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(54) **OPTOGENETIC INDUCTION OF NEURODEGENERATIVE DISEASE PATHOLOGIES**

OPTOGENETISCHE INDUKTION VON NEURODEGENERATIVEN KRANKHEITSPATHOLOGIEN

INDUCTION OPTOGÉNÉTIQUE DE PATHOLOGIES NEURODÉGÉNÉRATIVES

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Description

FIELD

[0001] The present disclosure relates to compounds, compositions, and methods for the inducing neurodegenerative disease pathologies.

BACKGROUND

[0002] The world is aging. By the year 2050, the proportion of individuals over the age of 60 will have doubled to 2 billion from 605 million in 2000. Unfortunately, aging is the single greatest risk factor for developing a fatal neurodegenerative disease. In turn, the number of individuals with dementias such as Alzheimer's disease (AD), Lewy Body Dementia (LBD), Frontotemporal Dementia (FTD), and movement disorders such as Parkinson's Disease (PD) and Amyotrophic Lateral Sclerosis (ALS) will significantly increase. Nearly 6.5 million individuals within the United States are currently living with one of these diseases and the associated costs are unsustainable.

[0003] In the United States, the current economic burden of AD, PD, and ALS is an estimated $241 billion dollars per year. AD and ALS/FTD patients can incur personal medical costs upwards of $100,000 - $250,000 per year. For AD, it is estimated that 13.8 million individuals in the United States will have been diagnosed by 2050, up from 4.7 million in 2010, while the worldwide number of ALS cases will rise ~31% by 2040 and no effective treatment currently exists for these disorders. Despite a variety of genetic mutations that contribute to these neurodegenerative disorders, there is no known single cause. However, despite this diversity, nearly all patients within each disease exhibit a common neuropathological hallmark in the form of intracellular protein aggregates. Animal models to recapitulate these neuropathologies currently require using either genetic mutations or grossly overexpressing proteins and these often do not mimic patient pathology. What is needed are new and improved methods for inducing neurodegenerative disease pathologies in cell lines and animal models.

[0004] The compounds, compositions, and methods disclosed herein address these and other needs.

SUMMARY

[0005] Disclosed herein are compounds, compositions, and methods for inducing neurodegenerative disease pathologies in a cell or animal. The inventors have developed new methods for inducing neurodegenerative disease pathologies in cells and animals without the need for genetic mutations or grossly overexpressing neurodegenerative disease proteins.

[0006] In one aspect, disclosed herein is a nucleotide sequence encoding a chimeric polypeptide, comprising: a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and a second nucleotide sequence encoding a low complexity domain from a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B 1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15.

[0007] In one aspect, disclosed herein is an expression vector encoding a chimeric polypeptide, comprising: a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2 and a second nucleotide sequence encoding a low complexity domain from a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15, wherein the first nucleotide sequence is operably linked to a promoter.

[0008] In one aspect, disclosed herein is a cell comprising a nucleotide sequence encoding a chimeric polypeptide, comprising: a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2 and a second nucleotide sequence encoding a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B 1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15.

[0009] In one aspect, disclosed herein is a chimeric polypeptide comprising: a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2; and a low complexity domain from a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B 1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15.

[0010] In one aspect, disclosed herein is a method of inducing a neurodegenerative disease pathology in a cell, comprising the steps:

introducing into the cell an expression vector encoding a chimeric polypeptide, comprising:
a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2 and
a second nucleotide sequence encoding a low complexity domain from a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B 1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15, wherein the first nucleotide sequence is operably linked to a promoter;
expressing the chimeric polypeptide; and
inducing oligomerization of the chimeric polypeptide by stimulation with blue light.

[0011] In another aspect, disclosed herein is a method of screening for an agent that modulates protein aggregation, comprising the steps:

introducing into a cell an expression vector encoding a chimeric polypeptide, comprising:
a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2 and
a second nucleotide sequence encoding a low complexity domain from a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B 1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15, wherein the first nucleotide sequence is operably linked to a promoter;
expressing the chimeric polypeptide;
introducing the agent into a culture media comprising the cell;
inducing oligomerization of the chimeric polypeptide by stimulation with blue light; and
determining modulation of protein aggregation by the agent.

[0012] In one embodiment, the light-induced oligomerization domain is selected from the group consisting of CRYPHR, CRY2OLIG, NcVVD, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2. In one embodiment, the light-induced oligomerization domain is selected from the list of domains in Table 2. In one embodiment, the light-induced oligomerization domain is NcVVDY50W. In one embodiment, the light-induced oligomerization domain is CRY2OLIG. In one embodiment, the light-induced oligomerization domain is CRYPHR.

[0013] In one embodiment, the light-induced oligomerization domain is selected from the group consisting of a CRY2 PHR domain (for example, CRY2PHR, CRY2OLIG) or a light-oxygen-voltage-sensing (LOV) domain (for example, NcVVD, NcVVDY50W, VfAU1, YtvA, EL222, RsLOV, AsLOV2).

[0014] In one embodiment, the low complexity domain from a neurodegenerative disease target protein is TDP-43. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is Alpha synuclein. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is Tau.

[0015] In one embodiment, the cell is a mammalian cell. In one embodiment, the cell is a human cell.

[0016] In one embodiment, the blue light has a wavelength between 405 nm and 499 nm. In one embodiment, the blue light has a wavelength of about 465 nm.

BRIEF DESCRIPTION OF THE DRAWINGS

[0017] The accompanying figures, which are incorporated in and constitute a part of this specification, illustrate several aspects described below.

FIG. 1 shows the examples of genetic causes of ALS and the common neuropathology. The left panel shows a graph of the number of ALS-causing genes on the Y axis, and the X axis indicates the year each mutation was discovered. FIG. 1, panel A shows that ALS exhibits extreme genetic heterogeneity, especially since these mutations are found in only ~10% of ALS cases. As described in Table 1, despite these genetic causes of ALS, nearly all patients show the same neuropathology in the motor cortex and spinal cord. The right panel shows an example of ALS neuropathology by H and E staining of paraffin tissue sections from an ALS patient motor cortex. Shown are cytoplasmic aggregates of TDP-43. TDP-43 is predominantly nuclear in normal cells as represented by *. In ALS, TDP-43 is absent from the nucleus and aggregates in the cytoplasm as shown by the arrow. Although ALS is used as an example, cytoplasmic aggregate neuropathology is a common feature of many neurodegenerative diseases, see Table 1.

FIGS. 2A-2B describe methods to generate neuropathological aggregate proteins containing an LCD/IDR/Prion-like domain with light using TDP-43 and CRY2OLIG as an example. Various protein arrangements and blue light exposure paradigms were developed to induce protein aggregation of proteins and protein fragments containing

LCD/IDR/prion-like domains, promote the mislocalization of nuclear proteins and recapitulate the neuropathology of neurodegenerative diseases. TDP-43 is a predominantly nuclear protein that contains an IDR/IDD/prion-like domain, and is mislocalized and aggregated in ALS, FTD, and some AD patients, as an example. DNA sequences were engineered to generate amino acid sequences that encode for a the CRY2OLIG protein that clusters when exposed to blue light generated a fusion protein either the entire TDP-43 protein (cry2-TDP43-mCh) or just the low complexity domain (LCD/IDD/prion-like domain), which makes TDP-43 aggregation prone (Cry2-274-mCh). As a control, CRY2OLIG alone was used. All constructs were fused to a fluorescent protein called mCherry (mCh) to visualize the proteins in live cells. CRY2OLIG-mCh reversibly clusters with blue light stimulation but the CRY2OLIG-TDP-43-mCh or the truncated CRY2OLIG-274-mCh forms irreversible aggregates with specific blue light stimulation paradigms. FIG. 2A shows examples of the CRY2OLIG-TDP-43 arrangements and truncated CRY2OLIG-274 arrangements used in this work. FIG. 2B shows a model of the described technology.

FIG. 3 shows a schematic describing blue light induced oligomerization and aggregation of proteins employing the NcVVD, NcVVDY50W or NcLOV photoreceptor. The NcVVD or LOV domain have only been shown to homodimerize with blue light stimulation. A light exposure paradigm to induce oligomerization and aggregation was developed. The top panel shows a schematic of how a single acute stimulation with blue light (405-499 nm) induces the homodimerization of the LOV protein when fused to a protein of interest. The bottom panel shows that chronic stimulation with blue light promotes the homooligomerization of NcVVD or LOV fusion proteins that contain a prion-like domain/LCD/IDD.

FIGS. 4A-4E show light-induced aggregation of low-complexity domain proteins. Optogenetic TDP-43 fragments containing the low-complexity domain (LCD) undergo progressive aggregation with light stimulation. (FIGS. 4A-4B) C-terminal fragments of TDP-43 (optoRRM2+LCD/optoLCD) rapidly oligomerize after a brief pulse (8 sec, 10% laser power, 488nm) of blue light when monitored by live confocal microscopy. These oligomers persist much longer than the Cry2 photoreceptor alone (~10 min disassembly). (FIGS. 4C-4D) Optogenetic LCD fragments also continue to aggregate following brief light pulses, growing in size over time. (FIG. 4E) Persistent blue light stimulation of the TDP-43 LCD forms intracellular aggregates in the cells. Fluorescent recovery after photobleaching (FRAP) experiments show that persistent light LCD inclusions do not recover from FRAP indicating that these are insoluble.

FIGS. 5A-5K show chronic blue light stimulation induces optoTDP43 mislocalization and aggregation that recapitulates pathological hallmarks seen in patient CNS tissue. HEK293 cells expressing optoTDP43-mCh were exposed to 488nm LED stimulation or darkness for up to 36 hours. (FIG. 5A-5C) Representative images showing optoTDP43 that (FIG. 5B) first experiences gradual cytoplasmic mislocalization, (FIG. 5C) which was confirmed by nuclear/cytoplasmic fractionation. (FIG. 5D) Mislocalization is followed by optoTDP43 aggregation, as measured by simultaneous chronic blue light exposure and high-throughput automated confocal microscopy, that increases in propensity with increasing light exposure. (FIG. 5E) Fluorescence recovery after photobleaching (FRAP) imaging was performed to assess dynamicity of optoTDP43 structures. Lack of fluorescence recovery shows that light-induced optoTDP43 aggregates are non-dynamic, immobile granules reminiscent of aggregated structures. (FIG. 5F) Detergent-solubility of optoTDP43 structures was assessed by subcellular fractionation to confirm aggregated state of light-induced optoTDP43 granules. (Left lanes) Non-optogenetic TDP-43 (TDP43-mCh) shows no changes in solubility with and without light treatment, while optoTDP43 (right lanes) displays a drastic shift to the insoluble fraction with chronic blue light stimulation. In addition to increased insolubility of exogenous, full-length optoTDP43 (top band), chronic blue light exposure also results in recruitment of aberrant optoTDP43 cleavage products (middle bands), as well as endogenous full-length TDP-43 and disease-relevant cleavage products (bottom bands), to the detergent-insoluble, urea-soluble fraction of cell lysates as is observed in patient tissue. (FIG. 5G) To confirm direct recruitment of non-optogenetic TDP-43 species to exogenous light-induced optoTDP43 inclusions, EGFP-tagged TDP-43 was co-expressed with optoTDP43 or the Cry2 photoreceptor-only control. In cells exposed to chronic blue light stimulation, strong co-localization is observed between optoTDP43 inclusions and EGFP-TDP43, confirming the ability of optoTDP43 inclusions to directly recruit other TDP-43 species. This recruitment appears to be dependent on TDP43 :TDP43 interactions, as no co-localization is observed with Cry2-mCh puncta following blue light exposure. (FIG. 5H-5J) Immunofluorescence analysis was performed on light-induced optoTDP43 aggregates to confirm pathological hallmarks seen in patient tissue. optoTDP43 inclusions appear to be (FIG. 5H) ubiquitinated, (FIG. 5I) hyperphosphorylated, and (FIG. 5J) p62-positive, all of which have been observed with TDP-43 inclusions in patient CNS. (FIG. 5K) Automated high-throughput confocal microscopy was performed to assess the neurotoxicity of light-induced optoTDP43 inclusions. Human ReN neurons expressing TDP43-mCh or optoTDP43 were exposed to chronic blue light stimulation and viability was simultaneously monitored by longitudinal imaging. Neurons expressing non-optogenetic TDP43-mCh showed no significant decrease in survival with or without blue light exposure. However, neurons expressing optoTDP43 that were exposed to blue light stimulation display significantly decreased viability over time, suggesting optoTDP43 inclusions are neurotoxic. * = $p < .05$, ** = $p < .01$

FIGS. 6A-6E show chronic stimulation of CRY2OLIG α-synuclein or a-synuclein LOV induces clustering and aggregation. Chronic stimulation of a CRY2-asyn-mCh was tested to induce clustering or the α -synuclein protein.

Figure 6A shows the chronic stimulation paradigm and Figure 6B shows representative images of a-synuclein clustering with light over time along with quantification of clustering in Figure 6C. These data indicate that this optogenetic system can be employed to induce the clustering and aggregation of multiple neurodegenerative disease proteins that are prone to aggregation, that is, contain prion-like domains/LCD/IDDs. Figure 6D shows that a-synuclein fused to the LOV (dimerizing photoreceptor) forms intracellular clusters of alpha synuclein. Figure 6E shows that light induced a-synuclein LOV aggregates exhibit pathological hallmarks of synucleinopathies including phosphorylation at serine 129 and p62 positivity.

FIGS. 7A-7D show Cry2-Tau fusion protein shows pathological markers for various tauopathies. (FIGS. 7A-7C) HEK293 cells expressing Cry2 photoreceptor-alone or Cry2-Tau fusion proteins were exposed to chronic blue light stimulation (16 hours, 488nm, 10mW). Cry2-Tau-expressing cells show fibril-like aggregates that co-stain with phospho-Tau antibodies AT8 (FIG. 7A) and PHF1 (FIG. 7B), as well as the pathological conformation-dependent Tau antibody MC1 (FIG. 7C). (FIG. 7D) Summary showing the various optogenetic Tau constructs that co-localize with pathological Tau antibodies after light-induction of neurofibrillary tangle formation.

FIGS. 8A-8E show LOV-Tau fusion proteins also show pathological markers for various tauopathies and are insoluble. (FIG. 8A- FIG. 8B) HEK293 cells expressing VVD-Tau or VfAU-Tau fusion proteins were exposed to chronic blue light stimulation (16 hours, 488nm, 10mW). Both fusion proteins co-stain with phospho-Tau antibodies AT8 and PHF1, and the pathological conformation-dependent Tau antibody MC1. (FIG. 8C) Differentiated MAP2+ human ReN neurons expressing VVD-Tau also shows neurofibrillary tangle formation following chronic light treatment that co-localizes with AT8. (FIG. 8D) Fluorescence recovery after photobleaching analysis was performed on light-induced tangles and shows a lack of fluorescence recovery, indicating a non-dynamic, immobile structure. (FIG. 8E) Urea extraction was next performed to confirm insoluble tau species with light treatment in HEK293 cells expressing VVD-Tau. Cells exposed to chronic light show increased levels of soluble and insoluble 150kDa tau species which is present in Alzheimer's Disease and Frontotemporal Dementia patient tissue.

FIGS. 9A-9B show the aggregation potential of CRY2 or VVD fusion proteins based on the protein arrangement and light stimulation paradigm combination. Studies indicate that the ability of Cry2 or VVD photoreceptor to stimulate clustering and activation are dependent on the protein arrangement as well as the light stimulation paradigm. Figure 9A shows that a TDP-43-CRY2OLIG-mCh protein mislocalizes but does not exhibit the ability to aggregate as the CRY2OLIG-TDP-43-mCh arrangement does. Similarly, Figure 9B shows that the mCh-aSyn-NvVVDY50W does not have the ability to aggregate. This data shows that the protein arrangement and light stimulation paradigms are important for inducing neuropathological protein aggregates as observed in the CNS tissue of patients with neurodegenerative disease.

FIGS. 10A-10B show that blue light induced TDP-43 aggregates or truncated LCD/IDR/prion-like domain aggregates are toxic to cells. FIG 10A shows that acute stimulation of HEK cells expressing CRY2OLIG-TDP274-mCh can induce the formation of pathological aggregates within 1 hour. These aggregates can grow in size and become toxic over time. FIG 10B is a schematic of a screening pipeline to use the induction of neurodegenerative disease pathology to identify therapeutic compounds that rescue toxicity and prevent or remove the formation of the induced neurodegenerative disease pathology.

DETAILED DESCRIPTION

[0018] Disclosed herein are compounds, compositions, and methods for inducing neurodegenerative disease pathologies in a cell or animal. The inventors have developed new methods for inducing neurodegenerative disease pathologies in cells and animals without the need for genetic mutations or grossly overexpressing neurodegenerative disease proteins.

[0019] Reference will now be made in detail to the embodiments of the invention, examples of which are illustrated in the drawings and the examples.

[0020] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which this disclosure belongs. The term "comprising" and variations thereof as used herein is used synonymously with the term "including" and variations thereof and are open, non-limiting terms. Although the terms "comprising" and "including" have been used herein to describe various embodiments, the terms "consisting essentially of" and "consisting of" can be used in place of "comprising" and "including" to provide for more specific embodiments and are also disclosed.

[0021] The following definitions are provided for the full understanding of terms used in this specification.

Terminology

[0022] As used herein, the article "a," "an," and "the" means "at least one," unless the context in which the article is used clearly indicates otherwise.

[0023] The term "about" as used herein when referring to a measurable value such as an amount, a percentage, and

the like, is meant to encompass variations of ±20%, ±10%, ±5%, or ±1% from the measurable value.

[0024] As used herein, the terms "may," "optionally," and "may optionally" are used interchangeably and are meant to include cases in which the condition occurs as well as cases in which the condition does not occur.

[0025] The term "nucleic acid" as used herein means a polymer composed of nucleotides, e.g. deoxyribonucleotides or ribonucleotides.

[0026] The terms "ribonucleic acid" and "RNA" as used herein mean a polymer composed of ribonucleotides.

[0027] The terms "deoxyribonucleic acid" and "DNA" as used herein mean a polymer composed of deoxyribonucleotides.

[0028] The term "oligonucleotide" denotes single- or double-stranded nucleotide multimers of from about 2 to up to about 100 nucleotides in length. Suitable oligonucleotides may be prepared by the phosphoramidite method described by Beaucage and Carruthers, Tetrahedron Lett., 22:1859-1862 (1981), or by the triester method according to Matteucci, et al., J. Am. Chem. Soc., 103:3185 (1981), or by other chemical methods using either a commercial automated oligonucleotide synthesizer or VLSIPS™ technology. When oligonucleotides are referred to as "double-stranded," it is understood by those of skill in the art that a pair of oligonucleotides exist in a hydrogen-bonded, helical array typically associated with, for example, DNA. In addition to the 100% complementary form of double-stranded oligonucleotides, the term "double-stranded," as used herein is also meant to refer to those forms which include such structural features as bulges and loops, described more fully in such biochemistry texts as Stryer, Biochemistry, Third Ed., (1988),

[0029] The terms "polynucleotide", "nucleotide sequence", and "nucleic acid sequence" are used interchangeably herein and refer to a single or double stranded polymer composed of nucleotide monomers.

[0030] The term "polypeptide" refers to a compound made up of a single chain of D- or L-amino acids or a mixture of D- and L-amino acids joined by peptide bonds.

[0031] The term "complementary" refers to the topological compatibility or matching together of interacting surfaces of a probe molecule and its target. Thus, the target and its probe can be described as complementary, and furthermore, the contact surface characteristics are complementary to each other.

[0032] The term "hybridization" refers to a process of establishing a non-covalent, sequence-specific interaction between two or more complementary strands of nucleic acids into a single hybrid, which in the case of two strands is referred to as a duplex.

[0033] The term "anneal" refers to the process by which a single-stranded nucleic acid sequence pairs by hydrogen bonds to a complementary sequence, forming a double-stranded nucleic acid sequence, including the reformation (renaturation) of complementary strands that were separated by heat (thermally denatured).

[0034] The term "melting" refers to the denaturation of a double-stranded nucleic acid sequence due to high temperatures, resulting in the separation of the double strand into two single strands by breaking the hydrogen bonds between the strands.

[0035] The term "promoter" or "regulatory element" refers to a region or sequence determinants located upstream or downstream from the start of transcription and which are involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. Promoters need not be of bacterial origin, for example, promoters derived from viruses or from other organisms can be used in the compositions, systems, or methods described herein. The term "regulatory element" is intended to include promoters, enhancers, internal ribosomal entry sites (IRES), and other expression control elements (e.g. transcription termination signals, such as polyadenylation signals and poly-U sequences). Such regulatory elements are described, for example, in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, Calif. (1990). Regulatory elements include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). A tissue-specific promoter may direct expression primarily in a desired tissue of interest, such as muscle, neuron, bone, skin, blood, specific organs (e.g. liver, pancreas), or particular cell types (e.g. lymphocytes). Regulatory elements may also direct expression in a temporal-dependent manner, such as in a cell-cycle dependent or developmental stage-dependent manner, which may or may not also be tissue or cell-type specific. In some embodiments, a vector comprises one or more pol III promoter (e.g. 1, 2, 3, 4, 5, or more pol I promoters), one or more pol II promoters (e.g. 1, 2, 3, 4, 5, or more pol II promoters), one or more pol I promoters (e.g. 1, 2, 3, 4, 5, or more pol I promoters), or combinations thereof. Examples of pol III promoters include, but are not limited to, U6 and H1 promoters. Examples of pol II promoters include, but are not limited to, the retroviral Rous sarcoma virus (RSV) LTR promoter (optionally with the RSV enhancer), the cytomegalovirus (CMV) promoter (optionally with the CMV enhancer) [see, e.g., Boshart et al, Cell, 41:521-530 (1985)], the SV40 promoter, the dihydrofolate reductase promoter, the β-actin promoter, the phosphoglycerol kinase (PGK) promoter, and the EF1α promoter. Also encompassed by the term "regulatory element" are enhancer elements, such as WPRE; CMV enhancers; the R-U5' segment in LTR of HTLV-I (Mol. Cell. Biol., Vol. 8(1), p. 466-472, 1988); SV40 enhancer; and the intron sequence between exons 2 and 3 of rabbit β-globin (Proc. Natl. Acad. Sci. USA., Vol. 78(3), p. 1527-31, 1981). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression desired, etc.

[0036] The term "recombinant" refers to a human manipulated nucleic acid (e.g. polynucleotide) or a copy or complement of a human manipulated nucleic acid (e.g. polynucleotide), or if in reference to a protein (i.e, a "recombinant protein"), a protein encoded by a recombinant nucleic acid (e.g. polynucleotide). In embodiments, a recombinant expression cassette comprising a promoter operably linked to a second nucleic acid (e.g. polynucleotide) may include a promoter that is heterologous to the second nucleic acid (e.g. polynucleotide) as the result of human manipulation (e.g., by methods described in Sambrook et al., Molecular Cloning-A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., (1989) or Current Protocols in Molecular Biology Volumes 1-3, John Wiley & Sons, Inc. (1994-1998)). In another example, a recombinant expression cassette may comprise nucleic acids (e.g. polynucleotides) combined in such a way that the nucleic acids (e.g. polynucleotides) are extremely unlikely to be found in nature. For instance, human manipulated restriction sites or plasmid vector sequences may flank or separate the promoter from the second nucleic acid (e.g. polynucleotide). One of skill will recognize that nucleic acids (e.g. polynucleotides) can be manipulated in many ways and are not limited to the examples above.

[0037] The term "expression cassette" refers to a nucleic acid construct, which when introduced into a host cell, results in transcription and/or translation of a RNA or polypeptide, respectively. In embodiments, an expression cassette comprising a promoter operably linked to a second nucleic acid (e.g. polynucleotide) may include a promoter that is heterologous to the second nucleic acid (e.g. polynucleotide) as the result of human manipulation (e.g., by methods described in Sambrook et al., Molecular Cloning-A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y., (1989) or Current Protocols in Molecular Biology Volumes 1-3, John Wiley & Sons, Inc. (1994-1998)). In some embodiments, an expression cassette comprising a terminator (or termination sequence) operably linked to a second nucleic acid (e.g. polynucleotide) may include a terminator that is heterologous to the second nucleic acid (e.g. polynucleotide) as the result of human manipulation. In some embodiments, the expression cassette comprises a promoter operably linked to a second nucleic acid (e.g. polynucleotide) and a terminator operably linked to the second nucleic acid (e.g. polynucleotide) as the result of human manipulation. In some embodiments, the expression cassette comprises an endogenous promoter. In some embodiments, the expression cassette comprises an endogenous terminator. In some embodiments, the expression cassette comprises a synthetic (or non-natural) promoter. In some embodiments, the expression cassette comprises a synthetic (or non-natural) terminator.

[0038] The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 60% identity, preferably 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% or higher identity over a specified region when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 10 amino acids or 20 nucleotides in length, or more preferably over a region that is 10-50 amino acids or 20-50 nucleotides in length. As used herein, percent (%) amino acid sequence identity is defined as the percentage of amino acids in a candidate sequence that are identical to the amino acids in a reference sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR) software. Appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared can be determined by known methods.

[0039] For sequence comparisons, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

[0040] One example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) Nuc. Acids Res. 25:3389-3402, and Altschul et al. (1990) J. Mol. Biol. 215:403-410, respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al. (1990) J. Mol. Biol.

215:403-410). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

[0041] The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-5787). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01.

[0042] The phrase "codon optimized" as it refers to genes or coding regions of nucleic acid molecules for the transformation of various hosts, refers to the alteration of codons in the gene or coding regions of polynucleic acid molecules to reflect the typical codon usage of a selected organism without altering the polypeptide encoded by the DNA. Such optimization includes replacing at least one, or more than one, or a significant number, of codons with one or more codons that are more frequently used in the genes of that selected organism.

[0043] Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are near each other, and, in the case of a secretory leader, contiguous and in reading phase. However, operably linked nucleic acids (e.g. enhancers and coding sequences) do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. In embodiments, a promoter is operably linked with a coding sequence when it is capable of affecting (e.g. modulating relative to the absence of the promoter) the expression of a protein from that coding sequence (i.e., the coding sequence is under the transcriptional control of the promoter).

[0044] The term "variant" or "derivative" as used herein refers to an amino acid sequence derived from the amino acid sequence of the parent protein having one or more amino acid substitutions, insertions, and/or deletions.

Chimeric Constructs

[0045] In one aspect, disclosed herein is a nucleotide sequence encoding a chimeric polypeptide, comprising: a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2 and a second nucleotide sequence encoding a low complexity domain from a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B 1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15.

[0046] In one aspect, disclosed herein is an expression vector encoding a chimeric polypeptide, comprising: a first nucleotide sequence encoding a light-induced oligomerization domain and a second nucleotide sequence encoding a low complexity domain from a neurodegenerative disease target protein, wherein the first nucleotide sequence is operably linked to a promoter.

[0047] In some embodiments, the expression vector encoding a chimeric polypeptide is comprised in a plasmid or in a virus or viral vector. A plasmid or a viral vector can be capable of extrachromosomal replication or, optionally, can integrate into the host genome. As used herein, the term "integrated" used in reference to an expression vector (e.g., a plasmid or viral vector) means the expression vector, or a portion thereof, is incorporated (physically inserted or ligated) into the chromosomal DNA of a host cell. As used herein, a "viral vector" refers to a virus-like particle containing genetic material which can be introduced into a eukaryotic cell without causing substantial pathogenic effects to the eukaryotic cell. A wide range of viruses or viral vectors can be used for transduction, but should be compatible with the cell type the virus or viral vector are transduced into (e.g., low toxicity, capability to enter cells). Suitable viruses and viral vectors

include adenovirus, lentivirus, retrovirus, among others. In some embodiments, the expression vector encoding a chimeric polypeptide is a naked DNA or is comprised in a nanoparticle (e.g., liposomal vesicle, porous silicon nanoparticle, gold-DNA conjugate particle, polyethylenimine polymer particle, cationic peptides, etc.).

[0048] The expression vectors disclosed herein are, in some embodiments, capable of inducing a neurodegenerative disease pathology in a cell (e.g., inducing aggregation of a protein) without substantially altering the expression level of a protein involved in the neurodegenerative disease pathology. For example and without limitation, the expression vector can induce aggregation of a protein having a low complexity domain from a neurodegenerative disease target protein without substantially increasing or decreasing the expression level of an endogenous target protein which comprises the same low complexity domain. As such, a cell comprising a herein disclosed nucleotide sequence encoding a chimeric polypeptide can have substantially unchanged expression levels of an endogenous neurodegenerative disease target protein comprising a low complexity domain, as compared to a cell of the same cell type which does not comprise the nucleotide sequence encoding a chimeric polypeptide. The term "substantially unchanged expression levels," as used herein, refers to a change in expression level, if any, to a degree not known or not suspected to cause or be associated with inducing a neurodegenerative disease pathology in a cell.

[0049] The expression vectors disclosed herein are, in some embodiments, are capable of inducing a neurodegenerative disease pathology in a cell (e.g., inducing aggregation of a protein) using a wild-type form of a low complexity domain from a neurodegenerative disease target protein. Thus, in some embodiments, the low complexity domain from a neurodegenerative disease target protein does not include a mutation which differs from the wild-type sequence and which is known or suspected to cause or be associated with inducing a neurodegenerative disease pathology in a cell. For example and without limitation, the expression vector can comprise a low complexity domain from a wild-type TDP-43 protein which does not contain a mutation such as Q331K, known to cause or be associated with ALS.

[0050] In one aspect, disclosed herein is a cell comprising a nucleotide sequence encoding a chimeric polypeptide, comprising: a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2 and a second nucleotide sequence encoding a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B 1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15.

[0051] In some embodiments, the cell is a cell which can be affected by a neurodegenerative disease. For example, the cell can be a glial cell or a neuronal cell.

[0052] In one aspect, disclosed herein is a chimeric polypeptide comprising: a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2; and a low complexity domain from a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B 1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15.

[0053] In one embodiment, the light-induced oligomerization domain is selected from the group consisting of CRYPHR, CRY2OLIG, NcVVD, NcVVDY50W, and NcLOV. In one embodiment, the light-induced oligomerization domain is selected from the group consisting of CRYPHR, CRY2OLIG, NcVVD, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2. In one embodiment, the light-induced oligomerization domain is selected from the list of domains in Table 2. In one embodiment, the light-induced oligomerization domain is selected from a variant of CRYPHR, CRY2OLIG, NcVVD, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, or AsLOV2. In one embodiment, the light-induced oligomerization domain is selected from a fragment of CRYPHR, CRY2OLIG, NcVVD, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, or AsLOV2.

[0054] In one embodiment, the light-induced oligomerization domain is NcVVDY50W. In one embodiment, the light-induced oligomerization domain is CRY2OLIG. In one embodiment, the light-induced oligomerization domain is CRYPHR. In one embodiment, the light-induced oligomerization domain comprises a LOV domain from the VVD protein. In one embodiment, the light-induced oligomerization domain comprises a LOV domain from the LOV protein. In one embodiment, the light-induced oligomerization domain comprises a PHR domain. In one embodiment, the light-induced oligomerization domain comprises a PHR domain, from the CRY2 protein. In one embodiment, the light-induced oligomerization domain is VfAU1. In one embodiment, the light-induced oligomerization domain is YtvA. In one embodiment, the light-induced oligomerization domain is EL222. In one embodiment, the light-induced oligomerization domain is RsLOV. In one embodiment, the light-induced oligomerization domain is AsLOV2.

[0055] Although not explicitly claimed, the disclosure also provides that the light-induced oligomerization domain is at least 90% identical to CRYPHR. Although not explicitly claimed, the disclosure also provides that the light-induced oligomerization domain is at least 90% identical to NcVVD. Although not explicitly claimed, the disclosure also provides that the light-induced oligomerization domain is at least 90% identical to NcVVDY50W. Although not explicitly claimed, the disclosure also provides that the light-induced oligomerization domain is at least 90% identical to NcLOV. Although not explicitly claimed, the disclosure also provides thatthe light-induced oligomerization domain is at least 90% identical to CRY2OLIG. Although not explicitly claimed, the disclosure also provides that the light-induced oligomerization domain

is at least 90% identical to VfAU1. Although not explicitly claimed, the disclosure also provides that the light-induced oligomerization domain is at least 90% identical to YtvA. Although not explicitly claimed, the disclosure also provides that the light-induced oligomerization domain is at least 90% identical to EL222. Although not explicitly claimed, the disclosure also provides that the light-induced oligomerization domain is at least 90% identical to RsLOV. Although not explicitly claimed, the disclosure also provides that the light-induced oligomerization domain is at least 90% identical to AsLOV2.

[0056] In some embodiments, the first nucleotide sequence can comprise a nucleotide sequence which encodes a light-induced oligomerization domain selected from the group consisting of CRYPHR, CRY2OLIG, NcVVD, NcVVDY50W, NcLOV, and VfAU1LOV.

[0057] Although not explicitly claimed, the disclosure also provides that the first nucleotide sequence can comprise a nucleotide sequence which encodes an amino acid sequence that is at least 70% identical to SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:99, SEQ ID NO: 100, SEQ ID NO: 101, or SEQ ID NO: 102. Although not explicitly claimed, the disclosure also provides that the first nucleotide sequence can encode an amino acid sequence which is at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 99% identical to SEQ ID NO: 1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, or SEQ ID NO:102. The first nucleotide sequence can comprise SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:99, SEQ ID NO: 100, SEQ ID NO: 101, or SEQ ID NO: 102. In some embodiments, the first nucleotide sequence can comprise SEQ ID NO:94. The nucleotide sequence can be that of the wild type nucleic acid sequence encoding an amino acid sequence disclosed herein. In some embodiments, the nucleotide sequence is modified from the wild type sequence, but due to the degeneracy of the genetic code, can still encode for the same amino acid sequence. In some embodiments, the nucleotide sequence is a variant of one of the sequences disclosed herein (or encodes of variant protein sequence). In some embodiments, the nucleotide sequence is a fragment of one of the nucleic acids herein, or encodes a fragment of one of the amino acids disclosed herein. In some embodiments, the nucleotide sequence is codon optimized (for example, to improve expression).

[0058] In one embodiment, the light-induced oligomerization domain is selected from the group consisting of a CRY2 PHR domain (for example, CRY2PHR, CRY2OLIG) or a light-oxygen-voltage-sensing (LOV) domain (for example, NcVVD, NcVVDY50W, VfAU1, YtvA, EL222, RsLOV, AsLOV2).

[0059] In one embodiment, the low complexity domain from a neurodegenerative disease target protein is selected from the group consisting of TDP-43, Alpha synuclein, Tau, Fus, TIA1, SOD1, Huntingtin, Ataxin 2, and hnRNPA2B1. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is selected from the group consisting of TDP-43, Alpha synuclein, Tau, Fus, TIA1, SOD1, Huntingtin, Ataxin 2, and hnRNPA2B1. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is selected from the group consisting of TDP-43, Alpha synuclein, Tau, Fus, TIA1, SOD1, Huntingtin, Ataxin 2,hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is selected from a variant of TDP-43, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B 1, EWS RNA Binding Protein 1, or TATA box binding protein factor 15. The low complexity domain from a neurodegenerative disease target protein is selected from a fragment of TDP-43, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS RNA Binding Protein 1, or TATA box binding protein factor 15. In one embodiment, the fragment of TDP-43, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2,hnRNPA2B1, EWS RNA Binding Protein 1, or TATA box binding protein factor 15 comprises a low complexity domain (or fragment thereof) within each neurodegenerative disease target protein.

[0060] The low complexity domain from a neurodegenerative disease target protein is selected from Table 3.

[0061] Although not explicitly claimed, the disclosure also provides that the low complexity domain from a neurodegenerative disease target protein is selected from the group consisting of an amino acid sequence with at least 90% identity to TDP-43, Alpha synuclein, Tau, Fus, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA1, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15. Although not explicitly claimed, the disclosure also provides that the low complexity domain from a neurodegenerative disease target protein is selected from the group consisting of an amino acid sequence with at least 90% identity to a low complexity domain from a neurodegenerative disease target protein is selected from Table 3. The low complexity domain from a neurodegenerative disease target protein is selected from an orthologue of the group consisting of TDP-43, Alpha synuclein, Tau, Fus, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B 1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15.

[0062] Although not explicitly claimed, the disclosure also provides that the low complexity domain from a neurodegenerative disease target protein is selected from the group consisting of an amino acid sequence with at least 60% (for example, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%) identity to TDP-43, Alpha synuclein, Tau, Fus, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA1, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15 (or a fragment thereof).

[0063] In one embodiment, the low complexity domain from a neurodegenerative disease target protein is TDP-43. In

one embodiment, the low complexity domain from a neurodegenerative disease target protein is Alpha synuclein. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is Tau. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is Fus. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is TIA1. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is SOD1. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is Huntingtin. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is Ataxin 2. Although not explicitly claimed, the disclosure also provides that the low complexity domain from a neurodegenerative disease target protein is hnRNPA1. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is hnRNPA2B1. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is EWS RNA Binding Protein 1. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is TATA box binding protein factor 15.

[0064] In one embodiment, a VVD light-induced oligomerization domain is fused to a low complexity domain of TDP-43. In one embodiment, a VVD light-induced oligomerization is fused to full length TDP-43 (comprising a low complexity domain). In one embodiment, a light-induced oligomerization domain is fused to a low complexity domain from any neurodegenerative disease target protein that aggregates in neurodegenerative diseases.

[0065] In one embodiment, a light-induced oligomerization domain is fused to a low complexity domain of TDP-43, wherein the sequence of the low complexity domain of TDP-43 comprises SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, or SEQ ID NO:98 (or a fragment thereof).

[0066] In one embodiment, the nucleotide sequence encoding the chimeric polypeptide may further comprise a third nucleotide sequence encoding a reporter protein such as a fluorescent protein (to allow visualization of the protein aggregates by fluorescence). In one embodiment, the fluorescent protein is mCherry (mCh). In some embodiments, the fluorescent protein is GFP or YFP. In some embodiments, the first nucleotide sequence can encode a light-induced oligomerization domain comprising a PHR domain of the *Arabidopsis* Cryptochrome 2 protein (e.g., CRYPHR). In some embodiments, the light-induced oligomerization domain can comprise a wild-type CRYPHR amino acid sequence as disclosed, for example, in SEQ ID NO:1, or optionally, can comprise a mutated CRYPHR amino acid sequence as disclosed, for example, in SEQ ID NO:2. In some embodiments, a mutated CRYPHR amino acid sequence can comprise a E490G mutation, which can increase efficiency of clustering upon blue light stimulation as compared to a wild-type CRYPHR amino acid sequence. Although not explicitly claimed, the disclosure also provides that the first nucleotide sequence can encode a light-induced oligomerization domain, wherein the light-induced oligomerization domain comprises a polypeptide sequence which is at least 70% identical to SEQ ID NO: 1 or SEQ ID NO:2. Although not explicitly claimed, the disclosure also provides that the first nucleotide sequence can encode a light-induced oligomerization domain, wherein the light-induced oligomerization domain comprises a polypeptide sequence which is at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 99% identical to SEQ ID NO:1 or SEQ ID NO:2. In some embodiments, the first nucleotide sequence can encode a light-induced oligomerization domain comprising the polypeptide sequence of SEQ ID NO:1 or SEQ ID NO:2.

[0067] In some embodiments, the first nucleotide sequence can encode a light-induced oligomerization domain comprising Light-Oxygen-Voltage-Sensing Domain (LOV) from Neurospora Vivid protein (e.g., LOV, NcVVD, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and/or AsLOV2). In some embodiments, the light-induced oligomerization domain can comprise a wild-type LOV amino acid sequence as disclosed, for example, in SEQ ID NO:3,SEQ ID NO:4, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, or SEQ ID NO: 102, or optionally, can comprise a mutated LOV amino acid sequence as disclosed, for example, in SEQ ID NO:5. In some embodiments, a mutated LOV amino acid sequence can comprise a Y50W mutation, which can reduce the rate of dissipation from a dimerized state as compared to a wild-type LOV amino acid sequence. Although not explicitly claimed, the disclosure also provides that the first nucleotide sequence can encode a light-induced oligomerization domain, wherein the light-induced oligomerization domain comprises a polypeptide sequence which is at least 70% identical to SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:99, SEQ ID NO: 100, SEQ ID NO: 101, or SEQ ID NO: 102. Although not explicitly claimed, the disclosure also provides that the first nucleotide sequence can encode a light-induced oligomerization domain, wherein the light-induced oligomerization domain comprises a polypeptide sequence which is at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 99% identical to SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, or SEQ ID NO:102. In some embodiments, the first nucleotide sequence can encode a light-induced oligomerization domain comprising the polypeptide sequence of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:99, SEQ ID NO: 100, SEQ ID NO: 101, or SEQ ID NO: 102.

[0068] In some embodiments, the first nucleotide sequence can encode a light-induced oligomerization domain comprising a PHR domain of the *Arabidopsis* Cryptochrome 2 protein (e.g., CRYPHR), and the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein. In some embodiments, the first nucleotide sequence can encode a light-induced oligomerization domain comprising a PHR domain of the *Arabidopsis* Cryptochrome 2 protein (e.g., CRYPHR), and the second nucleotide sequence can encode a low complexity domain

from a neurodegenerative disease target protein comprising TDP-43. In some embodiments, the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising full-length TDP-43 (e.g., SEQ ID NO:6 or SEQ ID NO:7). In some embodiments, the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising truncated TDP-43 (e.g., SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, or SEQ ID NO:13). In some embodiments, a truncated TDP-43 comprises or consists of amino acids 105-414, 191-414, or 274-414 of the full-length TDP-43 amino acid sequence. Although not explicitly claimed, the disclosure also provides that the first nucleotide sequence can encode a light-induced oligomerization domain comprising CRYPHR, and the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising full-length or truncated TDP-43, wherein the first nucleotide sequence and the second nucleotide sequence encode a chimeric polypeptide sequence which is at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 99% identical to SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, or SEQ ID NO: 13. In some embodiments, the first nucleotide sequence and the second nucleotide sequence encode a chimeric polypeptide sequence according to SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, or SEQ ID NO:13. In some embodiments, SEQ ID NO:6 is selected. In some embodiments, SEQ ID NO:11 is selected.

[0069] In some embodiments, a nucleotide sequence encoding a chimeric polypeptide comprising a first nucleotide sequence and a second nucleotide sequence can further contain a third nucleotide sequence encoding a reporter protein or fragment thereof (e.g., a fluorescent protein such as mCherry, also referred to as mCH). Thus, in some embodiments, a first nucleotide sequence can encode a light-induced oligomerization domain comprising CRYPHR, a second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising full-length or truncated TDP-43, and a third nucleotide sequence can encode a mCherry protein, wherein the first, second, and third nucleotide sequences encode a chimeric polypeptide sequence which is at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 99% identical to SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, or SEQ ID NO:25. In some embodiments, the first, second, and third nucleotide sequences encode a chimeric polypeptide sequence according to SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, or SEQ ID NO:25. In some embodiments, SEQ ID NO:14 is selected. In some embodiments, SEQ ID NO:23 is selected.

[0070] In some embodiments, the first nucleotide sequence can encode a light-induced oligomerization domain comprising a LOV photoreceptor domain (e.g., NcVVD, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2), and the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein. In some embodiments, the first nucleotide sequence can encode a light-induced oligomerization domain comprising a LOV photoreceptor domain (e.g., NcVVD, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2), and the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising TDP-43. In some embodiments, the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising full-length TDP-43 (e.g., SEQ ID NO:26 or SEQ ID NO:27). In some embodiments, the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising truncated TDP-43 (e.g., SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, or SEQ ID NO:33). In some embodiments, a truncated TDP-43 consists of amino acids 105-414, 191-414, or 274-414 of the full-length TDP-43 amino acid sequence. Although not explicitly claimed, the disclosure also provides that the first nucleotide sequence can encode a light-induced oligomerization domain comprising NcVVDY50W, and the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising full-length or truncated TDP-43, wherein the first nucleotide sequence and the second nucleotide sequence encode a chimeric polypeptide sequence which is at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 99% identical to SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, or SEQ ID NO:33. In some embodiments, the first nucleotide sequence and the second nucleotide sequence encode a chimeric polypeptide sequence according to SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, or SEQ ID NO:33.

[0071] In some embodiments, a nucleotide sequence encoding a chimeric polypeptide comprising a first nucleotide sequence and a second nucleotide sequence can further contain a third nucleotide sequence encoding a reporter protein or fragment thereof (e.g., a fluorescent protein such as mCherry). Thus, in some embodiments, a first nucleotide sequence can encode a light-induced oligomerization domain comprising NcVVDY50W, a second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising full-length or truncated TDP-43, and a third nucleotide sequence can encode a mCherry protein, wherein the first, second, and third nucleotide sequences encode a chimeric polypeptide sequence which is at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 99% identical to SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36,

SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, or SEQ ID NO:41. In some embodiments, the first, second, and third nucleotide sequences encode a chimeric polypeptide sequence according to SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID N0:40, or SEQ ID NO:41. In some embodiments, SEQ ID NO:34 is selected. In some embodiments, SEQ ID NO:41 is selected.

[0072] In some embodiments, the first nucleotide sequence can encode a light-induced oligomerization domain comprising a PHR domain of the *Arabidopsis* Cryptochrome 2 protein (e.g., CRY2OLIG), and the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising α-synuclein. Although not explicitly claimed, the disclosure also provides that the first nucleotide sequence can encode a light-induced oligomerization domain comprising CRY2OLIG, and the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising α-synuclein, wherein the first nucleotide sequence and the second nucleotide sequence encode a chimeric polypeptide sequence which is at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 99% identical to SEQ ID NO:42 or SEQ ID NO:43. In some embodiments, the first nucleotide sequence and the second nucleotide sequence encode a chimeric polypeptide sequence according to SEQ ID NO:42 or SEQ ID NO:43.

[0073] In some embodiments, a nucleotide sequence encoding a chimeric polypeptide comprising a first nucleotide sequence and a second nucleotide sequence can further contain a third nucleotide sequence encoding a reporter protein or fragment thereof (e.g., a fluorescent protein such as mCherry). Thus, in some embodiments, a first nucleotide sequence can encode a light-induced oligomerization domain comprising CRY2OLIG, a second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising α-synuclein, and a third nucleotide sequence can encode a mCherry protein, wherein the first, second, and third nucleotide sequences encode a chimeric polypeptide sequence which is at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 99% identical to SEQ ID NO:44, SEQ ID NO:45, or SEQ ID NO:46. In some embodiments, the first, second, and third nucleotide sequences encode a chimeric polypeptide sequence according to SEQ ID NO:44, SEQ ID NO:45, or SEQ ID NO:46. In some embodiments, SEQ ID NO:44 is selected.

[0074] In some embodiments, the first nucleotide sequence can encode a light-induced oligomerization domain comprising a LOV photoreceptor domain (e.g., NcVVD, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2), and the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising α-synuclein. Although not explicitly claimed, the disclosure also provides that the first nucleotide sequence can encode a light-induced oligomerization domain comprising NcVVDY50W, and the second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising α-synuclein, wherein the first nucleotide sequence and the second nucleotide sequence encode a chimeric polypeptide sequence which is at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 99% identical to SEQ ID NO:47 or SEQ ID NO:48. In some embodiments, the first nucleotide sequence and the second nucleotide sequence encode a chimeric polypeptide sequence according to SEQ ID NO:47 or SEQ ID NO:48.

[0075] In some embodiments, a nucleotide sequence encoding a chimeric polypeptide comprising a first nucleotide sequence and a second nucleotide sequence can further contain a third nucleotide sequence encoding a reporter protein or fragment thereof (e.g., a fluorescent protein such as mCherry). Thus, in some embodiments, a first nucleotide sequence can encode a light-induced oligomerization domain comprising NcVVDY50W, a second nucleotide sequence can encode a low complexity domain from a neurodegenerative disease target protein comprising α-synuclein, and a third nucleotide sequence can encode a mCherry protein, wherein the first, second, and third nucleotide sequences encode a chimeric polypeptide sequence which is at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 99% identical to SEQ ID NO:49, SEQ ID NO:50, or SEQ ID NO:51. In some embodiments, the first, second, and third nucleotide sequences encode a chimeric polypeptide sequence according to SEQ ID NO:49, SEQ ID NO:50, or SEQ ID NO:51. In some embodiments, SEQ ID NO:51 is selected.

[0076] In some embodiments, the first nucleotide sequence is positioned upstream of the second nucleotide sequence. In some embodiments, the first nucleotide sequence is positioned downstream of the second nucleotide sequence.

[0077] In some embodiments, where the sequences disclosed herein contain a methionine at the start of the protein, the protein without the methionine is also disclosed. In some embodiments, where the sequences disclosed herein do not contain a methionine at the start of the protein, the protein with the methionine at the start of the protein is also disclosed.

[0078] In some embodiments, the nucleotide sequence encoding a chimeric polypeptide comprises a sequence selected from SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, or SEQ ID NO:91.

Methods

[0079] In one aspect, disclosed herein is a method of inducing a neurodegenerative disease pathology in a cell, comprising the steps:

introducing into the cell an expression vector encoding a chimeric polypeptide, comprising:
a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2 and
a second nucleotide sequence encoding a low complexity domain from a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15, wherein the first nucleotide sequence is operably linked to a promoter;
expressing the chimeric polypeptide; and
inducing oligomerization of the chimeric polypeptide by stimulation with blue light.

[0080] In another aspect, disclosed herein is a method of screening for an agent that modulates protein aggregation, comprising the steps:

introducing into a cell an expression vector encoding a chimeric polypeptide, comprising:
a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2 and
a second nucleotide sequence encoding a low complexity domain from a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B 1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15, wherein the first nucleotide sequence is operably linked to a promoter;
expressing the chimeric polypeptide;
introducing the agent into a culture media comprising the cell;
inducing oligomerization of the chimeric polypeptide by stimulation with blue light; and
determining modulation of protein aggregation by the agent.

[0081] In one embodiment, the light-induced oligomerization domain is selected from the group consisting of a CRY2 PHR domain (for example, CRY2PHR, CRY2OLIG) or a light-oxygen-voltage-sensing (LOV) domain (for example, NcVVD, NcVVDY50W, VfAU1, YtvA, EL222, RsLOV, AsLOV2).

[0082] In one embodiment, the light-induced oligomerization domain is selected from the group consisting of CRYPHR, CRY2OLIG, NcVVD, NcVVDY50W, and NcLOV. In one embodiment, the light-induced oligomerization domain is selected from the group consisting of CRYPHR, CRY2OLIG, NcVVD, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2. In one embodiment, the light-induced oligomerization domain is selected from the list of domains in Table 2. Although not explicitly claimed, the disclosure also provides that the light-induced oligomerization domain is selected from a variant of CRYPHR, CRY2OLIG, NcVVD, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, or AsLOV2. Although not explicitly claimed, the disclosure also provides that the light-induced oligomerization domain is selected from a fragment of CRYPHR, CRY2OLIG, NcVVD, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, or AsLOV2.

[0083] In one embodiment, the light-induced oligomerization domain is NcVVDY50W. In one embodiment, the light-induced oligomerization domain is CRY2OLIG. In one embodiment, the light-induced oligomerization domain is CRYPHR. In one embodiment, the light-induced oligomerization domain comprises a LOV domain from the VVD protein. In one embodiment, the light-induced oligomerization domain comprises a LOV domain from the LOV protein. In one embodiment, the light-induced oligomerization domain comprises a PHR domain. In one embodiment, the light-induced oligomerization domain comprises a PHR domain, from the CRY2 protein. In one embodiment, the light-induced oligomerization domain is VfAU1. In one embodiment, the light-induced oligomerization domain is YtvA. In one embodiment, the light-induced oligomerization domain is EL222. In one embodiment, the light-induced oligomerization domain is RsLOV. In one embodiment, the light-induced oligomerization domain is AsLOV2.

[0084] In one embodiment, the low complexity domain from a neurodegenerative disease target protein is selected from the group consisting of TDP-43, Alpha synuclein, Tau, Fus, TIA1, SOD1, Huntingtin, Ataxin 2, and hnRNPA2B1. The low complexity domain from a neurodegenerative disease target protein is selected from the group consisting of TDP-43, Alpha synuclein, Tau, Fus, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15. Although not explicitly claimed, the disclosure also provides that the low complexity domain from a neurodegenerative disease target protein is selected from a variant of TDP-43, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA1, hnRNPA2B1, EWS RNA Binding Protein 1, or TATA box binding protein factor 15. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is selected

from a fragment of TDP-43, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS RNA Binding Protein 1, or TATA box binding protein factor 15. In one embodiment, the fragment of TDP-43, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS RNA Binding Protein 1, or TATA box binding protein factor 15 comprises the low complexity domain within each neurodegenerative disease target protein.

[0085] Although not explicitly claimed, the disclosure also provides that the low complexity domain from a neurodegenerative disease target protein is selected from Table 3.

[0086] Although not explicitly claimed, the disclosure also provides that the low complexity domain from a neurodegenerative disease target protein is selected from the group consisting of an amino acid sequence with at least 90% identity to TDP-43, Alpha synuclein, Tau, Fus, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA1, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15. Although not explicitly claimed, the disclosure also provides that the low complexity domain from a neurodegenerative disease target protein is selected from the group consisting of an amino acid sequence with at least 90% identity to a low complexity domain from a neurodegenerative disease target protein is selected from Table 3. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is selected from an orthologue of the group consisting of TDP-43, Alpha synuclein, Tau, Fus, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15.

[0087] Although not explicitly claimed, the disclosure also provides that the low complexity domain from a neurodegenerative disease target protein is selected from the group consisting of an amino acid sequence with at least 60% (for example, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%) identity to TDP-43, Alpha synuclein, Tau, Fus, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA1, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15 (or a fragment thereof).

[0088] In one embodiment, the low complexity domain from a neurodegenerative disease target protein is TDP-43. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is Alpha synuclein. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is Tau. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is Fus. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is TIA1. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is SOD1. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is Huntingtin. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is Ataxin 2. Although not explicitly claimed, the disclosure also provides that the low complexity domain from a neurodegenerative disease target protein is hnRNPA1. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is hnRNPA2B1. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is EWS RNA Binding Protein 1. In one embodiment, the low complexity domain from a neurodegenerative disease target protein is TATA box binding protein factor 15.

[0089] In one embodiment, the cell is a mammalian cell. In one embodiment, the cell is a human cell. In one embodiment, the cell is selected from the group consisting of yeast, insect, avian, fish, worm, amphibian, xenopus, bacteria, algae and mammalian cells. In one embodiment, disclosed herein is a non-human transgenic organism, wherein the organism is an insect, fish, bird, worm, amphibian, xenopus, or non-human mammal.

[0090] To induce a neurodegenerative disease pathology refers to the action of bringing about the neurodegenerative disease pathology, or increasing the phenotype, symptoms, or severity of the neurodegenerative disease pathology, as compared to refraining from performing the selected action.

[0091] The neurodegenerative disease pathology can include an array of pathologies known to be or suspected to be associated with any one or more neurodegenerative diseases. Examples of such pathologies include, but are not limited to, protein aggregation in the cytoplasm of a cell, mislocalization of nuclear proteins to, for example, the cytoplasm, increased expression of ubiquitin, cell degeneration and/or death, extracellular Amyloid Beta (Aβ) aggregation, and/or intracellular and/or cytoplasmic aggregation of Tau protein. Protein aggregates can, in some embodiments, be colocalized with p62 protein, can be hyper-phosphorylated, can include endogenous protein comprising the low complexity domain from a neurodegenerative disease target protein (e.g., endogenous TDP-43), or combinations thereof.

[0092] Increased ubiquitination or increased expression of ubiquitin can be a phenotypic feature of neurodegenerative diseases. Ubiquitin has numerous cellular roles, including "tagging" proteins (e.g., by covalent linkage) for degradation in a proteasome. Increased ubiquitin expression in a cell is typically compared to a control. In some embodiments, a cell having increased ubiquitin has at least 50% increased ubiquitin expression compared to a control. In some embodiments, a cell having increased ubiquitin has at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 98%, or at least 99% increased ubiquitin expression compared to a control.

[0093] Ubiquitin expression in a cell can be determined at the transcriptional level, the translational level, or combinations thereof, and can be measured via a wide array of methods used to measure gene or polypeptide expression levels. In some embodiments, ubiquitin expression can be measured at the gene transcription level. For example and without limitation, levels of ubiquitin mRNA transcripts can be determined by radiation absorbance (e.g., ultraviolet light absorption at 260, 280, or 230 nm), quantification of fluorescent dye or tag emission (e.g., ethidium bromide intercalation), quantitative polymerase chain reaction (qPCR) of cDNA produced from mRNA transcripts, southern blot analysis, gene

expression microarray, or other suitable methods. Increased levels of mRNA transcripts can be used to infer or estimate increased levels of polypeptide expression. In some embodiments, ubiquitin expression can be measured at the post-translational level. For example and without limitation, levels of ubiquitin polypeptide can be determined by radiation absorbance (e.g., ultraviolet light), bicinchoninic acid (BCA) assay, Bradford assay, biuret test, Lowry method, Coomassie-blue staining, functional or enzymatic assay, immunodetection methods and/or Western blot analysis, or other suitable methods.

[0094] As used herein, the term "introducing," "introduce," and grammatical variations thereof, as it relates to introducing an expression vector into a cell, refers to any method suitable for transferring the expression vector into the cell. The term includes as examples, but is not limited to, conjugation, transformation/transfection (e.g., divalent cation exposure, heat shock, electroporation), nuclear microinjection, incubation with calcium phosphate polynucleotide precipitate, high velocity bombardment with polynucleotide-coated microprojectiles (e.g., via gene gun), lipofection, cationic polymer complexation (e.g., DEAE-dextran, polyethylenimine), dendrimer complexation, mechanical deformation of cell membranes (e.g., cell-squeezing), sonoporation, optical transfection, impalefection, hydrodynamic polynucleotide delivery, Agrobacterium-mediated transformation, transduction (e.g., transduction with a virus or viral vector), natural or artificial competence, protoplast fusion, magnetofection, nucleofection, or combinations thereof. An introduced expression vector, or a polynucleotide therefrom, can be genetically integrated or exist extrachromosomally.

[0095] A range of blue light wavelengths can be used in the disclosed methods. In one embodiment, the blue light has a wavelength from about 400 nm to about 500 nm. In one embodiment, the blue light has a wavelength from about 405 nm to about 499 nm. In one embodiment, the blue light has a wavelength from about 420 nm to about 490 nm. In one embodiment, the blue light has a wavelength from about 450 nm to about 490 nm. In one embodiment, the blue light has a wavelength from about 460 nm to about 495 nm. In one embodiment, the blue light has a wavelength of about 488 nm. In one embodiment, the blue light has a wavelength of about 475 nm. In one embodiment, the blue light has a wavelength of about 465 nm.

[0096] In one embodiment, the blue light has a wavelength of about 405 nm, about 410 nm, about 415 nm, about 420 nm, about 425 nm, about 430 nm, about 435 nm, about 440 nm, about 445 nm, about 450 nm, about 455 nm, about 460 nm, about 465 nm, about 470 nm, about 475 nm, about 480 nm, about 485 nm, about 490 nm, about 495 nm, or about 500 nm.

[0097] The methods can include various degrees of blue light stimulation. In some embodiments, the stimulation is acute or, optionally, chronic. Acute stimulation refers stimulation with pulses of blue light from about 0.2 to about 60 seconds, wherein the wavelength of the blue light can be any herein disclosed blue light wavelength. In some embodiments, the acute stimulation includes pulses of blue light from about 0.5 second to about 30 seconds, from about 1 second to about 20 seconds, or about 5 seconds. The blue light can be provided by a blue light source or a broad-spectrum light source filtered for the disclosed wavelengths.

[0098] In some embodiments, acute stimulation can result in temporary aggregation of a light-induced oligomerization domain (e.g., cytoplasmic prion-like domains/LCD/IDD protein fragments). Temporary aggregation, in some embodiments, includes protein aggregation observable by the herein disclosed methods for less than about twenty minutes or, optionally, less than about fifteen minutes, less than about ten minutes, or about five minutes or less. In some embodiments, acute stimulation does not result in aggregation of cytoplasmic prion-like domains/LCD/IDD protein fragments for twenty minutes or more.

[0099] In some embodiments, acute stimulation can result in aggregation of a light-induced oligomerization domain which is shorter in duration than aggregation of a light-induced oligomerization domain fused with a low complexity domain from a neurodegenerative disease target protein. In some embodiments, acute stimulation can result in aggregation of a light-induced oligomerization domain fused with a low complexity domain from a neurodegenerative disease target protein which is shorter in duration than aggregation of the same protein having an amino acid mutation known to cause or be associated with a neurodegenerative disease (e.g., TDP-43 Q331K).

[0100] Chronic stimulation is defined by exposure to blue light having a wavelength from about 400 nm to about 500 nm for a duration of about 1 minute or longer (for example, at least 1 minute, at least 5 minutes, at least 10 minutes, at least 30 minutes, at least 60 minutes, at least 2 hours, at least 4 hours, at least 8 hours, at least 12 hours, at least 24 hours, at least 36 hours, or more) from about 0.1 mW/cm^2 to 8 mW/cm^2 (within 400 nm - 500 nm wavelength).

[0101] The methods disclosed herein can, in some embodiments, induce a neurodegenerative disease pathology in a cell (e.g., aggregation of a protein) without substantially altering the expression level of a protein involved in the neurodegenerative disease pathology. For example and without limitation, the methods can induce aggregation of a chimeric polypeptide comprising TDP-43 (which can include aggregation of endogenous TDP-43) without substantially increasing or decreasing the expression level of endogenous TDP-43. In some or further embodiments, the methods can induce a neurodegenerative disease pathology in a cell using a wild-type form of a low complexity domain from a neurodegenerative disease target protein. Thus, in some embodiments, the low complexity domain from a neurodegenerative disease target protein does not include a mutation which differs from the wild-type sequence and which is known or suspected to cause or be associated with inducing a neurodegenerative disease pathology in a cell. For example and

without limitation, the methods can induce aggregation of a chimeric polypeptide comprising wild-type TDP-43 protein, or fragment thereof, which does not contain a mutation such as Q331K, known to cause or be associated with ALS.

EXAMPLES

[0102] The following examples are set forth below to illustrate the compounds, compositions, methods, and results according to the disclosed subject matter. These examples are not intended to be inclusive of all aspects of the subject matter disclosed herein, but rather to illustrate representative methods and results.

Example 1. Optogenetic induction of neurodegenerative disease pathologies

[0103] The world is aging. By the year 2050, the proportion of individuals over the age of 60 will have doubled to 2 billion from 605 million in 2000. Unfortunately, aging is the single greatest risk factor for developing a fatal neurodegenerative disease. In turn, the number of individuals with dementias such as Alzheimer's disease (AD), Lewy Body Dementia (LBD), Frontotemporal Dementia (FTD), and movement disorders such as Parkinson's Disease (PD) and Amyotrophic Lateral Sclerosis (ALS) will significantly increase. Nearly 6.5 million individuals within the United States are currently living with one of these diseases and the associated costs are unsustainable. In the United States, the current economic burden of AD, PD, and ALS is an estimated $241 billion dollars per year. AD and ALS/FTD patients can incur personal medical costs upwards of $100,000 - $250,000 per year. For AD, it is estimated that 13.8 million individuals in the United States will have been diagnosed by 2050, up from 4.7 million in 2010, while the worldwide number of ALS cases will rise -31% by 2040. Moreover, no effective treatment currently exists for these disorders.

[0104] Two decades of genetic analysis has uncovered a number of neurodegenerative disease-associated mutations. However, these are found in only a fraction of AD, LBD, FTD, PD, and ALS patients (Table 1).

Table 1. List of common neurodegenerative diseases, pathology and contribution of genetic components.

Disease	Symptoms	Affected CNS Regions	Life Expectancy (years)	Primary Aggregate Pathology	Genetic Cause
AD	Memory loss, confusion	Entorhinal cortex, Hippocampus	8-10	Tau (100%), Aβ (100%)	2-3%
FTD	Personality change, compulsivity, aphasia	Frontal lobe, Temporal lobe	7-10	TDP-43 (45%), Tau (45%), Fus (5%)	20-25%
PD	Stiffness, muscle rigidity, slowing of movement	Substantia nigra	15-20+	α-synudein (99%)	10%
ALS	Muscle weakness, paralysis	Motor cortex, Spinal cord	3-5	TDP-43 (97%), SOD1 (2%), Fus (1%),	10%

[0105] Table 1 describes a selection of neurodegenerative diseases, the primary symptoms, the affected region of the central nervous system (CNS), the aggregate neuropathology observed in patient CNS, percent of patients exhibiting this pathology and the percent of patients that harbor some genetic component of the disease (known or unknown mutation within the family). Alzheimer's disease (AD) is characterized by memory loss and confusion due to degeneration of the hippocampus and entorhinal cortex. Only 1-3% of patients harbor a causal genetic mutation; however all patients show a common aggregate pathology in the affected tissue. This is characterized by the extracellular Amyloid Beta (Aβ) aggregates and intracellular and cytoplasmic aggregations of the Tau protein. Frontotemporal Dementia (FTD) is characterized by the progressive degeneration of the frontal and temporal lobes and while 20-25% of patients can harbor a genetic cause of the disease, the 80-75% of patients have no family history. However, all patients exhibit some form of cytoplasmic protein aggregation that are comprised of either TDP-43 (45% of cases), Tau (45% of cases), or FUS (5% of cases) proteins. Parkinson's Disease (PD), is characterized by the progressive degeneration of dopaminergic neurons in the substantia nigra and while only 10% of patients have a known genetic cause, nearly all patients (99%) show cytoplasmic aggregation of the α-synuclein protein. Amyotrophic Lateral Sclerosis (ALS) is characterized by the rapid degeneration of the motor neurons in the motor cortex in the spinal cord leading patient paralysis and death. Only 10% of ALS patients have a family history of the disease while nearly 90% of cases occur sporadically. To date, nearly 35 causative genetic mutations have been identified in various genes (see FIG. 1), however despite this genetic diversity,

nearly all ALS patients exhibit the same neuropathology. Nearly 97% of ALS patients show the cytoplasmic mislocalization of the predominantly nuclear TDP-43 protein in the affected regions. Patients with mutations in the SOD1 or FUS gene also show cytoplasmic aggregations of these proteins but this occurs in only 2% and 1% of all ALS cases, respectively.

[0106] Together, this table highlights that the principal unifying factor of many neurodegenerative diseases are the neuropathological hallmarks. These neuropathologies primarily occur in the form of intracellular protein aggregates and in the vast majority of cases these intracellular protein aggregations form regardless of any known genetic cause. Moreover, these neuropathologies predominantly form in the region and cell types most affected in each disease.

[0107] Interestingly, despite the lack of a common known genetic or environmental cause, these are universal neuropathological features among patients for each disease. Thus, the vast majority of patients (90-100% of all patients depending on the disease) exhibit the same pathology in the central nervous system despite no known genetic cause. These pathological hallmarks manifest in the form of insoluble protein clumps or aggregates in the central nervous system (Table 1, FIG. 1).

[0108] To date, it is not possible to accurately model neurodegenerative disease aggregation that mimics human neuropathology. For each neurodegenerative disease, there is a primary component of the intracellular protein aggregate which harbor protein domains which make these proteins aggregation prone when in a high local concentration (also known as: prion-like domain, low complexity domain, intrinsically disordered domain, intrinsically disordered region). Therefore, current methods to model these neurodegenerative disease aggregates rely on overexpressing these aggregate-prone proteins in vitro or in vivo that comprise the neurodegenerative disease aggregates as the high cellular concentration can, in some models, form aggregates. In addition to, or alternatively, another method of modeling these diseases is to express mutated forms of proteins that comprise neurodegenerative disease aggregates. These mutations are found in a very small subset of patients and typically enhance the ability of the protein to aggregate. Unfortunately, none of these methods recapitulate the cellular environment of patients because the vast majority of patients do not harbor any disease-causing mutation, nor do they grossly overexpress the components of the aggregates. In fact, despite gross overexpression of these proteins, many models still do not exhibit the human neuropathology. This disconnect between the patient biology and model systems has significantly contributed to the lack of translatability of current neurodegenerative disease models.

[0109] Described in this example are novel methods to spatially and temporally induce protein aggregates without simple overexpressing of aggregate prone genes or expressing mutant forms of these genes. Thus, this method better recapitulates the human disease condition. Here, an innovative approach has been undertaken to address this challenging biological problem by harnessing the power of optogenetics (controlling protein function with light). A series of novel DNA arrangements have been constructed that can induce neurodegenerative disease pathology as observed in patients only when the cells are exposed to specific light stimuli. This method is used to create in vitro and in vivo model systems to mimic the neuropathology observed in patients and induce this pathology only after the cells are exposed to specific light wavelengths. This novel approach can transform neurodegenerative disease modeling and, unlike the expression of mutant transgenes, can be used to generate various disease models that are applicable to the vast majority of patients and are temporally and spatially inducible.

[0110] A series of DNA arrangements have been developed comprising the PHR domain (CRY2OLIG or CRY2PHR) or light-oxygen-voltage-sensing (LOV) domain (NcVVD, NcVVDY50W, Vfau1, YtvA, EL222, RsLOV, AsLOV2) which cluster or homodimerize, respectively, in response to blue light exposure (Table 2) and the DNA sequence of genes that encode for proteins that contain low complexity domains (LCDs) and comprise neurodegenerative disease protein aggregates (Table 3).

Table 2. List of photoreceptors/light-induced oligomerization domains to optogenetically induce neurodegenerative pathologies in cells with blue light exposure.

Nomenclature	Protein Domain	Organism	Light Stimuli (nm)	Light Response	Features
CRYPHR	Photo lyase homology region (PHR)	*Arabidopsis*	405-499	Homooligomerization	Endogenous protein domain
CRY2OLIG	Photolyase homology region (PHR) with E490A mutation	*Arabidopsis*	405-499	Homooligomerization	E490G Mutation to enhance clustering
NcVVD	Light-oxygen-voltage-sensing (LOV) domain	*Neurospora*	405-499	Homodimerization	LOV domain of VVD gene

(continued)

Nomenclature	Protein Domain	Organism	Light Stimuli (nm)	Light Response	Features
NcVVDY50W	Light-oxygen-voltage-sensing (LOV) domain	*Neurospora*	405-499	Homodimerization	VVD Y50G Mutation to enhance clustering
NcLOV	Light-oxygen-voltage-sensing (LOV) domain	*Neurospora*	405-499	Homodimerization	Clustering LOV domain from NcVVD with no linker
Vfau1	Light-oxygen-voltage-sensing (LOV) domain	*Vucheric frigida*	405-499	Homodimerization	
YtvA	Light-oxygen-voltage-sensing (LOV) domain	*Bacillus subtillis*	405-499	Homodimerization	
EL222	Light-oxygen-voltage-sensing (LOV) domain	*Erythrobacter litoralis*	405-499	Homodimerization	
RsLOV	Light-oxygen-voltage-sensing (LOV) domain	*Rhodobacter sphaeroides*	405-499	Homodimerization	
AsLOV2	Light-oxygen-voltage-sensing (LOV) domain	*Avena sativa*	405-499	Intramolecular conformational change	

[0111] Table 2 shows a list of photoreceptors to be employed to optogenetically induce neurodegenerative pathologies in cells upon blue light exposure. Variations of the PHR domain of the Cryptochrome 2 protein found in the Arabidopsis plant will be one family of photoreceptors employed (named CRY2PHR and CRY2OLIG in this document). The PHR domain of the CRY2 protein and its variants have the ability to cluster/homo-oligomerize for ~5 minutes when exposed to a single pulse of blue light (within the 405-499 nm range). The CRY2PHR is an endogenous protein sequence found in *Arabidopsis.* While the CRY2OLIG is the endogenous amino acid sequence but has a E490G mutation and has been shown to exhibit a slightly increased efficiency of clustering upon blue light stimulation. The self-binding of CRY2PHR and CRY2OLIG act through the same mechanism and requires intracellular FAD+. Various arrangements of CRY2OLIG and target proteins that comprise neuropathological protein aggregates have been generated to show modulation of the light-induced clustering properties of CRY2OLIG to induce neurodegenerative disease pathology of both predominantly cytoplasmic and predominantly nuclear proteins. This includes inducing the cytoplasmic mislocalization of nuclear proteins as observed in patient neuropathology. In addition, these protein domains have been used to induce the aggregation of intrinsically disordered domains/prion-like domains/low complexity domains of truncated versions of these neurodegenerative proteins.

[0112] Vivid (VVD) is a protein generated in the Neurospora organism and is a photoreceptor that homodimerizes in response to blue light (within the 405-499 nm range). The Light-Oxygen-Voltage-Sensing (LOV) domain is common throughout many organisms but this domain is very small in this organism. NcLOV is only the LOV domain of the VVD protein but is conserved throughout other species. NcVVD comprises a small fragment of the N-term VVD protein and the VVD LOV domain. NcVVDY50W from the NcVVD protein sequence however is altered by a Y50W change that promotes a slower ability to dissipate from the dimerized state. It was shown here that persistent dimerization of LOV domains induces oligomerization with chronic light and when fused to an LCD containing protein (FIGS. 6, 8). Although LOV domains are not reported to form oligomers, a light stimulation paradigm to induce protein clustering of specific protein arrangements of these photoreceptors and specific target neurodegenerative disease proteins has been developed herein. Additional LOV domains used herein also include VfAU1, YtvA, EL222, RsLOV, and AsLOV2.

Table 3. Target neurodegenerative disease proteins.

Gene Symbol	Encoded Protein	Associated Disease	Human RefSeqGene	Predominant Cellular Localization
TARDBP	TDP-43	ALS, FTD, AD, CTE	NG_008734.1	Nuclear
SNCA	Alpha Synuclein	PD, LBD, AD, MSA	NG_011851.1	Cytoplasmic
MAPT	Tau	AD, FTD, CTE, PD	NG_007398.1	Cytoplasmic
FUS	FUS	FTD, ALS	NG_012889.2	Nuclear
SOD1	SOD1	ALS	NG_008689.1	Cytoplasmic
TIA1	TIA1	ALS	NG_029967.1	Cytoplasmic & Nuclear
ATXN2	Ataxin 2	ALS	NG_011572.2	Cytoplasmic
HNRNPA1	hnRNPA1	ALS	NG_033830.1	Nuclear
HNRNPA2B1	hnRNPA2B1	ALS	NG_029680.1	Nuclear
EWSR1	EWS RNA Binding Protein 1	ALS	NG_023240.1	Nuclear
TAF15	TATA box binding protein factor 15	ALS	NG_023279.1	Nuclear
Abbreviations: ALS, Amyotrophic Lateral Sclerosis; FTD, Frontotemporal Dementia; PD, Parkinsons Disease; AD, Alzheimer's Disease; CTE, Chronic Traumatic Encephalopathy; LBD, Lewy Body Dementia				

[0113] Table 3 describes a list of target neurodegenerative disease proteins to generate protein arrangements that recapitulate neurodegenerative disease pathology. Novel arrangements of the photoreceptors in Table 2 fused to neurodegenerative disease proteins such as those listed in Table 3 that respond to these various blue light exposure paradigms to recapitulate neurodegenerative disease pathologies are disclosed herein. This technology is also used to aggregate the prion-like domains/LCD/IDDs of truncated versions of these components that comprise neuropathological aggregates in patients. In this example, studies have been performed with CRY2OLIG and LOV fused to TDP-43, α-synuclein,and Tau proteins. In another example, the target neurodegenerative disease protein can be Huntingtin gene/protein (Accession Ref. NM_002111; NP_002102.4). However, a method was developed that can be applied to any photoreceptor with dimerizing or oligomerization capabilities due to the light treatment paradigms created. The primary purpose of this method is to control the local concentration of neurodegenerative disease proteins for specific periods of time forcing intramolecular crowding of proteins that contain LCDs and aggregate in neurodegenerative diseases. Each neurodegenerative disease protein and photoreceptor arrangement can require specific light stimulation parameters due to the nature of the protein. For example, cytoplasmic proteins or truncated versions of nuclear proteins to localize them to the cytoplasm typically (but not always) require short stimulation paradigms while predominantly nuclear proteins chronic stimulation since the protein will need to be trapped in the cytoplasm during translation (e.g. TDP-43, FUS). Details of the stimulation paradigms are discussed below.

[0114] Light exposure then forces these unique fusion protein arrangements into close proximity and employing chronic or repeated light stimulation, neurodegenerative disease aggregate pathologies of full length proteins or the LCDs alone can be obtained. This temporal and spatial control of neurodegenerative disease aggregates is novel since it does not require overexpression or mutation that are only relevant to a small subset of patients for each disease (Table 1). These proteins are forced to interact and form the disease pathology as occurs in human patients rather than filling the cell with these aggregate prone proteins.

[0115] Beyond protein aggregation, this system creates light-induced pathologies that mimic key pathological features found in patients making it unique compared to overexpression systems. The TDP-43 protein, which contains an LCD, was combined with the CRY2OLIG photoreceptor domain which clusters when exposed to blue light and becomes insoluble and aggregated with persistent light treatment. Fusion proteins of the full length and partial LCD sequence were generated to recapitulate human neurodegenerative disease pathology, including the cytoplasmic mislocalization of nuclear proteins that occurs in patients with ALS and FTD. This system could induce neurodegenerative disease protein aggregates in live HEK cells by exposing them to various blue light stimuli paradigms (FIGS. 4-5). In addition, biochemical hallmarks of ALS, FTD, and AD (FIG. 7) were produced showing that the cell is responding to the light-induced aggregates as observed in patient CNS despite the addition of these tags. Notably, TDP-43 neuropathology is one of the more complex neuropathologies to mimic since it is a predominantly nuclear protein but is found to be mislocalized to the cytoplasm in patients. Employing this DNA arrangement and light stimulation system as an example,

cytoplasmic TDP-43 aggregates were obtained that are also ubiquitinylated, cleaved, and hyperphosphorylated as observed in ALS, FTD, and AD patients. TDP-43 pathology is also found in AD as well as Chronic Traumatic Encephalopathy (CTE) thus highlighting the potential disease relevance of this work. In addition, a protein arrangement and light stimulation paradigm was developed to induce the aggregation of α-synuclein (FIG. 6), which is found in the CNS of patients diagnosed with Parkinson's Disease and Lewy Body Dementia. Methods were also developed to induce intracellular aggregation of Tau protein using both the Cry-PHR and LOV photoreceptors (FIG. 7) and persistent blue light stimulation. These tau tangles are pathological hallmarks of AD, FTD and CTE in HEK cells. These also exhibit pathological hallmarks of Tauopathy observed in patients including hyperphosphorylation using specific antibodies developed against pathological tau inclusions (FIGS. 7-8). Finally, it was shown that this method can be utilized to seed aggregations, as aggregates of TDP-43 formed using this method recruit endogenous TDP-43 to seed the pathogenic neuropathology (FIGS. 5F, 5G).

[0116] A novel methodology to force oligomerization and aggregation of LOV domain proteins fused to proteins that contain LCDs was also developed. The LOV domains, including NcVVDY50W has only been shown to dimerize with blue light stimulation. Using a chronic blue light stimulation paradigm (described in FIGS. 3 and 6-8), oligomerization and eventual aggregation of a LCD containing protein fused to the LOV sequence is induced. This amino acid sequence is significantly smaller than the PHR domain of CRY2 and may act as an alternative to CRY2 PHR since it is less likely to interfere with the endogenous target protein function.

[0117] In some embodiments, DNA arrangements are constructed that encode for the PHR domains (CRY2PHR or CRY2OLIG) or LOV photoreceptor proteins (NcVVD, NcVVDY50W, Vfau1, YtvA, EL222, RsLOV, AsLOV2) (or 90% similarity) fused to either the LCD fragment or full length neurodegenerative disease proteins listed in Table 3 (or 90% similarity). In some embodiments, disclosed herein are methods of employing blue light exposure treatment paradigms to induce these neurodegenerative disease pathologies. In other embodiments, the resulting protein aggregates and cell viability are used as a readout for neurodegenerative disease drug screening (FIG. 10). This system is used by pharmacologically or genetically mitigating neurodegenerative disease pathology formation or resident time can identify novel compounds for the treatment of specific neurodegenerative diseases. The following embodiments are also disclosed:

1. Generation of Novel Model Systems: These photoreceptor sequences are inserted into the genome of various in vitro and in vivo systems which can act as a new model to study neurodegenerative diseases. Some examples of in vitro uses include human and rodent cell lines, induced pluripotent stem cells (iPSCs), or yeast. Some examples of in vivo uses include invertebrates: Drosophila melanogaster (fruit fly), Caenorhabditis elegans (round worm), or Danio rerio (zebrafish). Other examples of in vivo uses include vertebrates: mouse, rat, or non-human primate.
2. These compounds, methods, and systems (such as iPSC) with edited genomes are used in high throughput drug screening systems. To achieve this, neurodegenerative disease pathologies are induced by stimulating cells with light. Cell viability and formation and residence time of protein aggregate/pathology in the presence of compound libraries are then examined. In addition, assays also involve employing survival and neuropathology of in vivo models following induction with light.

SEQUENCES

Amino Acid Sequences of Photoreceptor Tools:

[0118] Amino Acid Sequences of the Photolyase-Homologous Region (PHR) domain of the *Arabidopsis* Cryptochrome 2 protein:

SEQ ID NO: 1. *Cryptochrome 2 PHR Domain; Cry2PHR:*

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTREAQIMIGAA

SEQ ID NO: 2. *Cryptochrome 2 PHR Domain with E490G substitution; Cry2Olig:* (E490G in bold)

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTR**G**AQIMIGAA

[0119] Amino Acid Sequences containing the Light-Oxygen-Voltage-Sensing Domain (LOV) from *Neurospora* Vivid protein:

SEQ ID NO: 3. *VVD LOV Domain only:*

MTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQ
VEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETE

SEQ ID NO: 4. *NcVivid (NcVVD):*

HTLYAPGGYDIMGYLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPD
GMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETE

SEQ ID NO: 5. *NcVivid Y50W substitution; NcVVDY50W:* (Y50W in bold)

HTLYAPGGYDIMG**W**LIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPD
GMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETE

TDP-43 Protein Arrangements Generated:

1. Cry2olig Fusion Proteins Amino Acid Sequences:

A) Full Length TDP-43 Protein No Reporter

[0120]

SEQ ID NO: 6. Cry2olig-TDP-43:

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARGMSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQC
MRGVRLVEGILHAPDAGWGNLVYVVNYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTF
GEVLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMT
EDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGF
GNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGN
NQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGM

SEQ ID NO: 7. TDP-43-Cry2olig:

MSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVVNYP
KDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYE
TQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVT
FADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGG
GMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNS
GAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGM LEAT
MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK

KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAA

B) Truncated TDP-43 Proteins No Reporter

[0121]

SEQ ID NO: 8. TDP-43 $^{(AA274-414)}$-Cry2olig:

MGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLA
SQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWG
MLEATMKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALG
SDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSY
WKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYA
KNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSH
LRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDAD
LECDILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYA
KPIVDIDTARELLAKAISRTRGAQIMIGAA

SEQ ID NO: 9. TDP-43 $^{(AA191-414)}$-Cry2olig:

MRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNR
QLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMG
MLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSG
WGMLEATMKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLK
ALGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSF
NSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLI
DYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQS
LLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLL
DADLECDILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGT
NYAKPIVDIDTARELLAKAISRTRGAQIMIGAA

SEQ ID NO: 10. TDP-43 $^{(AA105-414)}$-Cry2olig:

MDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNS
KQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAE
PKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSS
WGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSS
MDSKSSGWGM
LEATMKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSD

LTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYW
KKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAK
NSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHL
RFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADL
ECDILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAK
PIVDIDTARELLAKAISRTRGAQIMIGAA

SEQ ID NO: 11. Cry2olig-TDP-43 (AA274-414):

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARGGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSI
NPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSA
SNAGSGSGFNGGFGSSMDSKSSGWGM

SEQ ID NO: 12. Cry2olig-TDP-43 (AA191-414):

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARGRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQI
AQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFG
AFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGW
GSASNAGSGSGFNGGFGSSMDSKSSGWGM

SEQ ID NO: 13. Cry2olig-TDP-43 (AA105-414):

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARGDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTE
YETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAF
VTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNM
GGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGS
NSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGM

C) Full Length TDP-43 Protein + mCherry Reporter

[0122]

SEQ ID NO: 14. Cry2olig-TDP-43-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARG
MSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVVNYP
KDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYE
TQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVT
FADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGG
GMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNS
GAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGMSRDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHE
FEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGV
VTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTY
KAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

SEQ ID NO: 15. TDP-43-Cry2olig-mCherry:

MSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVVNYP
KDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYE
TQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVT
FADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGG
GMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNS
GAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGMLEATMKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFI
WCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVK
EKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLEN
EAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARD
KNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWATGW
MHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIR
QWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELLAKAISRTRGAQIMIGAAARDPPVATMVSK
GEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHP

ADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYP
EDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

SEQ ID NO: 16. mCherry-TDP-43-Cry2olig:

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKMSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVV
NYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFT
EYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFA
FVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNM
GGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGS
NSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGMLEATMKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFP
VFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHT
VKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGL
ENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWA
RDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWAT
GWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGE
YIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELLAKAISRTRGAQIMIGAA

D) Truncated TDP-43 Proteins + mCherry Reporter

[0123]

SEQ ID NO: 17. TDP-43 $^{(AA274-414)}$-Cry2olig-mCherry:

MGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLA
SQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWG
MLEATMKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALG
SDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSY
WKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYA
KNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSH
LRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDAD
LECDILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYA
KPIVDIDTARELLAKAISRTRGAQIMIGAAARDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGR
PYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQ
DGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPG
AYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

SEQ ID NO: 18. TDP-43 $^{(AA191-414)}$-Cry2olig-mCherry:

MRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNR
QLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMG
MLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSG
WGMLEATMKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLK
ALGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSF
NSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLI
DYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQS
LLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLL
DADLECDILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGT
NYAKPIVDIDTARELLAKAISRTRGAQIMIGAAARDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEG
EGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDS
SLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQ
LPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

SEQ ID NO: 19. TDP-43 $^{(AA105-414)}$-Cry2olig-mCherry:

MDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNS
KQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAE
PKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSS
WGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSS
MDSKSSGWGMLEATMKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSL
AHLSQSLKALGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYC
EKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKL
LNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICF
NFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWG
MKYFWDTLLDADLECDILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTV
LKASGVELGTNYAKPIVDIDTARELLAKAISRTRGAQIMIGAAARDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVN
GHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFED
GGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEV
KTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

SEQ ID NO: 20. mCherry-Cry2olig-TDP-43 (AA274-414):

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYK
MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC

DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARGGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSI
NPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSA
SNAGSGSGFNGGFGSSMDSKSSGWGM

SEQ ID NO: 21. mCherry-Cry2olig-TDP-43 (AA191-414):

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYK
MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARGRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQI
AQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFG
AFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGW
GSASNAGSGSGFNGGFGSSMDSKSSGWGM

SEQ ID NO: 22. mCherry-Cry2olig-TDP-43 (AA105-414):

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKMKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSD
LTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYW
KKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAK
NSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHL
RFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADL
ECDILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAK
PIVDIDTARELLAKAISRTRGAQIMIGAAARGDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRF
TEYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAF
AFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSN
MGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYS
GSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGM

SEQ ID NO: 23. Cry2olig-TDP-43 $^{(AA274-414)}$-mCherry:

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARGGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSI
NPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSA
SNAGSGSGFNGGFGSSMDSKSSGWGMSRDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGR
PYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQ
DGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPG
AYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

SEQ ID NO: 24. Cry2olig-TDP-43 $^{(AA191-414)}$-mCherry:

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARGRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQI
AQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFG
AFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGW
GSASNAGSGSGFNGGFGSSMDSKSSGWGMSRDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEG
EGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDS
SLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQ
LPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

SEQ ID NO: 25. Cry2olig-TDP-43 $^{(AA105-414)}$-mCherry:

MDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNS
KQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAE
PKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSS
WGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSS
MDSKSSGWGMLEATMKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSL
AHLSQSLKALGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYC
EKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKL
LNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICF
NFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWG
MKYFWDTLLDADLECDILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTV
LKASGVELGTNYAKPIVDIDTARELLAKAISRTRGAQIMIGAASRDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVN

GHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFED
GGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEV
KTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

2.NcVVDY50W Fusion Proteins Amino Acid Sequences:

A) Full length TDP-43 Protein no reporter

[0124]

SEQ ID NO: 26. NcVVDY50W-TDP-43

MHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQS
PDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEAMS
EYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVVNYPKD
NKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYETQ
VKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFA
DDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGG
MNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSG
AAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGM

SEQ ID NO: 27. TDP-43-NcVVDY50W

MSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVVNYP
KDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYE
TQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVT
FADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGG
GMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNS
GAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGMFRAQRHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTS
CALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEV
VNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETE

B) Truncated TDP-43 protein no reporter

[0125]

SEQ ID NO: 28. TDP-43 $^{(AA105-414)}$- NcVVDY50W

MDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNS
KQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAE
PKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSS
WGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSS
MDSKSSGWGMFRAQRHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGY

SNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEY
RYSMGFQCETE

SEQ ID NO: 29. TDP-43 $^{(AA191-414)}$- NcVVDY50W

MRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNR
QLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMG
MLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSG
WGMFRAQRHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLG
RNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQ
CETE

SEQ ID NO: 30. TDP-43 $^{(AA274-414)}$- NcVVDY50W

MGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLA
SQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWG
MFRAQRHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNC
RFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCET
E

SEQ ID NO: 31. NcVVDY50W- TDP-43 $^{(AA105-414)}$

MHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQS
PDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEADLI
VLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQS
QDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKH
NSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWG
MMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMD
SKSSGWGM

SEQ ID NO: 32. NcVVDY50W- TDP-43 $^{(AA191-414)}$

MHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQS
PDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEARKV
FVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERS
GRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLAS
QQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGM

SEQ ID NO: 33. NcVVDY50W- TDP-43 (AA274-414)

HTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPD
GMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEAGRFGG
NPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQS
GPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGM

C) Full length TDP-43 Protein + mCherry Reporter

[0126]

SEQ ID NO: 34. NcVVDY50W-TDP-43-mCherry

MHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQS
PDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEAMS
EYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVVNYPKD
NKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYETQ
VKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFA
DDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGG
MNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSG
AAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGMFAPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIE
GEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVT
QDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKK
PVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

SEQ ID NO: 35. mCherry-TDP-43-NcVVDY50W

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLKMSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNL
VYVVNYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGF
VRFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPF
RAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQ
GSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNN
SYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGMFRAQRHTLYAPGGYDIMGWLIQIMNRPNPQVEL
GPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNA
EVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETE

D) Truncated TDP-43 protein + mCherry Reporter

[0127]

SEQ ID NO: 36. mCherry-TDP-43 $^{(AA105-414)}$- NcVVDY50W

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLKDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCD
CKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGIS
VHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAA
QAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGF
NGGFGSSMDSKSSGWGMFRAQRHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEA
FLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPV
RDETGEYRYSMGFQCETE

SEQ ID NO: 37. mCherry-TDP-43 $^{(AA191-414)}$- NcVVDY50W

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLKRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPK
HNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSW
GMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSM
DSKSSGWGMFRAQRHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYS
NAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYR
YSMGFQCETE

SEQ ID NO: 38. mCherry-TDP-43 $^{(AA274-414)}$- NcVVDY50W

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLKGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGM
MGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSK
SSGWGMFRAQRHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAE
VLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSM
GFQCETE

SEQ ID NO: 39. NcVVDY50W-TDP-43 $^{(AA105-414)}$-mCherry

MHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQS
PDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEADLI
VLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQS
QDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKH
NSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWG

MMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMD
SKSSGWGMFAPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFA
WDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPV
MQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQ
YERAEGRHSTGGMDELYK

SEQ ID NO: 40. NcVVDY50W-TDP-43 $^{(AA191-414)}$-mCherry

MHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQS
PDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEARKV
FVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERS
GRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLAS
QQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGM
FAPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFM
YGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMG
WEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRH
STGGMDELYK

SEQ ID NO: 41. NcVVDY50W-TDP-43 $^{(AA274-414)}$-mCherry

MHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQS
PDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEAGRF
GGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQN
QSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGMFAP
VATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGS
KAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEA
SSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTG
GMDELYK

Alpha Synuclein Protein Arrangements Generated:

1. Cry2olig Fusion Proteins Amino Acid Sequences:

A) Full Length alpha synuclein (asyn) Protein No Reporter

[0128]

SEQ ID NO: 42. Cry2olig-asyn

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC

LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAMDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVH
GVATVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYE
MPSEEGYQDYEPEA

SEQ ID NO: 43. Asyn-Cry2

MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQVTNVGGAVVTGVTA
VAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEADPPVATMKMDKK
TIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLIKTHNTISA
ILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKCLDMSIESV
MLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTS
LLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVD
KFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYIS
GSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELL
AKAISRTRGAQIMIGAA

B) Full Length alpha synuclein (asyn) Protein + mCherry Reporter

[0129]

SEQ ID NO: 44. Cry2olig-asyn-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAMDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVH
GVATVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYE
MPSEEGYQDYEPEADPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGG
PLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPS
DGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDY
TIVEQYERAEGRHSTGGMDELYK

SEQ ID NO: 45. Cry2olig-mCherry-Asyn

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPY
EGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQD
GEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGA
YNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYKMDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLY
VGSKTKEGVVHGVATVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILED
MPVDPDNEAYEMPSEEGYQDYEPEA

SEQ ID NO: 46. Asyn-Cry2-mCherry

MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQVTNVGGAVVTGVTA
VAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEADPPVATMKMDKK
TIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLIKTHNTISA
ILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKCLDMSIESV
MLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTS
LLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVD
KFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYIS
GSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELL
AKAISRTRGAQIMIGAAAMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLP
FAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDG
PVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIV
EQYERAEGRHSTGGMDELYK

1. NcVVD Fusion Proteins Amino Acid Sequences:

A) Full Length alpha synuclein (asyn) Protein No Reporter

[0130]

SEQ ID NO: 47. Asyn- *NcVVDY50W*

MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQVTNVGGAVVTGVTA
VAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEAFHTLYAPGGYDIM
GWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYV
DSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETE

SEQ ID NO: 48. *NcVVDY50W* -Asyn

MHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQS
PDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEAMD
VFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQVTNVGGAVVTGVTAVA
QKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEA

B) Full Length alpha synuclein (asyn) Protein + mCherry Reporter

[0131]

SEQ ID NO: 49. mCherry-Asyn- *NcVVDY50W*

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYSKMDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQVTNVGGAVV
TGVTAVAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEAFHTLYAPG
GYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPK
STRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETE

SEQ ID NO: 50. *mCherry-NcVVDY50W* -Asyn

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLRSRAQRHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAE
VLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSM
GFQCETEALEFCSRRYRGPMDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEK
TKEQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQ
DYEPEA

SEQ ID NO: 51. *NcVVDY50W* -Asyn-mCherry

MHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQS
PDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEAMD
VFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQVTNVGGAVVTGVTAVA
QKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEAFAPVATMVSKGEED
NMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPD
YLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGAL
KGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

SEQ ID NO: 52. Alphasynuclein-mCherry-NcVVD (wildtype)

MDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQVTNVGGAVVTGVTA
VAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEALLPVATMVSKGEE
DNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIP
DYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGA
LKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYKSGLRS
RAQASNSAVDGTAGPMHTLYAPGGYDIMGYLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGY
2SNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGE
YRYSMGFQCETEGIHRI*

SEQ ID NO: 53. mCherry-alphasynuclein-NcVVD (wildtype)

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLRSRAQMDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVAEKTKEQVTN
VGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEGYQDYEPEAS
NSAVDGTAGPMHTLYAPGGYDIMGYLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVL
GRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGF
QCETEGIHRI*

SEQ ID NO: 54. mCherry-NcVVD (wildtype)-alphasynuclein

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLRSRAQASNSAVDGTAGPMHTLYAPGGYDIMGYLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASE
AFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIP
VRDETGEYRYSMGFQCETEGMDVFMKGLSKAKEGVVAAAEKTKQGVAEAAGKTKEGVLYVGSKTKEGVVHGVATVA
EKTKEQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMPVDPDNEAYEMPSEEG
YQDYEPEAHRI*

Tau

[0132]

SEQ ID NO: 55. mCherry-Tau

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLRSRAQASNSAVDGTAGPMAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTP
TEDGSEEPGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVS

KSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPG
SRSRTPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNV
QSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGG
GNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLGIHRI*

SEQ ID NO: 56. mCherry-VfAU-Tau

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLRSRAQASNSAVDGTAGPMPDYSLVKALQMAQQNFVITDASLPDNPIVYASRGFLTLTGYSLDQILGRNCRFL
QGPETDPRAVDKIRNAITKGVDTSVCLLNYRQDGTTFWNLFFVAGLRDSKGNIVNYVGVQSKVSEDYAKLLVNEQNIEY
KGVRTSNMLRRKPGGIHRIMAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGS
EEPGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDG
TGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTP
SLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGS
KDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIET
HKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLITDHNQPYHICR
GFTCFKKPPTPPPEPET*

SEQ ID NO: 57. mCherry-(y50w)-Tau

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLRSRAQASNSAVDGTAGPMHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYAS
EAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMI
PVRDETGEYRYSMGFQCETEGMAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTED
GSEEPGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSK
DGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRS
RTPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSK
CGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNK
KIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLHRI*

SEQ ID NO: 58. mCherry-Tau-NcVVD(y50w)

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLTMAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDAKS
TPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGA

DGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKK
VAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGG
SVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKA
KTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLRRAQRHTLYAPGGYDIMGWLI
QIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNT
INTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEALEFCSRRYRGPGIHRI*

SEQ ID NO: 59. mCherry-NcVVD(y50w)-Tau

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLRSRAQRHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAE
VLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSM
GFQCETEALAMAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDA
KSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKG
ADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPK
KVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGG
GSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAK
AKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLRCSRRYRGPGIHRI*

SEQ ID NO: 60. Tau-mCherry-NcVVD(y50w)

MAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDAKSTPTAEDVT
APLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATP
RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPK
SPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPV
DLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIV
YKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLALPVATMVSKGEEDNMAIIKEFMRFKVHME
GSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVM
NFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHY
DAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYKSGLRSRAQRHTLYAPGGYDIM
GWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYV
DSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEALEFCSRRYRGPGIHRI*

SEQ ID NO: 61. Cry-mCherry-Tau

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF

PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPY
EGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQD
GEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGA
YNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYKSRMAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQ
EGDTDAGLKESPLQTPTEDGSEEPGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLE
DEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSG
DRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGG
GKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQ
SKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADE
VSASLAKQGLGDSRS*

SEQ ID NO: 62. Tau-mCherry

MAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDAKSTPTAEDVT
APLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATP
RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPK
SPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPV
DLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIV
YKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLFATMVSKGEEDNMAIIKEFMRFKVHMEGSV
NGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFE
DGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAE
VKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYKSGLRSRAQASNSAVDGTAGPGSTG
SR*

SEQ ID NO: 63. Tau-Cry2olig-mCherry

MAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDAKSTPTAEDVT
APLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATP
RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPK
SPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPV
DLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIV
YKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLALPDSDLEATMKMDKKTIVWFRRDLRIEDNP
ALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLIKTHNTISAILDCIRVTGATKVVF
NHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITA
AAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRH
VFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYP
LVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYISGSIPDGHELDRLDN
PALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELLAKAISRTRGAQIMI
GAAARDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDIL
SPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQK

KTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYER
AEGRHSTGGMDELYK*

SEQ ID NO: 64. Cry2Olig-Tau-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAPMAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESP
LQTPTEDGSEEPGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQAR
MVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPG
TPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLS
NVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVP
GGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLGD
PPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMY
GSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGW
EASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHST
GGMDELYK*

SEQ ID NO: 65. Cry-mCherry-Tau

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPY
EGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQD
GEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGA
YNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYKSRMAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQ
EGDTDAGLKESPLQTPTEDGSEEPGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLE
DEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSG
DRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGG
GKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQ
SKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADE
VSASLAKQGLGDSRS*

SEQ ID NO: 66. mCherry-Tau-NcVVD(y50w)

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLTMAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDAKS
TPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGA
DGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKK
VAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGG
SVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKA
KTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLRRAQRHTLYAPGGYDIMGWLI
QIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNT
INTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETEALEFCSRRYRGPGIHRI*

SEQ ID NO: 67. mCherry-NcVVD(y50w)-Tau

MVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAY
VKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSER
MYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMD
ELYKSGLRSRAQRHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAE
VLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSM
GFQCETEALAMAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDA
KSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKG
ADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPK
KVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGG
GSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAK
AKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLRCSRRYRGPGIHRI*

SEQ ID NO: 68. Cry-Tau

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAQMAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESP
LQTPTEDGSEEPGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQAR
MVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPG
TPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLS
NVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVP

GGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLATL
DHNQPYHICRGFTCFKKPPTPPPEPET*

SEQ ID NO: 69. NcVVD(y50w)-Tau

MHTLYAPGGYDIMGWLIQIMNRPNPQVELGPVDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQS
PDGMVKPKSTRKYVDSNTINTMRKAIDRNAEVQVEVVNFKKNGQRFVNFLTMIPVRDETGEMAEPRQEFEVMEDHA
GTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAA
QPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAPPGQKGQANA
TRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAPVP
MPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKVTSKCGSLGNI
HHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRH
LSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLHRI*

SEQ ID NO: 70. Tau-Cry

MAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDAKSTPTAEDVT
APLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATP
RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPK
SPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPV
DLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIV
YKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLMKMDKKTIVWFRRDLRIEDNPALAAAAHEG
SVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLIKTHNTISAILDCIRVTGATKVVFNHLYDPVSLV
RDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKCLDMSIESVMLPPPWRLMPITAAAEAIWACSI
EELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSKKVVGNSTSLLSPYLHFGEISVRHVFQCARMKQ
IIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFFPWDADVDKFKAWRQGRTGYPLVDAGMREL
WATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLECDILGWQYISGSIPDGHELDRLDNPALQGAKYD
PEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPIVDIDTARELLAKAISRTRGAQIMIGAAATLDHN
QPYHICRGFTCFKKPPTPPPEPET*

SEQ ID NO: 71. Tau-VfAU

MAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDAKSTPTAEDVT
APLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATP
RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPK
SPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPV
DLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIV
YKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLPDYSLVKALQMAQQNFVITDASLPDNPIVYA
SRGFLTLTGYSLDQILGRNCRFLQGPETDPRAVDKIRNAITKGVDTSVCLLNYRQDGTTFWNLFFVAGLRDSKGNIVNYV
GVQSKVSEDYAKLLVNEQNIEYKGVRTSNMLRRKPGLQSTVPRARDPPDLDN*

SEQ ID NO: 72. Tau-NcVVD(y50w)

MAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDAKSTPTAEDVT
APLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATP
RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPK
SPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPV
DLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIV
YKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLHTLYAPGGYDIMGWLIQIMNRPNPQVELGP
VDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEV
QVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETELQSTVPRARDPPDLDN*

SEQ ID NO: 73. Tau-NcVVD(wildtype)

MAEPRQEFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDAKSTPTAEDVT
APLVDEGAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATP
RGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPK
SPSSAKSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPV
DLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIV
YKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLHTLYAPGGYDIMGWLIQIMNRPNPQVELGP
VDTSCALILCDLKQKDTPIVYASEAFLYMTGYSNAEVLGRNCRFLQSPDGMVKPKSTRKYVDSNTINTMRKAIDRNAEV
QVEVVNFKKNGQRFVNFLTMIPVRDETGEYRYSMGFQCETELQSTVPRARDPPDLDN*

SEQ ID NO: 74. VfAU-Tau

MPDYSLVKALQMAQQNFVITDASLPDNPIVYASRGFLTLTGYSLDQILGRNCRFLQGPETDPRAVDKIRNAITKGVDTS
VCLLNYRQDGTTFWNLFFVAGLRDSKGNIVNYVGVQSKVSEDYAKLLVNEQNIEYKGVRTSNMLRRKPGSLMAEPRQ
EFEVMEDHAGTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQTPTEDGSEEPGSETSDAKSTPTAEDVTAPLVDE
GAPGKQAAAQPHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIATPRGAAP
PGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSSA
KSRLQTAPVPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNIKHVPGGGSVQIVYKPVDLSKV
TSKCGSLGNIHHKPGGGQVEVKSEKLDFKDRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSPV
VSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGLSNSAVDGTAGPGSTGSR*

SEQ ID NO: 75. Cry-TDP(F147L)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARGMSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQC

MRGVRLVEGILHAPDAGWGNLVYVVNYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTF
GEVLMVQVKKDLKTGHSKGLGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMT
EDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGF
GNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGN
NQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGMSRDPPVATMV
SKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKH
PADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMY
PEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELY
K*

SEQ ID NO: 76. Cry-TDP(F229L)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAARGMSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQC
MRGVRLVEGILHAPDAGWGNLVYVVNYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTF
GEVLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMT
EDELREFFSQYGDVMDVFIPKPFRALAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGF
GNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGN
NQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGMSRDPPVATMV
SKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKH
PADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMY
PEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELY
K*

SEQ ID NO: 77. Cry-TDP(S409,410A)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAQMSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCM
RGVRLVEGILHAPDAGWGNLVYVVNYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGE
VLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTED
ELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGN
QGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQ

NQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKAAGWGMWDPPVATMVSK
GEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHP
ADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYP
EDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK
*

SEQ ID NO: 78. Cry-TDP(S409,410D)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAAQMSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCM
RGVRLVEGILHAPDAGWGNLVYVVNYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGE
VLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTED
ELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGN
QGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQ
NQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKDDGWGMWDPPVATMVSK
GEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHP
ADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYP
EDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK
*

SEQ ID NO: 79. Cry-TDP(A321V)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAAQMSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCM
RGVRLVEGILHAPDAGWGNLVYVVNYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGE
VLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTED
ELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGN
QGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPVMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQ
NQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGWDPPVATMVSKGEE
DNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIP
DYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGA
LKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK*

SEQ ID NO: 80. Cry-TDP(m337V)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAAQMSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCM
RGVRLVEGILHAPDAGWGNLVYVVNYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGE
VLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTED
ELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGN
QGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMVGMLASQQNQSGPSGNNQN
QGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGWDPPVATMVSKGEED
NMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPD
YLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGAL
KGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK*

SEQ ID NO: 81. Cry-TDP(LCD, A321V)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAQGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSI
NPVMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSA
SNAGSGSGFNGGFGSSMDSKSSGWGMRDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRP
YEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQD
GEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGA
YNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK*

SEQ ID NO: 82. Cry-TDP(LCD, M337V)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI

VDIDTARELLAKAISRTRGAQIMIGAAAQGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSI
NPAMMAAAQAALQSSWGMVGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSA
SNAGSGSGFNGGFGSSMDSKSSGWGMRDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRP
YEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQD
GEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGA
YNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK*

SEQ ID NO: 83. Cry-TDP(LCD, S409,410A)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAQGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSI
NPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSA
SNAGSGSGFNGGFGSSMDSKAAGWGMRDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGR
PYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQ
DGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPG
AYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK*

SEQ ID NO: 84. Cry-TDP(LCD, S409,410D)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAPGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSIN
PAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSAS
NAGSGSGFNGGFGSSMDSKDDGWGMTRDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGR
PYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQ
DGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPG
AYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK*

SEQ ID NO: 85. Cry-TDP(SFL)-mcherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC

LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAQMSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCM
RGVRLVEGILHAPDAGWGNLVYVVNYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGE
VLMVQVKKDLKTGHSKGLGLVRFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVLVGRCTEDMTED
ELREFFSQYGDVMDVFIPKPFRALALVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGN
QGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQ
NQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGMWDPPVATMVSKG
EEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPA
DIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPE
DGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK*

SEQ ID NO: 86. Cry-TDP(RRM1)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAQDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEY
ETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEI
EGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTV
TQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAK
KPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK*

SEQ ID NO: 87. Cry-TDP(RRM2)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAQRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIA
QSLCGEDLIIKGISVHISNAEPRDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAK
LKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKL
RGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDI
TSHNEDYTIVEQYERAEGRHSTGGMDELYK*

SEQ ID NO: 88. Cry-TDP(RRM1+2)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAQDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEY
ETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFV
TFADDQIAQSLCGEDLIIKGISVHISNAEPRDPPVATMVSKGEEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRP
YEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQD
GEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGA
YNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK*

SEQ ID NO: 89. Cry-TDP(dLCD)-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAQMSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCM
RGVRLVEGILHAPDAGWGNLVYVVNYPKDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGE
VLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTED
ELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSRDPPVATMVSKG
EEDNMAIIKEFMRFKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPA
DIPDYLKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPE
DGALKGEIKQRLKLKDGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK*

FUS Protein Arrangements Generated:

1. Cry2olig Fusion Proteins Amino Acid Sequences:

[0133]

A) Full Length FUS Protein No Reporter

SEQ ID NO: 90. Cry2O1ig-FUS

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK

KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAQCRATMYPYDVPDYAMASNDYTQQATQSYGAYPTQPGQGYSQQSSQPY
GQQSYSGYSQSTDTSGYGQSSYSSYGQSQNTGYGTQSTPQGYGSTGGYGSSQSSQSSYGQQSSYPGYGQQPAPSSTS
GSYGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGGGGNYGQDQSS
MSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGRGGSGGGGGGGGGGYNRSSGGYEPRGRGGGRGGRGGM
GGSDRGGFNKFGGPRDQGSRHDSEQDNSDNNTIFVQGLGENVTIESVADYFKQIGIIKTNKKTGQPMINLYTDRETGK
LKGEATVSFDDPPSAKAAIDWFDGKEFSGNPIKVSFATRRADFNRGGGNGRGGRGRGGPMGRGGYGGGGSGGGGR
GGFPSGGGGGGGQQRAGDWKCPNPTCENMNFSWRNECNQCKAPKPDGPGGGPGGSHMGGNYGDDRRGGRGG
YDRGGYRGRGGDRGGFRGGRGGGDRGGFGPGKMDSRGEHRQDRRERPY

B) Full Length FUS Protein + mCherry Reporter
SEQ ID NO: 91. Cry2Olig-FUS-mCherry

MKMDKKTIVWFRRDLRIEDNPALAAAAHEGSVFPVFIWCPEEEGQFYPGRASRWWMKQSLAHLSQSLKALGSDLTLI
KTHNTISAILDCIRVTGATKVVFNHLYDPVSLVRDHTVKEKLVERGISVQSYNGDLLYEPWEIYCEKGKPFTSFNSYWKKC
LDMSIESVMLPPPWRLMPITAAAEAIWACSIEELGLENEAEKPSNALLTRAWSPGWSNADKLLNEFIEKQLIDYAKNSK
KVVGNSTSLLSPYLHFGEISVRHVFQCARMKQIIWARDKNSEGEESADLFLRGIGLREYSRYICFNFPFTHEQSLLSHLRFF
PWDADVDKFKAWRQGRTGYPLVDAGMRELWATGWMHNRIRVIVSSFAVKFLLLPWKWGMKYFWDTLLDADLEC
DILGWQYISGSIPDGHELDRLDNPALQGAKYDPEGEYIRQWLPELARLPTEWIHHPWDAPLTVLKASGVELGTNYAKPI
VDIDTARELLAKAISRTRGAQIMIGAAAQCRATMYPYDVPDYAMASNDYTQQATQSYGAYPTQPGQGYSQQSSQPY
GQQSYSGYSQSTDTSGYGQSSYSSYGQSQNTGYGTQSTPQGYGSTGGYGSSQSSQSSYGQQSSYPGYGQQPAPSSTS
GSYGSSSQSSSYGQPQSGSYSQQPSYGGQQQSYGQQQSYNPPQGYGQQNQYNSSSGGGGGGGGGGNYGQDQSS
MSSGGGSGGGYGNQDQSGGGGSGGYGQQDRGGRGRGGSGGGGGGGGGGYNRSSGGYEPRGRGGGRGGRGGM
GGSDRGGFNKFGGPRDQGSRHDSEQDNSDNNTIFVQGLGENVTIESVADYFKQIGIIKTNKKTGQPMINLYTDRETGK
LKGEATVSFDDPPSAKAAIDWFDGKEFSGNPIKVSFATRRADFNRGGGNGRGGRGRGGPMGRGGYGGGGSGGGGR
GGFPSGGGGGGGQQRAGDWKCPNPTCENMNFSWRNECNQCKAPKPDGPGGGPGGSHMGGNYGDDRRGGRGG
YDRGGYRGRGGDRGGFRGGRGGGDRGGFGPGKMDSRGEHRQDRRERPYWDPPVATMVSKGEEDNMAIIKEFMR
FKVHMEGSVNGHEFEIEGEGEGRPYEGTQTAKLKVTKGGPLPFAWDILSPQFMYGSKAYVKHPADIPDYLKLSFPEGFK
WERVMNFEDGGVVTVTQDSSLQDGEFIYKVKLRGTNFPSDGPVMQKKTMGWEASSERMYPEDGALKGEIKQRLKLK
DGGHYDAEVKTTYKAKKPVQLPGAYNVNIKLDITSHNEDYTIVEQYERAEGRHSTGGMDELYK

[0134] Amino Acid Sequences of the *Vaucheria frigida (Yellow-green alga) (Conferva frigida)* Aureochrome1 protein (Gene is AURE01):

SEQ ID NO: 92. *VfAU1 (A8QW55):*

MNGLTPPLMFCSRSDDPSSTSNINLDDVFADVFFNSNGELLDIDEIDDFGDNTCPKSSMSVDDDASSQVFQGHLFGNA
LSSIALSDSGDLSTGIYESQGNASRGKSLRTKSSGSISSELTEAQKVERRERNREHAKRSRVRKKFLLESLQQSVNELNHEN
NCLKESIREHLGPRGDSLIAQCSPEADTLLTDNPSKANRILEDPDYSLVKALQMAQQNFVITDASLPDNPIVYASRGFLTL

TGYSLDQILGRNCRFLQGPETDPRAVDKIRNAITKGVDTSVCLLNYRQDGTTFWNLFFVAGLRDSKGNIVNYVGVQSKV
SEDYAK LLVNEQNIEYKGVRTSNMLRRK

SEQ ID NO: 93. *VfAU1-LOV domain:*

PDYSLVKALQMAQQNFVITDASLPDNPIVYASRGFLTLTGYSLDQILGRNCRFLQGPETDPRAVDKIRNAITKGVDTSVC
LLNYRQDGTTFWNLFFVAGLRDSKGNIVNYVGVQSKVSEDYAKLLVNEQNIEYKGVRTS NMLRRK

SEQ ID NO: 94. *VfAU1 - DNA sequence - VfAU1-LOV domain (No Start codon):*

Cctgactacagtctcgtgaaggctctgcaaatggcacaacagaattttgtcattacagacgcctccctcccagacaaccctatcgtctacgccagtaga
gggtttctgacactgacaggctattctctcgaccagatcctgggcaggaactgcaggtttctgcaagggccagaaacagacccaagagctgtggataa
gatcaggaatgccatcaccaaaggcgttgataccagtgtctgtctgctgaattatagacaggatggcacaaccttctggaatctcttcttcgtggctgga
ctcagagattctaagggcaatattgtcaactacgtcggagtgcagtcaaaggtgagcgaagattatgccaagctgctggtcaacgagcagaacattg
agtacaaaggtgtgcgcaccagtaacatgctgcgcagaaag

SEQ ID NO:95. TDP-43 (TAR DNA-binding protein-43)

MSEYIRVTEDENDEPIEIPSEDDGTVLLSTVTAQFPGACGLRYRNPVSQCMRGVRLVEGILHAPDAGWGNLVYVVNYP
KDNKRKMDETDASSAVKVKRAVQKTSDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYE
TQVKVMSQRHMIDGRWCDCKLPNSKQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVT
FADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGG
GMNFGAFSINPAMMAAAQAALQSSWGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNS
GAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWGM

SEQ ID NO:96. TDP-43 (amino acids 105-414)

MDLIVLGLPWKTTEQDLKEYFSTFGEVLMVQVKKDLKTGHSKGFGFVRFTEYETQVKVMSQRHMIDGRWCDCKLPNS
KQSQDEPLRSRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAE
PKHNSNRQLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSS
WGMMGMLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSS
MDSKSSGWGM

SEQ ID NO:97. TDP-43 (amino acids 191-414)

MRKVFVGRCTEDMTEDELREFFSQYGDVMDVFIPKPFRAFAFVTFADDQIAQSLCGEDLIIKGISVHISNAEPKHNSNR
QLERSGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMG
MLASQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSG
WGM

SEQ ID NO:98. TDP-43 (amino acids 274 to 414)

MGRFGGNPGGFGNQGGFGNSRGGGAGLGNNQGSNMGGGMNFGAFSINPAMMAAAQAALQSSWGMMGMLA
SQQNQSGPSGNNQNQGNMQREPNQAFGSGNNSYSGSNSGAAIGWGSASNAGSGSGFNGGFGSSMDSKSSGWG
M

SEQ ID NO:99. AsLOV2

GEFLATTLERIEKNFVITDP RLPDNPIIFASDSFLQLTEY SREEILGRNCRFLQGPETDR ATVRKIRDAIDNQTEVTVQL
INYTKSGKKFWNLFHLQPMR DQKGDVQYFIGVQLDGTEHV RDAAEREGVMLIKKTAENID
EAAKELPDANLRPEDLWANH G

SEQ ID NO:100. EL222

MLDMGQDRPI DGSGAPGADD TRVEVQPPAQ WVLDLIEASP IASVVSDPRL ADNPLIAINQ AFTDLTGYSE EECVGRNCRF LAGSGTEPWL TDKIRQGVRE HKPVLVEILN YKKDGTPFRN AVLVAPIYDD DDELLYFLGS QVEVDDDQPN MGMARRERAA EMLKTLSPRQ LEVTTLVASG LRNKEVAARL GLSEKTVKMH RGLVMEKLNL KTSADLVRIA VEAGI

SEQ ID NO:101. Ytva

MASFQSFGIP GQLEVIKKAL DHVRVGVVIT DPALEDNPIV YVNQGFVQMT GYETEEILGK NCRFLQGKHT DPAEVDNIRT ALQNKEPVTV QIQNYKKDGT MFWNELNIDP MEIEDKTYFV GIQNDITKQK EYEKLLEDSL TEITALSTPI VPIRNGISAL PLVGNLTEER FNSIVCTLTN ILSTSKDDYL IIDLSGLAQV NEQTADQIFK LSHLLKLTGT ELIITGIKPE LAMKMNKLDA NFSSLKTYSN VKDAVKVLPI M

SEQ ID NO:102. RsLOV

MDQKQFEKIRAVFDRSGVALTLVDMSLPEQPVVLANPPFLRMTGYTEGQILGFNCRFLQRGDENAQARAD IRDALKLGRELQVVLRNYRANDEPFDNLLFLHPVGGRPDAPDYFLGSQFELGRSGNSEEAAAAGHAGALT GELARIGTVAARLEMDSRRHLAQAAAALVRAWERRG

[0135] Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of skill in the art to which the disclosed invention belongs.

Claims

1. A nucleotide sequence encoding a chimeric polypeptide, comprising: a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2, and a second nucleotide sequence encoding a low complexity domain from a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15.

2. An expression vector encoding a chimeric polypeptide, comprising: a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2 and a second nucleotide sequence encoding a low complexity domain from a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15, wherein the first nucleotide sequence is operably linked to a promoter.

3. A cell comprising a nucleotide sequence encoding a chimeric polypeptide, comprising: a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2 and a second nucleotide sequence encoding a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15.

4. A chimeric polypeptide comprising: a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2; and a low complexity domain from a neurodegenerative disease target protein selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15.

5. Use of an expression vector encoding a chimeric polypeptide in inducing a neurodegenerative disease pathology in a cell, comprising the steps:

introducing into the cell said expression vector encoding a chimeric polypeptide, comprising: a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2 and a second nucleotide sequence encoding a low complexity domain from a neurodegenerative disease target protein, selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15 wherein the first nucleotide sequence is operably linked to a promoter;
expressing the chimeric polypeptide; and inducing oligomerization of the chimeric polypeptide by stimulation with blue light.

6. The use of claim 5, wherein the cell is a mammalian cell, optionally a human cell; and/or wherein the blue light has a wavelength between 405 nm and 499 nm.

7. Use of an expression vector encoding a chimeric polypeptide in screening for an agent that modulates protein aggregation, comprising the steps:

introducing into a cell said expression vector encoding a chimeric polypeptide, comprising:
a first nucleotide sequence encoding a light-induced oligomerization domain selected from the group consisting of VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV, and AsLOV2 and a second nucleotide sequence encoding a low complexity domain from a neurodegenerative disease target protein, selected from the group consisting of TDP-43, FUS, Alpha synuclein, Tau, TIA1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B 1, EWS RNA Binding Protein 1, and TATA box binding protein factor 15 wherein the first nucleotide sequence is operably linked to a promoter;
expressing the chimeric polypeptide;
introducing the agent into a culture media comprising the cell;
inducing oligomerization of the chimeric polypeptide by stimulation with blue light; and
determining modulation of protein aggregation by the agent.

8. The use of claim 7, wherein the cell is a mammalian cell, optionally a human cell; and/or wherein the blue light has a wavelength between 405 nm and 499 nm.

9. The nucleotide sequence of claim 1, the expression vector of claim 2, the cell of claim 3, the chimeric polypeptide of claim 4, or the use of any one of claims 5-8, wherein the chimeric polypeptide comprises the amino acid sequence of any one of SEQ ID NOs: 6-41 and 75-89.

Patentansprüche

1. Nucleotidsequenz, die für ein chimäres Polypeptid kodiert, umfassend: eine erste Nucleotidsequenz, die für eine lichtinduzierte Oligomerisierungsdomäne kodiert, die aus der aus VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV und AsLOV2 bestehenden Gruppe ausgewählt ist, und eine zweite Nucleotidsequenz, die für eine Domäne geringer Komplexität aus einem Zielprotein einer neurodegenerativen Erkrankung kodiert, das aus der aus TDP-43, FUS, Alpha-Synuclein, Tau, T1A1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS-RNA-Bindungsprotein 1 und TATA-Box-Bindungsproteinfaktor 15 bestehenden Gruppe ausgewählt ist.

2. Expressionsvektor, der für ein chimäres Polypeptid kodiert, umfassend: eine erste Nucleotidsequenz, die für eine lichtinduzierte Oligomerisierungsdomäne kodiert, die aus der aus VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV und AsLOV2 bestehenden Gruppe ausgewählt ist, und eine zweite Nucleotidsequenz, die für eine Domäne geringer Komplexität aus einem Zielprotein einer neurodegenerativen Erkrankung kodiert, das aus der aus TDP-43, FUS, Alpha-Synuclein, Tau, T1A1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS-RNA-Bindungsprotein 1 und TATA-Box-Bindungsproteinfaktor 15 bestehenden Gruppe ausgewählt ist, wobei die erste Nucleotidsequenz operabel an einen Promotor gebunden ist.

3. Zelle, umfassend eine Nucleotidsequenz, die für ein chimäres Polypeptid kodiert, umfassend: eine erste Nucleotidsequenz, die für eine lichtinduzierte Oligomerisierungsdomäne kodiert, die aus der aus VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV und AsLOV2 bestehenden Gruppe ausgewählt ist, und eine zweite Nucleotidsequenz, die für ein Zielprotein einer neurodegenerativen Erkrankung

kodiert, das aus der aus TDP-43, FUS, Alpha-Synuclein, Tau, T1A1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS-RNA-Bindungsprotein 1 und TATA-Box-Bindungsproteinfaktor 15 bestehenden Gruppe ausgewählt ist.

4. Chimäres Polypeptid, umfassend: eine lichtinduzierte Oligomerisierungsdomäne, die aus der aus VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV und AsLOV2 bestehenden Gruppe ausgewählt ist; und eine Domäne geringer Komplexität aus einem Zielprotein einer neurodegenerativen Erkrankung, das aus der aus TDP-43, FUS, Alpha-Synuclein, Tau, T1A1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS-RNA-Bindungsprotein 1 und TATA-Box-Bindungsproteinfaktor 15 bestehenden Gruppe ausgewählt ist.

5. Verwendung eines Expressionsvektors, der für ein chimäres Polypeptid kodiert, beim Auslösen einer Pathologie einer neurodegenerativen Erkrankung in einer Zelle, umfassend die folgenden Schritte:
Einführen des Expressionsvektors, der für ein chimäres Polypeptid kodiert, in die Zelle, umfassend:

eine erste Nucleotidsequenz, die für eine lichtinduzierte Oligomerisierungsdomäne kodiert, die aus der aus VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV und AsLOV2 bestehenden Gruppe ausgewählt ist, und eine zweite Nucleotidsequenz, die für eine Domäne geringer Komplexität aus einem Zielprotein einer neurodegenerativen Erkrankung kodiert, das aus der aus TDP-43, FUS, Alpha-Synuclein, Tau, T1A1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS-RNA-Bindungsprotein 1 und TA-TA-Box-Bindungsproteinfaktor 15 bestehenden Gruppe ausgewählt ist, wobei die erste Nucleotidsequenz operabel an einen Promotor gebunden ist;
Exprimieren des chimären Polypeptids; und Induzieren der Oligomerisierung des chimären Polypeptids durch Stimulieren mit Blaulicht.

6. Verwendung nach Anspruch 5, wobei die Zelle eine Säugetierzelle, gegebenenfalls eine menschliche Zelle, ist; und/oder wobei das Blaulicht eine Wellenlänge zwischen 405 nm und 499 nm aufweist.

7. Verwendung eines Expressionsvektors, der für ein chimäres Polypeptid kodiert, beim Screenen auf ein Mittel, das die Proteinaggregation moduliert, umfassend folgende Schritte:

Einführen des Expressionsvektors, der für ein chimäres Polypeptid kodiert, in eine Zelle, umfassend:

eine erste Nucleotidsequenz, die für eine lichtinduzierte Oligomerisierungsdomäne kodiert, die aus der aus VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV und AsLOV2 bestehenden Gruppe ausgewählt ist, und eine zweite Nucleotidsequenz, die für eine Domäne geringer Komplexität aus einem Zielprotein einer neurodegenerativen Erkrankung kodiert, das aus der aus TDP-43, FUS, Alpha-Synuclein, Tau, T1A1, SOD1, Huntingtin, Ataxin 2, hnRNPA2B1, EWS-RNA-Bindungsprotein 1 und TATA-Box-Bindungsproteinfaktor 15 bestehenden Gruppe ausgewählt ist, wobei die erste Nucleotidsequenz operabel an einen Promotor gebunden ist;
Exprimieren des chimären Polypeptids;
Einführen des Mittels in ein Kulturmedium, umfassend die Zelle;

Induzieren der Oligomerisierung des chimären Polypeptids durch Stimulieren mit Blaulicht; und
Bestimmen der Modulation der Proteinaggregation durch das Mittel.

8. Verwendung nach Anspruch 7, wobei die Zelle eine Säugetierzelle, gegebenenfalls eine menschliche Zelle, ist; und/oder wobei das Blaulicht eine Wellenlänge zwischen 405 nm und 499 nm aufweist.

9. Nucleotidsequenz nach Anspruch 1, Expressionsvektor nach Anspruch 2, Zelle nach Anspruch 3, chimäres Polypeptid nach Anspruch 4 oder Verwendung nach einem der Ansprüche 5 bis 8, wobei das chimäre Polypeptid die Aminosäuresequenz einer beliebigen der SEQ ID NO: 6 bis 41 und 75 bis 89 umfasst.

Revendications

1. Séquence nucléotidique codant pour un polypeptide chimérique, comprenant : une première séquence nucléotidique codant pour un domaine d'oligomérisation induit par de la lumière choisi dans le groupe constitué de VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV et AsLOV2, et une seconde séquence nucléotidique codant pour un domaine de faible complexité provenant d'une protéine cible de maladie

neurodégénérative choisie dans le groupe constitué de TDP-43, FUS, Alpha synucléine, Tau, TIA1, SOD1, Huntingtine, Ataxine 2, hnRNPA2B1, une protéine EWS de liaison à l'ARN 1 et un facteur de la protéine de liaison à la boîte TATA 15.

2. Vecteur d'expression codant pour un polypeptide chimérique, comprenant : une première séquence nucléotidique codant pour un domaine d'oligomérisation induit par de la lumière choisi dans le groupe constitué de VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV et AsLOV2, et une seconde séquence nucléotidique codant pour un domaine de faible complexité provenant d'une protéine cible de maladie neurodégénérative choisie dans le groupe constitué de TDP-43, FUS, Alpha synucléine, Tau, TIA1, SOD1, Huntingtine, Ataxine 2, hnRNPA2B1, une protéine EWS de liaison à l'ARN 1 et un facteur de la protéine de liaison à la boîte TATA 15, dans lequel la première séquence nucléotidique est liée de manière opérationnelle à un promoteur.

3. Cellule comprenant Séquence nucléotidique codant pour un polypeptide chimérique, comprenant : une première séquence nucléotidique codant pour un domaine d'oligomérisation induit par de la lumière choisi dans le groupe constitué de VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV et AsLOV2, et une seconde séquence nucléotidique codant pour un domaine de faible complexité provenant d'une protéine cible de maladie neurodégénérative choisie dans le groupe constitué de TDP-43, FUS, Alpha synucléine, Tau, TIA1, SOD1, Huntingtine, Ataxine 2, hnRNPA2B1, une protéine EWS de liaison à l'ARN 1 et un facteur de la protéine de liaison à la boîte TATA 15.

4. Polypeptide chimérique comprenant : un domaine d'oligomérisation induit par de la lumière choisi dans le groupe constitué de VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV et AsLOV2, et une seconde séquence nucléotidique codant pour un domaine de faible complexité provenant d'une protéine cible de maladie neurodégénérative choisie dans le groupe constitué de TDP-43, FUS, alpha synucléine, Tau, TIA1, SOD1, Huntingtine, Ataxine 2, hnRNPA2B1, une protéine EWS de liaison à l'ARN 1 et un facteur de la protéine de liaison à la boîte TATA

5. Utilisation d'un vecteur d'expression codant pour un polypeptide chimérique dans l'induction d'une pathologie de maladie neurodégénérative dans une cellule, comprenant les étapes consistant à :
introduire dans la cellule ledit vecteur d'expression codant pour un polypeptide chimérique, comprenant :

une première séquence nucléotidique codant pour un domaine d'oligomérisation induit par de la lumière choisi dans le groupe comprenant VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV et AsLOV2, et une seconde séquence nucléotidique codant pour un domaine de faible complexité provenant d'une protéine cible de maladie neurodégénérative choisie dans le groupe constitué de TDP-43, FUS, alpha synucléine, Tau, TIA1, SOD1, Huntingtine, Ataxine 2, hnRNPA2B1, une protéine EWS de liaison à l'ARN 1 et un facteur de la protéine de liaison à la boîte TATA, la première séquence nucléotidique étant reliée de manière opérationnelle à un promoteur ;
exprimer le polypeptide chimérique ; et induire une oligomérisation du polypeptide chimérique par stimulation avec de la lumière bleue.

6. Utilisation selon la revendication 5, dans laquelle la cellule est une cellule de mammifère, facultativement une cellule humaine ; et/ou dans laquelle la lumière bleue présente une longueur d'onde comprise entre 405 nm et 499 nm.

7. Utilisation d'un vecteur d'expression codant pour un polypeptide chimérique dans le dépistage d'un agent qui module l'agrégation des protéines, comprenant les étapes consistant à :
introduire dans une cellule ledit vecteur d'expression codant pour un polypeptide chimérique, comprenant :

une première séquence nucléotidique codant pour un domaine d'oligomérisation induit par de la lumière choisi dans le groupe comprenant VVD LOV, NcVVD, CRY2OLIG, CRYPHR, NcVVDY50W, NcLOV, VfAU1, YtvA, EL222, RsLOV et AsLOV2, et une seconde séquence nucléotidique codant pour un domaine de faible complexité provenant d'une protéine cible de maladie neurodégénérative choisie dans le groupe constitué de TDP-43, FUS, alpha synucléine, Tau, TIA1, SOD1, Huntingtine, Ataxine 2, hnRNPA2B1, une protéine EWS de liaison à l'ARN 1 et un facteur de la protéine de liaison à la boîte TATA, la première séquence nucléotidique étant reliée de manière opérationnelle à un promoteur ;
exprimer le polypeptide chimérique ;
introduire l'agent dans un milieu de culture comprenant la cellule ;
induire l'oligomérisation du polypeptide chimérique par stimulation avec de la lumière bleue ; et déterminer la

modulation de l'agrégation de protéines par l'agent.

8. Utilisation selon la revendication 7, dans laquelle la cellule est une cellule de mammifère, facultativement une cellule humaine ; et/ou dans laquelle la lumière bleue présente une longueur d'onde comprise entre 405 nm et 499 nm.

9. Séquence nucléotidique selon la revendication 1, vecteur d'expression selon la revendication 2, cellule selon la revendication 3, polypeptide chimérique selon la revendication 4, ou utilisation selon l'une quelconque des revendications 5 à 8, le polypeptide chimérique comprenant la séquence d'acides aminés selon l'une quelconque des SEQ ID NOs : 6 à 41 et 75 à 89.

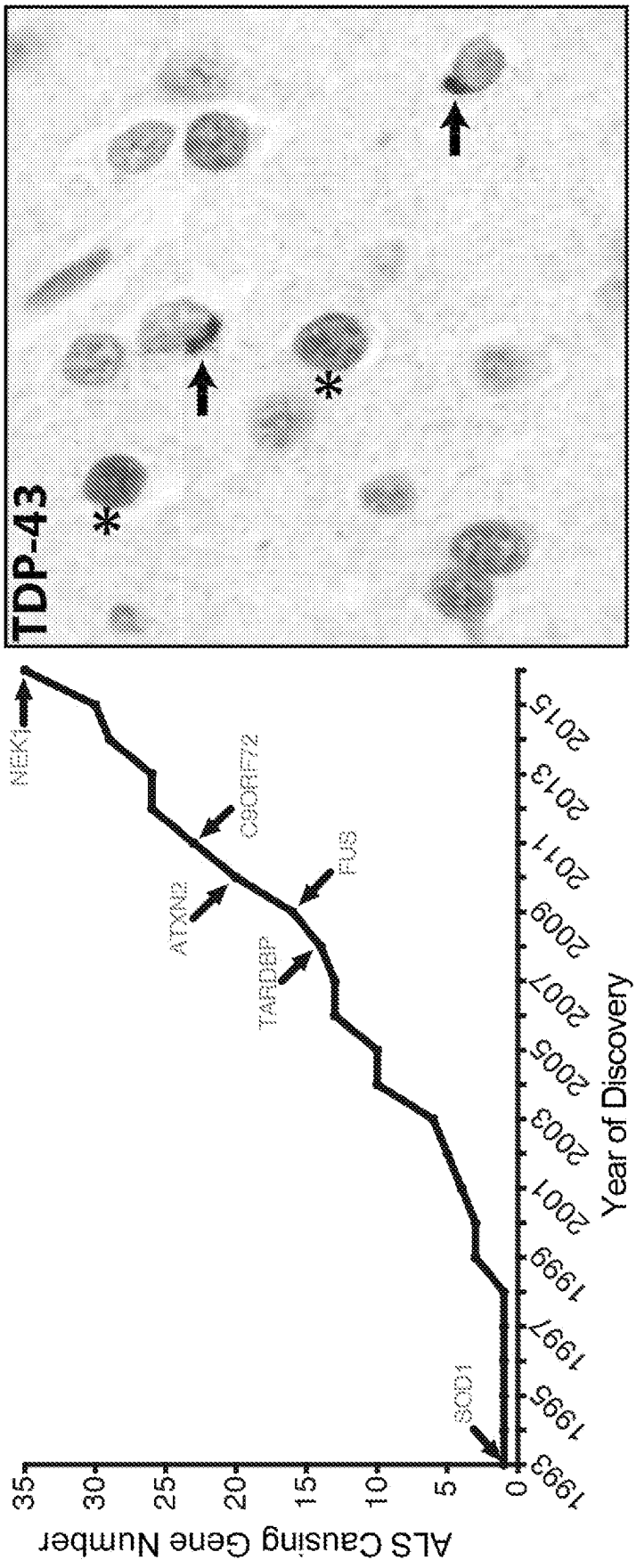

TDP-43
ALS Causing Gene Number
Year of Discovery
SOD1
TARDBP
FUS
ATXN2
C9ORF72
MEK1
0
5
10
15
20
25
30
35
1993
1995
1997
1999
2001
2003
2005
2007
2009
2011
2013
2015

FIGURE 1

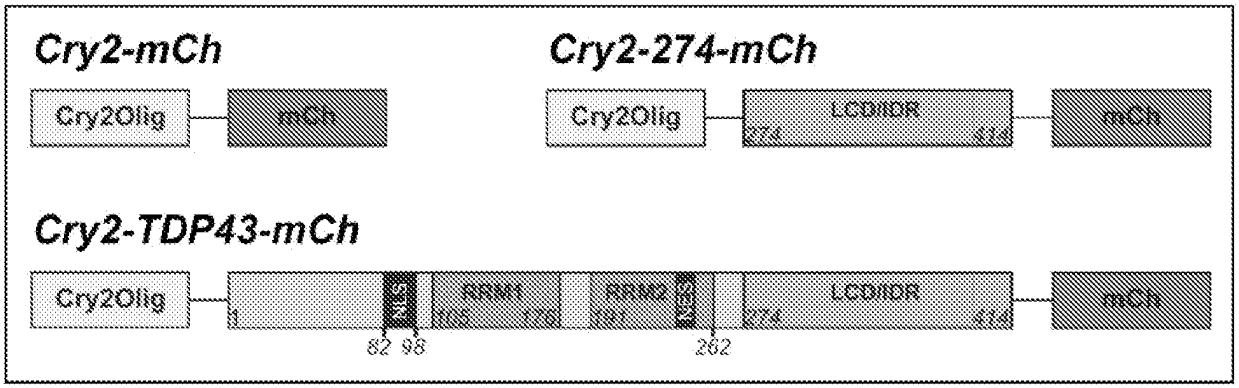


FIGURE 2A

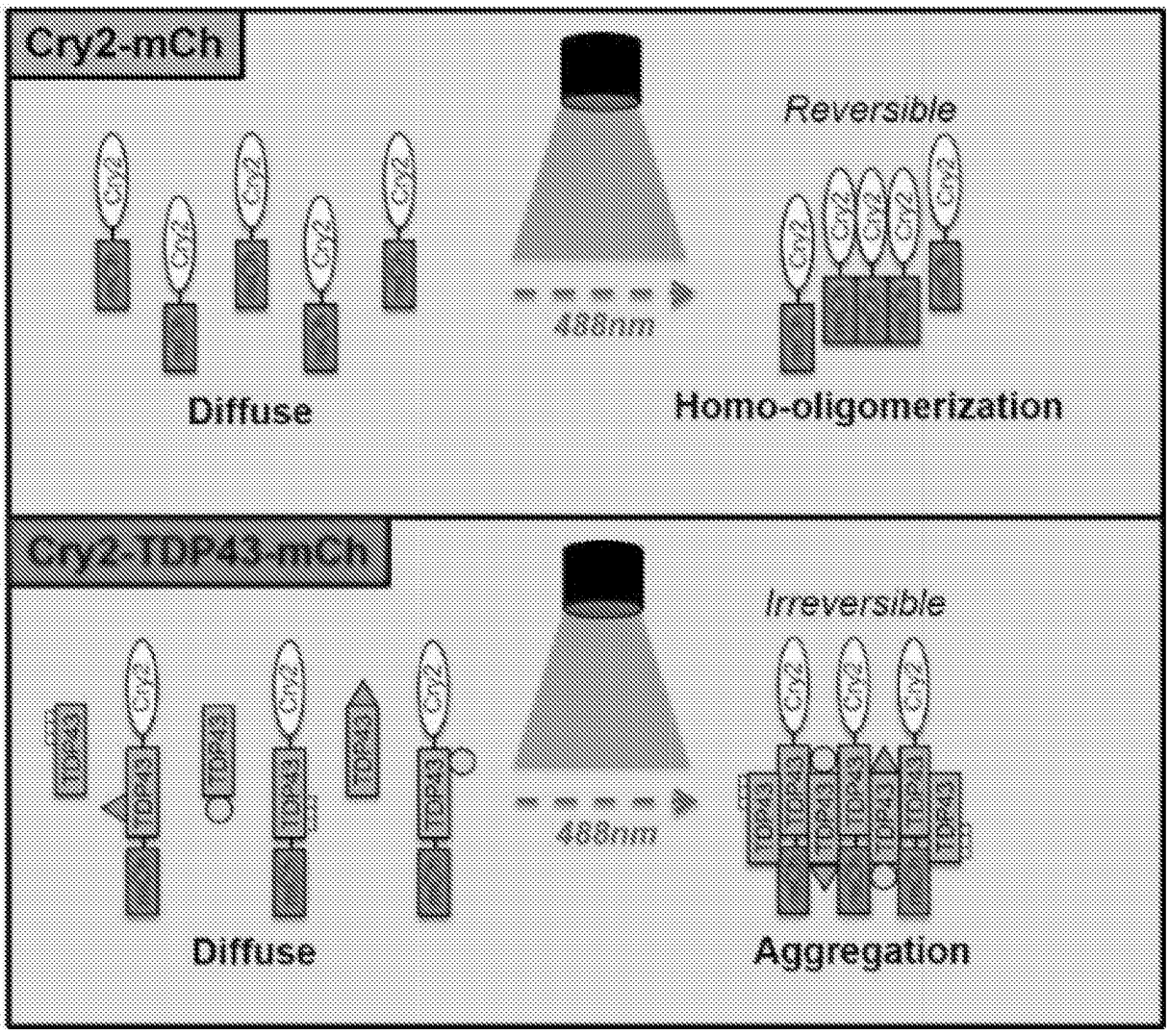


FIGURE 2B

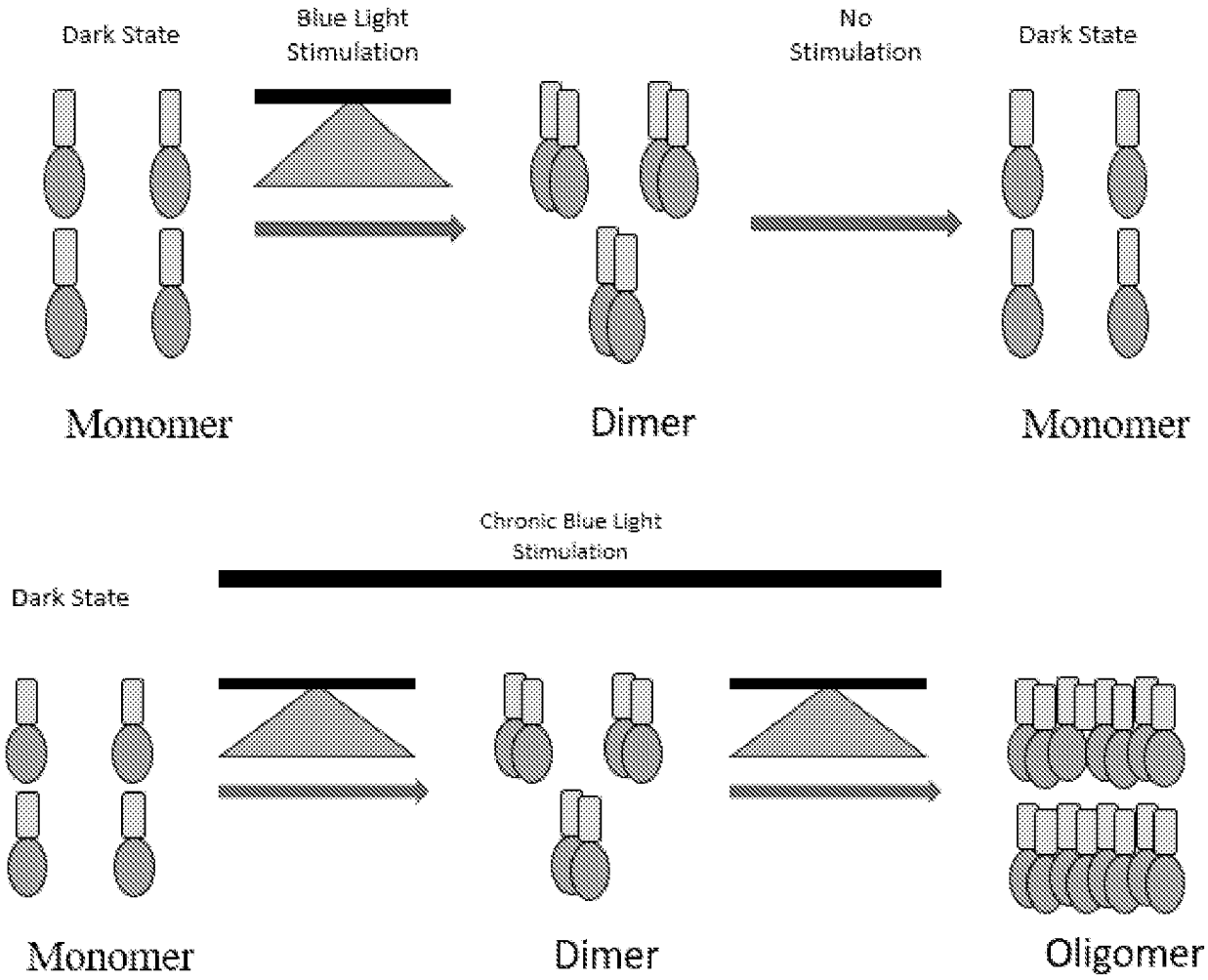

Dark State
Blue Light Stimulation
No Stimulation
Dark State
Monomer
Dimer
Monomer
Chronic Blue Light Stimulation
Dark State
Monomer
Dimer
Oligomer
Legend:
NcVVD/LOV + Protein with LCD/IDD/prion-like domain

FIGURE 3

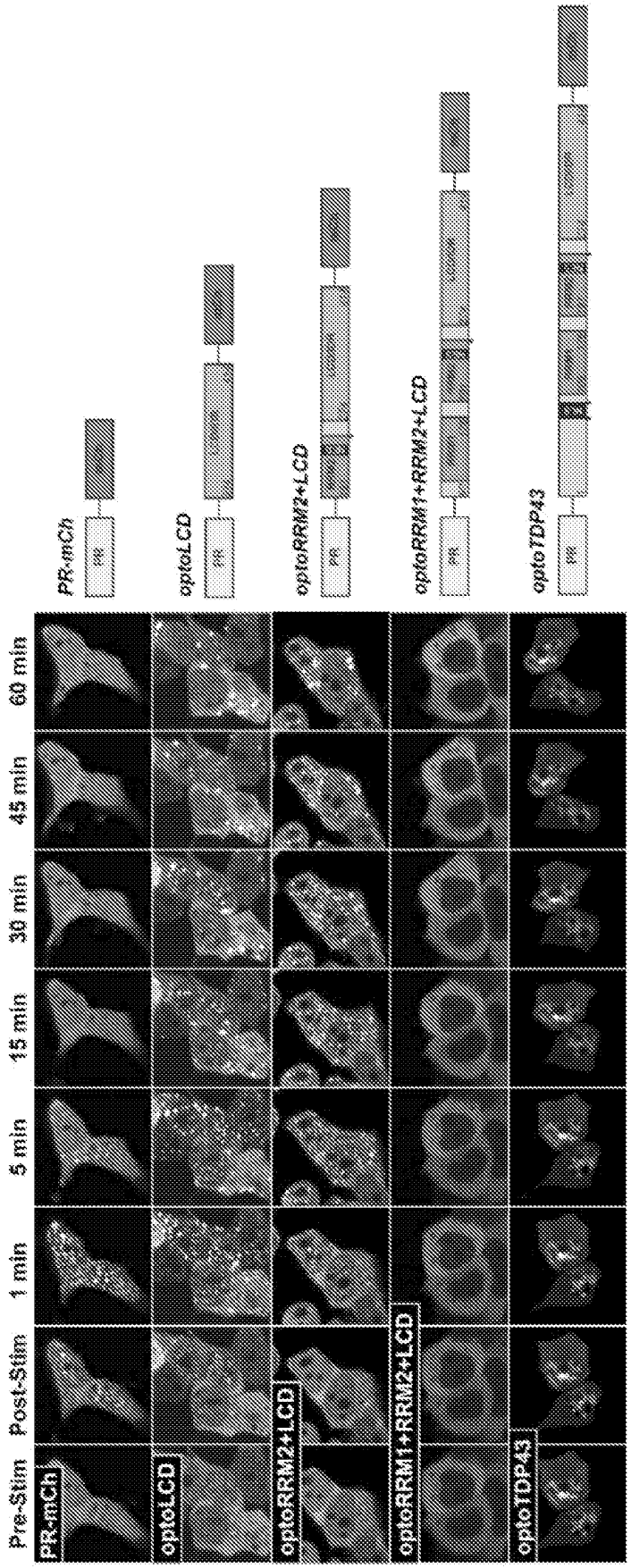

Pre-Stim
Post-Stim
1 min
5 min
15 min
30 min
45 min
60 min
PR-mCh
optoLCD
optoRRM2+LCD
optoRRM1+RRM2+LCD
optoTDP43
PR-mCh
optoLCD
optoRRM2+LCD
optoRRM1+RRM2+LCD
optoTDP43
PR

FIGURE 4A

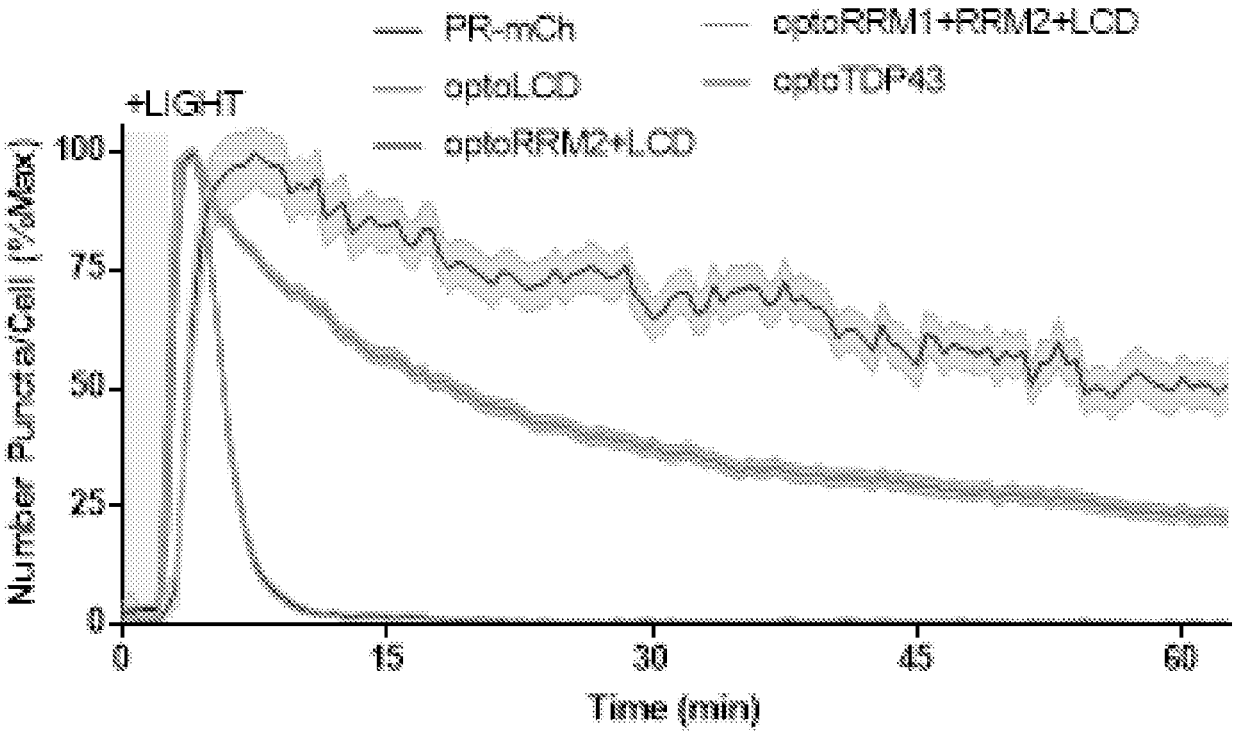

PR-mCh
optoLCD
optoRRM2+LCD
optoRRM1+RRM2+LCD
optoTDP43
+LIGHT
Number Puncta/Cell (%Max)
100
75
50
25
0
0
15
30
45
60
Time (min)

FIGURE 4B

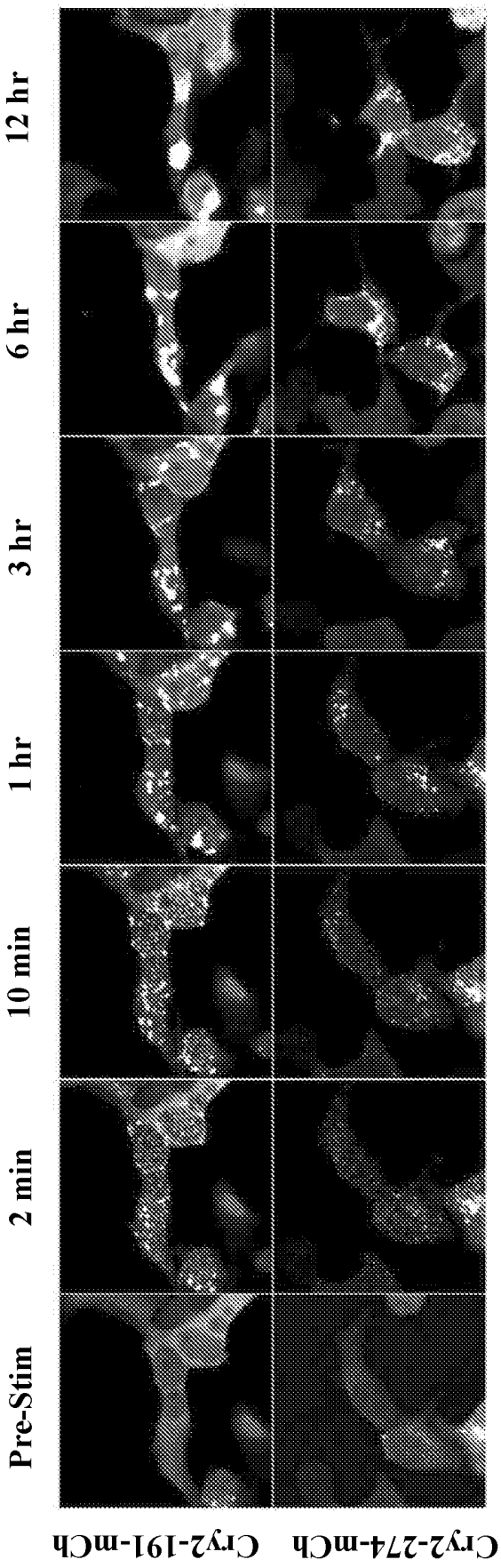


FIGURE 4C

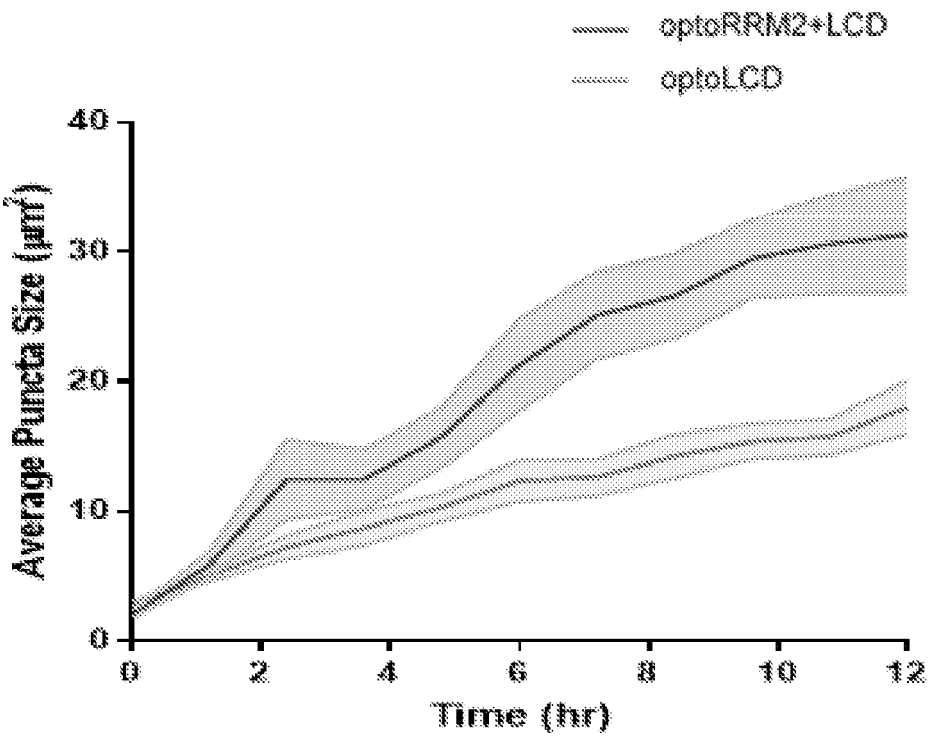


FIGURE 4D

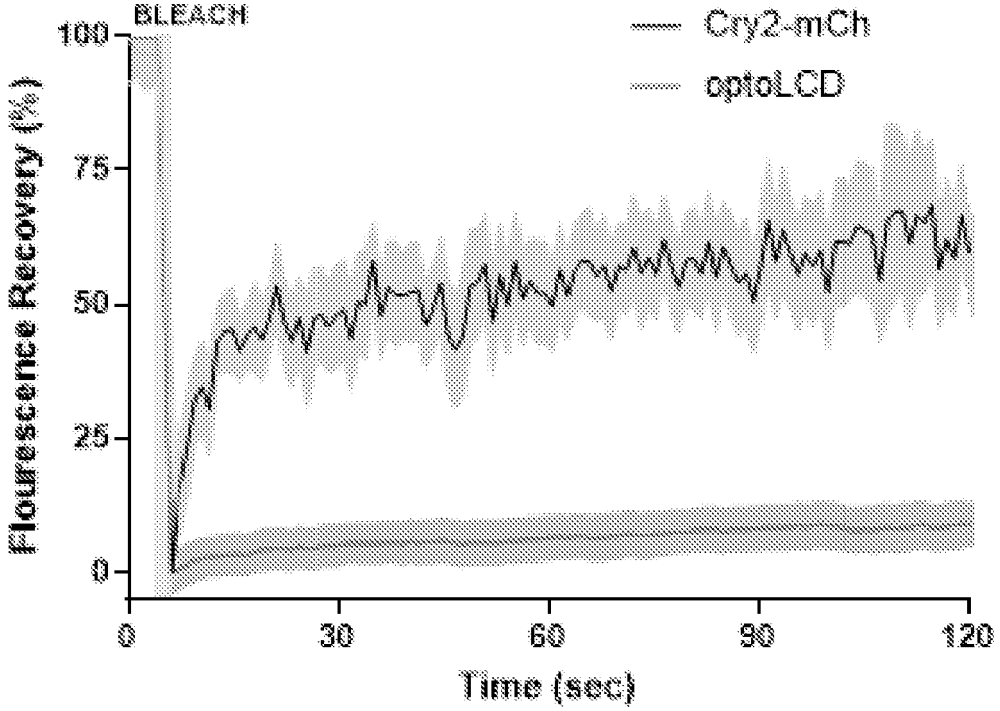


FIGURE 4E

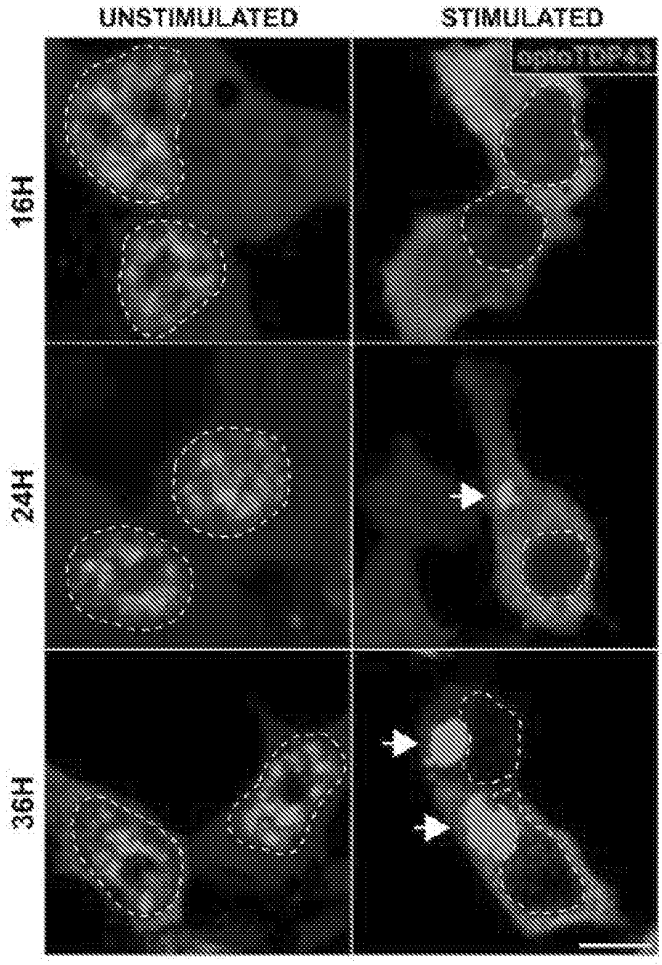


FIGURE 5A

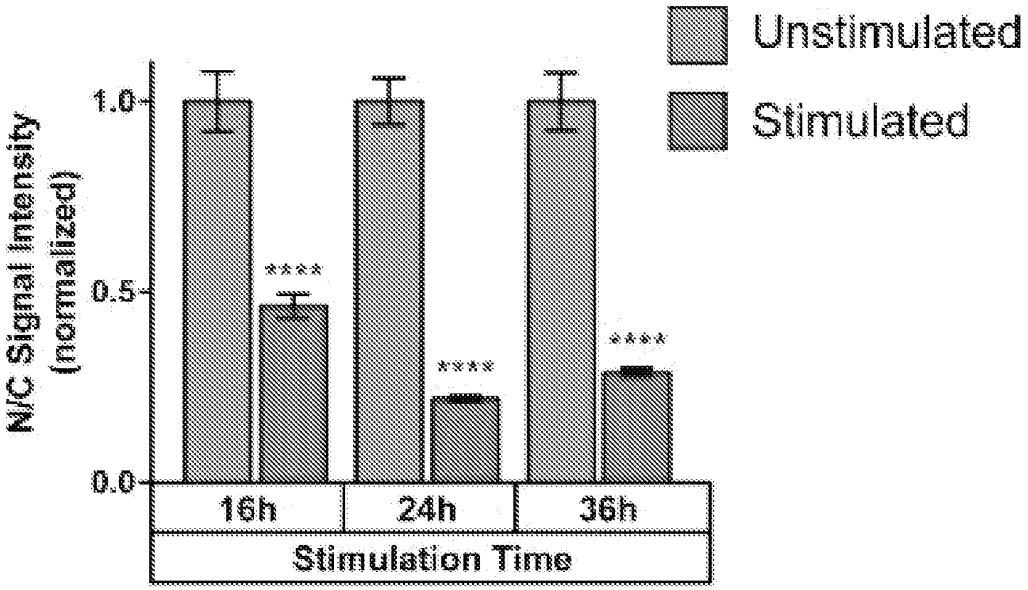


FIGURE 5B

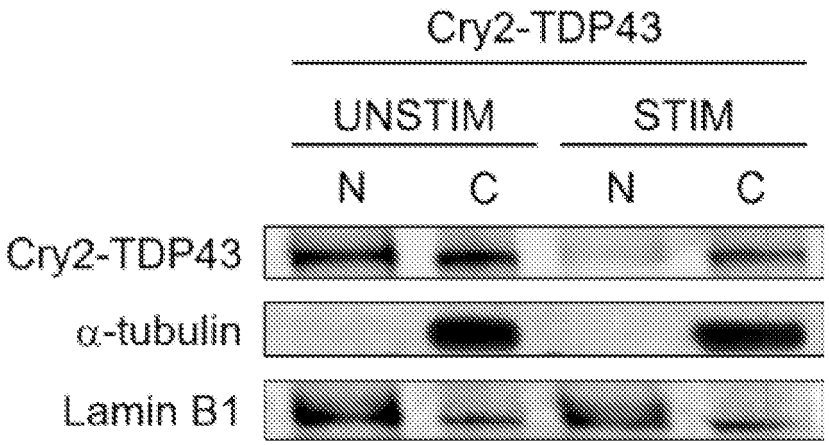


FIGURE 5C

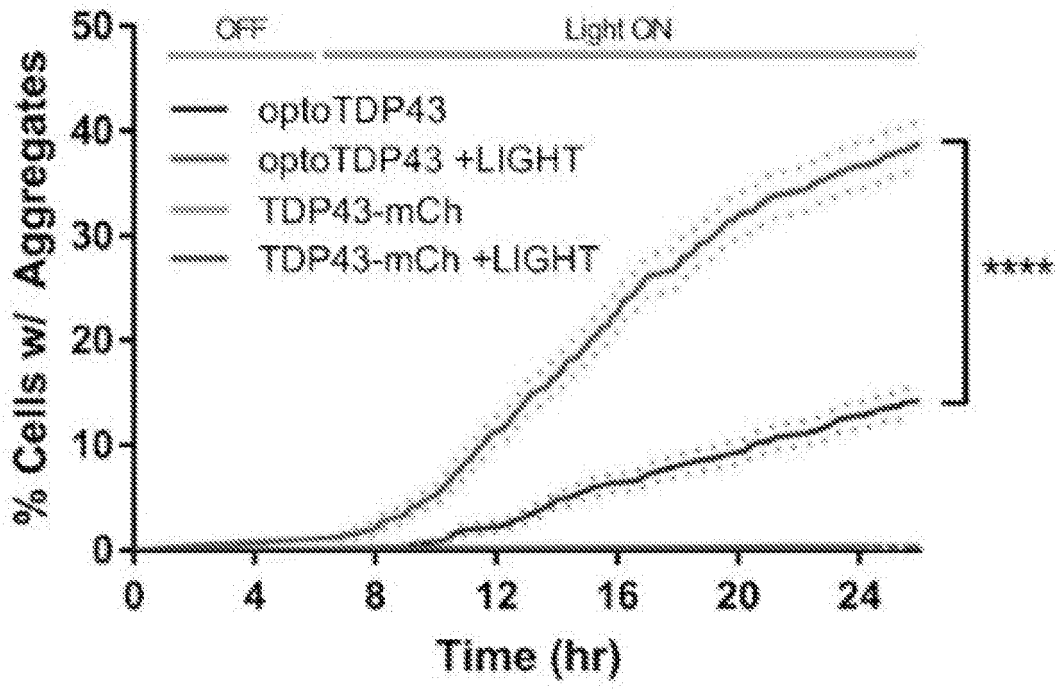


FIGURE 5D

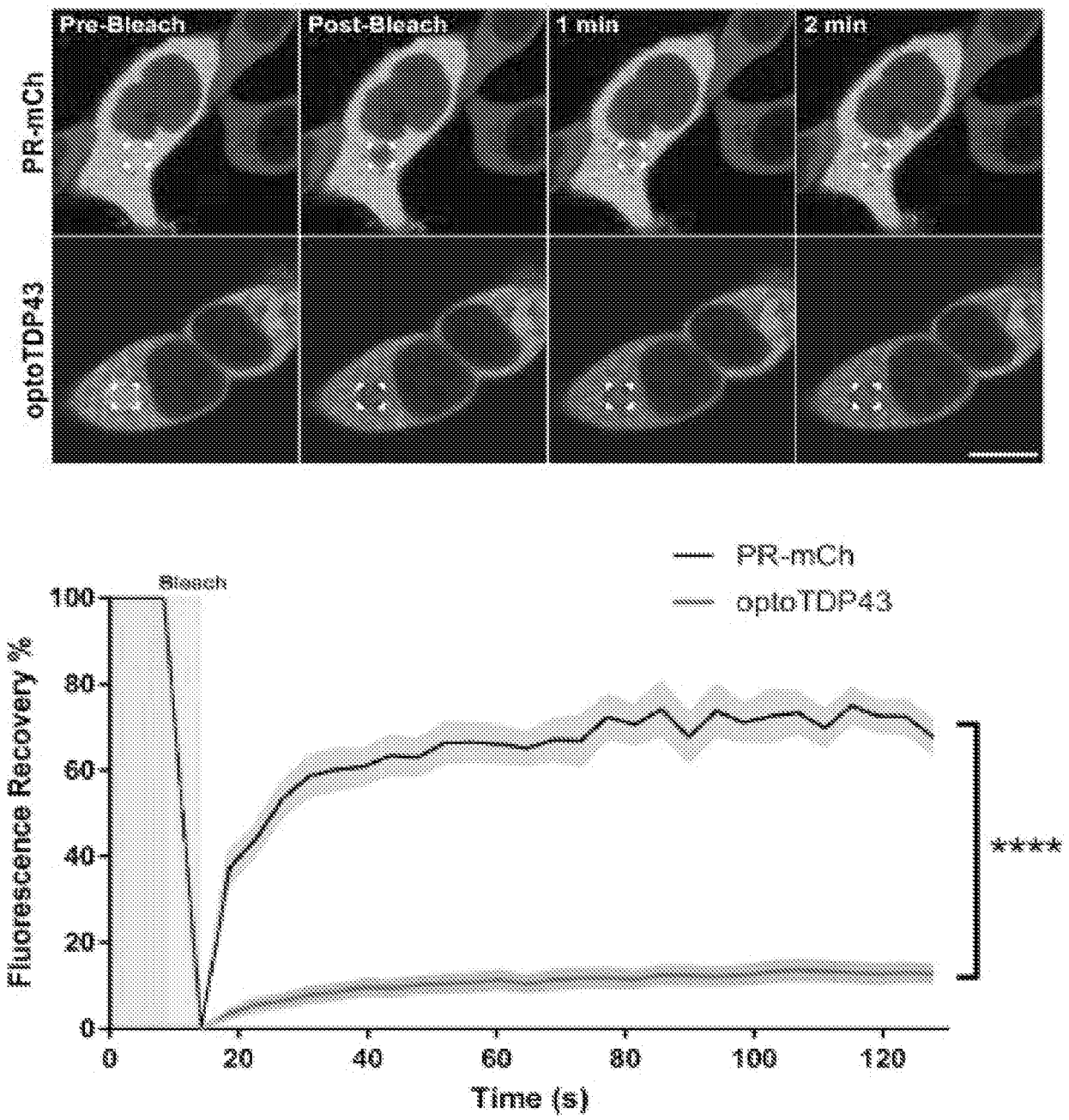

Pre-Bleach
Post-Bleach
1 min
2 min
PR-mCh
optoTDP43
PR-mCh
optoTDP43
Bleach
Fluorescence Recovery %
100
80
60
40
20
0
0
20
40
60
80
100
120
Time (s)
****

FIGURE 5E

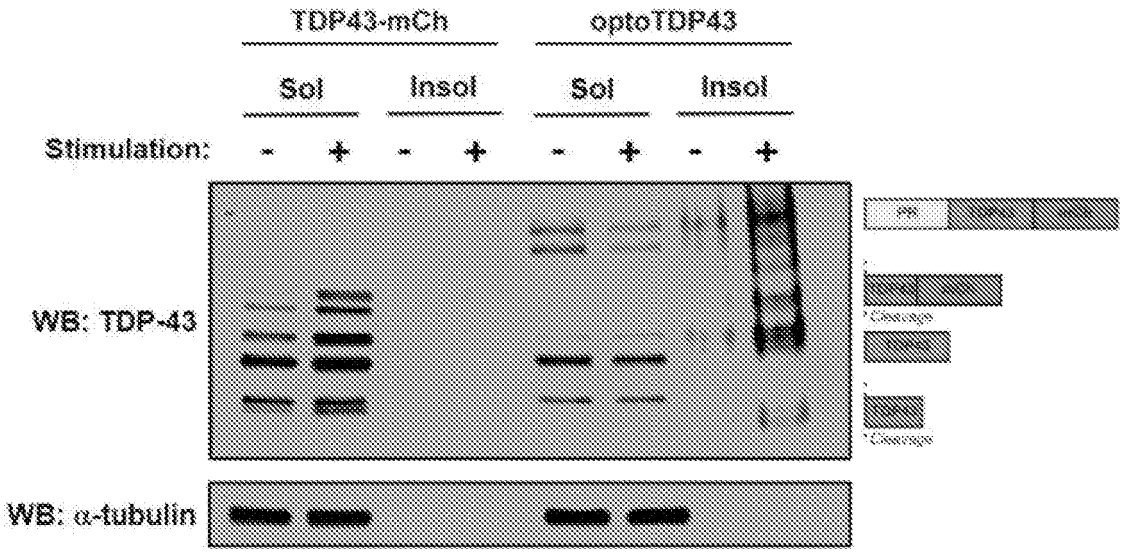


FIGURE 5F

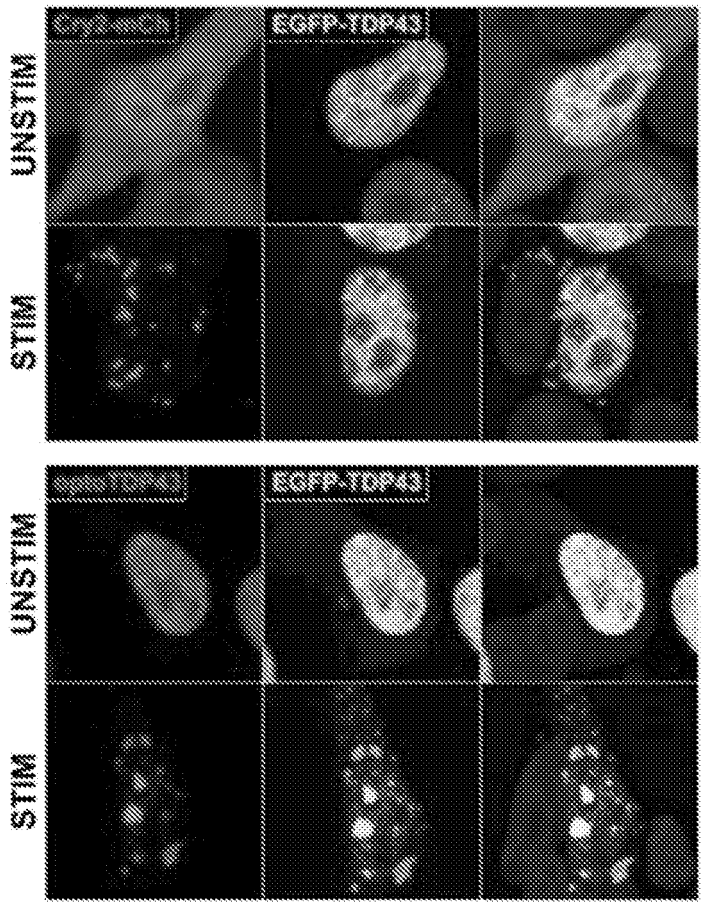


FIGURE 5G

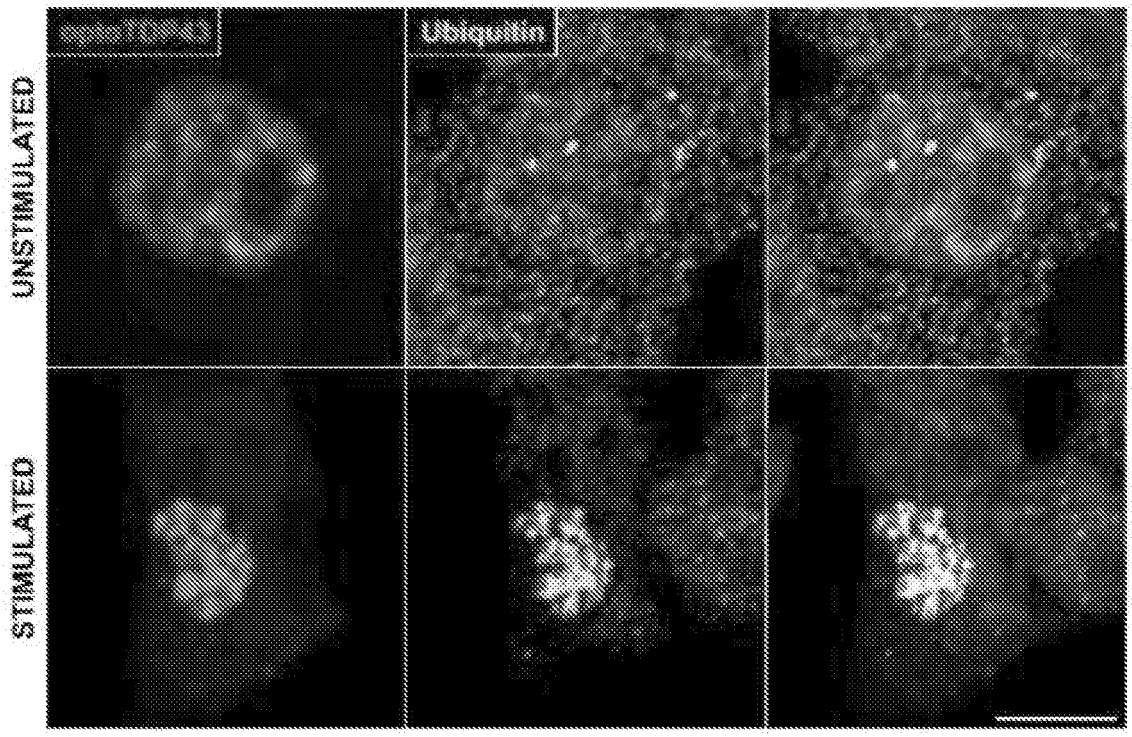


FIGURE 5H

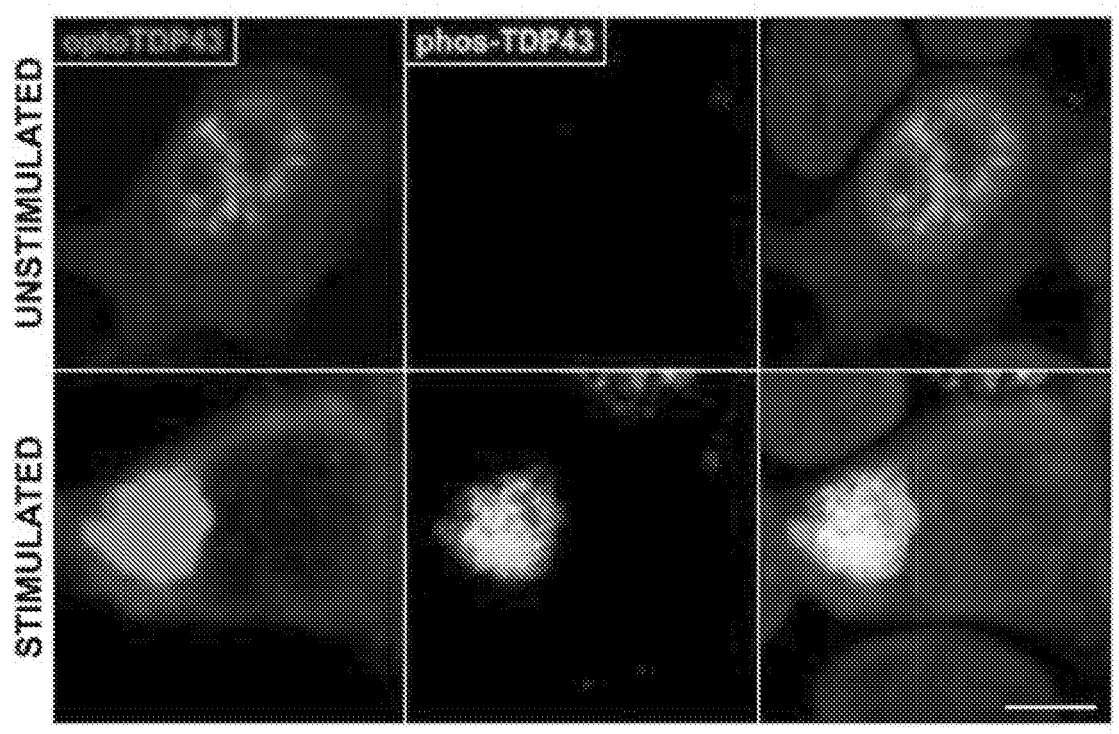


FIGURE 5I

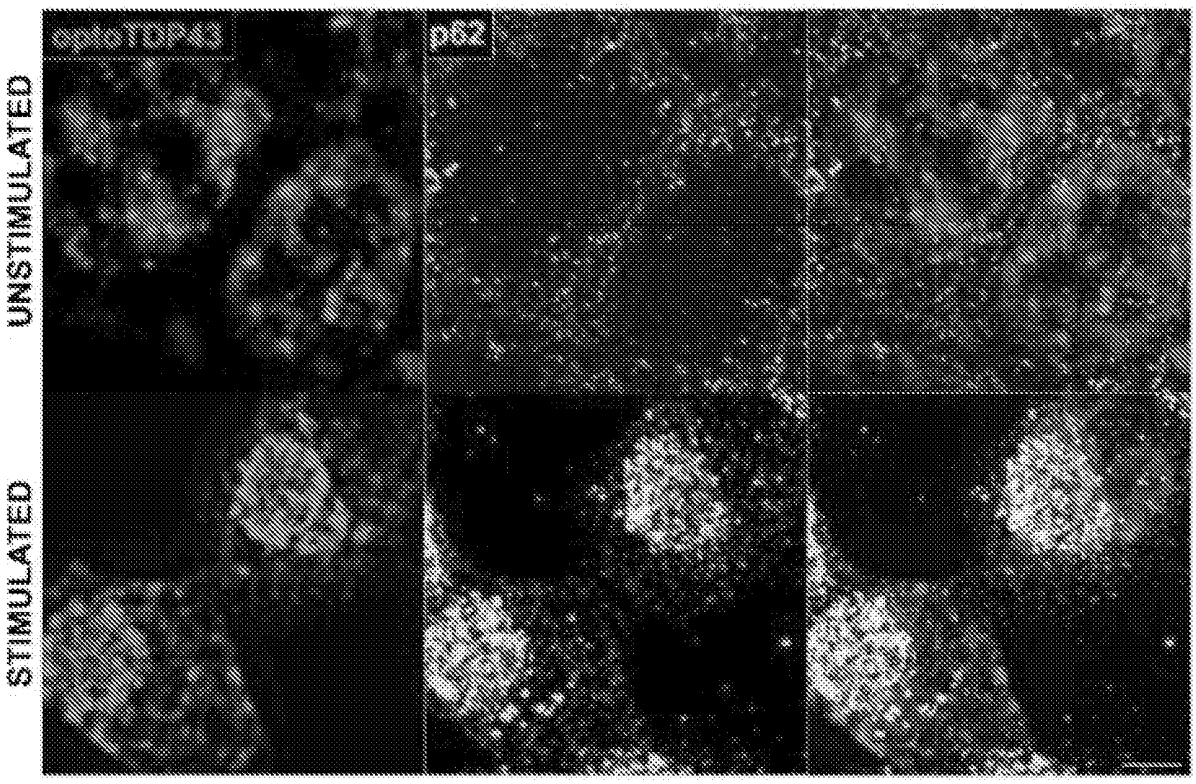


FIGURE 5J

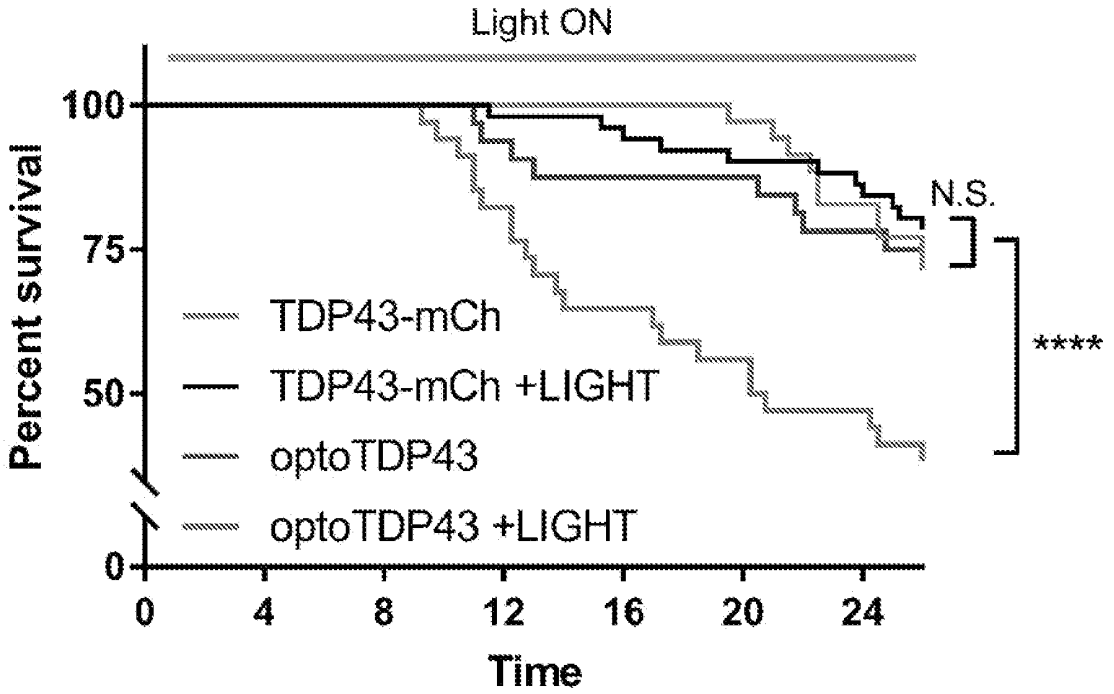


FIGURE 5K

FIGURE 6A

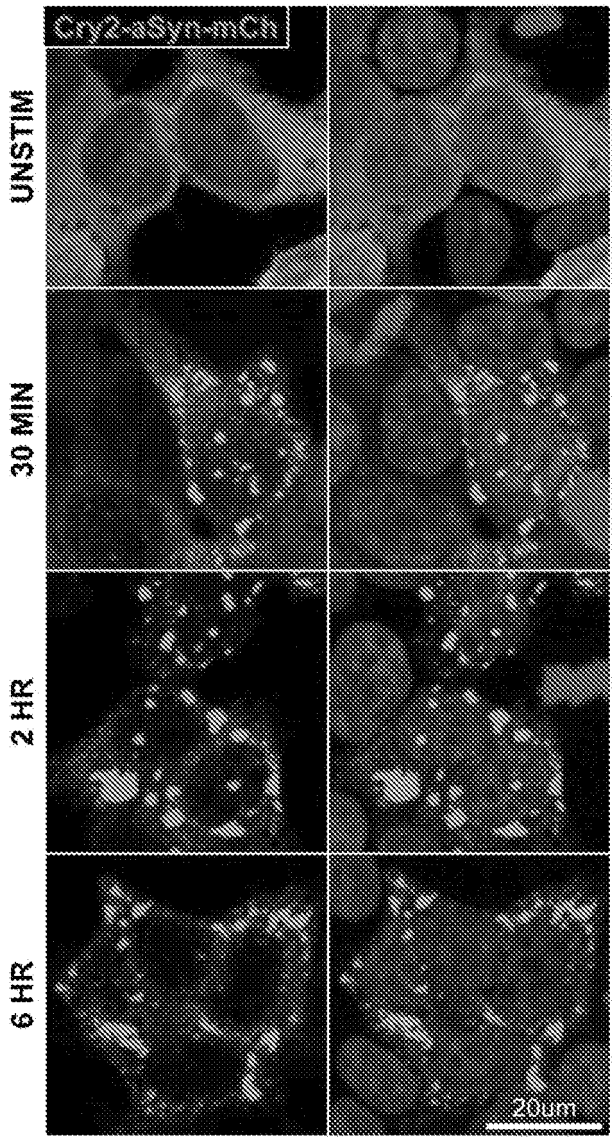


FIGURE 6B

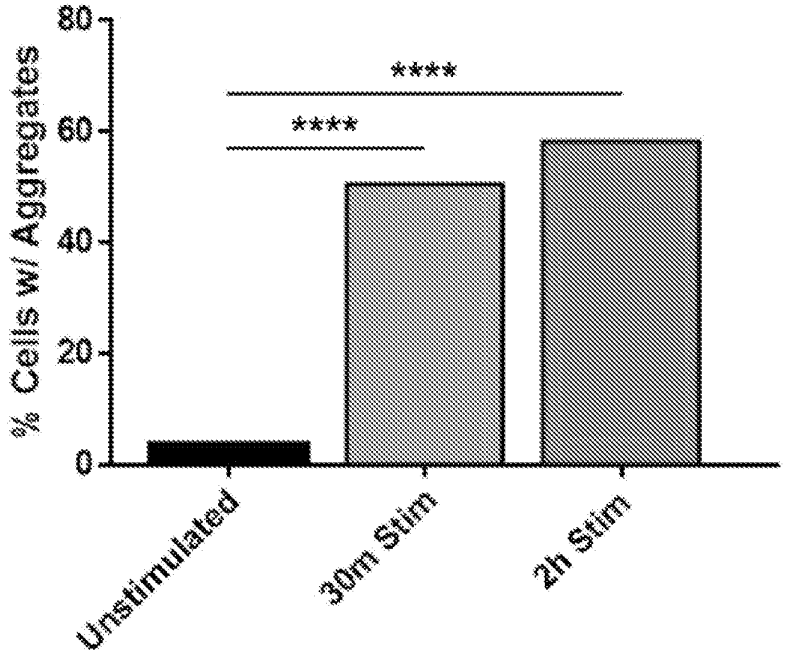


FIGURE 6C

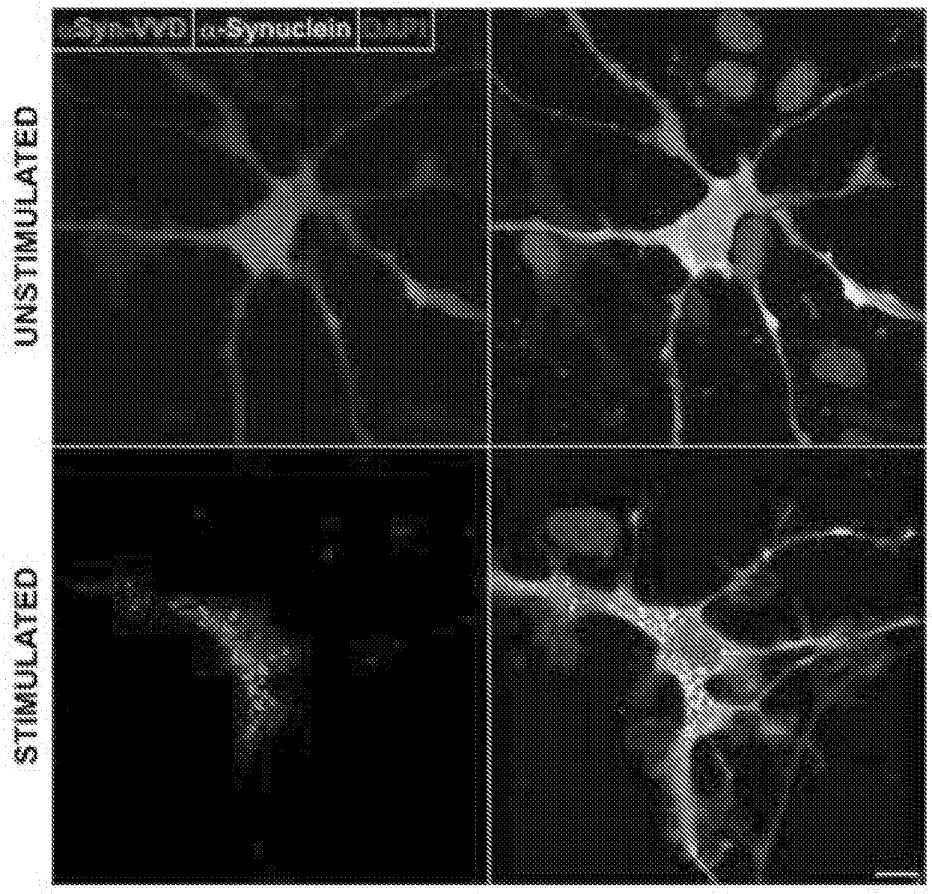


FIGURE 6D

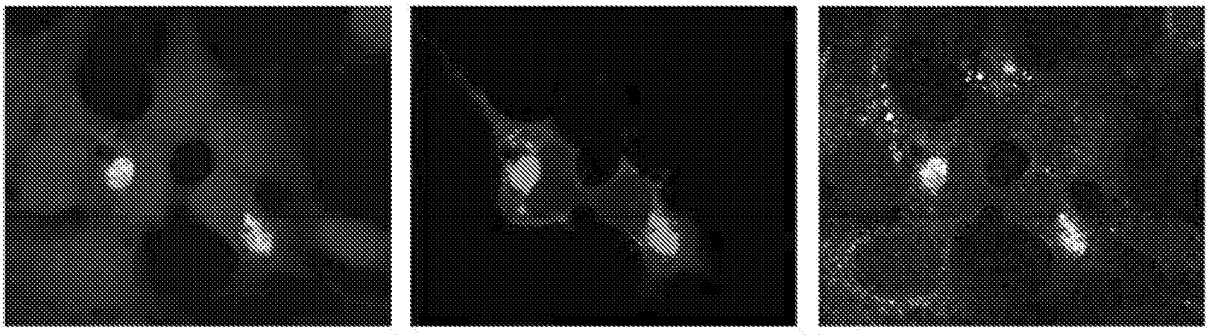


FIGURE 6E

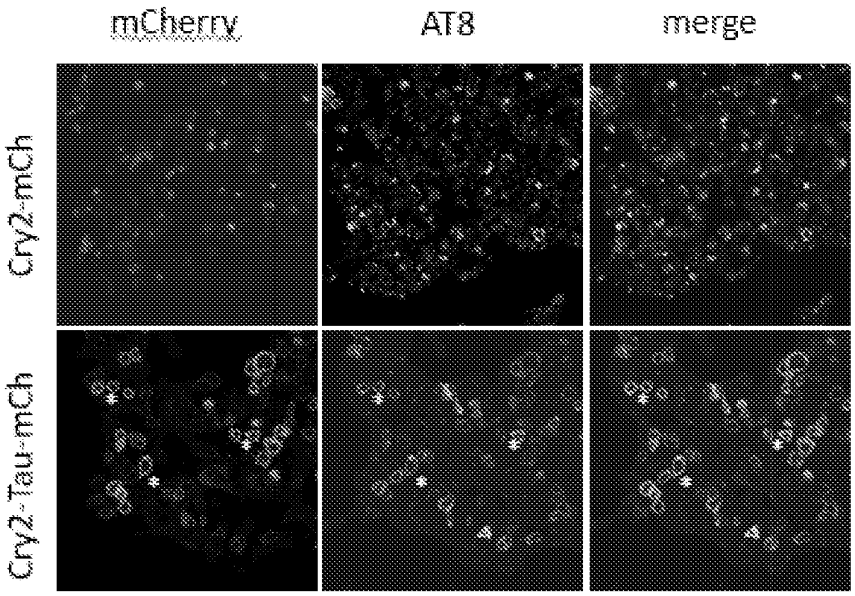


FIGURE 7A

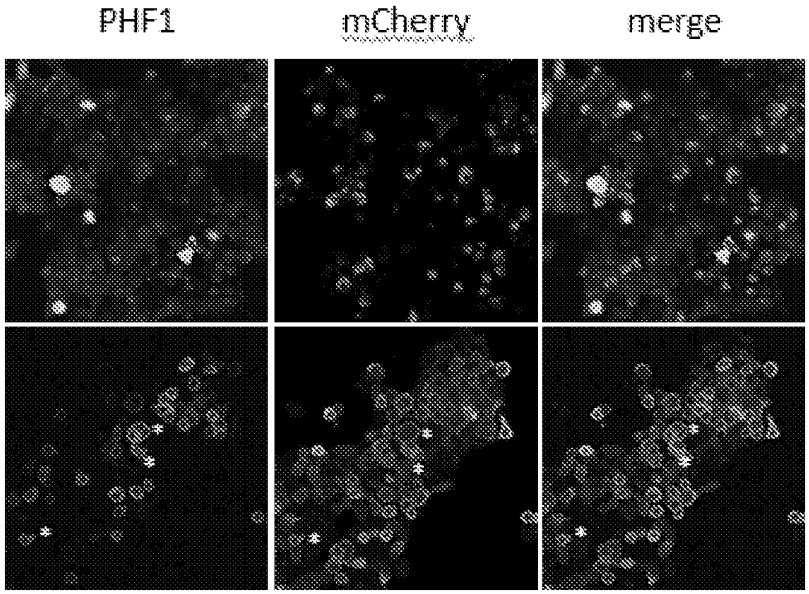


FIGURE 7B

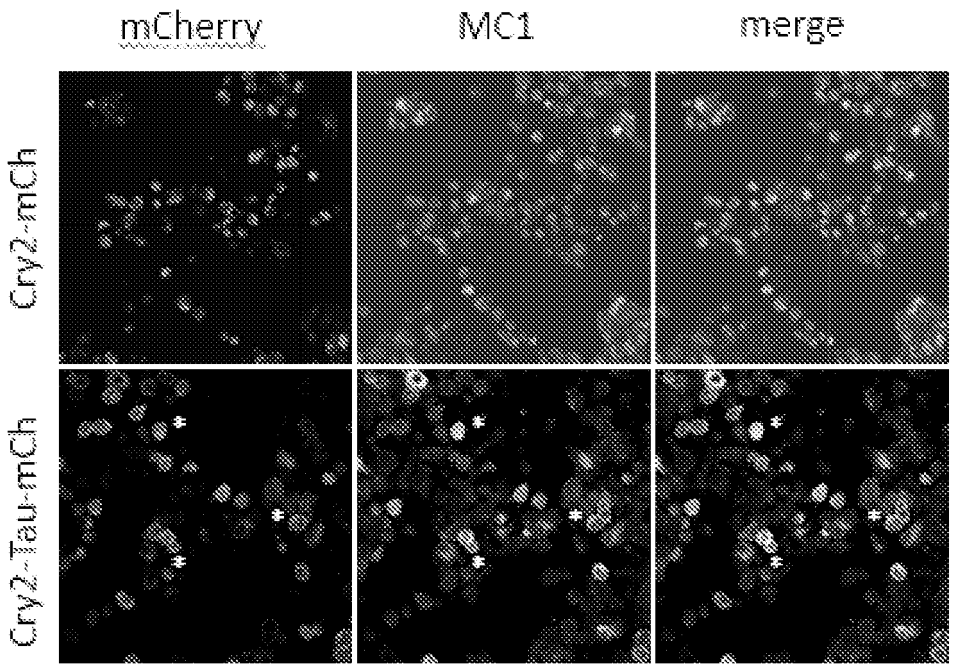


FIGURE 7C

	AT8	PHF1	MC1
VFAU-TAU(WT)-MCH	+	+	+
CRY-TAU(WT)-MCH	+	+	+
MCH-VVD-TAU(WT)	+	+	+

FIGURE 7D

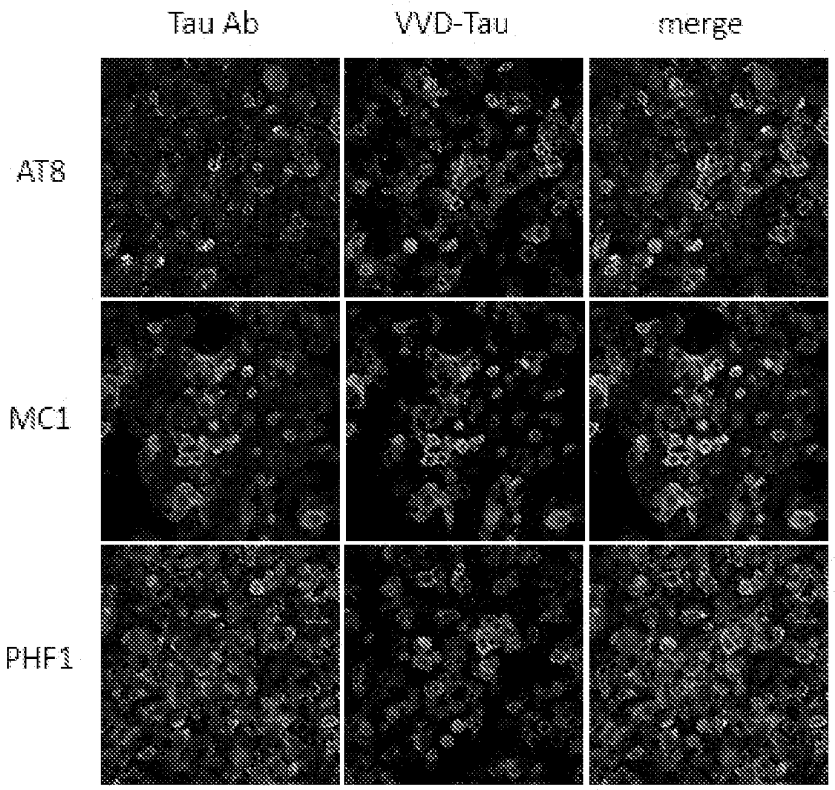


FIGURE 8A

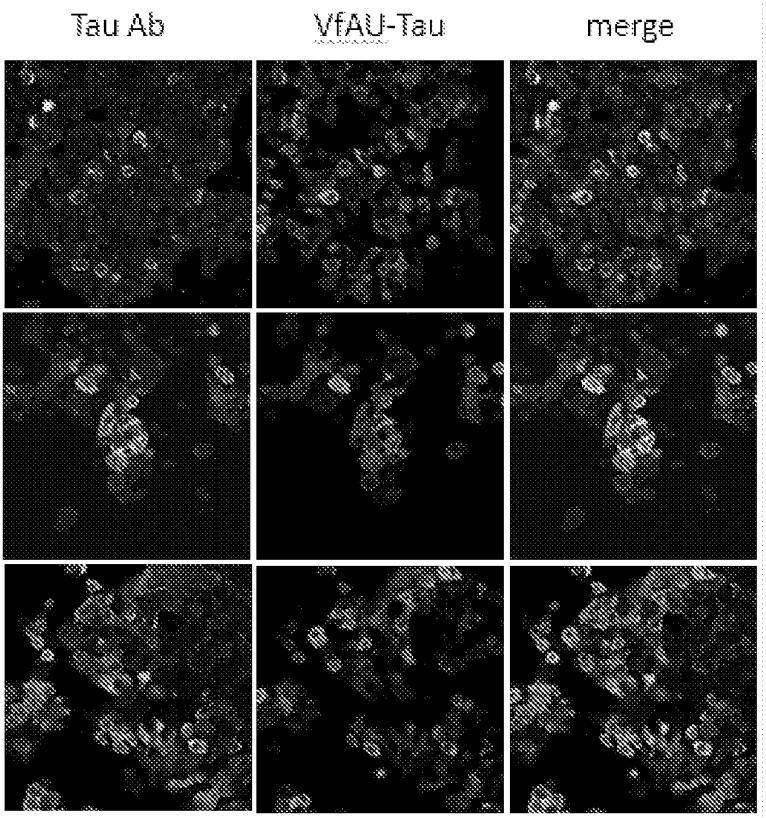


FIGURE 8B

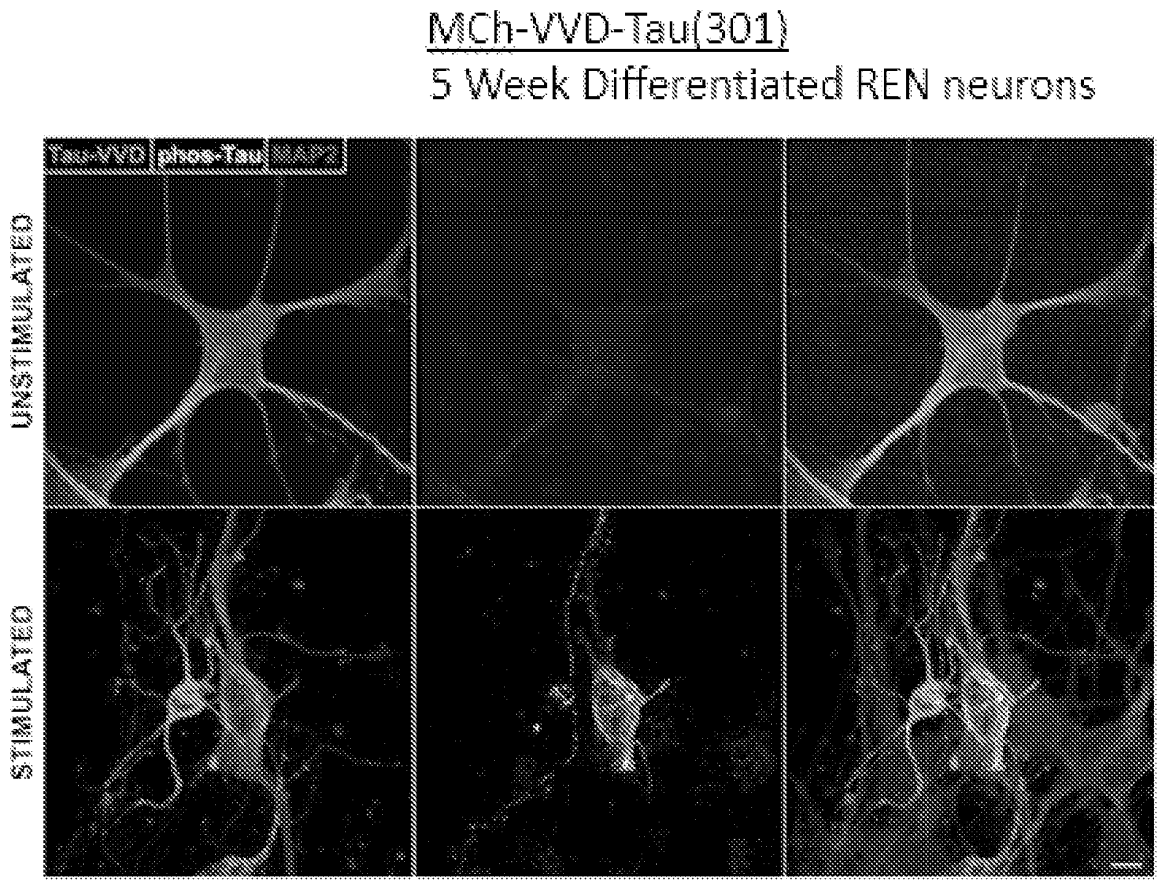


FIGURE 8C

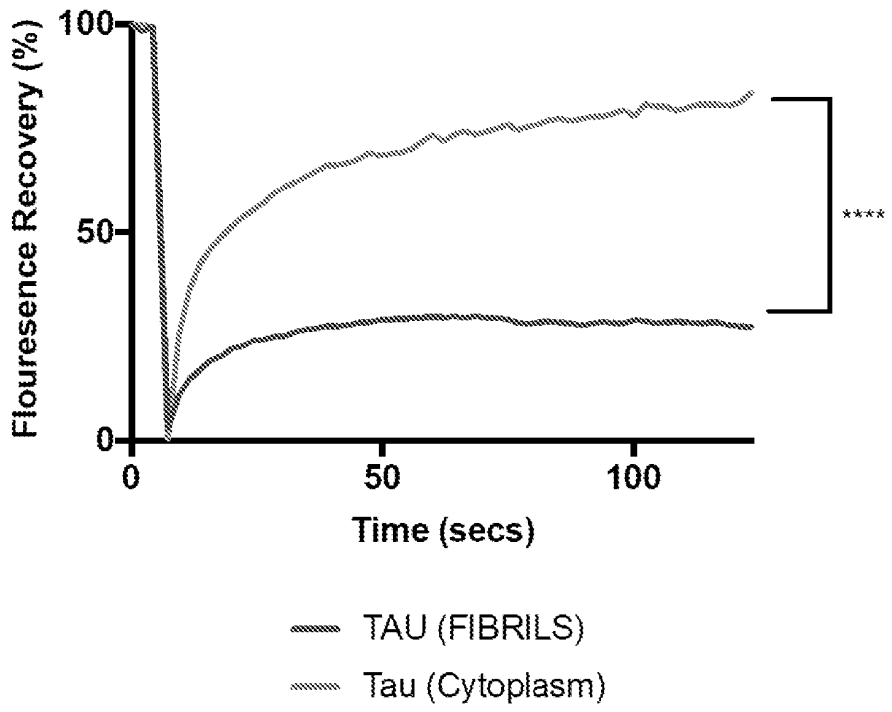


FIGURE 8D

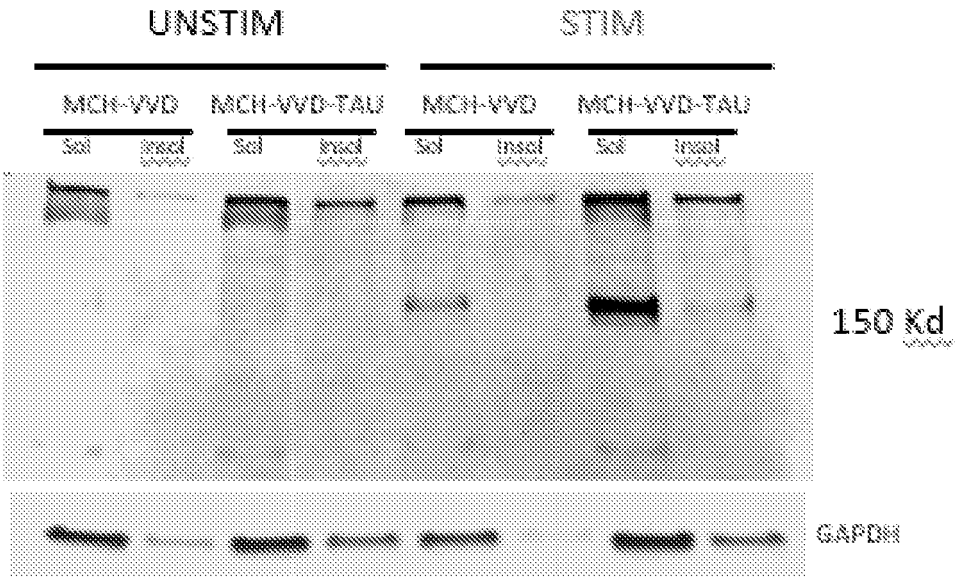


FIGURE 8E

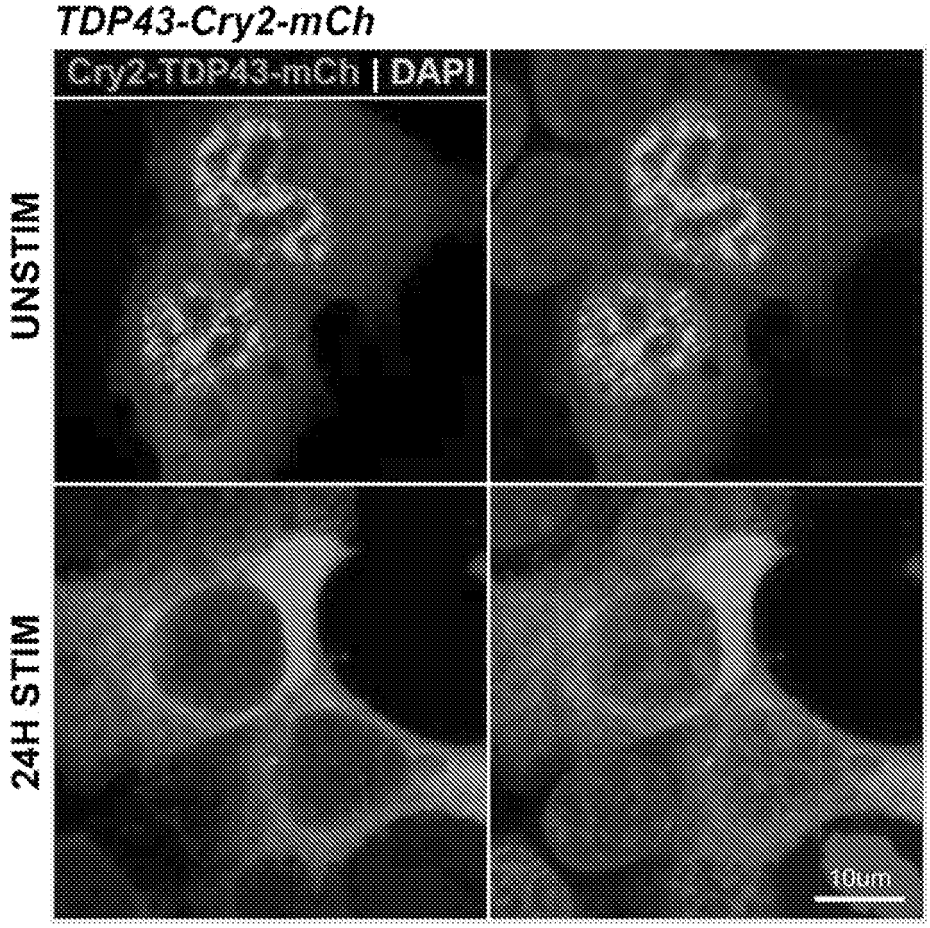


FIGURE 9A

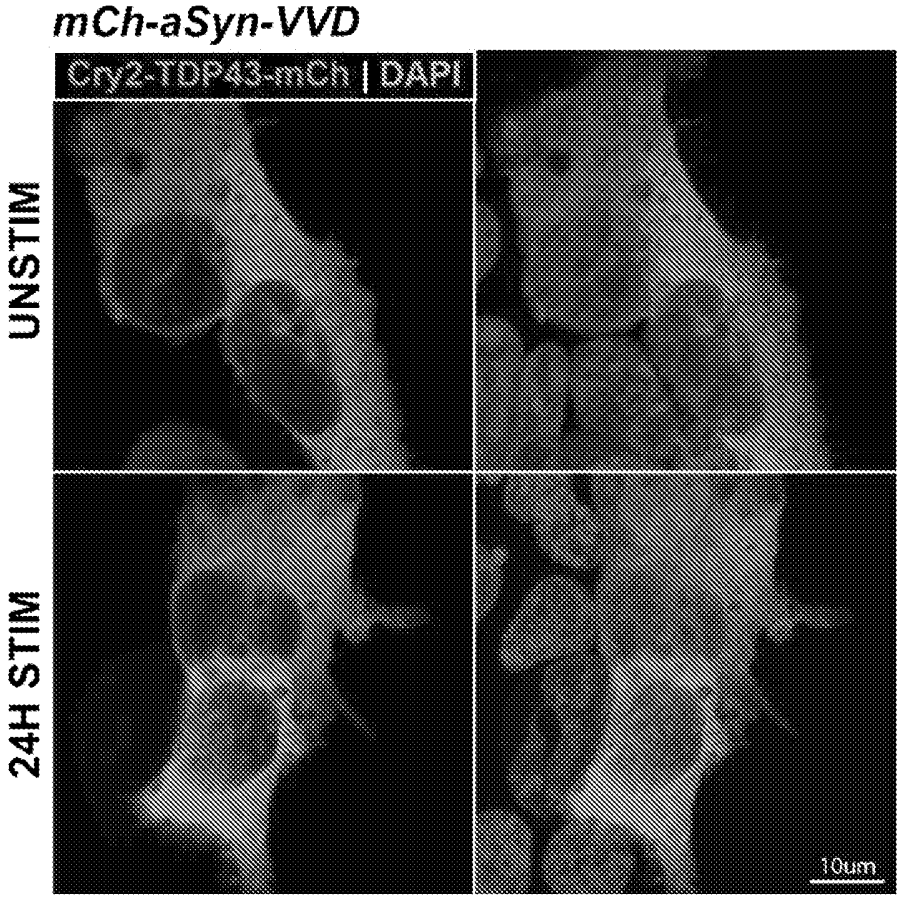


FIGURE 9B

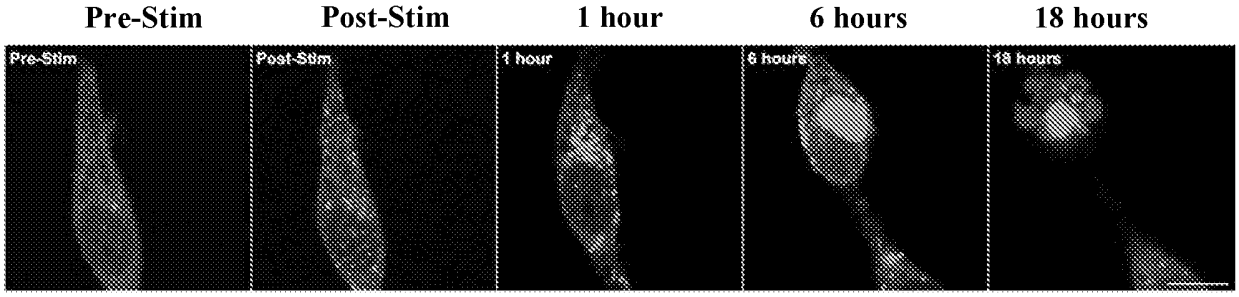
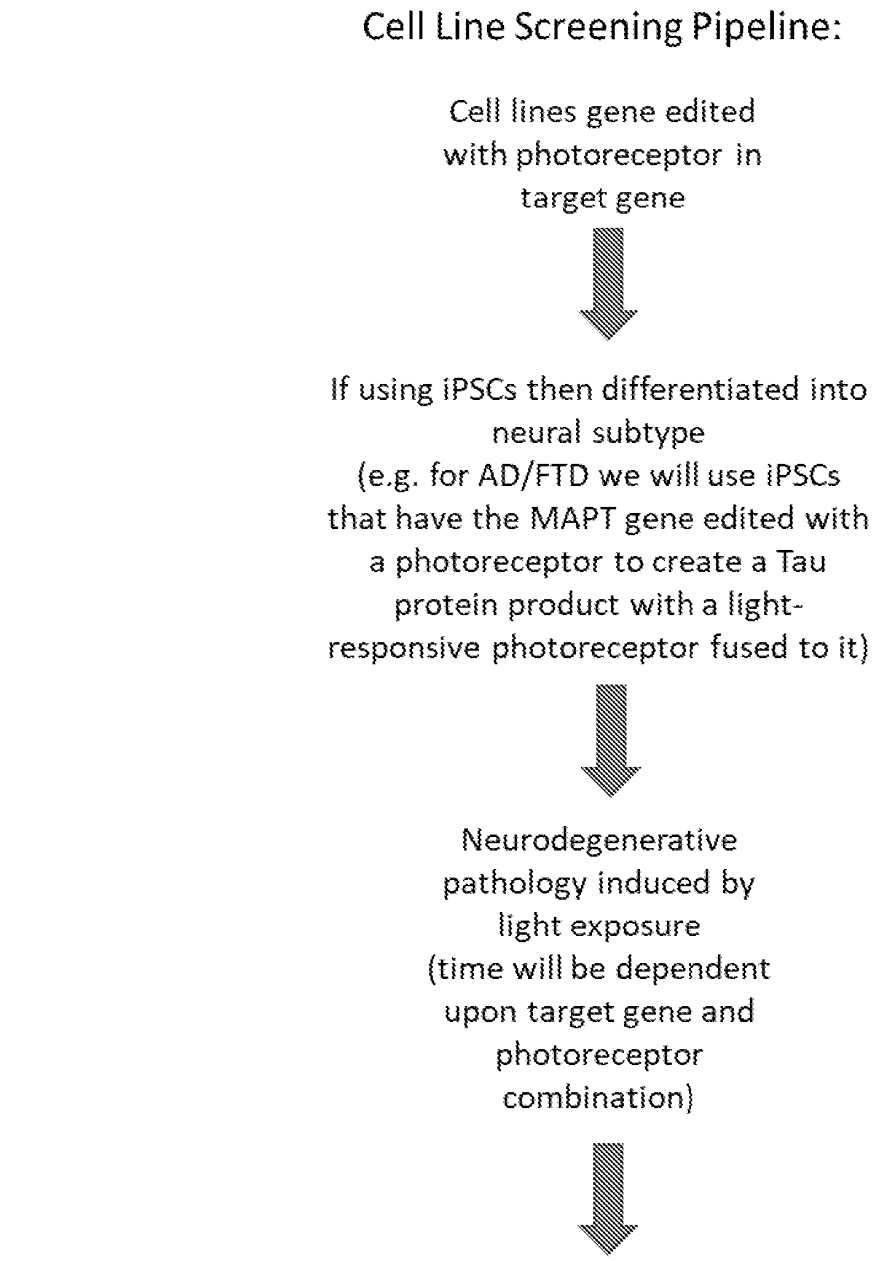


FIGURE 10A



ALS - spinal motor neurons
FTD, AD, LBD – cortical neurons
PD – dopaminergic neurons

FIGURE 10B

REFERENCES CITED IN THE DESCRIPTION

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Non-patent literature cited in the description

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- **KARLIN ; ALTSCHUL.** *Proc. Natl. Acad. Sci. USA,* 1993, vol. 90, 5873-5787 **[0041]**