

What is claimed is:

1. A fusion protein comprising a zinc finger protein (ZFP) domain and a transcription repressor domain, wherein the ZFP domain binds to a target region of a human alpha-synuclein gene (*SNCA* gene), wherein the ZFP domain comprises a DNA-binding recognition helix sequence shown in the Table below, wherein the SEQ ID NO of each sequence is indicated in parenthesis:

F1	F2	F3	F4	F5	F6
QSGHLAR (20)	QRKDLTQ (21)	RSDHLRS (22)	TRDGLRQ (23)	RSANLAR (24)	DSSDRKK (25)
RSDNLST (27)	RSDNLTR (28)	DRSDLSR (29)	RREHLRA (30)	TSGNLTR (31)	QRSHLSD (32)
ERGTLAR (34)	MACCRYA (35)	RSADLTR (36)	QSGDLTR (37)	QSGNLAR (38)	RQEHRVA (39)
RSAHLRS (41)	DRSDLSR (29)	MSCCRSA (42)	RSADLSR (43)	QSGDLTR (37)	QRSNLNI (44)
RSDNLSV (46)	ASWTLTQ (47)	DRSDLSR (29)	DRSNLTR (48)	DRSHLTR (49)	DRSNLTR (48)
LRHHLTR (51)	VAEYRYK (52)	RSDNLSV (46)	RHSHLTS (53)	RSDTLSA (54)	RSADLSR (43)
RSDNLST (27)	QSGHLRS (56)	DAHHLHR (57)	RSANLTR (58)	DRSNRTT (59)	HRSSLRR (60)
RSDDLTR (62)	QKFPRDS (63)	RSDHLTQ (64)	DSANLSR (65)	DRSNLSR (66)	DRTSLKW (67)
DRSNLSR (66)	HLCCCLR (69)	RSCCLHL (70)	RNASRTR (71)	QSSDLRS (72)	HRKSLRS (73)
DRSNLSR (66)	DRSHLAR (75)	RSDHLSE (76)	TSSDRTK (77)	DRSHLSR (78)	DRSHLAR (75)
DRSHLTR (49)	DRSHLAR (75)	QSGNLAR (38)	AKWNLDA (80)	QSGDLTR (37)	TQGYLRK (81)
TSGSLRS (83)	QAGHLAK (84)	DRSARTR (85)	QSGHLRS (56)	RSAHLRS (41)	QSSDLRR (86)
RSDHLRS (22)	QHHRNT (88)	RPDTLRD (89)	QNATRTK (90)	RSDALRS (91)	DRSALAR (92)
NNRDLIN (94)	TSSNLRS (95)	RSDTLSE (96)	NNRDRTK (97)	QSSDLRS (72)	HRSTRNR (98)
QNAHRKT (100)	DNSTRIK (101)	DRSNLSR (66)	HLCCCLR (69)	DRSNLSR (66)	TSANLSR (102)
QRNHRRT (104)	DRSNLTR (48)	MSCCRSA (42)	RSADLSR (43)	RSAHLRS (41)	TSANLSR (102)
QSSDLRS (72)	DRSALAR (92)	DRSYRNT (106)	RRSDLKR (107)	RSADLTR (36)	DRSALAR (92)
DSSTRKT (109)	QSATRTK (110)	ERGTLAR (34)	QSGDLTR (37)	QSSDLRS (72)	AASNRSK (111)
RSDNLSQ (113)	ASNDRKK (114)	YDYGRYT (115)	DRSHLAR (75)	QSGNLAR (38)	DRSALAR (92)
RSDHLSE (76)	QSNHRKT (117)	VYEGCLK (118)	QSGHLRS (56)	RSDVLSE (119)	DRSNRIK (120)
^RRADLSR (122)	YHWYLKK (123)	^QSSDLRS (72)	DRSHLAR (75)	^RSDHLSQ (124)	TSANRTT (125)
^RSDHLST (127)	RSDALAR (128)	^QSANRTT (129)	RSAHLRS (41)	DRSHLTR (49)	QSGNLHV (130)
^RSDHLST (127)	RSDALAR (128)	^QSANRTT (129)	RSAHLRS (41)	^DRSHLTR (49)	QSGNLHV (130)
^RSDHLSE (76)	AKHHRKT (132)	QSGNLAR (38)	RQEHRVA (39)	RSDNLSA (133)	QNRDRKN (134)
^RSDSLSV (136)	QANRKT (137)	RSAHLRS (41)	DRSHLAR (75)	QSANRTT (129)	RRSDLKR (107)

F1	F2	F3	F4	F5	F6
^RSDSLSV (136)	QNANRKT (137)	^RSAHLSR (41)	DRSHLAR (75)	QSANRTT (129)	RRSDLKR (107)
^QSANRTT (129)	RSAHLSR (41)	^QSGDLTR (37)	QSSDLRR (86)	DQSNLRA (139)	RSANLTR (58)
^QSANRTT (129)	RSAHLSR (41)	^QSGDLTR (37)	QSSDLRR (86)	^DQSNLRA (139)	RSANLTR (58)
^QSGDLTR (37)	QRSNLNI (44)	RSAHLSR (41)	QSGDLTR (37)	DSSTRKT (109)	QSATRTK (110)
^QSGDLTR (37)	QRSNLNI (44)	^RSAHLSR (41)	QSGDLTR (37)	DSSTRKT (109)	QSATRTK (110)
^MSCRSA (42)	RSADLSR (43)	^QSGDLTR (37)	QRSNLNI (44)	^RSAHLSR (41)	QSGDLTR (37)
^RSDNLAR (143)	DRSVLHR (144)	QSAHRKN (145)	RHSHLTS (53)	RSDHLSE (76)	RNDHRTT (146)
^QRNHRTT (104)	DRSNLTR (48)	MSCRSA (42)	RSADLSR (43)	RSDHLTR (22)	QGAHLGA (148)
^RSDALSV (150)	DSSHRTR (151)	DNRDLST (152)	DRSNLTR (48)	QSGDLTR (37)	TQGYLRK (81)
^RSDHLSQ (124)	DNSHRTR (154)	DRSDLSR (29)	RSTHLVR (155)	DRSHLTR (49)	DRSYRNT (106)
^DRSDLSR (29)	RSTHLVR (155)	DRSHLTR (49)	DRSYRNT (106)	QESDLVR (157)	DRSNLTR (48)
^RSDNLSV (46)	RRAHNLQ (159)	DQSNLRA (139)	RRSDLKR (107)	QSGHLAR (20)	QRVALQA (160)
^QSGNLAR (38)	AKWNLDA (80)	QSGDLTR (37)	TQGYLRK (81)	RSDNLSV (46)	QSGDLTR (37)
^TSGNLTR (31)	RSELLQS (163)	ARSTRIT (164)	QSGSLTR (165)	QSGSLTR (165)	AKWNLDA (80)
^TSGNLTR (31)	RSELLQS (163)	^ARSTRIT (164)	QSGSLTR (165)	QSGSLTR (165)	AKWNLDA (80)
^TSGNLTR (31)	RSELLQS (163)	^ARSTRIT (164)	QSGSLTR (165)	^QSGSLTR (165)	AKWNLDA (80)
^RPYTLRL (167)	DNSNRIK (168)	^RSANLAR (24)	TSGHLSR (169)	QSGHLAR (20)	RKWTLQG (170)
^RPYTLRL (167)	DNSNRIK (168)	^RSANLAR (24)	TSGHLSR (169)	^QSGHLAR (20)	RKWTLQG (170)
^QSADRTK (172)	DNSNRIK (168)	^RSDNLST (27)	DSANRIK (173)	^RSDHLSE (76)	QNANRIT (174)
^QSADRTK (172)	DNSNRIK (168)	RSANLSV (176)	DRANLSR (177)	RSDNLSV (46)	QKATRIT (178)
^QSADRTK (172)	DNSNRIK (168)	^RSANLSV (176)	DRANLSR (177)	RSDNLSV (46)	QKATRIT (178)
^QSADRTK (172)	DNSNRIK (168)	^RSANLSV (176)	DRANLSR (177)	^RSDNLSV (46)	QKATRIT (178)

2. The fusion protein of claim 1, wherein the target region is within 1 kb of a transcription start site (TSS) in the *SNCA* gene.

3. The fusion protein of claim 2, wherein the TSS is TSS1, 2a, or 2b.

4. The fusion protein of claim 3, wherein the target region is within 500 bps upstream of TSS 1, within 500 bps downstream of TSS 1, within 500 bps upstream of TSS 2a, and/or within 500 bps downstream of TSS 2b, of the *SNCA* gene.

5. The fusion protein of any one of the preceding claims, wherein the ZFP domain comprises six zinc fingers and the fusion protein optionally represses expression of the *SNCA* gene by at least 40%, 75%, 90%, 95%, or 99% with no or minimal detectable off-target binding or activity.
6. The fusion protein of any one of the preceding claims, wherein the transcription repressor domain comprises a KRAB domain amino acid sequence from human KOX1.
7. The fusion protein of any one of the preceding claims, wherein the ZFP domain is linked to the transcription repressor through a peptide linker.
8. The fusion protein of any one of the preceding claims, wherein the ZFP domain comprises the DNA-binding recognition helix sequences as shown in a single row of the Table in claim 1.
9. The fusion protein of any one of the preceding claims, wherein the ZFP domain comprises the DNA-binding recognition helix sequences as shown in a single row of the Table in claim 1 ordered from F1 to F6.
10. The fusion protein of any one of the preceding claims, wherein the ZFP domain comprises the F1 to F6 recognition helix regions, and the phosphate contact mutations, if present, of the DNA-binding recognition helix sequences selected from the group consisting of:

QSGHLAR (20), QRKDLTQ (21), RSDHLSR (22), TRDGLRQ (23), RSANLAR

(24), DSSDRKK (25) for F1 to F6, respectively;

RSDNLST (27), RSDNLTR (28), DRSDLSR (29), RREHLRA (30), TSGNLTR (31),

QRSHLSD (32) for F1 to F6, respectively;

ERGTLAR (34), MACCRYA (35), RSADLTR (36), QSGDLTR (37), QSGNLAR

(38), RQEHRVA (39) for F1 to F6, respectively;

RSAHLSR (41), DRSDLSR (29), MSCCRSA (42), RSADLSR (43), QSGDLTR
 (37), QRSNLNI (44) for F1 to F6, respectively;

RSDNLSV (46), ASWTLTQ (47), DRSDLSR (29), DRSNLTR (48), DRSHLTR
 (49), DRSNLTR (48) for F1 to F6, respectively;

LRHHLTR (51), VAEYRYK (52), RSDNLSV (46), RHSHLTS (53), RSDTLA
 (54), RSADLSR (43) for F1 to F6, respectively;

RSDNLST (27), QSGHLSR (56), DAHHLHR (57), RSANLTR (58), DRSNRTT
 (59), HRSSLRR (60) for F1 to F6, respectively;

RSDDLTR (62), QKFPRDS (63), RSDHLTQ (64), DSANLSR (65), DRSNLSR
 (66), DRTSLKW (67) for F1 to F6, respectively;

DRSNLSR (66), HLCCLGR (69), RSCCLHL (70), RNASRTR (71), QSSDLSR (72),
 HRKSLSR (73) for F1 to F6, respectively;

DRSNLSR (66), DRSHLAR (75), RSDHLSE (76), TSSDRTK (77), DRSHLSR (78),
 DRSHLAR (75) for F1 to F6, respectively;

DRSHLTR (49), DRSHLAR (75), QSGNLAR (38), AKWNLDA (80), QSGDLTR
 (37), TQGYLRK (81) for F1 to F6, respectively;

TSGSLSR (83), QAGHLAK (84), DRSARTR (85), QSGHLSR (56), RSAHLSR
 (41), QSSDLRR (86) for F1 to F6, respectively;

RSDHLSR (22), QHAHRNT (88), RPDTLRD (89), QNATRTK (90), RSDALSR
 (91), DRSALAR (92) for F1 to F6, respectively;

NNRDLIN (94), TSSNLSR (95), RSDTLSE (96), NNRDRTK (97), QSSDLSR (72),
 HRSTRNR (98) for F1 to F6, respectively;

QNAHRKT (100), DNSTRIK (101), DRSNLSR (66), HLCCLGR (69), DRSNLSR
 (66), TSANLSR 102) for F1 to F6, respectively;

QRNHRTT (104), DRSNLTR (48), MSCCRSA (42), RSADLSR (43), RSAHLSR (41), TSANLSR (102) for F1 to F6, respectively;

QSSDLSR (72), DRSALAR (92), DRSYRNT (106), RRSDLKR (107), RSADLTR (36), DRSALAR (92) for F1 to F6, respectively;

DSSTRKT (109), QSATRTK (110), ERGTLAR (34), QSGDLTR (37), QSSDLSR (72), AASNRSK (111) for F1 to F6, respectively;

RSDNLSQ (113), ASNDRKK (114), YDYGRTY (115), DRSHLAR (75), QSGNLAR (38), DRSALAR (92) for F1 to F6, respectively;

RSDHLSE (76), QSNHRKT (117), VYEGCLKK (118), QSGHLSR (56), RSDVLSE (119), DRSNRIK (120) for F1 to F6, respectively;

^RRADLSR (122), YHWYLLKK (123), ^QSSDLSR (72), DRSHLAR (75), ^RSDHLSQ (124), TSANRTT (125) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1, F3, and F5;

^RSDHLST (127), RSDALAR (128), ^QSANRTT (129), RSAHLSR (41), DRSHLTR (49), QSGNLHV (130) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1 and F3;

^RSDHLST (127), RSDALAR (128), ^QSANRTT (129), RSAHLSR (41), ^DRSHLTR (49), QSGNLHV (130) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1, F3, and F5;

^RSDHLSE (76), AKHHRKT (132), QSGNLAR (38), RQEHRVA (39), RSDNLSA (133), QNRDRKN (134) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1;

^RSDSLSV (136), QNANRKT (137), RSAHLSR (41), DRSHLAR (75), QSANRTT (129), RRSDLKR (107) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1;

[^]RSDSLSV (136), QNANRKT (137), [^]RSAHLSR (41), DRSHLAR (75),
 QSANRTT (129), RRSDLKR (107) for F1 to F6, respectively, and an R-to-Q
 substitution at the (-5) position of F1 and F3;
[^]QSANRTT (129), RSAHLSR (41), [^]QSGDLTR (37), QSSDLRR (86), DQSNLRA
 (139), RSANLTR (58) for F1 to F6, respectively, and an R-to-Q substitution at the (-
 5) position of F1 and F3;
[^]QSANRTT (129), RSAHLSR (41), [^]QSGDLTR (37), QSSDLRR (86), [^]DQSNLRA
 (139), RSANLTR (58) for F1 to F6, respectively, and an R-to-Q substitution at the (-
 5) position of F1, F3, and F5;
[^]QSGDLTR (37), QRSNLNI (44), RSAHLSR (41), QSGDLTR (37), DSSTRKT
 (109), QSATRTK (110) for F1 to F6, respectively, and an R-to-Q substitution at the (-
 5) position of F1;
[^]QSGDLTR (37), QRSNLNI (44), [^]RSAHLSR (41), QSGDLTR (37), DSSTRKT
 (109), QSATRTK (110) for F1 to F6, respectively, and an R-to-Q substitution at the (-
 5) position of F1 and F3;
[^]MSCCRSA (42), RSADLSR (43), [^]QSGDLTR (37), QRSNLNI (44), [^]RSAHLSR
 (41), QSGDLTR (37) for F1 to F6, respectively, and an R-to-Q substitution at the (-5)
 position of F1, F3, and F5;
[^]RSDNLAR (143), DRSVLHR (144), QSAHRKN (145), RHSHLTS (53),
 RSDHLSE (76), RNDHRTT (146) for F1 to F6, respectively, and an R-to-Q
 substitution at the (-5) position of F1;
[^]QRNHRTT (104), DRSNLTR (48), MSCCRSA (42), RSADLSR (43), RSDHLSR
 (22), QGAHLGA (148) for F1 to F6, respectively, and an R-to-Q substitution at the (-
 5) position of F1;

^RSDALSV (150), DSSHRTR (151), DNRDLST (152), DRSNLTR (48), QSGDLTR (37), TQGYLRK (81) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1;

^RSDHLSQ (124), DNSHRTR (154), DRSDLSR (29), RSTHLVR (155), DRSHLTR (49), DRSYRNT (106) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1;

^DRSDLSR (29), RSTHLVR (155), DRSHLTR (49), DRSYRNT (106), QESDLVR (157), DRSNLTR (48) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1;

^RSDNLSV (46), RRAHLNQ (159), DQSNLRA (139), RRSDLKR (107), QSGHLAR (20), QRVALQA (160) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1;

^QSGNLAR (38), AKWNLDA (80), QSGDLTR (37), TQGYLRK (81), RSDNLSV (46), QSGDLTR (37) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1;

^TSGNLTR (31), RSELLQS (163), ARSTRIT (164), QSGSLTR (165), QSGSLTR (165), AKWNLDA (80) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1;

^TSGNLTR (31), RSELLQS (163), ^ARSTRIT (164), QSGSLTR (165), QSGSLTR (165), AKWNLDA (80) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1 and F3;

^TSGNLTR (31), RSELLQS (163), ^ARSTRIT (164), QSGSLTR (165), ^QSGSLTR (165), AKWNLDA (80) for F1 to F6, respectively, and an R-to-Q substitution at the (-5) position of F1, F3, and F5;

^RPYTLRL (167), DNSNRIK (168), ^RSANLAR (24), TSGHLSR (169),
 QSGHLAR (20), RKWTLQG (170) for F1 to F6, respectively, and an R-to-Q
 substitution at the (-5) position of F1 and F3;
 ^RPYTLRL (167), DNSNRIK (168), ^RSANLAR (24), TSGHLSR (169),
 ^QSGHLAR (20), RKWTLQG (170) for F1 to F6, respectively, and an R-to-Q
 substitution at the (-5) position of F1, F3, and F5;
 ^QSADRTK (172), DNSNRIK (168), ^RSDNLSV (27), DSANRIK (173),
 ^RSDHLSR (76), QNANRIT (174) for F1 to F6, respectively, and an R-to-Q
 substitution at the (-5) position of F1, F3, and F5;
 ^QSADRTK (172), DNSNRIK (168), RSANLSV (176), DRANLSR (177),
 RSDNLSV (46), QKATRIT (178) for F1 to F6, respectively, and an R-to-Q
 substitution at the (-5) position of F1;
 ^QSADRTK (172), DNSNRIK (168), ^RSANLSV (176), DRANLSR (177),
 RSDNLSV (46), QKATRIT (178) for F1 to F6, respectively, and an R-to-Q
 substitution at the (-5) position of F1 and F3; and
 ^QSADRTK (172), DNSNRIK (168), ^RSANLSV (176), DRANLSR (177),
 ^RSDNLSV (46), QKATRIT (178) for F1 to F6, respectively, and an R-to-Q
 substitution at the (-5) position of F1, F3, and F5.

11. The fusion protein of any one of the preceding claims, wherein the wherein the ZFP domain comprises a DNA-binding recognition helix sequence set forth in a single row of the Table below wherein the DNA-binding recognition helix sequences are in boldface, intramodule and intermodule linkers are underlined and R(-5)Q backbone mutations are indicated by boldface and underline:

SEQ ID NO	Amino Acid Sequences
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179	MAPKKKRKVGVPAAEAERPFQCRICMRNFS <u>QSGHLAR</u> HIRTHTGEKPFAC DICGRKFA <u>QRKDLTQ</u> HHTKIHTHPRAPIPKPFQCRICMRNFS <u>RSDDL</u> SRHI RTHHTGEKPFACDICGRKFAT <u>TRDGLRQ</u> HHTKIHTGSQKPFQCRICMRNFS <u>RS</u> <u>ANLAR</u> HIRTHTGEKPFACDICGRKFAD <u>SSDRKKHTKIHLRQKDAARGSGG</u> DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
180	MAPKKKRKVGVPAAEAERPFQCRICMRNFS <u>RSDDL</u> STHIRTHTGEKPFAC DICGRKFA <u>RSDDL</u> TRHTKIHTGSQKPFQCRICMRNFS <u>DRSDDL</u> SRHIRTHT GEKPFACDICGRKFAR <u>REHLRA</u> HHTKIHTGSQKPFQCRICMRNFS <u>TSGNLT</u> <u>R</u> HIRTHTGEKPFACDICGRKFA <u>QRSHLSD</u> HHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
181	MAPKKKRKVGVPAAEAERPFQCRICMRNFS <u>ERGTLAR</u> HIRTHTGEKPFAC DICGRKFAM <u>ACCRYA</u> HHTKIHTGSQKPFQCRICMRNFS <u>RSADL</u> TRHIRTHT GEKPFACDICGRKFA <u>QSGDL</u> TRHTKIHTHPRAPIPKPFQCRICMRNFS <u>QS</u> <u>GNLAR</u> HIRTHTGEKPFACDICGRKFAR <u>QEHRVA</u> HHTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
182	MAPKKKRKVGVPAAEAERPFQCRICMRNFS <u>RSAHL</u> SRHIRTHTGEKPFAC DICGRKFAD <u>RSDDL</u> SRHTKIHTGSQKPFQCRICMRNFS <u>MSCCR</u> SAHIRTHT GEKPFACDICGRKFARS <u>ADL</u> SRHTKIHTGSQKPFQCRICMRNFS <u>QSGDL</u> T <u>R</u> HIRTHTGEKPFACDICGRKFA <u>QRSNLNI</u> HHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
183	MAPKKKRKVGVPAAEAERPFQCRICMRNFS <u>RSDDL</u> SVHIRTHTGEKPFAC DICGRKFA <u>ASWTLTQ</u> HHTKIHTGSQKPFQCRICMRNFS <u>DRSDDL</u> SRHIRTHT GEKPFACDICGRKFAD <u>RSNL</u> TRHTKIHTGSQKPFQCRICMRNFS <u>DRSHLT</u> <u>R</u> HIRTHTGEKPFACDICGRKFAD <u>RSNL</u> TRHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
184	MAPKKKRKVGVPAAEAERPFQCRICMRNFS <u>LRHHL</u> TRHIRTHTGEKPFAC DICGRKFVA <u>EYRYK</u> HHTKIHTGSQKPFQCRICMRNFS <u>RSDDL</u> SVHIRTHT GEKPFACDICGRKFAR <u>HSHLT</u> SHHTKIHTGSQKPFQCRICMRNFS <u>RSDTLS</u> <u>A</u> HIRTHTGEKPFACDICGRKFARS <u>ADL</u> SRHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
185	MAPKKKRKVGVPAAEAERPFQCRICMRNFS <u>RSDDL</u> STHIRTHTGEKPFAC DICGRKFA <u>QSGHL</u> SRHTKIHTGSQKPFQCRICMRNFS <u>DAHHL</u> RHIRTHT GEKPFACDICGRKFARS <u>ANL</u> TRHTKIHTGSQKPFQCRICMRNFS <u>DRSNRT</u> <u>T</u> HIRTHTGEKPFACDICGRKFA <u>HRS</u> SLRRHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
186	MAPKKKRKVGVPAAEAERPFQCRICMRNFS <u>RSDDL</u> TRHIRTHTGEKPFAC DICGRKFA <u>QKFPRDS</u> HHTKIHTGSQKPFQCRICMRNFS <u>RSDDL</u> TQHIRTHT GEKPFACDICGRKFAD <u>SANL</u> SRHTKIHTGSQKPFQCRICMRNFS <u>DRSNLS</u> <u>R</u> HIRTHTGEKPFACDICGRKFAD <u>RTSLKW</u> HHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS

187	MAPKKRKRKVGVPAAEAERPFQCRICMRNFS <u>DRSNLSR</u> HIRTHTGEKPFAC DICGRKFA <u>HLCC</u> <u>LR</u> HTKIHTHPRAPIPKPFQCRICMRNFS <u>RS</u> <u>CCL</u> <u>HL</u> HI RTHTGEKPFACDICGRKFARNASRTRHTKIHTGSQKPFQCRICMRNFS <u>QS</u> <u>SDLSR</u> HIRTHTGEKPFACDICGRKFA <u>HRKS</u> <u>LSR</u> HTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
188	MAPKKRKRKVGVPAAEAERPFQCRICMRNFS <u>DRSNLSR</u> HIRTHTGEKPFAC DICGRKFA <u>DRSHL</u> ARHTKIHTHPRAPIPKPFQCRICMRNFS <u>RS</u> <u>DHL</u> SEHI RTHTGEKPFACDICGRKFATSSDRTKHTKIHTGSQKPFQCRICMRNFS <u>SDR</u> <u>SHLSR</u> HIRTHTGEKPFACDICGRKFAD <u>DRSHL</u> ARHTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
189	MAPKKRKRKVGVPAAEAERPFQCRICMRNFS <u>DRSHL</u> TRHIRTHTGEKPFAC DICGRKFAD <u>DRSHL</u> ARHTKIHTHPRAPIPKPFQCRICMRNFS <u>QS</u> <u>GNL</u> ARHI RTHTGEKPFACDICGRKFAAKWNLDAHTKIHTGSQKPFQCRICMRNFS <u>QS</u> <u>GDLTR</u> HIRTHTGEKPFACDICGRKFATQGYLRKHTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
190	MAPKKRKRKVGVPAAEAERPFQCRICMRNFS <u>TSGSL</u> SRHIRTHTGEKPFAC DICGRKFAQAGHLAKHTKIHTGSQKPFQCRICMRNFS <u>DRS</u> ARTRHIRTHT GEKPFACDICGRKFAQSGHLSRHTKIHTHPRAPIPKPFQCRICMRNFS <u>SRS</u> <u>AHLSR</u> HIRTHTGEKPFACDICGRKFAQSSDLRRHTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
191	MAPKKRKRKVGVPAAEAERPFQCRICMRNFS <u>RS</u> <u>DHL</u> SRHIRTHTGEKPFAC DICGRKFAQHHRNTHTKIHTGSQKPFQCRICMRNFS <u>RPD</u> TLRDHIRTHT GEKPFACDICGRKFAQONATRTKHTKIHTHPRAPIPKPFQCRICMRNFS <u>SRS</u> <u>DALS</u> RHIRTHTGEKPFACDICGRKFADRSALARHTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
192	MAPKKRKRKVGVPAAEAERPFQCRICMRNFS <u>NNRD</u> LINHIRTHTGEKPFAC DICGRKFATSSNLSRHTKIHTHPRAPIPKPFQCRICMRNFS <u>RS</u> <u>DTL</u> SEHI RTHTGEKPFACDICGRKFANNRDRTKHTKIHTGSQKPFQCRICMRNFS <u>QS</u> <u>SDLSR</u> HIRTHTGEKPFACDICGRKFAHRSTRNRHTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
193	MAPKKRKRKVGVPAAEAERPFQCRICMRNFSQNAHRKTHIRTHTGEKPFAC DICGRKFADNSTRIKHTKIHTHPRAPIPKPFQCRICMRNFS <u>DRSNLSR</u> HI RTHTGEKPFACDICGRKFA <u>HLCC</u> <u>LR</u> HTKIHTHPRAPIPKPFQCRICMRNFS <u>SDR</u> <u>SNLSR</u> HIRTHTGEKPFACDICGRKFATSANLSRHTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
194	MAPKKRKRKVGVPAAEAERPFQCRICMRNFSQNRHRTTHIRTHTGEKPFAC DICGRKFADRSNLTRHTKIHTGSQKPFQCRICMRNFS <u>MSC</u> CRSAHIRTHT GEKPFACDICGRKFARSADLSRHTKIHTGSQKPFQCRICMRNFS <u>RS</u> <u>AHLS</u> <u>R</u> HIRTHTGEKPFACDICGRKFATSANLSRHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS

195	MAPKKRKVGVPAAEAERPFQCRICMRNFS <u>QSSDLSR</u> HIRTHTGEKPFAC DICGRKFADRSALARHTKIHTHPRAPIPKPFQCRICMRNFS <u>DRSYRNTHI</u> RTHTGEKPFACDICGRKFAR <u>RSDLKR</u> HTKIHTGSQKPFQCRICMRNFS <u>SRS</u> <u>ADLTR</u> HIRTHTGEKPFACDICGRKFADRSALARHTKIHLRQKDAARGSGG DAKSLTAWSRITLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
196	MAPKKRKVGVPAAEAERPFQCRICMRNFS <u>DSSTRKT</u> HIRTHTGEKPFAC DICGRKFQ <u>SATRTK</u> HTKIHTHPRAPIPKPFQCRICMRNFS <u>ERGTLARHI</u> RTHTGEKPFACDICGRKFQ <u>SGDLTR</u> HTKIHTGSQKPFQCRICMRNFS <u>QS</u> <u>SDLSR</u> HIRTHTGEKPFACDICGRKFQ <u>AASNRSK</u> HTKIHLRQKDAARGSGG DAKSLTAWSRITLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
197	MAPKKRKVGVPAAEAERPFQCRICMRNFS <u>RS DNLSQ</u> HIRTHTGEKPFAC DICGRKFQ <u>AASNDRKK</u> HTKIHTGSQKPFQCRICMRNFS <u>YDYGRT</u> HIRTHT GEKPFACDICGRKFADRSALARHTKIHTHPRAPIPKPFQCRICMRNFS <u>QS</u> <u>GNLAR</u> HIRTHTGEKPFACDICGRKFADRSALARHTKIHLRQKDAARGSGG DAKSLTAWSRITLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
198	MAPKKRKVGVPAAEAERPFQCRICMRNFS <u>RS DHLSE</u> HIRTHTGEKPFAC DICGRKFQ <u>SNHRKT</u> HTKIHTGSQKPFQCRICMRNFS <u>VYEGLKK</u> HIRTHT GEKPFACDICGRKFQ <u>SGHLSR</u> HTKIHTHPRAPIPKPFQCRICMRNFS <u>SRS</u> <u>DVLSE</u> HIRTHTGEKPFACDICGRKFADRSNRIKHTKIHLRQKDAARGSGG DAKSLTAWSRITLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
199	MAPKKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS <u>RRADLSR</u> HIRTHTGEKPFAC DICGRKFQ <u>YHWYLKK</u> HTKIHTGSQKPFQCRICM <u>Q</u> NFS <u>QSSDLSR</u> HIRTHT GEKPFACDICGRKFADRSALARHTKIHTHPRAPIPKPFQCRICM <u>Q</u> NFS <u>SRS</u> <u>DHLSQ</u> HIRTHTGEKPFACDICGRKFQ <u>TSANRT</u> HTKIHLRQKDAARGSGG DAKSLTAWSRITLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
200	MAPKKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS <u>RS DHLST</u> HIRTHTGEKPFAC DICGRKFARSDALARHTKIHTGSQKPFQCRICM <u>Q</u> NFS <u>QSANRTT</u> HIRTHT GEKPFACDICGRKFARSAHLSRHTKIHTGSQKPFQCRICMRNFS <u>DRSHLT</u> <u>R</u> HIRTHTGEKPFACDICGRKFQ <u>SGNLHV</u> HTKIHLRQKDAARGSGGDAKS LTAWSRITLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
201	MAPKKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS <u>RS DHLST</u> HIRTHTGEKPFAC DICGRKFARSDALARHTKIHTGSQKPFQCRICM <u>Q</u> NFS <u>QSANRTT</u> HIRTHT GEKPFACDICGRKFARSAHLSRHTKIHTGSQKPFQCRICM <u>Q</u> NFS <u>DRSHLT</u> <u>R</u> HIRTHTGEKPFACDICGRKFQ <u>SGNLHV</u> HTKIHLRQKDAARGSGGDAKS LTAWSRITLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
202	MAPKKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS <u>RS DHLSE</u> HIRTHTGEKPFAC DICGRKFQ <u>AKHHRKT</u> HTKIHTGSQKPFQCRICMRNFS <u>QSGNLAR</u> HIRTHT GEKPFACDICGRKFQ <u>RQEHVA</u> HTKIHTHPRAPIPKPFQCRICMRNFS <u>SRS</u> <u>DNLSA</u> HIRTHTGEKPFACDICGRKFQ <u>QNRDRKN</u> HTKIHLRQKDAARGSGG DAKSLTAWSRITLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS

203	MAPKKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS RS <u>DSL</u> SVHIRTHTGEKPFAC DICGRKFA <u>Q</u> NANRKT HHTKIHTGSQKPFQCRICMRNFS RS <u>AHL</u> SRHIRTHT GEKPFACDICGRKF ADRSHLAR HHTKIHTGSQKPFQCRICMRNFS Q <u>SANRT</u> T HIRTHTGEKPFACDICGRKF ARRSD LKRHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFVDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
204	MAPKKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS RS <u>DSL</u> SVHIRTHTGEKPFAC DICGRKFA <u>Q</u> NANRKT HHTKIHTGSQKPFQCRICM <u>Q</u> NFS RS <u>AHL</u> SRHIRTHT GEKPFACDICGRKF ADRSHLAR HHTKIHTGSQKPFQCRICMRNFS Q <u>SANRT</u> T HIRTHTGEKPFACDICGRKF ARRSD LKRHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFVDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
205	MAPKKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS Q <u>SANRT</u> T HIRTHTGEKPFAC DICGRKF ARSAHL SRHTKIHTGSQKPFQCRICM <u>Q</u> NFS Q <u>SGDLTR</u> HIRTHT GEKPFACDICGRKFA Q <u>SSDLRR</u> HHTKIHTGSQKPFQCRICMRNFS D <u>QSNLR</u> A HIRTHTGEKPFACDICGRKF ARSANL TRHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFVDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
206	MAPKKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS Q <u>SANRT</u> T HIRTHTGEKPFAC DICGRKF ARSAHL SRHTKIHTGSQKPFQCRICM <u>Q</u> NFS Q <u>SGDLTR</u> HIRTHT GEKPFACDICGRKFA Q <u>SSDLRR</u> HHTKIHTGSQKPFQCRICM <u>Q</u> NFS D <u>QSNLR</u> A HIRTHTGEKPFACDICGRKF ARSANL TRHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFVDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
207	MAPKKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS Q <u>SGDLTR</u> HIRTHTGEKPFAC DICGRKFA Q <u>RSNLNI</u> HHTKIHTGSQKPFQCRICMRNFS RS <u>AHL</u> SRHIRTHT GEKPFACDICGRKFA Q <u>SGDLTR</u> HHTKIHTHPRAPIPKPFQCRICMRNFS SDS STRKT HIRTHTGEKPFACDICGRKFA Q <u>SATRTK</u> HHTKIHLRQKDAARGSGG DAKSLTAWSTRLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
208	MAPKKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS Q <u>SGDLTR</u> HIRTHTGEKPFAC DICGRKFA Q <u>RSNLNI</u> HHTKIHTGSQKPFQCRICM <u>Q</u> NFS RS <u>AHL</u> SRHIRTHT GEKPFACDICGRKFA Q <u>SGDLTR</u> HHTKIHTHPRAPIPKPFQCRICMRNFS SDS STRKT HIRTHTGEKPFACDICGRKFA Q <u>SATRTK</u> HHTKIHLRQKDAARGSGG DAKSLTAWSTRLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
209	MAPKKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS MS <u>CCRSA</u> HIRTHTGEKPFAC DICGRKF ARSAD LSRHTKIHTGSQKPFQCRICM <u>Q</u> NFS Q <u>SGDLTR</u> HIRTHT GEKPFACDICGRKFA Q <u>RSNLNI</u> HHTKIHTGSQKPFQCRICM <u>Q</u> NFS RS <u>AHL</u> R HIRTHTGEKPFACDICGRKFA Q <u>SGDLTR</u> HHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFVDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
210	MAPKKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS RS <u>DN</u> LARHIRTHTGEKPFAC DICGRKF ADRSVL HRHTKIHTGSQKPFQCRICMRNFS Q <u>SAHR</u> KNHIRTHT GEKPFACDICGRKF ARHSHL TSHTKIHTGSQKPFQCRICMRNFS RS <u>DHLS</u> E HIRTHTGEKPFACDICGRKF ARN DHRTTHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFVDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS

211	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS <u>Q</u> RNHRTTHIRTHTGEKPFAC DICGRKFAD <u>RSNLTR</u> HTKIHTGSQKPFQCRICMRNFS <u>MSCCRSA</u> HIRTHT GEKPFACDICGRKF <u>ARSADLSR</u> HTKIHTHPRAPIPKPFQCRICMRNFS <u>SRS</u> <u>DHLSR</u> HIRTHTGEKPFACDICGRKFA <u>QGAHLGA</u> HTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
212	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS <u>RS</u> DALSVHIRTHTGEKPFAC DICGRKFAD <u>SSHRTR</u> HTKIHTGSQKPFQCRICMRNFS <u>DN</u> RDLS <u>TH</u> IRTHT GEKPFACDICGRKFAD <u>RSNLTR</u> HTKIHTGSQKPFQCRICMRNFS <u>QSGDLT</u> <u>R</u> HIRTHTGEKPFACDICGRKFAT <u>QGYLRK</u> HTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
213	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS <u>RS</u> DHLSQHIRTHTGEKPFAC DICGRKFAD <u>NSHRTR</u> HTKIHTHPRAPIPKPFQCRICMRNFS <u>DRSDLSR</u> HI RTHTGEKPFACDICGRKFAR <u>STHLVR</u> HTKIHTGSQKPFQCRICMRNFS <u>DR</u> <u>SHLTR</u> HIRTHTGEKPFACDICGRKFAD <u>RSYRN</u> THTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
214	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS <u>DRSDLSR</u> HIRTHTGEKPFAC DICGRKFAR <u>STHLVR</u> HTKIHTGSQKPFQCRICMRNFS <u>DRSHLTR</u> HIRTHT GEKPFACDICGRKFAD <u>RSYRN</u> THTKIHTGSQKPFQCRICMRNFS <u>QESDLV</u> <u>R</u> HIRTHTGEKPFACDICGRKFAD <u>RSNLTR</u> HTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
215	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS <u>RS</u> DNLSVHIRTHTGEKPFAC DICGRKFAR <u>RAHLN</u> QHTKIHTGSQKPFQCRICMRNFS <u>SDQSNLRA</u> HIRTHT GEKPFACDICGRKFAR <u>RSDLKR</u> HTKIHTGSQKPFQCRICMRNFS <u>QSGHLA</u> <u>R</u> HIRTHTGEKPFACDICGRKFA <u>Q</u> RVALQAHTKIHLRQKDAARGSGGDAKS LTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
216	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS <u>QSGNLAR</u> HIRTHTGEKPFAC DICGRKFA <u>AKWNLDA</u> HTKIHTGSQKPFQCRICMRNFS <u>QSGDLTR</u> HIRTHT GEKPFACDICGRKFAT <u>QGYLRK</u> HTKIHTHPRAPIPKPFQCRICMRNFS <u>SRS</u> <u>DNLSV</u> HIRTHTGEKPFACDICGRKFA <u>QSGDLTR</u> HTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
217	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS <u>TSGNLTR</u> HIRTHTGEKPFAC DICGRKFAR <u>SELLQ</u> SHTKIHTGSQKPFQCRICMRNFS <u>ARSTRIT</u> HIRTHT GEKPFACDICGRKFA <u>QSGSLTR</u> HTKIHTHPRAPIPKPFQCRICMRNFS <u>QS</u> <u>GSLTR</u> HIRTHTGEKPFACDICGRKFA <u>AKWNLDA</u> HTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
218	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS <u>TSGNLTR</u> HIRTHTGEKPFAC DICGRKFAR <u>SELLQ</u> SHTKIHTGSQKPFQCRICM <u>Q</u> NFS <u>ARSTRIT</u> HIRTHT GEKPFACDICGRKFA <u>QSGSLTR</u> HTKIHTHPRAPIPKPFQCRICMRNFS <u>QS</u> <u>GSLTR</u> HIRTHTGEKPFACDICGRKFA <u>AKWNLDA</u> HTKIHLRQKDAARGSGG DAKSLTAWSRTLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS

219	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS TSGNLTR HIRTHTGEKPFAC DICGRKFAR SELLQ SHTKIHTGSQKPFQCRICM <u>Q</u> NFS ARSTRIT HIRTHT GEKPFACDICGRKFA QSGSLTR HHTKIHTHPRAPIPKPFQCRICM <u>Q</u> NFS QS GSLTR HIRTHTGEKPFACDICGRKFA AKWNLDA HHTKIHLRQKDAARGSGG DAKSLTAWSRTRLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
220	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS RPYTLRL HIRTHTGEKPFAC DICGRKFAD NSNRIK HHTKIHTGSQKPFQCRICM <u>Q</u> NFS RSANLAR HIRTHT GEKPFACDICGRKFA TSGHLSR HHTKIHTGSQKPFQCRICM <u>Q</u> NFS QSGHLA R HIRTHTGEKPFACDICGRKF ARKWTLQ GHTKIHLRQKDAARGSGGDAKS LTAWSRTRLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
221	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS RPYTLRL HIRTHTGEKPFAC DICGRKFAD NSNRIK HHTKIHTGSQKPFQCRICM <u>Q</u> NFS RSANLAR HIRTHT GEKPFACDICGRKFA TSGHLSR HHTKIHTGSQKPFQCRICM <u>Q</u> NFS QSGHLA R HIRTHTGEKPFACDICGRKF ARKWTLQ GHTKIHLRQKDAARGSGGDAKS LTAWSRTRLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
222	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS QSA DRTHIRTHTGEKPFAC DICGRKFAD NSNRIK HHTKIHTGSQKPFQCRICM <u>Q</u> NFS RS DNLS TH IRTHT GEKPFACDICGRKFAD SANRIK HHTKIHTGSQKPFQCRICM <u>Q</u> NFS RS DHLS E HIRTHTGEKPFACDICGRKFA Q NANR IT HHTKIHLRQKDAARGSGGDAKS LTAWSRTRLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLVSLGY QLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
223	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS QSA DRTHIRTHTGEKPFAC DICGRKFAD NSNRIK HHTKIHTGSQKPFQCRICM <u>Q</u> NFS RSANLSV HIRTHT GEKPFACDICGRKFAD RANLSR HHTKIHTHPRAPIPKPFQCRICM <u>Q</u> NFS RS DNLSV HIRTHTGEKPFACDICGRKFA QKATRIT HHTKIHLRQKDAARGSGG DAKSLTAWSRTRLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
224	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS QSA DRTHIRTHTGEKPFAC DICGRKFAD NSNRIK HHTKIHTGSQKPFQCRICM <u>Q</u> NFS RSANLSV HIRTHT GEKPFACDICGRKFAD RANLSR HHTKIHTHPRAPIPKPFQCRICM <u>Q</u> NFS RS DNLSV HIRTHTGEKPFACDICGRKFA QKATRIT HHTKIHLRQKDAARGSGG DAKSLTAWSRTRLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS
225	MAPKKRKRKVGVPAAEAERPFQCRICM <u>Q</u> NFS QSA DRTHIRTHTGEKPFAC DICGRKFAD NSNRIK HHTKIHTGSQKPFQCRICM <u>Q</u> NFS RSANLSV HIRTHT GEKPFACDICGRKFAD RANLSR HHTKIHTHPRAPIPKPFQCRICM <u>Q</u> NFS RS DNLSV HIRTHTGEKPFACDICGRKFA QKATRIT HHTKIHLRQKDAARGSGG DAKSLTAWSRTRLVTFKDVFDFTREEWKLLDTAQQIVYRNVMLENYKNLV SLGYQLTKPDVILRLEKGEEPWLVEREIHQETHPDSETAFEIKSSVRS

12. A nucleic acid construct comprising a coding sequence for the fusion protein of any one of claims 1-11, wherein the coding sequence is linked operably to a transcription regulatory element.
13. The nucleic acid construct of claim 12, wherein the transcription regulatory element is a mammalian promoter that is constitutively active or inducible in a brain cell, and wherein the promoter is optionally a human synapsin I promoter.
14. A recombinant virus comprising the nucleic acid construct of claim 12 or 13.
15. The recombinant virus of claim 14, wherein the recombinant virus is an adeno-associated viral vector, an adenoviral vector, or a lentiviral vector.
16. A pharmaceutical composition comprising the nucleic acid construct of claim 12 or 13 or the recombinant virus of claim 14 or 15, and a pharmaceutically acceptable carrier.
17. A host cell comprising the nucleic acid construct of claim 12 or 13, or the recombinant virus of claim 14 or 15.
18. The host cell of claim 17, wherein the host cell is a human cell.
19. The host cell of claim 17, wherein the host cell is a brain cell or a pluripotent stem cell, wherein the stem cell is optionally an embryonic stem cell or an inducible pluripotent stem cell (iPSC).
20. Use of a fusion protein of any one of claims 1-11 in the manufacture of a medicament for inhibiting expression of alpha-synuclein in a human brain cell of a patient suffering from or at risk of developing Parkinson's disease, Lewy body dementia, Alzheimer's disease, multiple system atrophy, or another synucleinopathy, wherein the fusion protein of any one of claims 1-11 is to be introduced to the cell, optionally through introduction of a nucleic acid construct of claim 12 or 13 or a recombinant virus of claim 14 or 15.
21. The use of claim 20, wherein the human brain cell is a neuron, a glial cell, an ependymal cell, or a neuroepithelial cell.

22. The use of any one of claims 20-21, wherein the fusion protein is to be introduced into the cell through a recombinant virus that expresses the fusion protein.

23. The use of claim 22, wherein the recombinant virus is an adeno-associated virus (AAV), optionally of serotype 9.

24. Use of a recombinant AAV encoding a fusion protein of any one of claims 1-11 in the manufacture of a medicament for treating a synucleinopathy in a patient, wherein the recombinant AAV encoding a fusion protein of any one of claims 1-11 is to be administered to the patient.

25. The use of claim 24, wherein the recombinant AAV is to be introduced to the patient via intravenous, intrathecal, intracerebroventricular, intra-cisternal magna, intrastriatal, or intranigral injection, or injection into any brain region.

26. The use of claim 24 or 25, wherein the synucleinopathy is Parkinson's disease, Lewy body dementia, Alzheimer's disease, or multiple system atrophy.

27. A fusion protein of any one of claims 1-11, a nucleic acid construct of claim 12 or 13, a recombinant virus of claim 14 or 15, a pharmaceutical composition of claim 16, for use as a medicament.

28. A fusion protein comprising a zinc finger protein (ZFP) domain and a transcription repressor domain, wherein the ZFP domain binds to capital letters in a genomic target sequence in the following table of a human alpha-synuclein gene (*SNCA* gene), and the fusion protein is capable of repressing *SNCA* gene expression, wherein the SEQ ID NO of each genomic target sequence is indicated in parenthesis:

ZFP name	Binding Sequence (capital letters)
19	aTCCGAGATAGGGaCGAGGAg
26	cCGAGATAGGGACGAGGAGc
33	cAGGGAAaGCAGCGAGCGCCg
40	gAAAGCAGCGAGCGCCGGGa

ZFP name	Binding Sequence (capital letters)
45	gGACGGCGACGACCAGAAGg
50	cGCGACGCGGAAGTGAGGTg
55	cGCTCACGAGGGTGGAAAGg
61	aTTCGACGACAGGTTAGCGg
68	gGCCGCTGTGAGCcGGCGACg
74	aGGCGGCACCCGgGGGGACT
79	gAGCGCACAGGAAGGGCGAGg
82	gGCGGGGaGGAGTCGGAGTTg
87	gGTCGTGgGCACCGGGAGGGg
93	gGCTGCTTCTCCGgGATCCGc
99	gGAGGACGGCGACgACCAGAA
103	aGAGGGGGCGAGCGACCGAg
105	cGTCGCGGCGCTCgGTCGCTc
108	cTGCGCTGCAGCCcGCACGCa
112	cGTCGAAtGGCCACTCCCAGt
116	gTACCTGtGGATCTAAACGGg
121	aAAGTGGgGGCGCTTTTGCGc
126	gCAAGGCGGAAAGTGGGGg
126	gCAAGGCGGAAAGTGGGGg
131	gCGCAAGgCGGGAAAGTGGGg
135	cGCGCAAGGCGGAAAGTGg
135	cGCGCAAGGCGGAAAGTGg
138	gGAGCACGCTGCAGGGAAAg
138	gGAGCACGCTGCAGGGAAAg
140	aGCACGctGCAGGGAAAGCAg
140	aGCACGctGCAGGGAAAGCAg
141	tGCAGGGAAAGCAGCGAGCg
142	gTGGGGGCGGAGAGCCGAGg
147	gAGAGGGgGCGAGCGACCGAg
149	gcAGCGCAGACCCCGGCCGg
153	tCTCGGAGGGGCCgGGCCGGg
156	gGACGCTCTCGGAGGGGCCg
158	aAAAGGAGCGCACAGGAAGg
161	gGAAAAGgAGCGCACAGGAAGg

ZFP name	Binding Sequence (capital letters)
162	tCAGGTAaGTACCTGTGGATc
162	tCAGGTAaGTACCTGTGGATc
162	tCAGGTAaGTACCTGTGGATc
166	tCTGGGAGGTGAGTACTTGt
166	tCTGGGAGGTGAGTACTTGt
171	cCAAAGGGACAAGTACTCAc
175	cCCAAAGgGACAAGTACTCAc
175	cCCAAAGgGACAAGTACTCAc
175	cCCAAAGgGACAAGTACTCAc