>472</td>
<td>470</td>
<td>456</td>
<td>457</td>
</tr>
<tr>
<td>CTZ fcp</td>
<td>472</td>
<td>466</td>
<td>471</td>
<td>471</td>
</tr>
<tr>
<td>CTZ f</td>
<td>472</td>
<td>490</td>
<td>473</td>
<td>471</td>
</tr>
<tr>
<td>CTZ n</td>
<td>472</td>
<td>487</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CTZ native</td>
<td>472</td>
<td>474</td>
<td>471</td>
<td>471</td>
</tr>
</tbody>
</table>

* All values, except wild type aequorin, were calculated from the average of 3 trials (wild type with 2). All mutants were, except Aeq5 purified to >95% purity. CTZ analogues diluted to 100 micrograms/ml methanol.
Fig. 2
Emission Spectra of Aeq3 and Native Aeq With CTZ, hcp

- Aeq3 CTZ 1 (491 nm)
- Aeq3 CTZ hcp (448 nm)
- NTV Aeq CTZ (472 nm)

Emitted Wavelength (nm)

RLU (Counts)

Fig. 6
Native Aequorin with Coelenterazine (CTZ) Analogues

RLU (counts)

Emitted Wavelength (nm)
Fig. 7

Fig. 7 is a table showing the emission wavelength maximum (nm) of aequorin mutant Mutant S Y132I, Mutant S having a 3-fluoro-1-tyrosine aequorin or a 5-fluoro-1-tyrosine non-natural amino acid in position 132 in conjunction with coelenterazine analogues CTZ i, ip, n, h, hcp, cp, fcp, f and native CTZ.

<table>
<thead>
<tr>
<th>Coelenterazine Analogue</th>
<th>Wild Type Aequorin</th>
<th>Aequorin Mutant S Tyr132lle</th>
<th>Aequorin Mutant S Tyr132 3-fluoro-l-tyr</th>
<th>Aequorin Mutant S Tyr132 5-fluoro-l-trp</th>
</tr>
</thead>
<tbody>
<tr>
<td>CTZ i</td>
<td>472</td>
<td>491</td>
<td>511</td>
<td>495</td>
</tr>
<tr>
<td>CTZ ip</td>
<td>472</td>
<td>452</td>
<td>471</td>
<td></td>
</tr>
<tr>
<td>CTZ n</td>
<td>472</td>
<td>491</td>
<td>500</td>
<td></td>
</tr>
<tr>
<td>CTZ h</td>
<td>472</td>
<td>472</td>
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<td>471</td>
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<tr>
<td>CTZ hcp</td>
<td>472</td>
<td>452</td>
<td>471</td>
<td>468</td>
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<tr>
<td>CTZ cp</td>
<td>472</td>
<td>457</td>
<td>471</td>
<td>471</td>
</tr>
<tr>
<td>CTZ fcp</td>
<td>472</td>
<td>463</td>
<td>471</td>
<td></td>
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<tr>
<td>CTZ f</td>
<td>472</td>
<td>472</td>
<td>500</td>
<td>497</td>
</tr>
<tr>
<td>CTZ native</td>
<td>472</td>
<td>471</td>
<td>495</td>
<td>472</td>
</tr>
</tbody>
</table>
Fig. 11
SEQ ID NO: 1 cDNA encoding wild type apoaequorin

1 aatgcaattc atctttgcat caaagaatta catcaaatct
c tagttgatc aactaaattg
61 tctcgacaac aacaagcaaa cagt gacaagc aaacaatact
cagtcaagct tacatcagac
c 121 ttgacacaacc caagatggat tggacgacac aagcataatgt
tcaatccct tgaatcagaac
181 cacaatggaa aatactctct tgaacgagatg gctatacaagc
catctgatat tgcataacat
c 241 aaccttggag caacacctga gcaagcctaa cgacacacaag
atgctgtgata agccctctcc
c 301 ggaagggctg gtaaatgaata tggagttggaa actgatttgcc
c tgcatatat tgaaggtagg
361 aaaaaattgg ctactgtgta atggagaaaa tacgccaaa
acgaaccacac gctcatccgt
c 421 atatggggtg atggttttgt tgtatctctg gcaaaagatc
aaaatggagc cattacaactg
481 gatgaatggaa aagcatacac caaaagctgt ggtatcatcc
aattcatcaga agattgccag
541 gaaacattca gagtctgcga tattgatgaa agtggtcaca
tcgatgttga tgagatgca
601 agacaacatt taggatttgg tgtacaccatg gatcctgtct
gcgaagactc tctagtttga
661 gctgctcccct aagaagcctct acggttttgta tcgaccccttg
gaagatgtatg tgtttttgaa
721 taaaaaaaaa atgaatttca tcaatatttt attttttttttt
aadgatcttca ttcgatggtt
gtatgagttt gttaattagga acagattaaa tgaagttttt
tagtttttt ttaatatcaac
841 gaacctaaa atcgaaaaaag t

Fig. 12
SEQ ID NO: 2 amino acid sequence for wild type apoaequorin
VKLTSDFDNP RWIGRHKHMF NFLDYNHNGK ISLDAMYKA SDIVINNLGA
TPEQAKRKHD AVEAFFGAGG MKYGVTEDWP AYIEGWJKLA TDELEKYAKN
EPTLIRIWGD ALFDIVDQ NGAITLDEWK AYTGAAGGIIQ SSEDCEETFR
VCDIDESQQL DVDEMTRQHL GFWYTMNPAC EKLYGGAVP
Fig. 13
SEQ ID NO: 3 cDNA encoding Mutant S apoaequorin

1 aatgcaattc atctttgcat caaagaatta catcaaatct
ctaggtaac aactaaattg
61 ttctgacaac aacaagccaa catgacaagc aaacaatact
cagtcaagct tacagtagac
121 ttgaccaacc caagatggtg tggacgacac aagcatatgt
tcaatttcct tgaattcaac
181 cacaatggaa aaatctctct tgacgagatg gtctacaagg
catctgatat tgcatacaat
241 aacccgagag caacacctga gcaagccaa caacaccaag
atgcttgtaga agcccttttc
301 ggaggagctg gaatggaaata tgggttgaa atcgattggc
cctcaatatg tgaagagatgg
361 aaatgagttg cctagtgaag aatggagaaa tacgccaaaa
acgaaaccaac gtcctcctgt
421 atgtggttgt atgtcttttt tggatcttgt gcaaagatcg
aaatggagac cattacaactg
481 gatgagtggg aagcatacaac caaagctttg ggtatttaccc
aatcataca gaagacgcag
541 gaaacattca gactgagctga atttgatgaa atgggcaaac
tcgatcttga tgagctctac
601 agacaacatt taggattttgt tgaacattatg gatcctgtca
gcgaagaagct ctacgggttga
661 gctgtccccct agaagctct acgggttgta tgccacccctgg
gaagatgtag tgaattttgaa
721 taaaacacttg atgaaattca tcaaaatattt ccacattttt
gaacgatttc aatcggttggt
781 tggatttttt gtaattagga acagattaa tcgaatgatt
tagtttttttt ttaatcaaca
841 gaaaccttacaa atcgaaaaag t

Fig. 14
SEQ ID NO: 4 amino acid sequence for "Mutant S" apoaequorin
VKLTSDFDPN RWIGRHKHMF NFLDVNHNCK ISLDEMYKA SDIVINNLGA
TPEQAKRHKD AVEAFFGGAG MKYGVTDSWP AYIEGWKCLA TDELEKAYKN
EPTLIRWGD ALFDIVKDQ NGAITLDE WK AYTKAAGIIQ SSDSEETFR
VSDIDESGLV DVDEMTRQHL GFYTMDSAP EKLYGGAVP
Plasmid construct for the expression of the aequorin fusion protein and schematic representation of the fusion protein showing the HIV-1 protease cleavage site. B represents biotin and NA represents Neutravidin immobilized on the wells.
Fig. 17. Non-natural amino acids

<table>
<thead>
<tr>
<th>Non-natural Amino Acid Analogue</th>
<th>Representative Example</th>
<th>Effect</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fluoro-analogue</td>
<td><img src="image" alt="3-fluoro-L-tyrosine" /></td>
<td>Altered pK_a and H-bonding strength</td>
</tr>
<tr>
<td>Amine-analogue</td>
<td><img src="image" alt="p-amino-L-phenylalanine" /></td>
<td>Altered electrostatic charge and H-bonding strength</td>
</tr>
<tr>
<td>Alkyl-analogue</td>
<td><img src="image" alt="p-methoxy-L-phenylalanine" /></td>
<td>Altered H-bonding capability, increased bulkiness</td>
</tr>
<tr>
<td>Nitro-analogue</td>
<td><img src="image" alt="2-nitro-L-tyrosine" /></td>
<td>Altered (\pi)-character, altered pK_a, altered H-bonding strength, and steric effects</td>
</tr>
<tr>
<td>Hydroxyl-analogue</td>
<td><img src="image" alt="2-amino-5-hydroxy-4-methyl pentanoic acid" /></td>
<td>Altered pK_a, loss of (\pi-\pi) interactions</td>
</tr>
</tbody>
</table>
Fig. 18  SEQ ID NO: 5, Obelin cDNA sequence

1 acgatcgaac caaacaactc agctcacagc tactgaacaa
cctttgttgt gtcaaatcaa
61 aatgtcttca aaatacgcag ttaaactcaa gactgaacctt
gataatccac gatggatcaa
121 aagacacaag cacatgttttg atttcctcga catcaatgga
aatggaaaaa tcaccctcga
181 tgaatatttg tccagggcat ctgatgacat atgtgccaag
cctgaagccca caccagaaca
241 aacaaaaacgc catcaagttt gtgttgaagc tttcttttga
ggtgtggaa tggatatatg
301 taaaagaatt gcctccccac aatccctcga tggatggaaa
ciaattgcgca ctccagaact
361 caagaaatgg gcaagaaacg aacctactct cattcgtgaa
tggggagatg ctgcttttga
421 tatattcgcac aaagatggaa gttgtacaat cactttggac
gaatggaaag cttatgaaaa
481 aatctctcgt atctctccat cacaagaaga ttgtgaaacg
acatccgac attgcgattt
541 ggacacacagt ggtgaccttg atgttgacga gatgacaaga
cacactcttg gatctctggta
601 caaccttcac ccacaagctg atgtctctca tggcaacgga
gttccctaaag ctttttttcc
661 aa
Fig. 19. SEQ ID NO: 6, Native Obelin Amino Acid Sequence

MSSKYAVKLK TDFDNPRWI K RHKHMFDFLD INGNGKITLD EIVSKASDDI
CAKLETPEQ TKRHQVCEA FFRGCMEYG KEIAFPQFLD GWKQLATSEL
KKWARNEPTL IREWGDAVFD IFDKDGSGTI TLDEWKAYGK ISGISPSQED
CEATFRHCDL DNSGDLDVDE MTRQHLGFYW TLDEPAGLY GNGVP
Fig. 20 Obelin mutants with Coelenerazine analogues.

<table>
<thead>
<tr>
<th>Obelin Mutant</th>
<th>$i$</th>
<th>$ip$</th>
<th>$h$</th>
<th>$hcp$</th>
<th>$cp$</th>
<th>$fcp$</th>
<th>$f$</th>
<th>$ctz$</th>
</tr>
</thead>
<tbody>
<tr>
<td>C75S-C51S</td>
<td>521</td>
<td>478</td>
<td>503</td>
<td>478</td>
<td>472</td>
<td>497</td>
<td>503</td>
<td>491</td>
</tr>
<tr>
<td>C75S-C67S</td>
<td>505</td>
<td>471</td>
<td>500</td>
<td>471</td>
<td>471</td>
<td>487</td>
<td>504</td>
<td>491</td>
</tr>
<tr>
<td>C158S</td>
<td>506</td>
<td>472</td>
<td>497</td>
<td>478</td>
<td>472</td>
<td>475</td>
<td>497</td>
<td>491</td>
</tr>
<tr>
<td>C151S</td>
<td>497</td>
<td>471</td>
<td>490</td>
<td>471</td>
<td>471</td>
<td>474</td>
<td>493</td>
<td>491</td>
</tr>
</tbody>
</table>
AEOQUORIN AND OBELIN MUTANTS WITH DIFFERING WAVELENGTHS AND BIOLUMINESCENCE

BACKGROUND OF THE INVENTION

1. Field of the Invention

This invention relates to the fields of bioluminescent labels for microanalysis and drug discovery.

2. Background

The increased demand for simultaneously detecting more than one analyte in physiological fluids has generated a greater interest in array detection methodologies. Accurate determination of several biomolecules in a sample allows a more accurate diagnosis. In these assays, the label that gives a distinguishable signal is one of the most important parts of the assay. For an array detection to be successful, each analyte must generate a distinguishable signal from the signals generated by the other analytes. Fluorescent labels have been previously used extensively in array detection. The inherent disadvantage of fluorescent detection for biological samples is the background fluorescence that is inherent with the nature of this type of labels.

Bioluminescent labels offer several advantages over fluorescence detection. Bioluminescent labels, being rare in nature, have much smaller interference from biological and other matrices. They are not prone to photo degradation. The phenomenon of bioluminescence, unlike fluorescence, is relatively rare in biological systems, thus, the sample does not produce any significant background signal. However, the bioluminescent labels have similar emission characteristics i.e., they emit light at roughly the same wavelength. Therefore, wild-type bioluminescent labels are not useful for array detection. New proteins that are capable of producing light at different wavelengths would be very beneficial as labels in array detection.

Aequorin is a calcium sensitive photo protein isolated from the jellyfish, Aequorea victoria. It is widely used as a label in immunnoassays and to monitor intracellular levels of free calcium. The X-ray crystal structure of aequorin reveals three EF-hand Ca$^{2+}$-binding sites, a hydrophilic pocket in which the chromophore, coelenterazine, resides. In the presence of molecular oxygen, coelenterazine and apoaequorin form a stable aequorin complex. The addition of calcium causes a conformational change in the aequorin. This conformational change results in the oxidation of the non-covalently bound chromoprotein unit, the coelenterazine to an excited coelenteramide. As the excited coelenteramide relaxes, light is emitted at 469 nm.

Aequorea victoria uses the blue light emitted from aequorin as an excitation light source to stimulate the emission of green light from Aequorea victoria's more famous and scientifically ubiquitous protein, Green Fluorescent Protein (GFP). GFP has long been used as a label in various scientific fields. Extensive research concerning GFP's structural and photochemical properties has resulted in the production of many spectrally shifted GFP mutants. The spectral shifts in GFP have proved extremely useful, allowing for single well multiple analyte analysis, multicolor reporting of cellular processes, and FRET measurements to study protein-protein interactions Backer et al., J Biomed Opt. 2003 Jul; 8(3): 368-75.

An advantage of using aequorin and other bioluminescent proteins instead of GFP is that since the bioluminescence emitted by these proteins is measured over virtually zero background, the proteins can be detected at extremely low levels (levels less than 10^{-18} moles). Additionally, this photoprotein retains its bioluminescence in a variety of buffers with a number of different additives. It can be stored in solution at 4°C for over a month while still retaining 85% of its original activity. Lyophilization of the protein allows for its storage up to one year. Accordingly, the creation of aequorin variants with significantly different emission maximum would result in a biochemical label that is superior to GFP.


Of particular relevance to the subject matter are U.S. Pat. Nos. 5,798,441; 5,766,941; 5,744,579; 5,541,309; 5,491,084; 5,422,266; and 5,360,728. Deo et al., Anal Biochem. 2000 May 15; 281(1):87-94; Malikova et al., FEBS Lett. 2003 Nov 6; 554(1-2):184-8; Vysotski et al., Biochemistry.
3


The use of aequorin as a label for multiple analyte single well analysis and multicolor reporting of cellular processes has been limited because of recombinant aequorin's single emission maximum wavelength of 469 nm. Wild type aequorin emits at a constant wavelength regardless which coelenterazine variant is used. By using different chromophore analogues, incorporation of non-natural amino acids and site-directed mutagenesis, the inventors have discovered a number of mutants that can be used to make superior biochemical labels because they have a bioluminescent emission shifted with respect to wild type aequorin.

Obelin is another bioluminescent protein from the marine hydroid Obelia longissima consisting of a single 22.2 kDa polypeptide chain. The primary sequences of obelin, aequorin and other photoproteins are highly homologous so presumably generate bioluminescence by a common chemical mechanism. There is also sequence homology in regions corresponding to the EF-hand structures of calcium-binding proteins such as calmodulin and troponin C, suggesting that some resemblance in three dimensional structures might also ensue. Obelin, along with a number of other photoproteins, is available in an efficient expression system.

All references cited within this document are explicitly incorporated by reference for all purposes.

SUMMARY OF THE INVENTION

One aspect of the invention relates to an isolated nucleic acid capable of hybridizing to SEQ ID NO: 3 under stringent conditions and encoding a protein which is capable of binding coelenterazine and molecular oxygen and emitting light, the protein having an isoleucine residue in a first position corresponding to position 132 of SEQ ID NO: 4.

Another aspect of the invention relates to an isolated nucleic acid capable of hybridizing to SEQ ID NO: 3 under stringent conditions and encoding a protein which is capable of binding coelenterazine and molecular oxygen and emitting light and having a non-natural amino acid incorporated into a position corresponding to 132 of SEQ ID NO: 4.

In one embodiment of this aspect of the invention the non natural amino acid is fluorotyrosine or fluorotryptophan. In a further embodiment the nucleic acid of claim 36 wherein the fluorotyrosine is 3-fluoro-1-tyrosine. In yet another embodiment, the non natural amino is 5-fluoro-1-tryptophan.

Another aspect of the invention relates to an isolated nucleic acid capable of hybridizing to SEQ ID NO: 3 under stringent conditions and encoding a protein which is capable of binding coelenterazine and molecular oxygen and emitting light, the protein having a cysteine residue in a first position corresponding to position 69 of SEQ ID NO: 4.

One embodiment of this aspect of the invention relates to an aequorin mutant protein conjugated to a fluorophore. In another embodiment, the fluorophore is IANBD ester.

Another aspect of the invention relates to an isolated nucleic acid capable of hybridizing to SEQ ID NO: 3 under stringent conditions and encoding a protein which is capable of binding coelenterazine and molecular oxygen and emitting light, the protein having a cysteine residue in a first position corresponding to position 70 of SEQ ID NO: 4.
selected from the group consisting of coelenterazine (CTZ) i, ip, h, hcp, cp, fcp, f, n, and native coelenterazine.

Another aspect of the invention relates to a method of identifying inhibitors of bond-breaking enzymes comprising immobilizing a fusion protein encoded by a fusion protein nucleic acid comprising any one of the nucleic acids of claims 1 to 13; operably linked to a second nucleic acid encoding a bond-breaking enzyme recognition site; in a first locus and a second locus; contacting said fusion protein with a candidate compound in the presence of the bond-breaking enzyme in said first locus; contacting said fusion protein with the bond-breaking enzyme in said second locus; and determining whether there is an increase in the intensity of light emission at said first locus relative to light emission in said second locus.

Another aspect of the invention relates to a method of identifying inhibitors of HIV-1 protease comprising: immobilizing a fusion protein encoded by a fusion protein nucleic acid comprising a nucleic acid capable of hybridizing to SEQ ID NO: 3 under stringent conditions and encoding a protein which is capable of binding coelenterazine and molecular oxygen and emitting light; operably linked to a second nucleic acid encoding an HIV-1 enzyme recognition site; in a first locus and a second locus; contacting said fusion protein with a candidate compound in the presence of the bond-breaking enzyme in said first locus; contacting said fusion protein with the bond-breaking enzyme in said second locus; and determining whether there is an increase in the intensity of light emission at said first locus relative to light emission in said second locus.

In one embodiment of this aspect of the invention, the recognition site is Ser-Glu-Asn-Tyr-Pro-Ile-Val (SEQ ID NO:5). In another embodiment, the fusion protein is conjugated to a fluorophore. In yet another embodiment, the fusion protein comprises a non-natural amino acid. In a further embodiment, the non-natural amino acid is fluoro-tyrosine and is at a position corresponding to 132 of SEQ ID NO: 4.

Another aspect of the invention relates to obelin mutants with altered emission patterns.

In one embodiment of this aspect of the invention, an isolated nucleic acid capable of hybridizing to SEQ ID NO: 5 under stringent conditions and encoding a protein which is capable of binding coelenterazine and molecular oxygen and emitting light, said protein having an serine residue in a first position corresponding to position 51, and a serine residue in a second position corresponding to position 75 of SEQ ID NO: 6.

Another embodiment of this aspect of the invention relates to an isolated nucleic acid capable of hybridizing to SEQ ID NO: 5 under stringent conditions and encoding a protein which is capable of binding coelenterazine and molecular oxygen and emitting light, said protein having an serine residue in a first position corresponding to position 67, and a serine residue in a second position corresponding to position 75 of SEQ ID NO: 6.

Another embodiment of this aspect of the invention relates to an isolated nucleic acid capable of hybridizing to SEQ ID NO: 5 under stringent conditions and encoding a protein which is capable of binding coelenterazine and molecular oxygen and emitting light, said protein having an serine residue in a first position corresponding to position 158 of SEQ ID NO: 6.

Another embodiment of this aspect of the invention relates to an isolated nucleic acid capable of hybridizing to SEQ ID NO: 5 under stringent conditions and encoding a protein which is capable of binding coelenterazine and molecular oxygen and emitting light, said protein having a serine residue in a first position corresponding to position 151 of SEQ ID NO: 6.

Another aspect of the invention relates to kit comprising the obelin mutants and a coelenterazine selected from the group consisting of CTZ i, ip, h, hcp, cp, fcp, f, n, and native coelenterazine.

Another aspect of the invention relates to method of identifying inhibitors of bond-breaking enzymes comprising immobilizing a fusion protein encoded by a fusion protein nucleic acid comprising an obelin encoding nucleic acids operably linked to a second nucleic acid encoding a bond-breaking enzyme recognition site; in a first locus and a second locus; contacting said fusion protein with a candidate compound in the presence of the bond-breaking enzyme in said first locus; contacting said fusion protein with the bond-breaking enzyme in said second locus; and determining whether there is an increase in the intensity of light emission at said first locus relative to light emission in said second locus.

In one embodiment of this aspect of the invention, the inhibitors are inhibitors of HIV-1 protease.

Additional advantages of the present invention will become readily apparent to those skilled in this art from the following detailed description, wherein only the preferred embodiment of the invention is shown and described, simply by way of illustration of the best mode contemplated of carrying out the invention. As will be realized, the invention is capable of other and different embodiments, and its several details are capable of modifications in various obvious respects, all without departing from the invention. The present invention may be practiced without some or all of these specific details. In other instances, well known process operations have not been described in detail, in order not to unnecessarily obscure the present invention. Accordingly, the drawings and description are to be regarded as illustrative in nature, and not as restrictive.

**BRIEF DESCRIPTION OF THE DRAWINGS**

FIG. 1. is a table showing the emission wavelength maximum (nm) of aequorin mutants with coelenterazine analogues.

FIG. 2. is a graph showing the emission spectrum of native and Aeq3 (aequorin Mutant S) with CTZ i and hcp.

FIG. 3. is a graph showing the emission spectrum of Aeq3 with coelenterazine analogues CTZ i, ip, h, hcp, cp, fcp, f and native CTZ.

FIG. 4. is a graph showing the emission spectrum of Aeq5 (aequorin Mutant S with a Cys residue at position 5) with coelenterazine analogues CTZ i, cp, fcp, f, h, hcp, ip, i and native CTZ.

FIG. 5. is a graph showing the emission spectrum of aequorin Mutant S Y132I with coelenterazine analogues CTZ i, ip, h, hcp, cp, fcp, f and native CTZ.

FIG. 6. is a graph showing the emission spectrum of native aequorin with coelenterazine analogues CTZ i, ip, h, hcp, cp, fcp, f and native CTZ.

FIG. 7. is a table showing the emission wavelength maximum (nm) of aequorin mutant S Y132I, Mutant S having a 3-fluoro-1-tyrosine aequorin or a 5-fluoro-1-tyrosine non-natural amino acid in position 132 in conjunction with coelenterazine analogues CTZ i, ip, n, h, hcp, cp, fcp, f and native CTZ.
FIG. 8. is a graph showing the emission spectrum of aequorin Mutant S with a 3-fluoro-1-tyrosine in position 132 with coelenterazine analogues CTZ f, n, fcp, h, cp, ip, ihp and native CTZ.

FIG. 9. is a graph showing the emission spectrum of aequorin Mutant S with a 5-fluoro-1-tyrosine in position 132 with coelenterazine analogues CTZ i, f, n, fcp, h, cp, ip, ihp and native CTZ.

FIG. 10. is a graph showing the emission spectrum of aequorin Mutant S Ala69Cys, aequorin Mutant S Gly70Cys, aequorin Mutant S Ala74Cys, and aequorin Mutant S Glu76Cys conjugated to the IANBD fluorophore.

FIG. 11. shows the cDNA sequence of wild type aequorin.

FIG. 12. shows the amino acid sequence of wild type aequorin.

FIG. 13. shows the cDNA sequence of aequorin Mutant S.

FIG. 14. shows the amino acid sequence of aequorin Mutant S.

FIG. 15. is a cartoon illustrating the use of an aequorin fusion protein having an HIV-1 protease recognition site in an assay to identify inhibitors of HIV-1 protease.

FIG. 16. is an illustration of the structures of various coelenterazine analogues.

FIG. 17. shows a list of non-natural amino acids contemplated for use in the invention.

FIG. 18. shows the cDNA sequence of wild type obelin.

FIG. 19. shows the amino acid sequence of wild type obelin.

FIG. 20. Obelin mutants with Coelenterazine analogues

DETAILED DESCRIPTION OF THE INVENTION

There is a clear need for assays that can be adapted to the small volumes imposed by the new emerging microanalytical instrumentation. Bioluminescence provides a powerful detection system that can be employed in the development of assays with high sensitivity and very low detection limits. As the volumes become smaller, in order to be able to detect the target biomolecule, labels must become more sensitive and varied.

Accordingly, the subject invention provides aequorin and obelin mutants suitable for multianalyte microanalysis capable of emission of light at different wavelengths with respect to wild type.

Before describing the invention in greater detail the following definitions are set forth to illustrate and define the meaning and scope of the terms used to describe the invention herein:

"Emission" as used herein refers to photons emitted in a chemical reaction resulting from discrete energy states of electrons, as they pass from one excited level to another. Each photon emitted is associated with a fixed amount of energy expressed as a wavelength of light.

"Shifted emission" with respect to wild type as used herein refers to the fact that the aequorin mutants disclosed herein are capable of emitting light at a wavelength different, i.e., shifted from that of the wild type aequorin or obelin. The aequorin and obelin photoproteins consists of an apoprotein, a chromophoric unit (coelenterazine), and molecular oxygen, which when combined form a stable complex. Binding to Ca²⁺ ions causes the photoprotein to undergo a conformational change, which results in the catalytic oxidation of the noncovalently bound coelenterazine. The coelenterazine is converted to coelenteramide with the release of CO₂ and a flash of light (λmax=about 469 to about 472 nm) lasting less than 10 s. The different structures of coelenterazine chromophores alone should result in spectral shifts since the energy difference between the excited coelenteramide and relaxed coelenteramide should change according to the structure of the original coelenterazine.

Coelenterazine variants (e.g., i, f, n, h, ihp, cp, cp, fcp, f, native) have either different ring structure and/or functional groups attached. However, wild type aequorin emits at a constant wavelength regardless which coelenterazine variant is used (λmax=about 469 to about 472 nm). The mutants disclosed herein are capable of emitting light at a predictably shifted wavelength when used with various coelenterazine variants. For example, whereas FIG. 1 shows a wild type aequorin emissions peak of 472 nm regardless of which coelenterazine variant (i, ip, h, cp, cp, fcp, f, n, or native) is used. Alternatively, aequorin Mutant S Y132I emits light at wavelengths ranging from 456 nm to 487 nm depending on the coelenterazine variant used.

"Chromophore" as used herein refers to group or substructure on a molecule that is responsible for the absorption of light. In the context of aequorin, the chromophore is coelenterazine (abbreviated CTZ) or an analog thereof. In addition to native coelenterazine there are several derivatives of coelenterazine designated i, ip, h, ihp, cp, fcp, f, or n. For chemical structures see FIG. 16.

The chromophore is stabilized by H-bonding to the three triads consisting of tyrosine, tryptophan, and histidine residues within the aequorin protein. Alteration of the structure of these H-bonds may affect the stability of the chromophore, inducing a change in the emission characteristics.

The rationally designed aequorin and obelin mutants disclosed herein also shift the emission maximum wavelength by changing the electronic and H-bonding network within the chromophore binding pocket of aequorin. Combining aequorin and obelin mutants disclosed herein with various coelenterazine analogues allows for spectral shifting.

As used herein, "wild type" refers to the nucleic acid or amino acid sequence of a particular protein as it most commonly occurs in nature as a normal functional protein. Nonetheless, it is elementary to one of skill in the art that such functional proteins have allelic variations. An allele is one of several alternate forms of a gene that can have the same locus on homologous chromosomes and are responsible for alternative traits. Some alleles are dominant over others. Such normal variation is encompassed within this term. The wild type aequorin nucleic acid sequence is provided in SEQ ID NO: 1 and the wild type amino acid sequence is provided in SEQ ID NO: 2. The wild type obelin nucleic acid sequence is provided in SEQ ID NO: 5 and the wild type amino acid sequence is provided in SEQ ID NO: 6.

Aequorin "Mutant S" or "Aeq³" as used herein refers to an aequorin mutant where site-specific mutagenesis was used to replace the three cysteine residues with serine (at positions 145, 152, and 180). The starting point of the inventive aequorin mutants is aequorin Mutant S. Kurose et al., (Proc. Natl. Acad. Sci. USA, Vol. 86, pp. 80-84, Jan 1989), showed that the time required for the regeneration of the triplicated substituted aequorin was substantially increased compared to the time required for the regeneration of the wild-type aequorin. They also showed that cysteine plays an important role in the regeneration of aequorin but not in its catalytic activity. The aequorin Mutant S nucleic acid sequence is provided in SEQ ID NO: 3 and the aequorin Mutant S amino acid sequence is provided in SEQ ID NO: 4.

Of course, as will be obvious to one skilled in the art, various degenerate codons can be substituted into SEQ ID
NO: 3 that will result in the identical amino acid sequence of SEQ ID NO: 4. All such substitutions of degenerate codons are equivalent because they result in identical amino acid sequences, and are, therefore, encompassed within the scope of the appended claims. Additionally, the sequence for apoaerugin is subject to significant microheterogeneity where variation in the amino acid and/or nucleotide sequence occurs at specific points in the sequence. Functional apoaerugin proteins may have variations relative to SEQ ID NO: 3 at one or more of the microheterogeneous residues. The positions of microheterogeneity, and the specific variations that occur at each, are shown in Table 1.

<table>
<thead>
<tr>
<th>Residue</th>
<th>Amino Acid Variations</th>
</tr>
</thead>
<tbody>
<tr>
<td>4</td>
<td>Giu, Lys</td>
</tr>
<tr>
<td>12</td>
<td>Ser, Pro</td>
</tr>
<tr>
<td>15</td>
<td>Asp, Asn</td>
</tr>
<tr>
<td>18</td>
<td>Arg, Lys</td>
</tr>
<tr>
<td>33</td>
<td>Lys, Arg</td>
</tr>
<tr>
<td>70</td>
<td>Gia, Gyi</td>
</tr>
<tr>
<td>71</td>
<td>Ais, Asp</td>
</tr>
<tr>
<td>85</td>
<td>Asp, Gia, Gia</td>
</tr>
<tr>
<td>86</td>
<td>Gia, Ala</td>
</tr>
<tr>
<td>95</td>
<td>Arg, Lys</td>
</tr>
<tr>
<td>98</td>
<td>Ser, Thr</td>
</tr>
<tr>
<td>99</td>
<td>Gia, Asp, Cys</td>
</tr>
<tr>
<td>102</td>
<td>Gia, Gia</td>
</tr>
<tr>
<td>103</td>
<td>Lys, Arg</td>
</tr>
<tr>
<td>105</td>
<td>Ais, Ser</td>
</tr>
<tr>
<td>108</td>
<td>Gia, Gia</td>
</tr>
<tr>
<td>109</td>
<td>Pro, Ile</td>
</tr>
<tr>
<td>113</td>
<td>Ile, Leu</td>
</tr>
<tr>
<td>120</td>
<td>Val, Ile</td>
</tr>
<tr>
<td>132</td>
<td>Ser, Thr</td>
</tr>
<tr>
<td>142</td>
<td>Ais, Ser</td>
</tr>
<tr>
<td>148</td>
<td>Ser, Thr</td>
</tr>
<tr>
<td>151</td>
<td>Arg, Lys</td>
</tr>
<tr>
<td>164</td>
<td>Ser, Asp</td>
</tr>
</tbody>
</table>

“Fluorophore” as used herein refers to a molecule capable of exhibiting fluorescence. The inventors have discovered that aerugin and obelin could be modified through the attachment of selected fluorophores capable of accepting energy transferred from aerugin. Preferably, fluorophores are chosen so the spectral bands of the overlap with the one corresponding to the bioluminescence emission of the Mutant S and wild type aerugin. Following energy transfer, the emission of light is shifted toward the maximum wavelength (λmax) of emission of the attached fluorophore. Thus, by modifying the aerugins with different fluorophores, bioluminescent labels will be produced with different emission maxima, allowing for the simultaneous detection of multiple analytes.

The conjugation of the fluorophore can be directed towards the lysine residues on aerugin or obelin by employing an N-hydroxysuccinimide ester derivative of the fluorophore. Alternatively, the fluorophore can be conjugated to unique cysteine residues introduced at sites on aerugin close to the coelenterazine binding site when a maleimide or an iodoacetamide derivative of the fluorophore is employed. Preferably, fluorescein, nitrobenz-2-oxa-1,3-diazole (NBD) or (3-(4-carboxybenzoyl)quinoline-2-carboxaldehyde (CBQCA), are employed as fluorophores. More preferably, an iodoacetamide-derivative of the fluorophore, N-(2-iodoacetamidoethyl)-N-methylamino-7-nitrobenz-2-oxa-1,3-diazole (IANBD ester) is attached to a unique cysteine rationally selected and inserted into aerugin Mutant S. Most preferably, an iodosuccinimide-derivative of the fluorophore, N-(2-iodoacetamidoethyl)-N-methylamino-7-nitrobenz-2-oxa-1,3-diazole (IANBD ester) is attached to a unique cysteine either at position 69, 70, 74 or 76 of aerugin Mutant S.

As used herein, “non-natural amino acid” refers to any amino acid that is chemically modified, preferably by the addition of a fluorine moiety, yet are similarly recognized by translation-competent enzymes and incorporated, site-specifically or otherwise, into proteins with marked effects on spectroscopic properties. Site-specific incorporation allows for the insertion of a non-natural amino acid at a specific place in the amino acid sequence. For example, this would allow for the placement of a non-natural tyrosine analog to be placed only at one position rather than replacing all tyrosine residues in a protein with the non-natural tyrosine analog. See Wang et al., Proc Natl. Acad. Sci. USA, 2003, 100, 56–61, Wang et al., J. Org. Chem., 2003, 68, 174–176.

Zhang et al., Biochem., 2003, 42, 6735–6746. Fluorinated amino acids such as 3- and 5-fluorotyrosine and 3- and 5-fluorotryptophan are among the non-natural amino acids that can be incorporated into proteins by microorganisms at reasonable levels.

The incorporation of fluorinated aromatic amino acids such as 3-fluoro-1-tyrosine, 5-fluoro-1-typtophan, and 6-fluoro-1-typtophan into aerugin alters the conformation of the protein, the H-bond network, and/or catalytic activity. Incorporation of 5-fluoro-1-typtophan resulted in an inactive aerugin, whereas both 5-fluoro-1-typtophan and 3-fluoro-1-tyrosine displayed varied activity and shifted wavelengths. Fluorine atoms in tyrosine can also act as H-bond acceptors from —NH and —OH donors. This ability of fluorine facilitates fluorotyrosine residues in forming novel H-bonds, further stabilizing the structure. In aerugin, the stability of the chromophore residing within the hydrophobic pocket defines the spectral properties of aerugin and obelin, as well as their overall thermal stability. In aerugin, coelenterazine is stabilized by the H-bonds formed between the residues Tyr, His and Trp. The strength of these H-bonds defines the stability of coelenterazine. Therefore, incorporation of fluorinated residues such as tyrosine, tryptophan, and histidine should affect the spectral properties of aerugin.

Additional non-natural amino acids contemplated for use in the present invention are p-amino-L-phenylalanine, p-methoxy-L-phenylalanine, 2-nitro-L-tyrosine, 2-amino-5-hydroxy-4-methyl pentanoic acid. See FIG. 17.

Preferably, the non-natural amino acid to be incorporated into aerugin Mutant S is fluorotyrosine, more preferably 3-fluoro-L-tyrosine. Most preferably, fluorotyrosine is incorporated into position 132 of aerugin Mutant S.

In addition to fluorinated tyrosine, other moieties may change the acidity an amino acid for example of the phenolic proton in tyrosine. For example, nitro group at position 3, is a more effective electron acceptor, hence the pKa of phenolic proton would even be lower. A nitro group is also sterically more bulky therefore the spatial arrangement of the residues within the active site can change. An —OCH3 group at position 2 in tyrosine, on the other hand, has an opposite effect due to the electron donating property of the group. Incorporation of non-natural amino acids into proteins can help expand the chemical and biological diversity of proteins.

In order to detect the inventive aerugin mutants, the use of an instrument capable of detecting flash-type bioluminescence over a wide range of wavelengths is envisaged. For
example, a fiber optic sensor collects the bioluminescence signal emitted by the aequorin and transmits it to a grating that directs the beam of light to an optical array detector. In one embodiment, the system to acquire the spectra from the flash kinetics of aequorin and obelin luminescence consists of a microtiter plate reader. The optical path of the instrument is replaced with a high collecting efficiency fiber optic bundle. Fiber optic bundle carries the emitted light into an Oriel Instruments Fixed Imaging Compact Spectrograph, the dispersed light is then fed into an ANDOR cooled CCD detector. See for example the SpectroSystem By Sciencesware, Inc (East Falmouth, Mass.).

The term “operably linked” refers to the linkage of a DNA segment to another DNA segment in such a way as to allow the segments to function in their intended manners. A DNA sequence encoding a gene product is operably linked to another DNA sequence encoding a different gene product when they are ligated in a manner which allows transcription and subsequent translation of both DNA sequences to yield a functional protein. Preferably, such coding DNA sequences are linked “in frame.” Additionally, a short stretch of coding DNA may be inserted between the two DNA sequences to encode a small number of spacer amino acids that facilitate proper functioning of the fusion protein by minimizing steric interference. Linkage of coding DNA sequences other coding DNA sequences or to regulatory sequences is typically accomplished by ligation at suitable restriction sites or via adapters or linkers inserted in the sequence using restriction endonucleases known to one of skill in the art.

Amino acid residue positions “corresponding” to one another as used herein, refers to the fact that there are conserved amino acid residues among orthologous proteins or among structurally similar aequorins that are encoded by substantially identical nucleic acids. Corresponding amino acids may be the same amino acids or they may be differing amino acids sharing one or more characteristics with respect to charge, polarity, acidity, hydrophilicity, hydrophobicity, or size. Corresponding amino acid positions may easily be determined in conjunction with standard protein alignment or 3-D modeling software common in the art. As such, one of skill in the art would readily be able to determine the location of other corresponding amino acids residues between properly aligned amino acid sequences encoded by nucleic acids that are substantially identical to one another.

The invention includes substantially identical polynucleotides that hybridize under stringent conditions (as defined herein) to all or a portion of the invention’s mutagen aequorin or obelin sequences (i.e., target sequences) or their complements. Under stringent hybridization conditions, only highly complementary, i.e., substantially similar nucleic acid sequences, hybridize. Preferably, such conditions prevent hybridization of nucleic acids having 4 or more mismatches out of 20 contiguous nucleotides, more preferably 2 or more mismatches out of 20 contiguous nucleotides, most preferably one or more mismatch out of 20 contiguous nucleotides. The hybridizing portion of the hybridizing nucleic acid is at least about 80%, preferably at least about 95%, or most preferably about at least about 98%, identical to the sequence of a target sequence, or its complement.

Hybridization of a nucleic acid to a nucleic acid sample under stringent conditions is defined below. Nucleic acid duplex or hybrid stability is expressed as a melting temperature (T_m), which is the temperature at which the probe dissociates from the target DNA. This melting temperature is defined to use the required stringency conditions. If sequences are to be identified that are substantially identical to the probe, rather than identical, then it is useful to first establish the lowest temperature at which only homologous hybridization occurs with a particular concentration of salt (e.g., SSC or SSPE). Then assuming that 1% mismatching results in a 1° C. decrease in T_m, the temperature of the final wash in the hybridization reaction is reduced accordingly (for example, if sequences having >95% identity with the probe are sought, the final wash temperature is decrease by 5° C.). In practice, the change in T_m can be between 0.5° C. and 1.5° C. per 1% mismatch.

Stringent conditions involve hybridizing at 68° C. in 5×SSC/5× Denhart’s solution/1.0% SDS, and washing in 0.2×SSC/0.1% SDS at room temperature. Moderately stringent conditions include washing in 3×SSC at 42° C. The parameters of salt concentration and temperature be varied to achieve optimal level of identity between the primer and the target nucleic acid. Additional guidance regarding such conditions is readily available in the art, for example, Sambrook, Fischer and Maniatis, Molecular Cloning, a laboratory manual, (2nd ed.), Cold Spring Harbor Laboratory Press, New York, (1989) and F. M. Ausubel et al eds., Current Protocols in Molecular Biology, John Wiley and Sons (1994).

The invention relates to aequorin mutants that emit light at a wavelength shifted with respect to wild type aequorin. Table 1 below is a list of exemplary aequorin mutants inventors have discovered to have an emission profile shifted with respect to wild type.

<table>
<thead>
<tr>
<th>Mutant Name</th>
<th>Mutant Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mutant S Tyr132Le</td>
<td>Mutant S Tyr132Le</td>
</tr>
<tr>
<td>Mutant S Tyr132-fluorotyrosine</td>
<td>Mutant S Tyr132-fluorotyrosine</td>
</tr>
<tr>
<td>Mutant S Ala69Cys</td>
<td>Mutant S Ala69Cys</td>
</tr>
<tr>
<td>Mutant S Gly70Cys</td>
<td>Mutant S Gly70Cys</td>
</tr>
<tr>
<td>Mutant S Ala74Cys</td>
<td>Mutant S Ala74Cys</td>
</tr>
<tr>
<td>Mutant S His76Cys</td>
<td>Mutant S His76Cys</td>
</tr>
<tr>
<td>Mutant S Tyr132Phe</td>
<td>Mutant S Tyr132Phe</td>
</tr>
</tbody>
</table>

The invention also relates to obelin mutants that emit light at a wavelength shifted with respect to wild type obelin. Table 2 below is a list of exemplary obelin mutants inventors have discovered to have an emission profile shifted with respect to wild type.

<table>
<thead>
<tr>
<th>Mutant Name</th>
<th>Mutant Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cys55Ser/Cys518er</td>
<td>Cys55Ser/Cys518er</td>
</tr>
<tr>
<td>Cys55Ser/Cys67Ser</td>
<td>Cys55Ser/Cys67Ser</td>
</tr>
</tbody>
</table>

One aspect of the invention relates to aequorin Mutants S that have been modified at position 132. As opposed to wild type aequorin which emits light at the same wavelength irrespective of the coelenterazine analogue used, these mutants’ emission is varied with the use of different coelenterazine analogues. Embodiments of this aspect of the invention include but are not limited to Mutant S Tyr132Le and Mutant S Tyr132Phe.

Another embodiment of this aspect of the invention is aequorin Mutant S with a non-natural amino acid in position 132. Preferably, the non-natural amino acid is a structural analogue of tyrosine. More preferably, the non-natural amino acid is fluorotyrosine or fluorotryptophan and most preferably, the fluorotryosine is 3-fluoro-1-tyrosine.
Another aspect of the invention relates to aequorin Mutants S and obelin that have been modified at other amino acid positions. As opposed to wild type aequorin which emits light at the same wavelength irrespective of the coelenterazine analogue used, these mutants’ emission is varied with the use of different coelenterazine analogues. Embodiments of this aspect of the invention include but are not limited to Mutant S Trp86Tyr, Mutant S Tyr82Trp, Mutant S His16Tyr, Mutant S Tyr82Phe, Mutant S Phe66Cys and Mutant S Phe65Cys and obelin mutants: Cys75Ser/Cys51Ser, Cys158Ser, Cys75Ser/Cys67Se, and Cys151Ser.

Another aspect of the invention relates to obelin and aequorin Mutants S that have been conjugated to a fluorophore which is excited by the emission of bioluminescent light from the aequorin such that it fluoresces at a different wavelength than wild type aequorin. Preferably, a fluorophore is selected that is excited by light having a wavelength similar to that at which wild type or Mutant S aequorin emits light. Aequorin Mutant S emits at a wavelength of about 445 nm to about 495 nm depending on the coelenterazine analogue employed. As such, it would be preferable to use a fluorophore that has an excitation wavelength of about 400 nm and about 520 nm, preferably about 420 nm to about 500 nm and most preferably about 440 nm to about 495 nm. In one embodiment of the invention, the native coelenterazine is used and therefore a fluorophore having an excitation wavelength of about 469 nm to about 472 nm would be ideal. For example, an iodacetamide-derivative of the fluorophore, N-(2-iodoacetoxyethyl)-(N-methyl)-amino-7-nitrobenz-2-oxa-1,3-diazole (IAND ester) is employed. However, other fluorophores may be selected based on the coelenterazine that is to be used with aequorin mutant and the resulting shift in emission.

In another embodiment of this aspect of the invention, the fluorophore is conjugated to a unique cysteine inserted into the aequorin Mutant S primary structure. Preferably, the fluorophore is linked to the unique cysteine in aequorin Mutant S Ala69Cys, Mutant S Gly70Cys, Mutant S Ala74Cys, or Mutant S Glu76Cys. Most preferably, aequorin Mutant S Ala69Cys and Mutant S Gly70Cys are used.

In another aspect of the invention, the obelin or aequorin mutants are used in the development of different competitive and non-competitive assays for physiologically important molecules, such as peptides, drugs, etc., and for the high-throughput screening of biopharmaceuticals.

In one embodiment of this aspect of the invention, the obelin or aequorin mutant is tethered to an analyte by conventional covalent attachment. Preferably, attachment to an analyte of interest is mediated by the free amine groups of the lysine residues on the aequorin mutant. Preferably, pure aprotinin is be conjugated to an analyte of interest by reacting, for example, an N-hydroxysuccinimide derivative of the analyte with the lysine residues on the photoprotein (Kendall, Trends Biotechnol 1998, 16, 216-24). The commercial availability of a number of analytes that are already derivatized with N-hydroxysuccinimide derivatives makes this conjugation approach quite generic. Conjugation of these analytes through other derivatives is also possible and would be readily apparent to one of ordinary skill in the art.

Additionally, the attachment of other analytes to unique cysteines added to aequorin Mutant S may be accomplished in the following manner. Analytes of interest, such as digoxin, fluoxetine, phenytoin, phenobarbitone, theophylline, amitriptyline, chlorpromazine and carbamazepine containing maleimido or iodacetamide groups may be reacted with the modified apoaequorin using a sulfhydryl-specific reaction. This reaction scheme may also be followed for analytes that are commercially available as maleimido or, iodacetamide derivatives. If the ligands contain a free amino group, then they can be reacted with a heterobifunctional reagent such as sulfo-N-succinimidyl 4-[N-maleimidomethyl]-cyclohexane-1-carboxylate (sulfo-SMCC) to introduce a maleimido coupling group (Hashida, J. Appl. Biochem. 1984, 56, 56-63). For example, a derivative of carbamazepine that contains a free amino group, carbamazepine-N-β-ethylamine will be prepared (Sidki, Clin. Chem. 1984, 30, 1348-1352). This derivative will then be coupled to sulfo-SMCC. If the ligand of interest contains a free carboxyl group, then a ligand hydrazide derivative will be prepared by reaction with thionyl chloride and hydrazine. This will introduce a free amino group, which can subsequently be reacted with sulfo-SMCC to introduce the desired maleimido moiety.

In another embodiment, the aequorin mutant proteins disclosed herein are part of a fusion protein wherein either the mutant obelin or aequorin cDNA and the cDNA of the target analyte are operably linked, i.e., transcribed and/or translated together in frame. Preferably, specifically designed oligonucleotide linkers may be employed to operably link the mutant aequorin cDNA to the cDNA of the target analyte. Standard molecular biology techniques known to those of skill in the art enable the investigator to create expression vectors encoding such aequorin mutant—analyte fusion proteins.

Another aspect of the invention relates to methods of using the aequorin mutants disclosed herein to identify drug lead compounds. In one embodiment of the invention, candidate drug lead compounds are small molecules generated for example, by combinatorial chemistry techniques well documented in the art.

One embodiment of this aspect of the invention relates to a method of identifying compounds that inhibit bond breaking enzymes such as proteases. Proteases catalyze the cleavage of amide bonds of proteins producing small oligopeptides or free amino acids, and thus, these enzymes play a critical role in various cell processes. The actions of certain proteases within the cell are important in that they are involved in metabolic digestion, complement activation, fertilization, and the production of peptide hormones. For example, serine proteases are essential for coagulation and fibrinolysis in blood plasma. Therefore, considerable interest has been placed on the study of proteases and detecting the cleavage of peptide bonds.

In another embodiment of this aspect of the invention, the detection of protease activity involves the preparation of mutant aequorin fusion protein that will incorporate a recognition site for the particular bond breaking enzyme or protease within its structure that can be cleaved in the presence of the bond breaking enzyme or protease.

In another embodiment, this aspect of the invention relates to a method of identifying inhibitors of HIV-1 protease. The HIV-1 protease encoded by the human immunodeficiency virus plays a key role in the development of AIDS, and has been extensively studied. The protease has been identified as a prime target for the design of inhibitors to be used as potential treatment for the AIDS virus. The assay for the detection of HIV-1 protease activity involves the preparation of mutant aequorin fusion protein that will incorporate and thereby be operably linked to a recognition site for the protease within its structure that can be cleaved in the presence of the bond breaking enzyme. In one embodiment, the recognition site incorporated and tested for
cleavage is Ser-Glu-Asn-Tyr-Pro-Ile-Val (SEQ ID NO: 5), which corresponds to an optimum natural substrate for the HIV-1 protease located on the gag-pol polyprotein. Preferably, spacers amino acids will be introduced before and after the recognition site present within the fusion protein to limit the possibility of steric hindrance, and produce a more accessible cleavage site for the protease. Any of the mutant aequorins disclosed herein are suitable for use in this assay. Preferably, the fusion protein is prepared by ligating the operably linked mutant aequorin and recognition site DNAs into the expression vector pSOD110 to yield pSOD1001. Preferably, Bacillus subtilis cells is then transformed with the plasmid. The expressed protein is preferably purified using perfluorionion-exchange chromatography. The purity and concentration of the protein may be determined by SDS-PAGE and the bicinechonic acid-based protein assay, respectively.

Preferably, the purified fusion protein is biotinylated using a maleimide-activated biotin that reacts selectively with the unique sulphydryl group at the N-terminus of the fusion protein. Following the biotinylation reaction, the aequorin fusion protein will preferably be generated by addition of an excess amount of coelenterazine. Preferably, the biotinylated fusion protein is immobilized onto a Neutravidin-coated 384-well microtiter plate. Bioluminescence studies are then undertaken to characterize the protein in terms of its luminescence properties. In order to determine the amount of the HIV-1 protease substrate to be used in subsequent experiments, preferably a binder-saturation study is performed. Preferably, the ability of the protease to cleave the recognition site is evaluated by using different concentrations of the enzyme on the substrate. To evaluate the bioluminescence system developed for assessing the activity of inhibitors of the HIV-1 protease, preferably a dose-response curve is generated for known inhibitors of this protease. Preferably, these include, for example, acetyl pepstatin and pepstatin A, competitive inhibitors of HIV-1 protease, as well as, a non-competitive inhibitor Ac-Leu-Val-phenylalaninal. At higher concentrations of the inhibitor, the bioluminescence signal should be higher since the protease is inhibited from cleaving at the recognition site. In contrast, as the concentration of the inhibitor decreases, the light intensity emitted by the solid phase should decrease because the protease will not be inhibited, and thus, it should catalyze the cleavage of the peptide bond (see FIG. 15).

Several strategies have been reported for the detection of amide bond cleavage by HIV-1 protease, including high performance liquid chromatography (HPLC), spectrophotometric analysis, fluorescence-based methods, ELISA with either chromogenic or fluorogenic substrate, and cell-based assays. Many of these methods employ synthetic substrates and require further confirmation of protease activity using naturally occurring substrates. These synthetic substrates may pose solubility problems in aqueous solutions at higher concentrations. In the proposed work, we postulate that a bioluminescence-based strategy can be employed in the sensitive detection of peptide bond cleavage by proteases. The assay designed should be readily adaptable to automation, and is essentially a single step, direct assay for proteolytic bond cleavage. Another advantage of the methods taught herein is that the labeled-substrate for the protease is genetically engineered, which allows for the production of a highly reproducible labeled-substrate in unlimited quantities. Since the label used is a protein, the system does not suffer from any solubility problems under the aqueous conditions of the assay.

Furthermore, the methods taught herein detect protease activity are versatile in that different recognition sites for other physiologically and pharmacologically important proteases, such as caspases, could be incorporated into the assay design through the preparation of other bioluminescent fusion proteins. Moreover, the system may find application in the high-throughput screening of biopharmaceutical drugs that are potential inhibitors of a target protease.

EXAMPLE 1

Aequorin Mutants with Coelenterazine Analouges

Cysteine free aequorin (Mutant S), Y1321 Mutant S aequorin, Acq5 (Mutant S with a cysteine at position 5), and wild type Aequorin were purified and multiple spectra taken and averaged (See FIG. 1). Wild type aequorin showed the same emission maxima for all coelenterazines analogues. Mutant S had emission maxima ranging from 448 nm to 491 nm. Y1321 Mutant S has emission maxima ranging from 453 nm to 487 nm. Aequorin 5 had emission maxima ranging from 466 nm to 491 nm. The greatest spread in emission maximum thus far has been between MutS/CTZ i and MutS/CTZ hcp (448 nm, 491 nm, respectively (43 nm range)). As can be seen on the graph the two peaks are starting to separate significantly. The greatest spread in emission maximum wavelengths so far with the same coelenterazine is CTZ hcp with Acq5 (476 nm) and MutS (448 nm) being 28 nm. Also, the maximum spread with the same CTZ’s and different aequorins is 19 nm for i, ip, and f.

Mutant S, Mutant S Y1321 and Acq5 final emission spectrums were the result of the average of three trials. Wild type aequorins final spectrum was the result of two trials. All mutants, except Acq5, were purified to >95% purity using SDS-PAGE and silver staining. All coelenterazine analogues were diluted to 100 micrograms/ML methanol. Solvent composition, coelenterazine concentration, temperature, and incubation time, were the same for all trials except with N coelenterazine, which required a higher concentration of aequorin than the other coelenterazines to show activity. Concentrations of the different mutants were not identical. Half life determination of Y1321 Mut S with coelenterazines i, ip, h, hcp, cp, fcp, f, and native were 23, 0.9, 0.4, 0.2, 0.6, 0.7, 2.6, and 1.2 seconds, respectively. The largest spread of emission wavelengths thus far is 43 nm between MutS/CTZi and MutS/CTZhcp. As can be seen on the graph this shift is starting to significantly separate the peaks. Further separation of the peaks will increase the practicality of the use of these mutant/ctz pairs. For single well multiple analyze analysis different aequorin mutants having separate emission maximum when using the same coelenterazine will be preferred. The 28 nm spread between Mut S and Acq5 with CTZ hcp is the most promising for single well analysis applications thus far.

The emission spectrum of native recombinant aequorin encoded by SEQ ID NO: 1 and purchased commercially (Aqualite from Molecular Probes), showed identical emission maximum (472 nm) for all coelenterazine analogues, contrary to previously published results (Shimomura et al., Cell Calcium, (1993) 14:373-378). It is likely that the older, more indirect method of finding emission maximum used by Shimomura somehow yielded inaccurate results. Additionally, previously published results were obtained using protein that was isolated directly from jellyfish, leading to the collection of different protein isoforms yielding results different from the native recombinant form.
Interesting observations in the spectrum are the similarity in the shape and relative intensity of the emission spectrum of some mutants with the same coelenterazine. For example, the CTZi spectrum with MutS and Y132I MutS is very similar in shape and relative intensity, yet in AeqS the CTZi spectrum shape and intensity is quite different. The most notable difference between these 3 mutants being that AeqS contains one cysteine whereas MutS and Y132I MutS contain none. Also, the maximum spread with the same CTZi’s and different aequorins is 19 nm for CTZi, CTZip, and CTZE. CTZi and CTZip similarity could be explained by the presence of an electron withdrawing halogen in the same position, but the 19 nm spread in CTZip, with an aliphatic side chain in a different position, is curious.

EXAMPLE 2

Aequorin Mutants with Non-Natural Amino Acids

In order to incorporate selected non-natural amino acids into the aequorin, E. coli cells containing a plasmid that has the genetic information for aequorin were grown in minimal media. This medium was supplemented with essential amino acids and vitamins minus the amino acid of the analogue would be incorporated. After cells were grown to a certain optical density the analogue and the inducer IPTG, was added in order to express aequorin. As the protein expression takes place, the amino acid residues are replaced by the analogue present in the medium. The percent incorporation depends largely on the type and nature of the amino acid analogue used and can range from about 10 to about 75%. The cells were harvested and lysed by sonication. The cell debris was separated from the supernatant. The supernatant was then incubated with different coelenterazine analogues and the emission spectra were taken. The results are shown in the following table.

The results are shown in FIG. 7 which is a table showing the emission wavelength maximum (nm) of aequorin mutant Mutant S Y132I, Mutant S having a 3-fluoro-1-tyrosine aequorin or a 5-fluoro-1-tryptophan non-natural amino acid in position 132 in conjunction with coelenterazine analogues CTZ i, f, n, h, hcp, cp, fcp, f and native CTZ. FIG. 8, is a graph showing the emission spectrum of aequorin Mutant S with a 3-fluoro-1-tyrosine in position 132 with coelenterazine analogues CTZ i, f, n, fcp, h, cp, ip, hcp and native CTZ. When 3-fluoro-1-tyrosine is incubated with coelenterazine i an emission wavelength of 511 nm is observed. This to date is the largest shift observed in aequorin emission with respect to wild type aequorin.

EXAMPLE 3

Aequorin Mutants Conjugated to Fluorophores

The aequorin variants: Mutant S Ala69Cys, Mutant S Gly70Cys, Mutant S Ala74Cys, Mutant S Gly76Cys were generated by site-directed mutagenesis. The iodoacetamide-derivative of the fluorophore, N-((2-iodoacetoxy)ethyl)-N-methylamino-7-nitrobenz-2-oxa-1,3-diazole (IANDB ester) is attached to a unique cysteine either at position 69, 70, 74 or 76. This fluorophore was selected because it has a light absorption maximum of 472 nm which is close to the maximum emission of aequorin. IANDB ester has an emission wave length of 536 nm which is sufficient far from wild type aequorin’s emission of 469-472 nm to be easily detectable. Conjugation was performed using a maleimide derivative of the fluorophore. The aequorin mutant—IANDB conjugation was incubated in excess of native coelenterazine and tested for photoemission by adding calcium ions. The results are shown in FIG. 10. Labeled Mutant S Ala69Cys and Mutant S Gly70Cys showed and emission peak of the fluorophore in the 530-540 nm range as well as a peak at corresponding to aequorin emission. When 3-fluoro-1-tyrosine is incubated with coelenterazine i an emission wave length of 511 is observed. This to date is the largest shift observed in aequorin emission with respect to wild type aequorin. This indicates that the transfer of energy from aequorin to the fluorophore occurred, thus resulting in a mutant aequorin with an emission shifted with respect to wild type aequorin.

EXAMPLE 4

Obelin Mutants with Coelenterazine Analogues

Obelin mutants C75S/C51S, C75S/C67, C158S, C151S, and wild type obelin were purified and multiple spectra taken and averaged (See FIG. 20). Wild type obelin showed the same 469 nm emission maxima for all coelenterazines analogues. The results of the different obelin mutants used with different coelenterazines analogues is shown in FIG. 20.

SEQUENCE LISTING
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Gly Ala Thr Pro Glu Gln Ala Lys Arg His Lys Asp Ala Val Glu Ala 50 55 60
Phe Phe Gly Gly Ala Gly Met Lys Tyr Gly Val Glu Thr Asp Trp Pro 65 70 75 80
Ala Tyr Ile Glu Gly Trp Lys Leu Ala Thr Asp Glu Leu Gly Lys 85 90 95
Tyr Ala Lys Ann Glu Pro Thr Leu Ile Arg Ile Trp Gly Asp Ala Leu 100 105 110
Phe Asp Ile Val Asp Lys Glu Ann Gly Ala Ile Thr Leu Asp Glu 115 120 125
Trp Lys Ala Tyr Thr Lys Ala Gly Ile Ile Glu Ser Glu Asp 130 135 140
Cys Glu Glu Thr Phe Arg Val Cys Asp Ile Asp Glu Ser Gly Gln Leu 145 150 155 160
Asp Val Asp Glu Met Thr Arg Glu His Leu Gly Phe Trp Tyr Thr Met 165 170 175
Asp Pro Ala Cys Glu Lys Leu Tyr Gly Gly Ala Val Pro 180 185
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20    25    30
Leu Asp Glu Met Val Tyr Lys Ala Ser Asp Ile Val Ile Aaa Aen Leu
35    40    45
Gly Ala Thr Pro Glu Gin Ala Lys Arg His Lys Asp Ala Val Glu Ala
50    55    60
Phe Phe Gly Gly Ala Gly Met Tyr Gly Val Glu Thr Asp Trp Pro
65    70    75    80
Ala Tyr Ile Glu Gly Trp Lys Leu Ala Thr Asp Glu Leu Glu Lys
85    90    95
Tyr Ala Lys Aen Glu Pro Thr Leu Ile Arg Ile Trp Gly Asp Ala Leu
100   105   110
Phe Asp Ile Val Asp Lys Gin Aen Gly Ala Ile Thr Leu Asp Glu
115   120   125
Trp Lys Ala Tyr Thr Lys Ala Gly Ile Ile Gin Ser Ser Glu Aen
130   135   140
Ser Glu Glu Thr Phe Arg Val Ser Asp Ile Asp Glu Ser Gly Gin Leu
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What is claimed is:

1. An isolated nucleic acid having at least 95% sequence identity to SEQ ID NO: 3 wherein said nucleic acid encodes a protein that binds coelenterazine and molecular oxygen and emits light, said protein having a tryptophan residue in a first position corresponding to position 82 of SEQ ID NO: 4.

2. An isolated nucleic acid having at least 95% sequence identity to SEQ ID NO: 3 wherein said nucleic acid encodes a protein that binds coelenterazine and molecular oxygen and emits light, said protein having a phenylalanine residue in a first position corresponding to position 82 of SEQ ID NO: 4.