FIGURE 1A

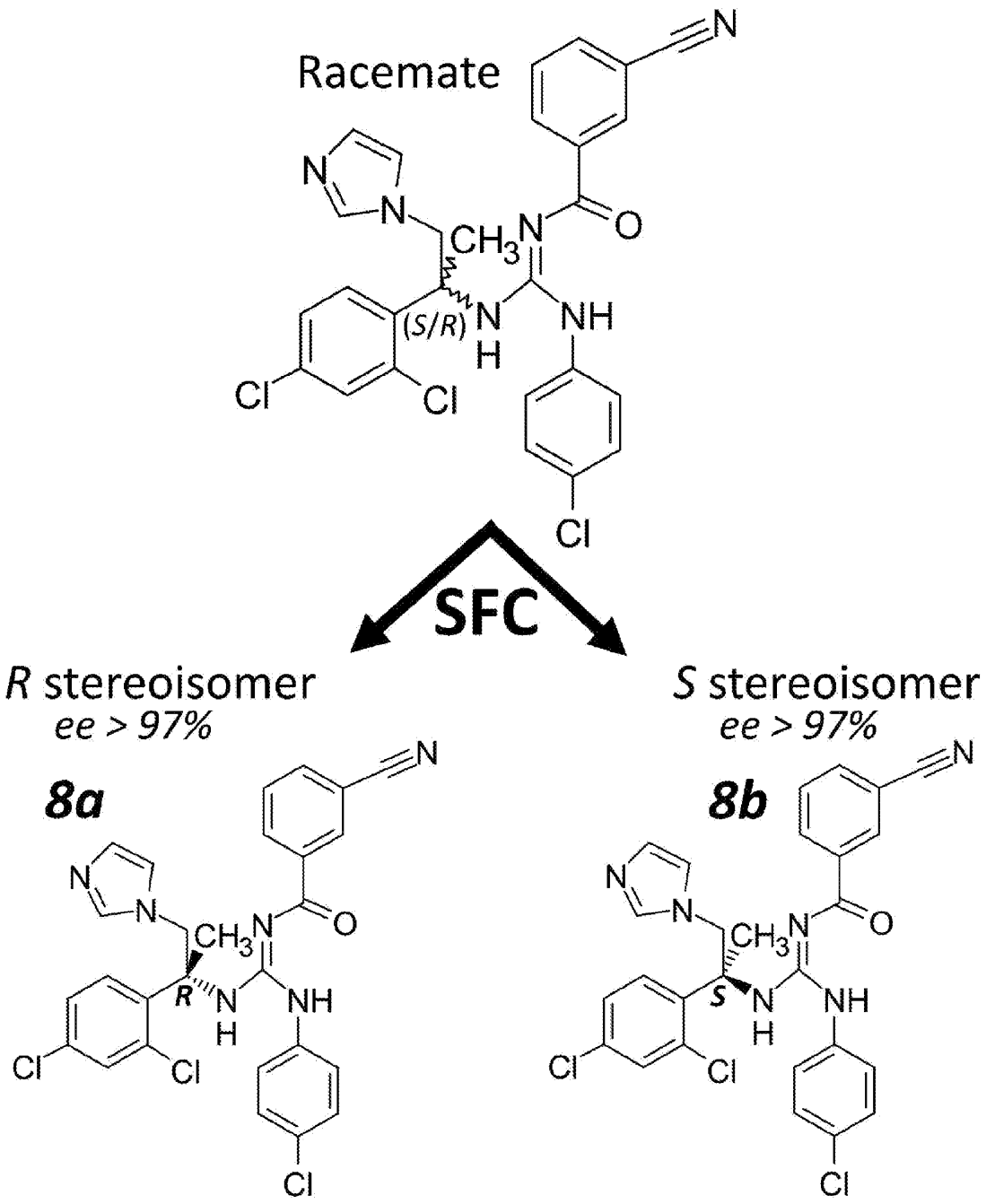


FIGURE 1B

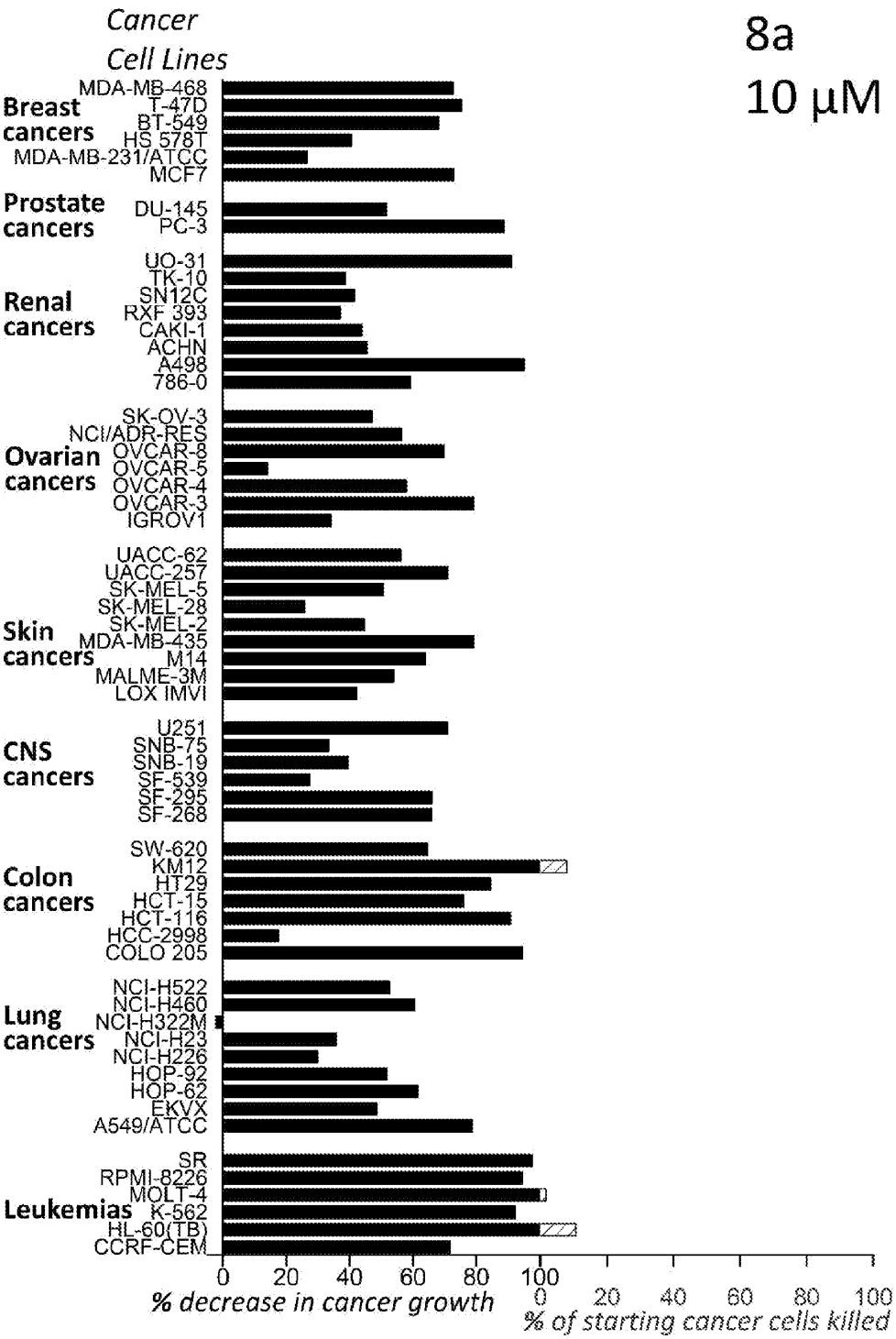

Cancer Cell Lines
8a
10 µM
Breast cancers
MDA-MB-468
T-47D
BT-549
HS 578T
MDA-MB-231/ATCC
MCF7
Prostate cancers
DU-145
PC-3
Renal cancers
UO-31
TK-10
SN12C
RXF 393
CAKI-1
ACHN
A498
786-0
Ovarian cancers
SK-OV-3
NCI/ADR-RES
OVCAR-8
OVCAR-5
OVCAR-4
OVCAR-3
IGROV1
Skin cancers
UACC-62
UACC-257
SK-MEL-5
SK-MEL-28
SK-MEL-2
MDA-MB-435
M14
MALME-3M
LOX IMVI
CNS cancers
U251
SNB-75
SNB-19
SF-539
SF-295
SF-268
Colon cancers
SW-620
KM12
HT29
HCT-15
HCT-116
HCC-2998
COLO 205
Lung cancers
NCI-H522
NCI-H460
NCI-H322M
NCI-H23
NCI-H226
HOP-92
HOP-62
EKVX
A549/ATCC
Leukemias
SR
RPMI-8226
MOLT-4
K-562
HL-60(TB)
CCRF-CEM
0 20 40 60 80 100
% decrease in cancer growth
0 20 40 60 80 100
% of starting cancer cells killed

FIGURE 1C

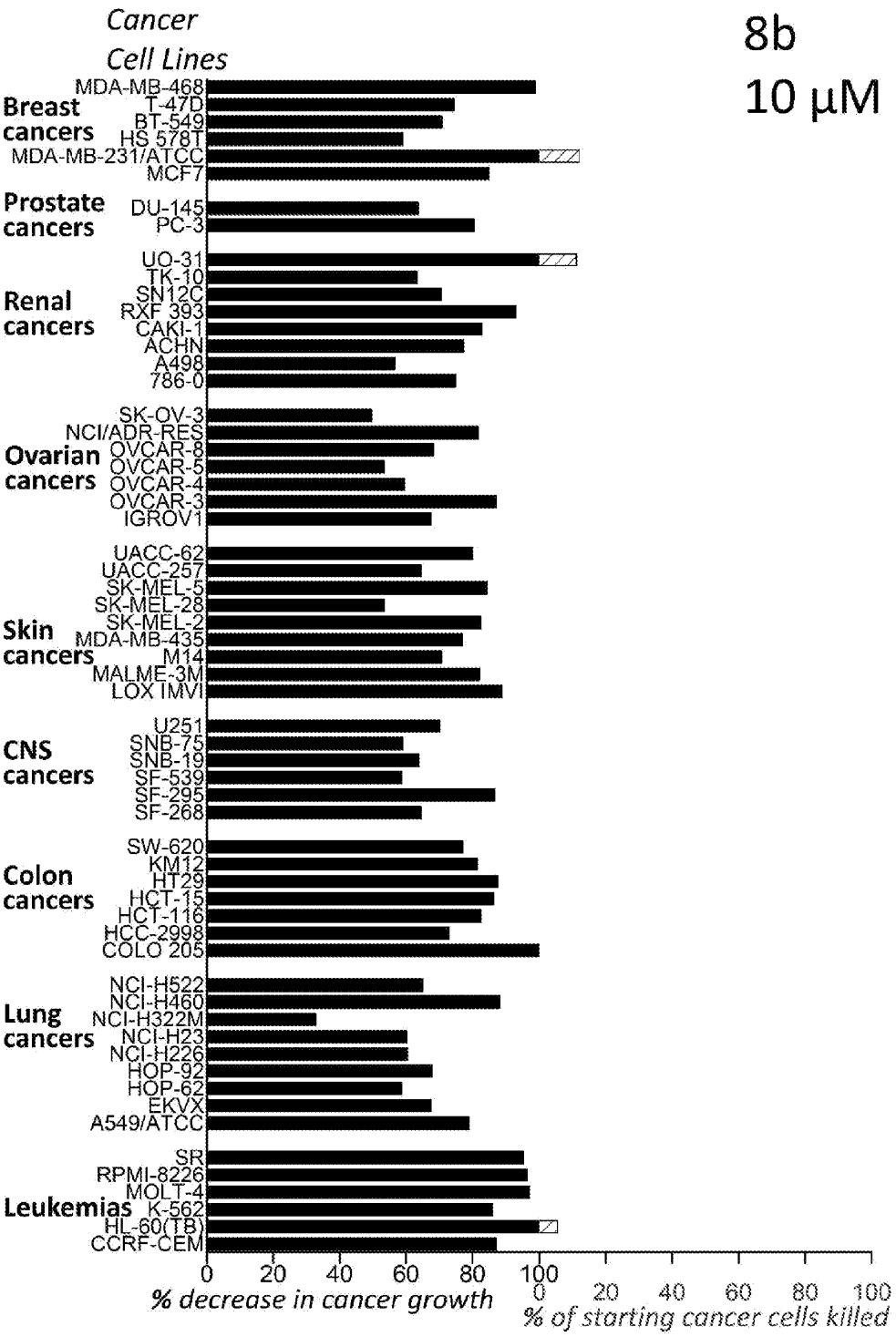

Cancer
Cell Lines
8b
10 µM
Breast cancers
MDA-MB-468
T-47D
BT-549
HS 578T
MDA-MB-231/ATCC
MCF7
Prostate cancers
DU-145
PC-3
Renal cancers
UO-31
TK-10
SN12C
RXF 393
CAKI-1
ACHN
A498
786-0
Ovarian cancers
SK-OV-3
NCI/ADR-RES
OVCAR-8
OVCAR-5
OVCAR-4
OVCAR-3
IGROV1
Skin cancers
UACC-62
UACC-257
SK-MEL-5
SK-MEL-28
SK-MEL-2
MDA-MB-435
M14
MALME-3M
LOX IMVI
CNS cancers
U251
SNB-75
SNB-19
SF-539
SF-295
SF-268
Colon cancers
SW-620
KM12
HT29
HCT-15
HCT-116
HCC-2998
COLO 205
Lung cancers
NCI-H522
NCI-H460
NCI-H322M
NCI-H23
NCI-H226
HOP-92
HOP-62
EKVX
A549/ATCC
Leukemias
SR
RPMI-8226
MOLT-4
K-562
HL-60(TB)
CCRF-CEM
0 20 40 60 80 100
% decrease in cancer growth
0 20 40 60 80 100
% of starting cancer cells killed

FIGURE 1D

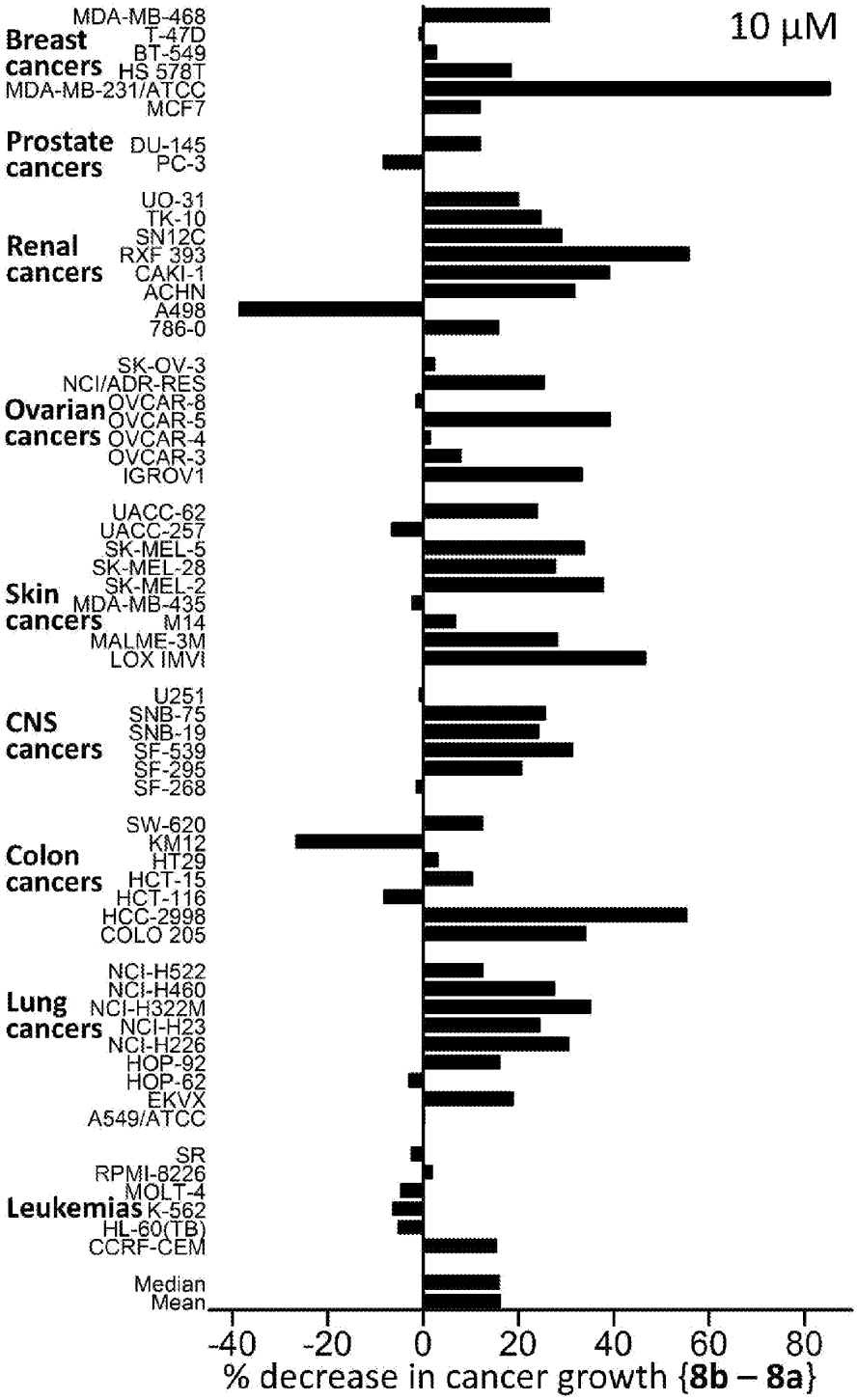

10 µM
Breast cancers
MDA-MB-468
T-47D
BT-549
HS 578T
MDA-MB-231/ATCC
MCF7
Prostate cancers
DU-145
PC-3
Renal cancers
UO-31
TK-10
SN12C
RXF 393
CAKI-1
ACHN
A498
786-0
Ovarian cancers
SK-OV-3
NCI/ADR-RES
OVCAR-8
OVCAR-5
OVCAR-4
OVCAR-3
IGROV1
Skin cancers
UACC-62
UACC-257
SK-MEL-5
SK-MEL-28
SK-MEL-2
MDA-MB-435
M14
MALME-3M
LOX IMVI
CNS cancers
U251
SNB-75
SNB-19
SF-539
SF-295
SF-268
Colon cancers
SW-620
KM12
HT29
HCT-15
HCT-116
HCC-2998
COLO 205
Lung cancers
NCI-H522
NCI-H460
NCI-H322M
NCI-H23
NCI-H226
HOP-92
HOP-62
EKVX
A549/ATCC
Leukemias
SR
RPMI-8226
MOLT-4
K-562
HL-60(TB)
CCRF-CEM
Median
Mean
-40
-20
0
20
40
60
80
% decrease in cancer growth {8b – 8a}

FIGURE 1E

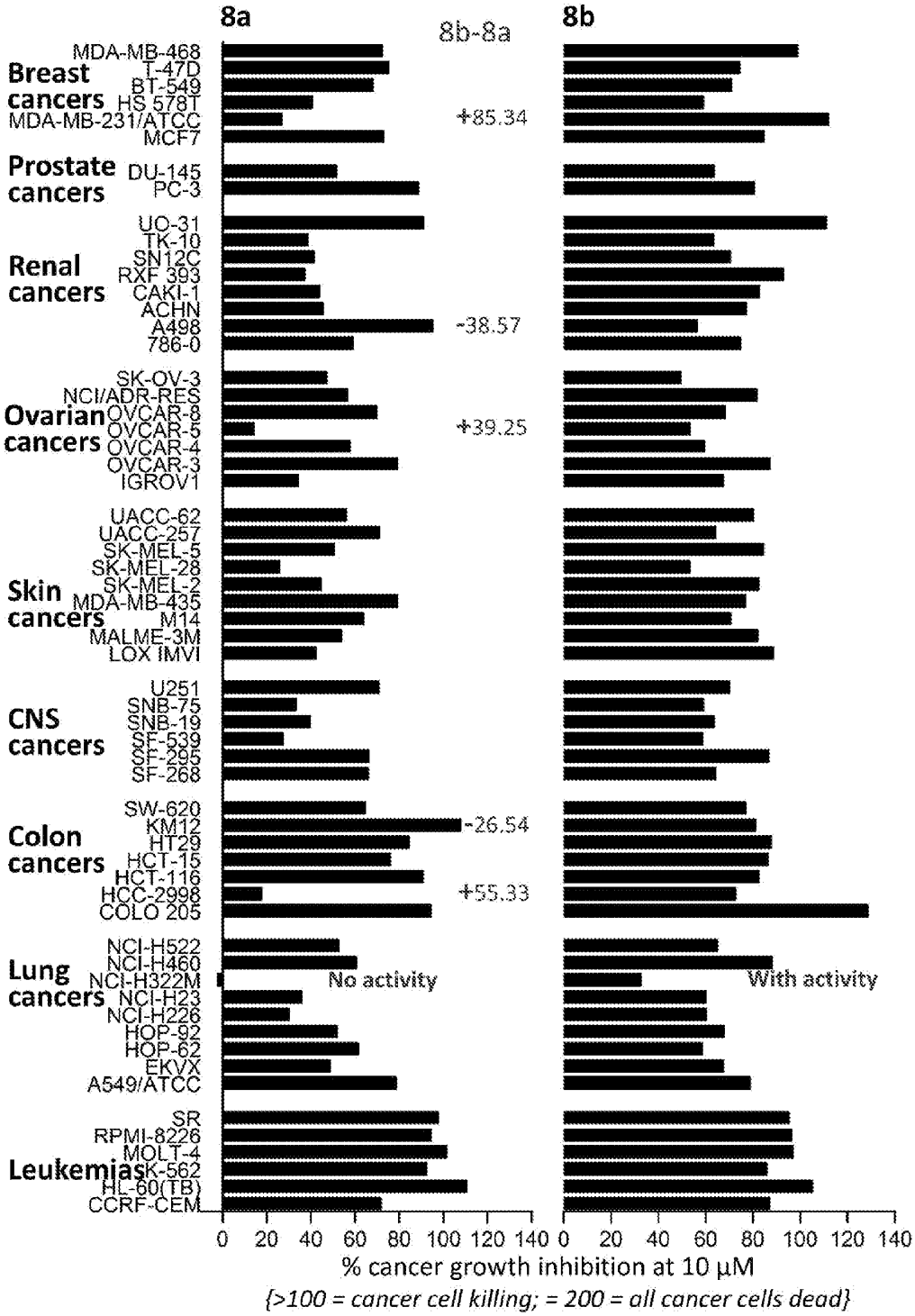
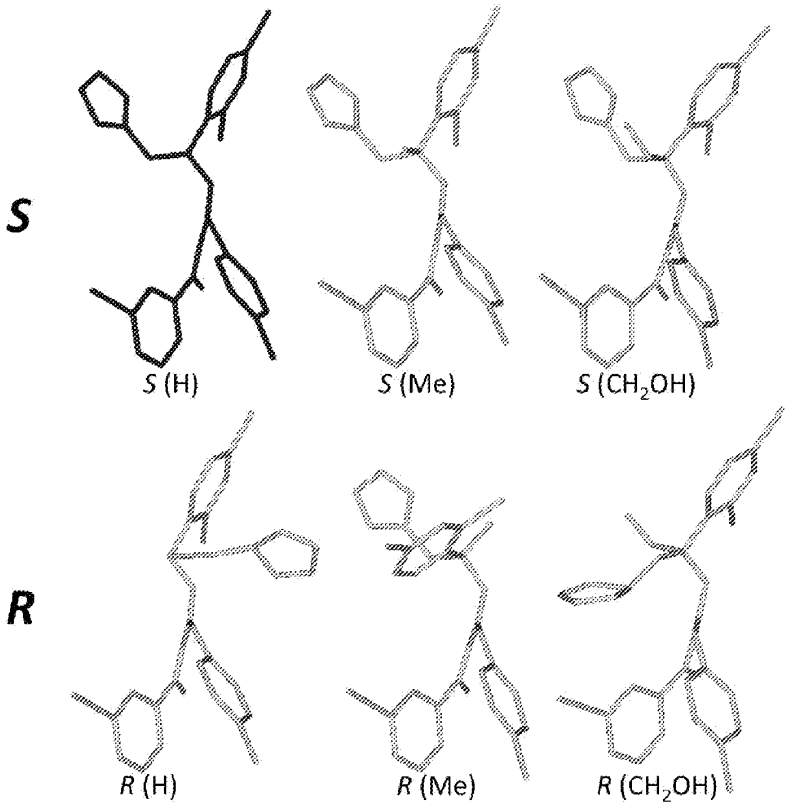
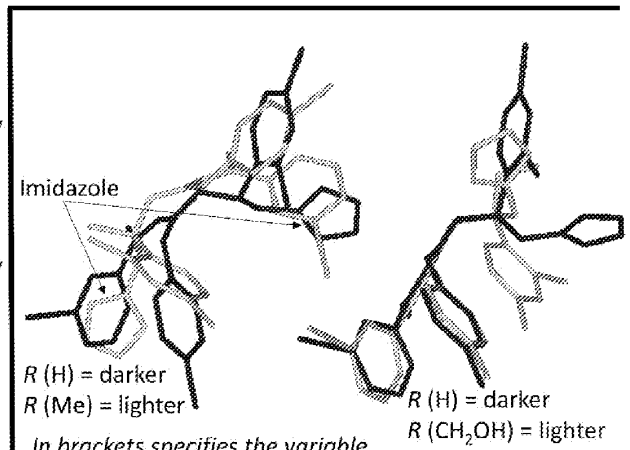

8a
8b-8a
8b
Breast cancers
MDA-MB-468
T-47D
BT-549
HS 578T
MDA-MB-231/ATCC
MCF7
+85.34
Prostate cancers
DU-145
PC-3
Renal cancers
UO-31
TK-10
SN12C
RXF 393
CAKI-1
ACHN
A498
786-0
-38.57
Ovarian cancers
SK-OV-3
NCI/ADR-RES
OVCAR-8
OVCAR-5
OVCAR-4
OVCAR-3
IGROV1
+39.25
Skin cancers
UACC-62
UACC-257
SK-MEL-5
SK-MEL-28
SK-MEL-2
MDA-MB-435
M14
MALME-3M
LOX IMVI
CNS cancers
U251
SNB-75
SNB-19
SF-539
SF-295
SF-268
Colon cancers
SW-620
KM12
HT29
HCT-15
HCT-116
HCC-2998
COLO 205
-26.54
+55.33
Lung cancers
NCI-H522
NCI-H460
NCI-H322M
NCI-H23
NCI-H226
HOP-92
HOP-62
EKVX
A549/ATCC
No activity
With activity
Leukemias
SR
RPMI-8226
MOLT-4
K-562
HL-60(TB)
CCRF-CEM
0 20 40 60 80 100 120 140
0 20 40 60 80 100 120 140
% cancer growth inhibition at 10 µM
{>100 = cancer cell killing; = 200 = all cancer cells dead}

FIGURE 1F



Lighter structures are the best computationally predicted alignment with the computationally predicted structure of *S* (H), the darker structure (top left).



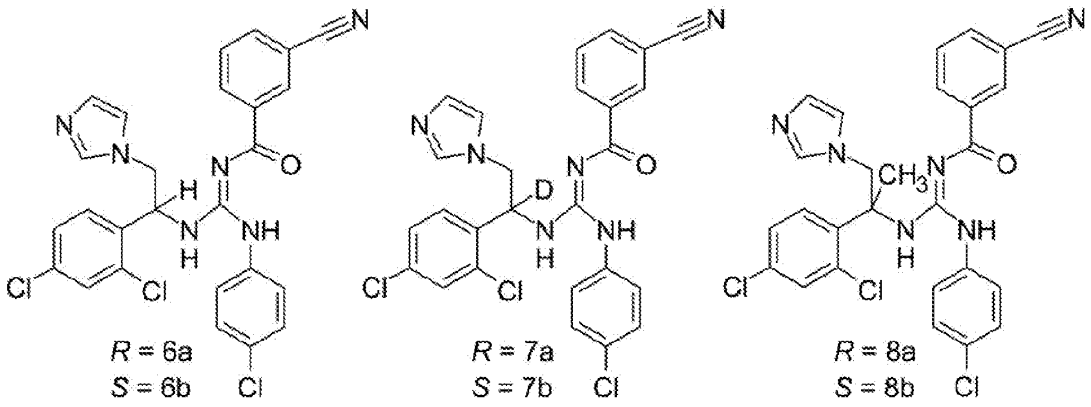
In brackets specifies the variable group attached to the chiral carbon.

Lighter structures are the best computationally predicted alignment with the computationally predicted structure of *R* (H) [darker structure].

All alignments here by "rigid alignment" with the "align by common scaffold (MCS)" algorithm (*initial conformation count = 999*) in MarvinSketch 16.6.20.0 (ChemAxon Ltd.).

In brackets specifies the variable group attached to the chiral carbon.

FIGURE 2

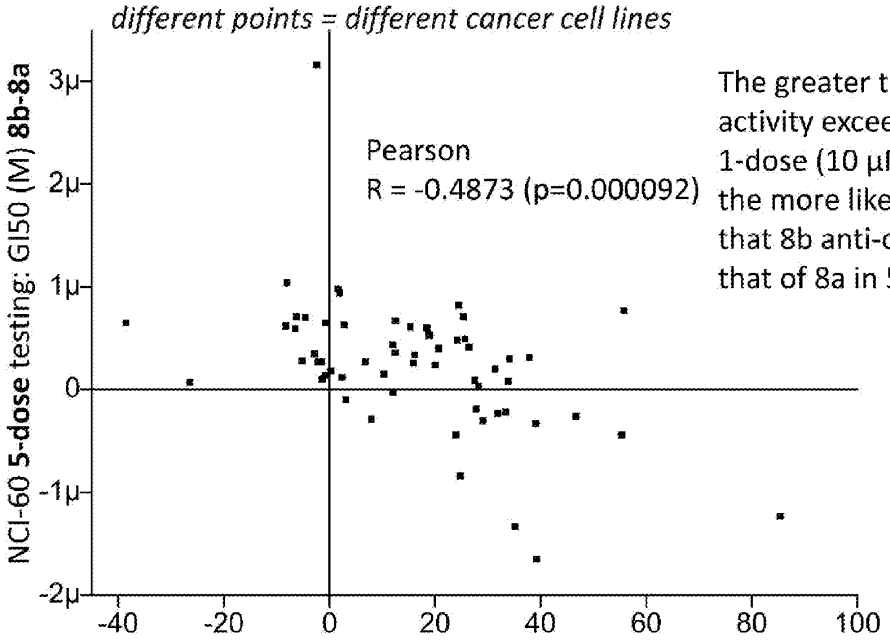


Cancer growth inhibition (%) at 10 µM						
	6a	6b	7a	7b	8a	8b
Mean	57.3	66.15	52.35	72.81	60.32	76.51
Median	58.62	66.9	52.09	74.51	59.83	76.99
Optical rotation	*D*		*D*		*D*	
		6b-6a		7b-7a		8b-8a
Mean		8.85		20.46		16.19
Median		8.28		22.42		17.16
Pearson correlation coefficient						
	6a	6b	7a	7b	8a	8b
6a	1					
6b	0.7991	1				
7a	0.7693	0.5205	1			
7b	0.6614	0.6451	0.8049	1		
8a	0.4882	0.3162	0.6544	0.547	1	
8b	0.5844	0.6342	0.5734	0.6581	0.5669	1

P values: 6b, 8a = 0.013845; 6a, 8a = 0.000076; all others <0.00001; all significant at p < 0.05.

FIGURE 3

*y-axis: **5-dose NCI-60 testing:** 8b=(GI50 for 8b), 8a=(GI50 for 8a): **Mostly** (not exclusively): 8b-8a>0 because 8b>8a because **8b has less anti-cancer activity than 8a.***



*x-axis: **1-dose (10 μM) NCI-60 testing**: 8b=% cancer growth inhibition with 8b, 8a=% cancer growth inhibition with 8a: **Mostly** (not exclusively): (8b-8a)>0 because **8b has more anti-cancer activity than 8a.***

The greater that 8b anti-cancer activity exceeds that of 8a in 1-dose (10 μM) NCI-60 testing, the more likely (and thence greater) that 8b anti-cancer activity exceeds that of 8a in 5-dose NCI-60 testing.

However, whilst 8b is the stronger against the majority (45/60) of cancer cell lines in 1-dose (10 μM) NCI-60 testing, 8a is the stronger against the majority (44/59) of cancer cell lines in 5-dose NCI-60 testing (less some of the cancer cell lines that 8b exerts much greater activity against than 8a in 1-dose testing, for which the risen tide of 8a anti-cancer activity isn't sufficient to overtake).

FIGURE 4

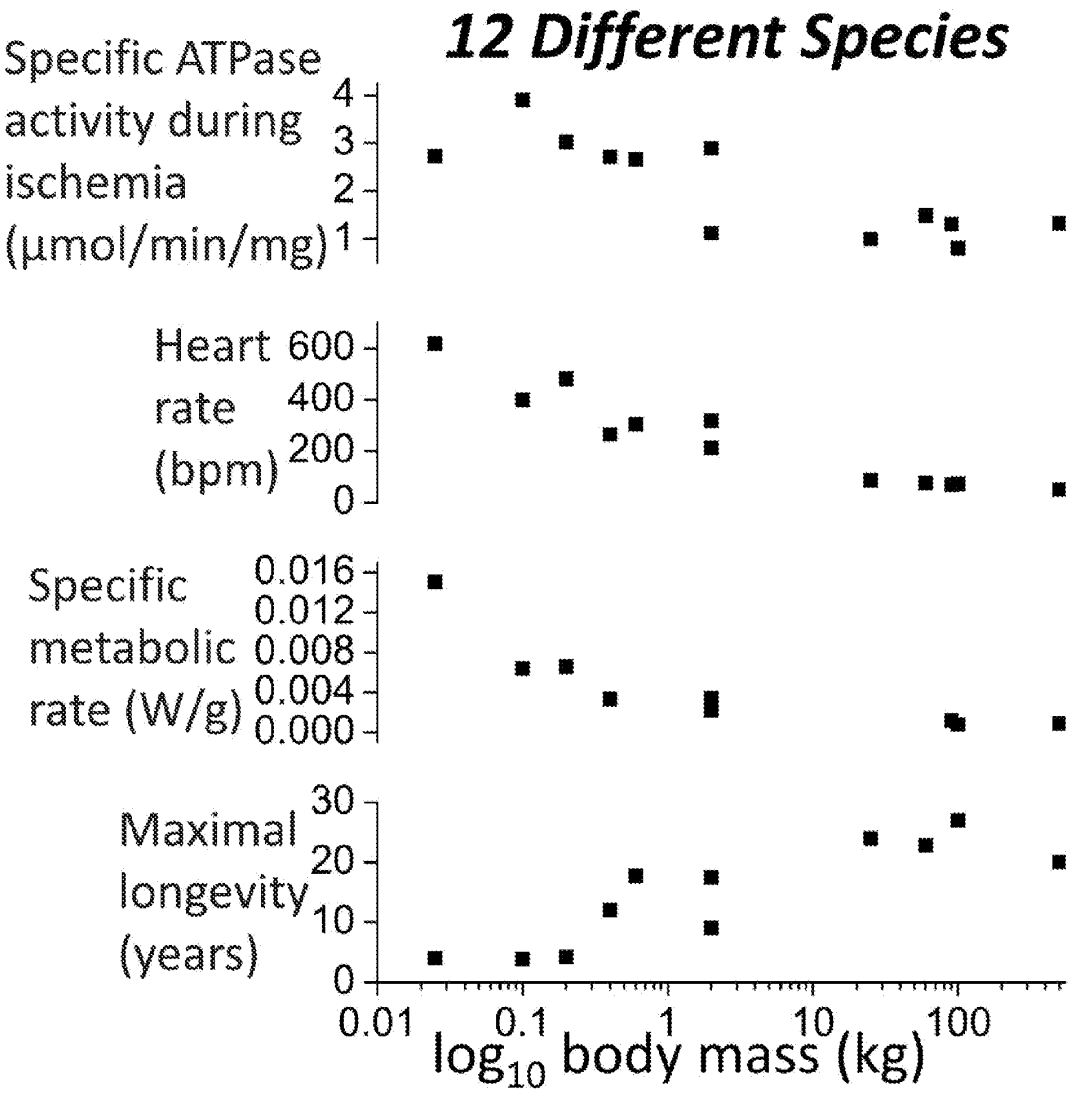
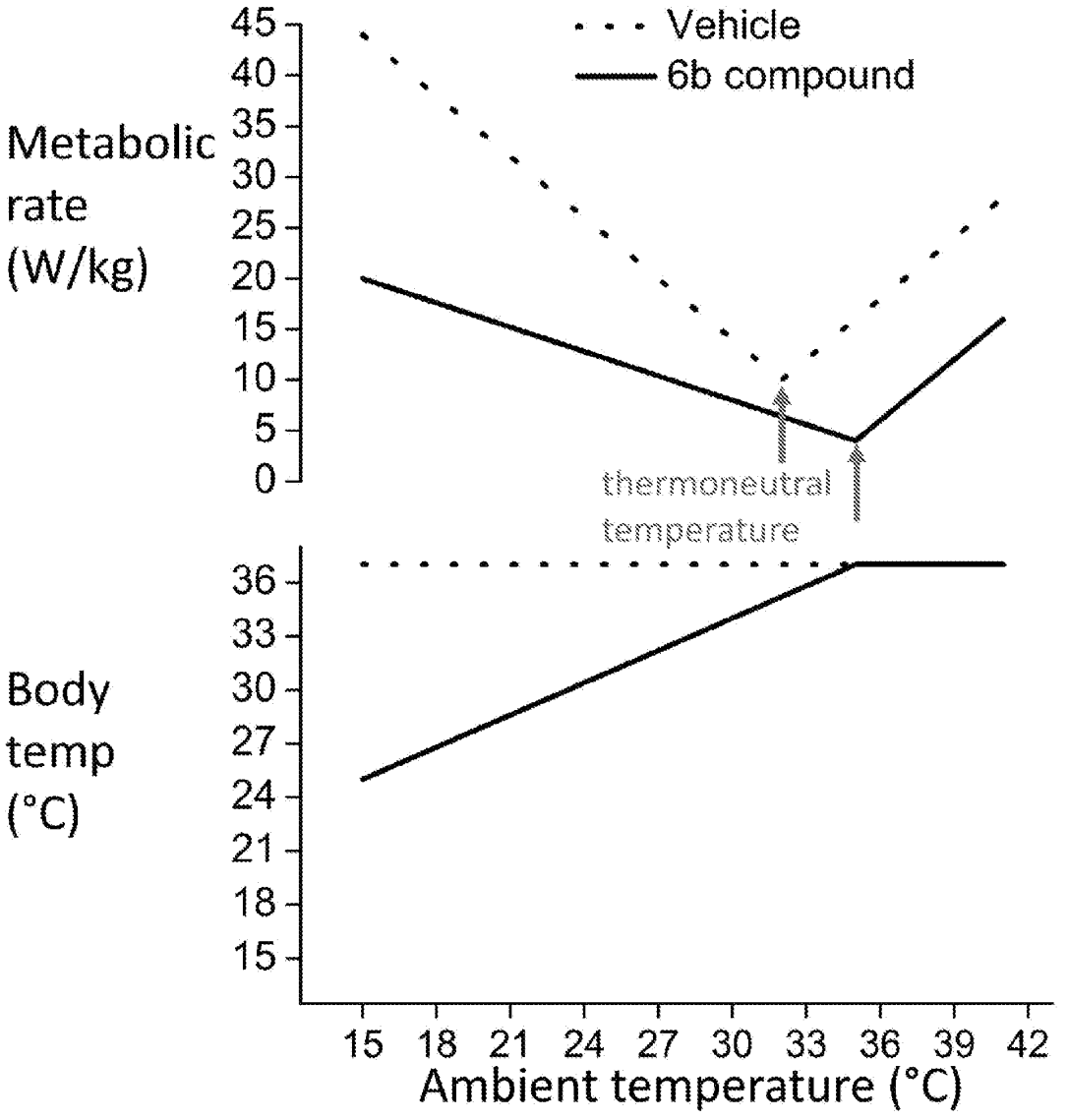

12 Different Species
Specific ATPase activity during ischemia (µmol/min/mg)
4
3
2
1
Heart rate (bpm)
600
400
200
0
Specific metabolic rate (W/g)
0.016
0.012
0.008
0.004
0.000
Maximal longevity (years)
30
20
10
0
0.01
0.1
1
10
100
log10 body mass (kg)

FIGURE 5



THIS IS A DIAGRAM, **NOT** REAL DATA

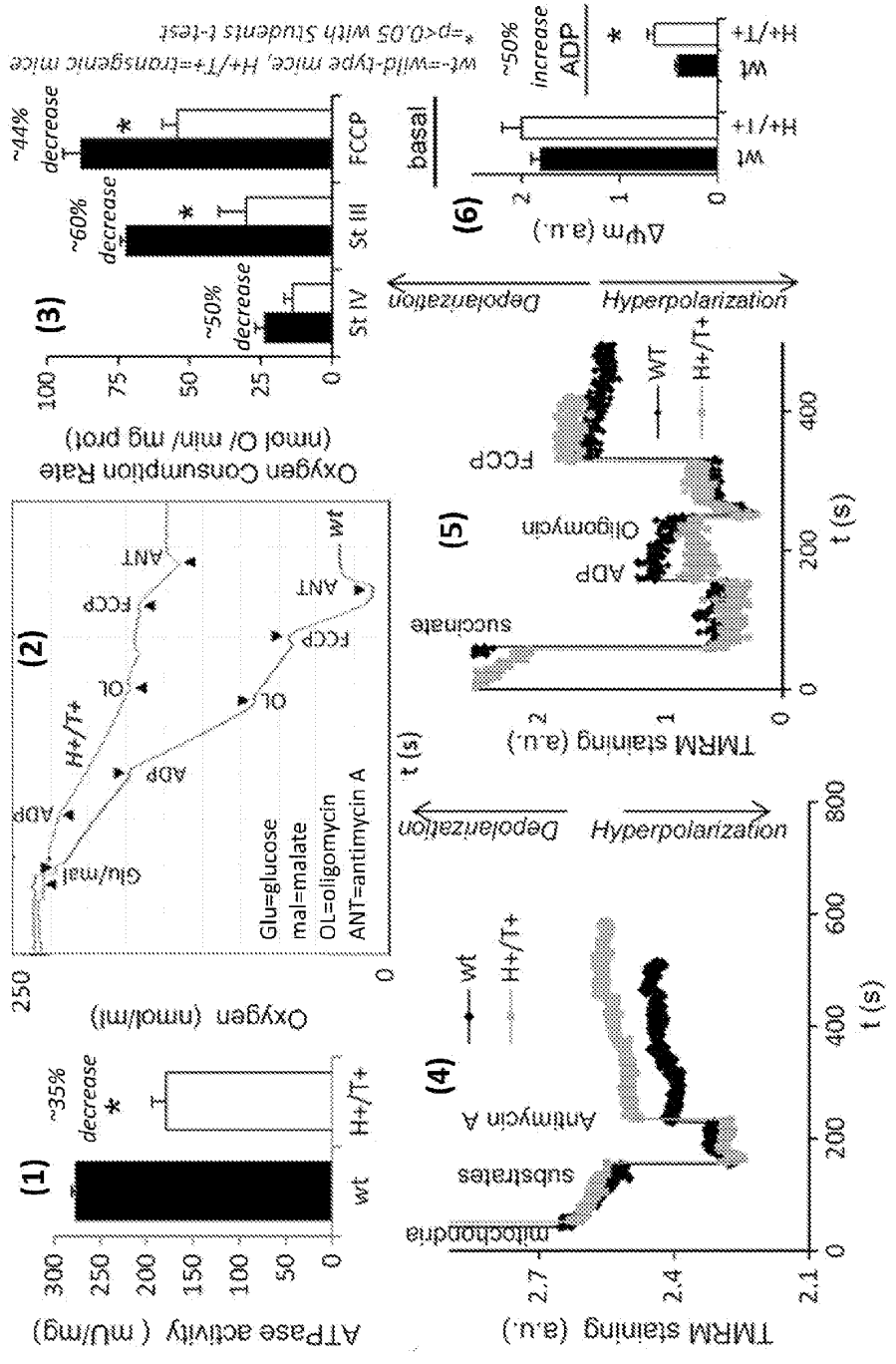

(1)
ATPase activity (mU/mg)
~35% decrease
wt
H+/T+
(2)
Oxygen (nmol/ml)
Glu/mal
ADP
H+/T+
OL
FCCP
ANT
Glu=glucose
mal=malate
OL=oligomycin
ANT=antimycin A
(3)
Oxygen Consumption Rate (nmol O/ min/ mg prot)
~50% decrease
~60% decrease
~44% decrease
St IV
St III
FCCP
(4)
TMRM staining (a.u.)
mitochondria
substrates
Antimycin A
wt
H+/T+
t (s)
Depolarization
Hyperpolarization
(5)
TMRM staining (a.u.)
succinate
ADP
Oligomycin
FCCP
WT
H+/T+
t (s)
(6)
ΔΨm (a.u.)
basal
ADP
~50% increase
wt
H+/T+
wt=wild-type mice, H+/T+=transgenic mice
*=p<0.05 with Students t-test

FIGURE 6A

FIGURE 6B

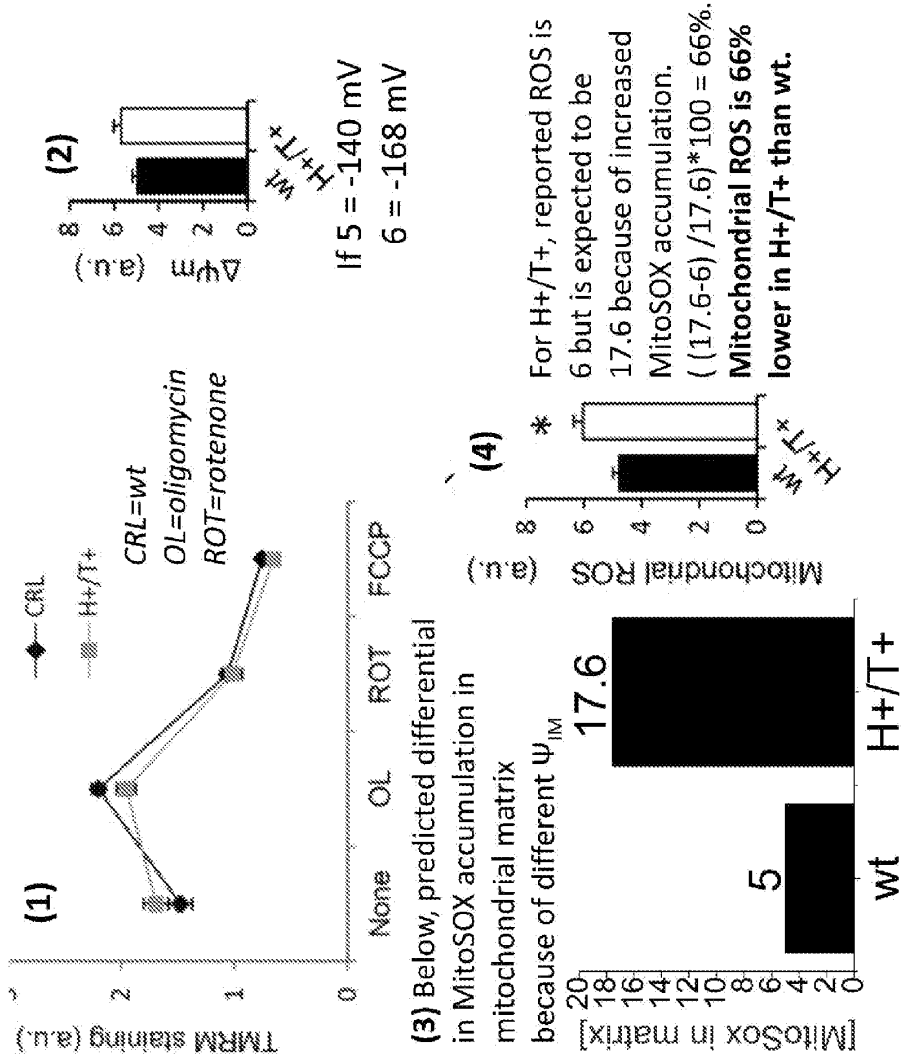
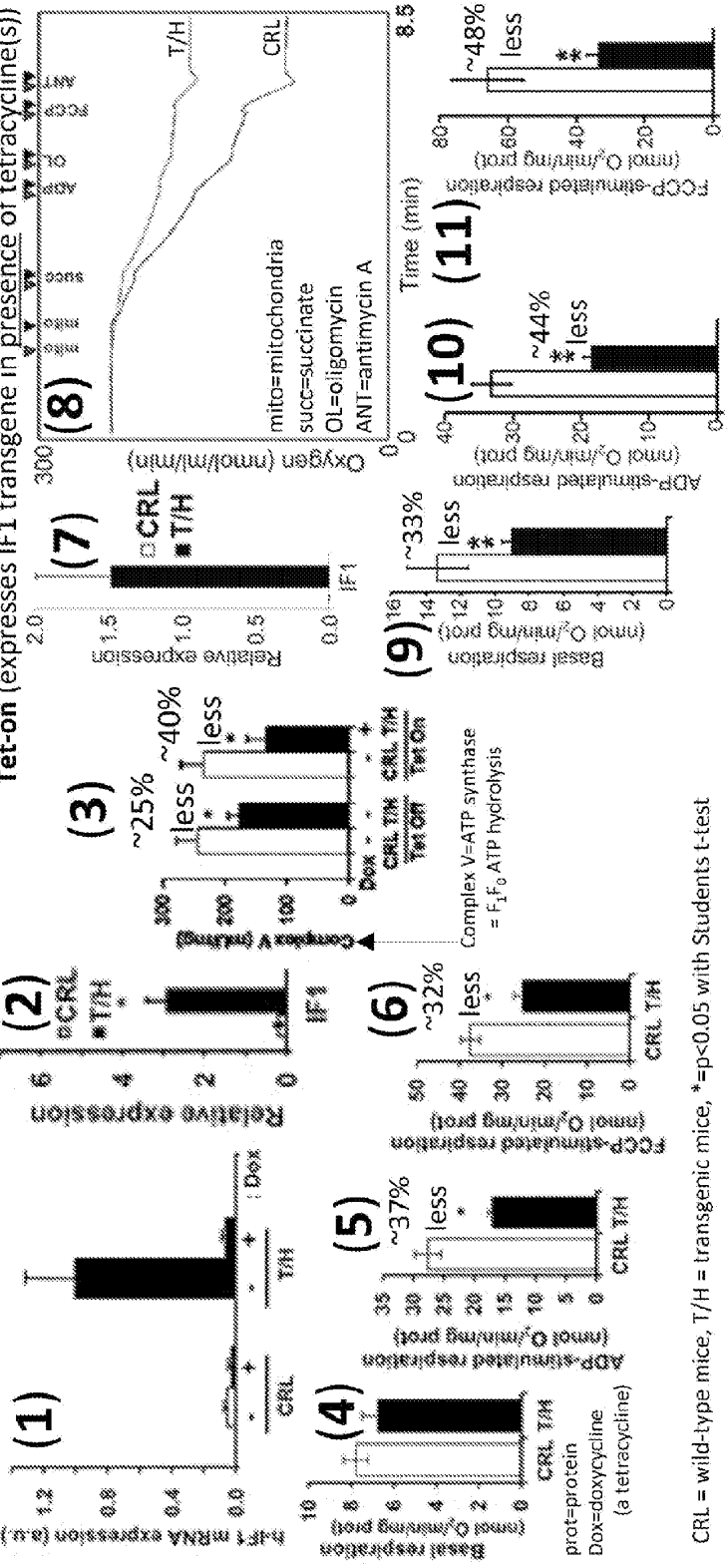

(1)
CRL
H+/T+
CRL=wt
OL=oligomycin
ROT=rotenone
TMRM staining (a.u.)
None
OL
ROT
FCCP
(2)
ΔΨm (a.u.)
wt
H+/T+
If 5 = -140 mV
6 = -168 mV
(3) Below, predicted differential in MitoSOX accumulation in mitochondrial matrix because of different Ψ_IM
[MitoSox in matrix]
5
17.6
wt
H+/T+
(4)
Mitochondrial ROS (a.u.)
*
For H+/T+, reported ROS is 6 but is expected to be 17.6 because of increased MitoSOX accumulation.
((17.6-6) /17.6)*100 = 66%.
Mitochondrial ROS is 66% lower in H+/T+ than wt.

FIGURE 7


Tet-off (expresses IF1 transgene in absence of tetracycline(s))
Tet-on (expresses IF1 transgene in presence of tetracycline(s))
(1)
(2)
(3)
(4)
(5)
(6)
(7)
(8)
(9)
(10)
(11)
CRL
T/H
IF1
Dox
prot=protein
Dox=doxycycline
(a tetracycline)
Complex V=ATP synthase
= F1F0 ATP hydrolysis
mito=mitochondria
succ=succinate
OL=oligomycin
ANT=antimycin A
Time (min)
Oxygen (nmol/ml/min)
~25% less
~40% less
~32% less
~37% less
~33% less
~44% less
~48% less
CRL = wild-type mice, T/H = transgenic mice, *=p<0.05 with Students t-test

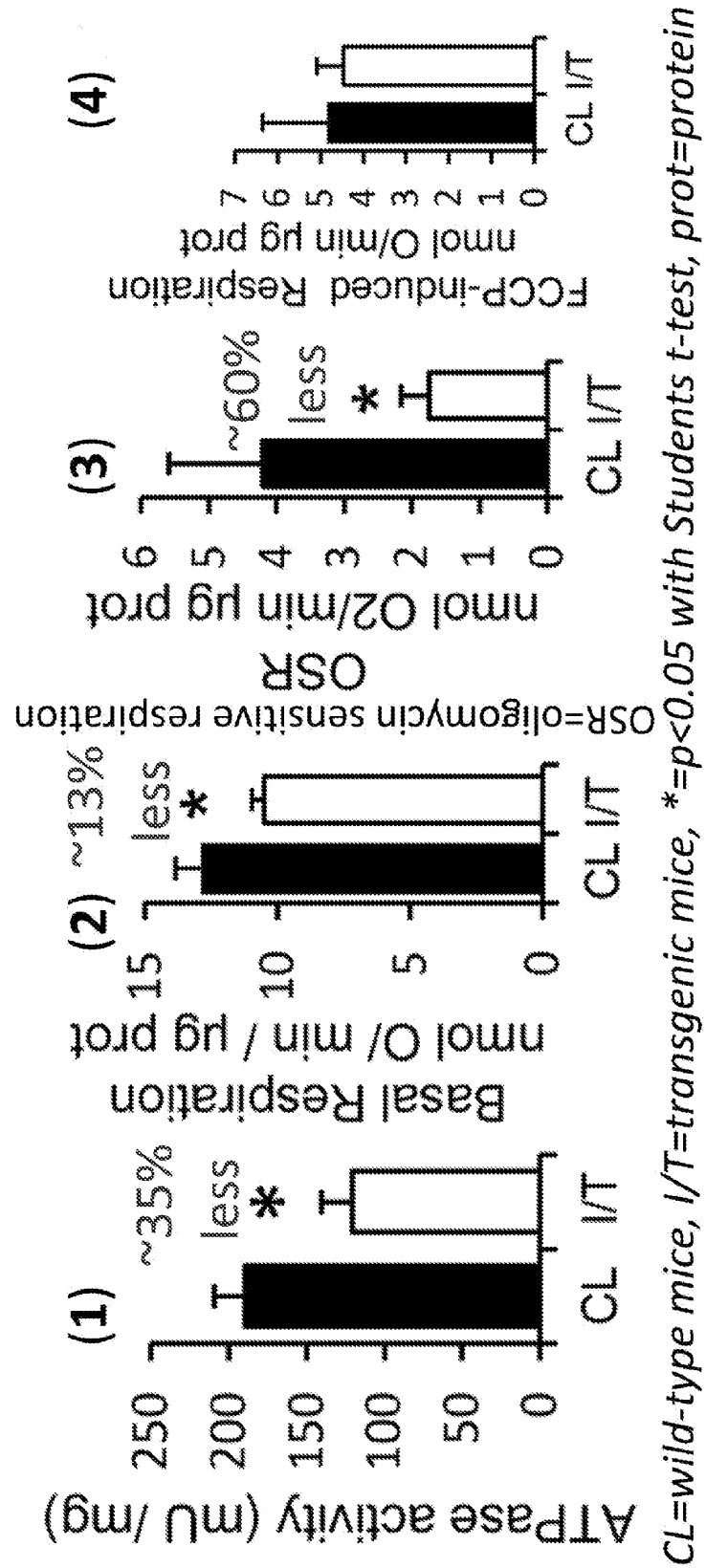

(1)
ATPase activity (mU /mg)
250
200
150
100
50
0
~35% less
*
CL I/T
(2)
Basal Respiration
nmol O/ min / µg prot
15
10
5
0
~13% less
*
CL I/T
(3)
OSR
nmol O2/min µg prot
6
5
4
3
2
1
0
~60% less
*
CL I/T
(4)
FCCP-induced Respiration
nmol O/min µg prot
7
6
5
4
3
2
1
0
CL I/T
OSR=oligomycin sensitive respiration
CL=wild-type mice, I/T=transgenic mice, *=p<0.05 with Students t-test, prot=protein

FIGURE 8

FIGURE 9

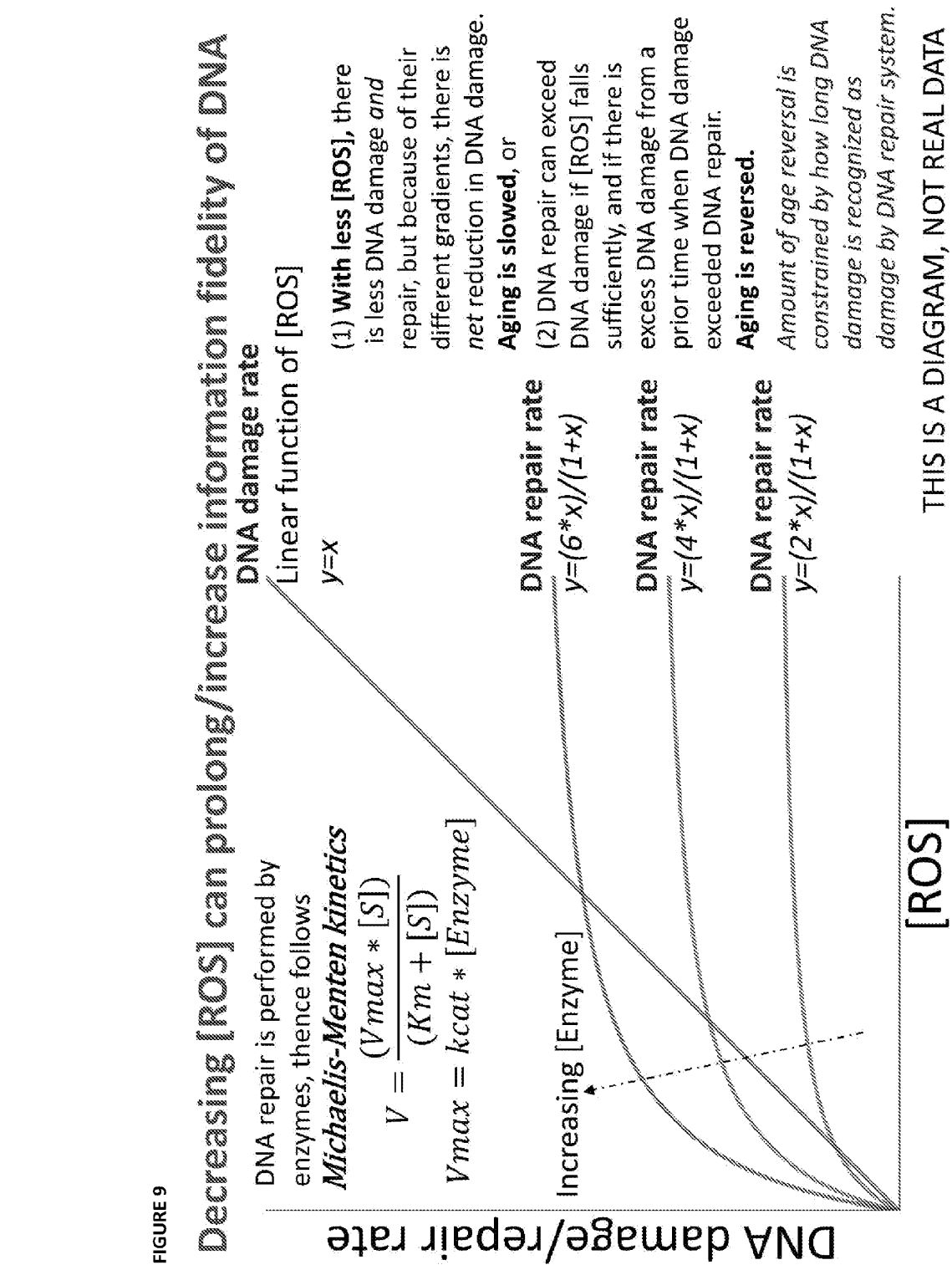
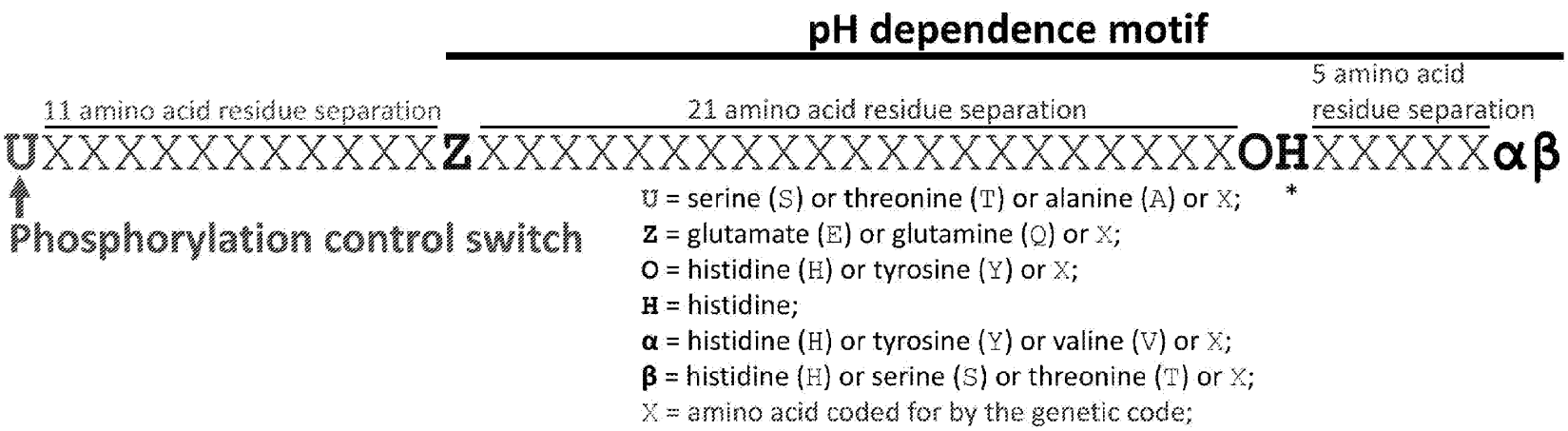

Decreasing [ROS] can prolong/increase information fidelity of DNA
DNA damage/repair rate
DNA damage rate
Linear function of [ROS]
y=x
(1) With less [ROS], there is less DNA damage and repair, but because of their different gradients, there is net reduction in DNA damage.
Aging is slowed, or
(2) DNA repair can exceed DNA damage if [ROS] falls sufficiently, and if there is excess DNA damage from a prior time when DNA damage exceeded DNA repair.
Aging is reversed.
Amount of age reversal is constrained by how long DNA damage is recognized as damage by DNA repair system.
DNA repair is performed by enzymes, thence follows
Michaelis-Menten kinetics
$V = \frac{(Vmax * [S])}{(Km + [S])}$
$Vmax = kcat * [Enzyme]$
Increasing [Enzyme]
DNA repair rate
y=(6*x)/(1+x)
DNA repair rate
y=(4*x)/(1+x)
DNA repair rate
y=(2*x)/(1+x)
[ROS]
THIS IS A DIAGRAM, NOT REAL DATA

FIGURE 10A

```
a) Human                MAVTALAARTWLGVWGYRTMQARGFGSDQSENVDRGAGSIREAGSAFGKKEQAEEERYTRAQSREQLAALKKHHEEEIVHHKKGIERLQKEIERHKQKIKMLKHDD
b) Chimpanzee           MAVTALAARTWLGVWGYRTMQARGFGSEQSENVDRGAGSIREAGSAFGKKEQAEEERYTRAQSREQLAALKKHHEEEIVHHKKGIERLQKEIERHKQKIKMLKHDD
c) Gorilla              MAVTALAARTWLGVWGYRTMQARGFGSDQSENVDRGAGSIREAGSAFGKKEQAEEERVTRAQSREQLAATLKNHHEEEIVHHKKGIERLQKEIERHKQKIKMLKHDD
d) Rhesus Macaque       MAVTALAARVRLGVWGYRTMQARGFGSDQSENVDRGAGSIREAGSAFGKKEQAEEERYTRARTKEQLATLKKHHEEEITHHIGIERLQKEIERHKKGIKHLKHDDDD
e) Walrus                  MAVTALAARVRLGVWGYRTMQARGFGSSERSDSGAGSIREAGSAFGKKEQAEEERYTRAQSREQLAALKKYHEEEIVHSKKGIERLQKEIERHKQKIKKLKHDD
f) West Indian Manatee  MAVTALAARVRLSVLGSRAMQAQGFSSDQSEDLDRRAGSIREAGSAFARKEQAEEERYTRAQAREQLAALKKYHEEEITHHKEEIERLQKEIERHKKKIKHLKHDD
g) Giant Panda          MAVTALAARVRLGVWSYRAMQARGFSSERPDYPGGSAGSIREAGSAFGKKEQAEEERYTRARNKEQEALRKHHEEEITHHKEEIERLQKEIERHKKKIKHLKHDD
h) Dog                     MAVSAVSSRVWLGMWGVRALQTRGFGSERSEDPGSAGSIREAGSAFGKKEQAEEERYTRARTREQLAALKKHHEDEISHHIKGIERLQKEIERHKKKIKNLKSDD
i) Cat                  MAVTATAASVRLGVWGVRAMQARGFSSERSEDSRAGSIREAGSAFGKKEQAEEERYTRARTREQLAALKKHHEDEISHHIKGIERLQKEIERHKNKIKHLKRDEEDD
j) Horse                MAVTALAASQMRLGVWGARVMQARGFSSDRSKDHDSPAGSIREAGSAFGKKEQAEEERYTRKTREQLAALKNHHEDEISHHVKGIELQKEIERHKQRIKTLKDHDDD
k) Polar Bear              MAVTAIAARVRLGVWSLRAMQARGFSSERPDSSAGSIREAGSAFGKKEQAEEERYTRARNKEQEALRKHHEDEITHHKEGIERLQKEIERHKKKIKHLKHDD
l) Rat                  MAGSALAVPARLGVWGMRVLQTRGFGSESSEGMDSGAGSIREAGSAFGKKEKAEEDSYTRKKTREQLAALKKHHEDEITDHHSKGIERLQKQIKSLKNSEH
m) Beluga Whale         MAATALAARTRFGVWSVRAMQGRGFGSESADNLGSSAGAVRDAGSAFGKKEQAEEERYTRARAEQLAALKNHHENEISHHMKGIERLQKEIKQKIKHLKHDD
n) Elephant (African)   MATTALAARVRLCALGVRTVQAQGFSSDQPHDLDRGAGAIREAGSAFAKKEAAEEERYTRAQAKQLAALKKYHEEEITHTKGIERLQKEIERHKQKIKKLKHDD
o) Sperm Whale          MAATALAARTRFGVWSVRAMQGRGFGSESADNLGSSAGAVRDAGSAFGKKEQAEEERYTRARAKEQLAALKKHHENEISHHVKGIERLQKEIERHKQSIKKLKHDED
p) Rabbit               MAGSALVARARLGTWSGRAAIQTRGFVSDKPEDLHGKAGSIREAGSAFGKKEQAEEERVTRAKTKEQLAALKKHHEDEIVHHKKGIERLQKEIKSLKNSDD
q) Guinea Pig              MAGTALASRARLGVWGVRAMQTRGFGSDKDHDGSGSIREAGSAFGKKEQAEEERFTRQKTREQLEALKNHHEDEIVHHKKGIERLQKEIKQKIKHLKHDD
r) Dolphin              MAATALAARTRFGVWSVRAMQGRGFGSESADNLGSSAGAVRDAGSAFGKKEQAEEERYTRARAKEQLAALKKHHENEISHHMSIEHLQKEIERHKQSIKKLKNDDD
s) Minke Whale          MAATALAARTRFGVWSVRAMQGRGFGSESADNLGSSAGAVRDAGSAFGKKEQAEEERYTRARAKEQLAALKKHHENEISHHVKGIENLQKEIERHKQSIKKLKRDED
t) Ferret                  MAVATSAARIWLGVGGFRALQARGFSSEKPDSSAGSIREAGSAFGKKEQAEEERVTRAKTNEQLAALKNHHEEEITHHLKEIERLQMEIERHKKKIKHLKDDDD
u) Pig                  MAATALAVSRRIGAWSVWAMQSRGFSSDTPECVRSGAGAVRDAGSAFGKKEQADEERVTRARARKEQLAALKKHHENEISHHVKGIERLQKEIERHKYKIKDLKDDD
v) Cow                  MAATALAARTRQAVWSVWAMQGRGFGSESGDNVRSSAGAVRDAGSAFGKKEQAEEERYTKARAKEQLAALKKHHENEISHHASGIERLQKEIERHKQSIKKLKQSEDD
w) Bovine "Minimal Inhibitory Sequence"                                AVRDAGSAFGKKEQAEEERYTRARAKEQLAALKK
x) Naked Mole Rat          MAGTALASRARLGVWGVRAMQTKGFSSDEGHESSGSIRDAGSAFGKKEQAEEERFTRQKTKEQLEALKKHHEDEIYHHKKAIEAMEKEIERHKQKIKQLKHDD
y) Mouse                MAGSALAVRARFSVWGWKVLQTRGTVESSSDSMDTGAGSIREAGSAFGKKEKAEEDRYTREKTKEQLAALRKHHEDEIDHHSKEIERLQRCIERHKKIQQLKNNH
z) Camel                MAATALAVETRFGVWSVWAMQGKGFSSDKPDSVRPSEGAVRDAGSAFGKKEQAEEERYTRARTREQLAALKKHHENEISHHHQAIEHLQKEIERHKQAIKKLKQHDDD
aa) Hedgehog            MAVSAVVAARMRLHVWGATALRAKGFSSDQPSSHDSSGGSIREAGSAFGKNEQAEEERYTRARTKEQLALAKKHHEDEIGHHVKEIERLQKEIERHKQRIKSLKRHDDDE
bb) Hamster             MAGSALAIRARLGVWGVRVLQTRGFGSGSGSSESAIDTSAGSIREAGSAFGKKEKAEEDRYFREKTKEQLAILKKHHLDEIQHHEQEIERLQKQIERHKKKIKNLKSHH
cc) Little Brown Bat    MAVTATAARLRLGAWGVRAMRAGGFGCGRSARFSTDSGALIKEAGSSFARNEKAEEERYFLERITKEQLAALKKHHLEEIDHHKKQIDLLKQKEIERHKYKIKKLKNDDDDE
dd) Alligator           MAAGVLRSSLRGAFLMQQQRGWSSSSGADQLGELGKGAGKGGGGGGSIREAGSAFGKKQAAEEERYTREKEESQIAALRKHHEEEIDHHKKQIDLLKQKEIERHKYKIKKLANDDDDE
ee) Snake               MAAVSAIFSSGLRGAMAFPQQGFAWSSGPDQLGELGKGAGKGGGGGGSIREAGSAFGKKEAAEERYTKKEKEESQIAMLRKHHEEEISHHKKGIERLQKEIERHKYKIKDLKDDD
ff) Puffer Fish            MSFLLLGTNIRRCVTSQIPMFSDQLGELGKGAGKGGGGGGSLREAGSAFGRSAAAEEERYTRQREEQIEMLRNHHEEEIEHHRNSIERLQREIDRHKGNIRKLKDDD
gg) Frog                MAGSSSLLRAGITNVLLMQMRESSDQLGELGKGAGKGGGGGGSVREAGSAFGRQQAAEEERIFRQKEQSIASLRNHHEEEIRHHGGIERLQKEIERHSSAIKKLKDD
hh) Piranha                MSTCRLIKTPNLRNFFATQIKMSSDQLGELLGKGVGKGGGGGGAVREAGSAFGRGQAAEEMYTKRKEHSQIAVLRKHHQQPEIDHHKEQIQRLKRGKVIRKLKDD
ii) Chicken             MAAVLALRGGLRGALLAQGGRAWSSGSGLGELGKGAGKGGGGGGSIREAGSAFGKKQAAEEERYTREKEKEESQIAALRKHHEEEIDHHKKQIDLLKQKEIERHKWKIKKLKDDD
jj) Zebrafish              MARLLARRGFFSSHIPMSSDQLGELGTGAGKGGGGGGSVRAAGSSFGRREAAEEERYTRQKEESQIAALKNHHEEEIDHHKKSIERLQREIDRHKGNIRKLKDD
kk) Eel                 MSRILKSNLKGFLTTQIRMSSDQLGELGKGAGNGGGGGGSVREAGSALGRRQAAEEERYTKREEQEQIAALRKHHEEEIDHHKKGIERLQREIDRHKGKIRKLKHDD
```

FIGURE 10B



Across many different species, O, α, and β are each typically histidine (H), with some exceptions

FIGURE 10C

```
# Original Human IFI protein sequence
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
At the 5 bolded positions, can be original residue or alanine (A), 2 options, 2^5=32 possible sequences:
# Single change
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKRAQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKAHEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHAEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVAHKKEIERLQKEIERHRQKIKMLKHED
# Double change
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKRAQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKAHEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKRAQAEEERYFRAQSREQLAALKKHAEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVAHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKRAQAEEERYFRAQSREQLAALKKAHEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHAEEEIVAHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKRAQAEEERYFRAQSREQLAALKKAHEEEIVAHKKEIERLQKEIERHRQKIKMLKHED
# Triple change
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKRAQAEEERYFRAQSREQLAALKKAHEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHAEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKRAQAEEERYFRAQSREQLAALKKHHEEEIVAHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKAAEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKRAQAEEERYFRAQSREQLAALKKAHEEEIVAHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHAEEEIVAHKKEIERLQKEIERHRQKIKMLKHED
# Quadruple change
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKRAQAEEERYFRAQSREQLAALKKAHEEEIVHHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKAAEEEIVAHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKRAQAEEERYFRAQSREQLAALKKHAEEEIVAHKKEIERLQKEIERHRQKIKMLKHED
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKRAQAEEERYFRAQSREQLAALKKAAEEEIVAHKKEIERLQKEIERHRQKIKMLKHED
# Quintuple change
MAVTALAARTWLGVWSVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKRAQAEEERYFRAQSREQLAALKKAAEEEIVAHKKEIERLQKEIERHRQKIKMLKHED
```

FIGURE 10D

```
a)
b)
c)
d)
e)
f)
g)
h)
i)
j)
k)
l)
m)
n)
o)
p)
q)
r)
s)
t)
u)
v)
w)
x)
y)MAVTALVARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKRESIVHHKEIERLQKEIERHKQKIKMLKHDD
z)MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKRESIVHHKEIERLQKEIERHKQKIKMLKHDD
aa)
bb)
cc)
dd)
ee)
ff)
gg)
hh)
ii)
jj)
```

FIGURE 10E

FIGURE 10F

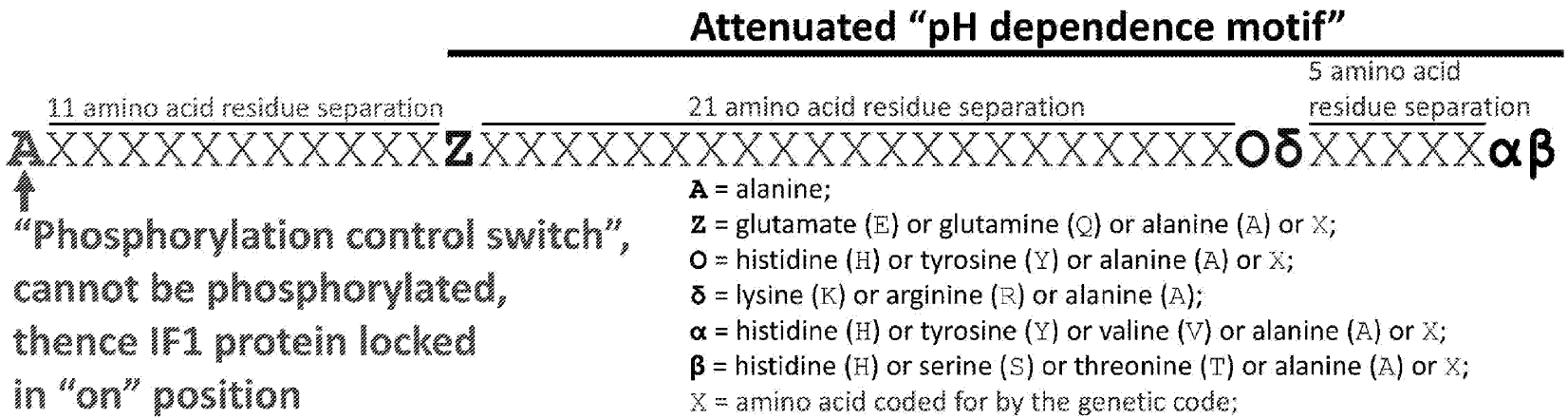

Attenuated "pH dependence motif"
11 amino acid residue separation
21 amino acid residue separation
5 amino acid residue separation
AXXXXXXXXXXXZXXXXXXXXXXXXXXXXXXXXXOδXXXXXαβ
"Phosphorylation control switch", cannot be phosphorylated, thence IF1 protein locked in "on" position
A = alanine;
Z = glutamate (E) or glutamine (Q) or alanine (A) or X;
O = histidine (H) or tyrosine (Y) or alanine (A) or X;
δ = lysine (K) or arginine (R) or alanine (A);
α = histidine (H) or tyrosine (Y) or valine (V) or alanine (A) or X;
β = histidine (H) or serine (S) or threonine (T) or alanine (A) or X;
X = amino acid coded for by the genetic code;

FIGURE 10G

a) MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIEMLKEDD
b) MAATALAARTPQAVWSVWAMQGRGFGSESGDMVRSSAGAVKDAGGAFGKREQAEEERYFRARAKEQLAALKKHKENEISHHAKEIERLQKEIERHKQSIEKLKQSEDDD
c) MAGSALAVRAPFGVVGMKVLQTRGFVSDSSDGMDTGAGAIREAGGAFGKREKAEEDRYFREKTKEQLAALRKHKEIEIDHHSKEIERLQKQIERHKKNIQQLKNNH
d) MAGSALAVRAPLGVVGMRVLQTRGFGSDSSESEMDSGAGAIREAGGAFGKREKAEEDRYFREKTKEQLAALKKHKDEIDHHSKEIERLQKQIERHKKNIKYLKNSEE
e) MAGSALVARARLGTWGARAIQTRGFVSDKPEDIHGKAGAIREAGGAFGKREQAEEERYFRARTKEQLAALKKHKEDEIVHHKKEIERLQKEIERHKQNIESLNSDD
f) MAGTALASRARLGVWGVRAMQTRGFGSDKDMDGSSGAIREAGGAFGKREQAEEERYFRARTKEQLEALKKHKEDEIVHHKKEIERMKEIERHKQNIEQLKED
g) MAVSAVSSRVWLGMWGVRALQTRGFGSERSEDPGSAGAIREAGGAFGKREQAEEERYFRARTREQLAALKKHKEDEISHHIKEIERLQKEIERHKEKNIKHLKRDSEDD
h) MAVTAFAARVRLGVWGVRAMQARGFSSERSEDSKAGAIREAGGAFGKREQAEEERYFRARTREQLAALKKHKEDEISHHIKEIERHKEKNIKHLKRDSEDD
i) MAVTALAAQMRLGVWGARVMQARGFSSDRSKDHDSPAGAIREAGGAFGKREQAEEERYFRKRTREQLAALKKHKEDEISHHVKEIERHKQNIKQLKEDD
j) MAGTALASFARLGVWGVRAMQTRGFSSDKDHESSSGAIRDAGGAFGKREQAEEERTTRQKTKEQLEALKKHKEDEIYHHKAIEMKEKIERHKQNIKQLKEDD
k) MAGSALAIRARLGAWGVRVLQTRGFGSDSSGSTESGAGAIREAGGAFGKREKSEEDRYFRERTKEQLAALKKHKEDEIQYHEQEIERLQKQIERHKKKMENLKNND
l) MAGSALAIRARLGVWGVRVLQTRGFGSGSSSSESIDTSAGAIREAGGAFGKREKAEEDRYFRERTKEQLAILKKHKEDEIQHHEQEIERLQKQIERHKKKIKMWLKSHH
m) MAVATSAAARIWLGVGGFRALQARGFSSERPDSSAGAIREAGGAFGKREQAEEERYFRARTKEQLAALKKHKEEEITHHLKEIERLQKEIERHEKKIKHHLKDDDD
n) MAATALAARTKFGVWSVWAMQGRGFGSESADMLGSSAGAVKDAGGAFGKREQAEEERYFRARAKEQLAALKKHKENEISHHMKEIERLQKEIERHKQSIEKLKEDDD
o) MATTALAARVRLCALGVGRTVQAQGFSSDQPHDLDRGAGAIREAGGAFAKREAAEEERYFRAQAKEQLAALKKHKEEEIVHHKKEIERLQKEIERHKQNIEKLKEDD
p) MAATALAARTRFGVWSVWAMQGRGFGSESADMLGSSAGAVKDAGGAFGKREQAEEERYFRARAKEQLAALKKHKENEISHHTVKEIEMLQKEIERHKQSIEKLKEDDD
q) MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQNIKEMLKEDD
r) MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQNIKEMLKEDD
s) MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQNIKEMLKEDD
t) MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQNIKEMLKEDD
u) MAVTALAARTWLGVWGVRTMQARGFGSDQSDNVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQNIKEMLKEDD
v) MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLATLKKHKEDEIVHHKKEIERLQKEIERHKQNIKEMLKEDD
w) MAVTALVARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQNIKTTLKEDD
x) MAVTALVARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQNIKTTLKEDD
y) MAVTALVARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQKIKTTLKEDD
z) MAVTALVARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQNIKTTLKEDD
aa) MAVTALVARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQNIKTTLKEDD
bb) MAVTALVARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQNIKTTLKEDD
cc) MAVTALVARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQNREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQKIKTTLKEDD
dd) MAVTALVARTWLGVWGVRTMQARGFGSDQSENIDRGAGAIREAGGAFGKREQAEEERYFRTQSREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQKIKTTLKEDD
ee) MAVTALVARTWLGVWGVRTMQARGFGSDQSENIDRGAGAIREAGGAFGKREQAEEERYFRTQSREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQKIKTTLKEDD
ff) MAVTALAARTWLGVWGVRTMQARSFGSDQSENLDRGAGAIREAGGAFGKREQAEEERYFRAQTREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQKIKILKEDD
gg) MAVTALAARTWLGVWGVRTMQARSFGSDQSENLDRGAGAIREAGGAFGKREQAEEERYFRAQTREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQKIKILKEDD
hh) MAVTALVARTWLGVWGVRTIQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRTQSREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQKIKTTLKEDD
ii) MAVTALAARTWLGVWGVRTMQARSFGSDQSENLDRGAGAIREAGGAFGKREQAEEERYFRAQTREQLAALKKHKEDEIVHHKKEIERLQKEIERHKQKIKILKEDD

FIGURE 10H

```
# Original Human IF1 protein sequence
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKPEQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
# More preferred sequence
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKPEQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
# More preferred sequence
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKPEQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
# Variants:
# Single change
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKPAQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKPEQAEEERYFRAQSREQLAALKKAKEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKPEQAEEERYFRAQSREQLAALKKHKEEEIVAHKKEIERLQKEIERHKQKIKMLKHDD
# Double change
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKPAQAEEERYFRAQSREQLAALKKAKEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKPAQAEEERYFRAQSREQLAALKKHKEEEIVAHKKEIERLQKEIERHKQKIKMLKHDD
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKPEQAEEERYFRAQSREQLAALKKAKEEEIVAHKKEIERLQKEIERHKQKIKMLKHDD
# Triple change
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKPAQAEEERYFRAQSREQLAALKKAKEEEIVAHKKEIERLQKEIERHKQKIKMLKHDD
                    ----------------------
                    # Original Human IF1 protein sequence, without mitochondrial targeting sequence
                    GSDQSENVDRGAGSIREAGGAFGKPEQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
                    # More preferred sequence
                    GSDQSENVDRGAGSIREAGGAFGKPEQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
                    # More preferred sequence
                    GSDQSENVDRGAGAIREAGGAFGKPEQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
                    # Variants:
                    # Single change
                    GSDQSENVDRGAGAIREAGGAFGKPAQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
                    GSDQSENVDRGAGAIREAGGAFGKPEQAEEERYFRAQSREQLAALKKAKEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
                    GSDQSENVDRGAGAIREAGGAFGKPEQAEEERYFRAQSREQLAALKKHKEEEIVAHKKEIERLQKEIERHKQKIKMLKHDD
                    # Double change
                    GSDQSENVDRGAGAIREAGGAFGKPAQAEEERYFRAQSREQLAALKKAKEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
                    GSDQSENVDRGAGAIREAGGAFGKPAQAEEERYFRAQSREQLAALKKHKEEEIVAHKKEIERLQKEIERHKQKIKMLKHDD
                    GSDQSENVDRGAGAIREAGGAFGKPEQAEEERYFRAQSREQLAALKKAKEEEIVAHKKEIERLQKEIERHKQKIKMLKHDD
                    # Triple change
                    GSDQSENVDRGAGAIREAGGAFGKPAQAEEERYFRAQSREQLAALKKAKEEEIVAHKKEIERLQKEIERHKQKIKMLKHDD
```

FIGURE 10I

```
# Bovine IF1 protein, and some non-limiting IF1 sub-sequence embodiments of the invention, wherein all IF1 (all species) sub-sequences are componentry to this invention
                                1                                                                                                49                                                                                                84
    MAATALAARTRQAVWSVWAMQGRGFGSESGDNVRSSAGAVRDAGGAFGKREQAEEERYFRARAKEQLAALKKHHENEISHHAKEIERLQKEIERHHKQSIKKLKQSEDDD
Without mitochondrial import sequence    GSESGDNVRSSAGAVRDAGGAFGKREQAEEERYFRARAKEQLAALKKHHENEISHHAKEIERLQKEIERHHKQSIKKLKQSEDDD
1-60 (monomer, can't dimerize)           GSESGDNVRSSAGAVRDAGGAFGKREQAEEERYFRARAKEQLAALKKHHENEISHHAKEI
1-56                                     GSESGDNVRSSAGAVRDAGGAFGKREQAEEERYFRARAKEQLAALKKHHENEISHH
10-84                                        SSAGAVRDAGGAFGKREQAEEERYFRARAKEQLAALKKHHENEISHHAKEIERLQKEIERHHKQSIKKLKQSEDDD
10-47                                        SSAGAVRDAGGAFGKREQAEEERYFRARAKEQLAALKK
10-46 (10-fold less activity than 10-47, so 47 is important) SSAGAVRDAGGAFGKREQAEEERYFRARAKEQLAALK
14-47                                        AVRDAGGAFGKREQAEEERYFRARAKEQLAALKK
22-46 (only inhibits F1 alone, not F1F0 complex)             FGKREQAEEERYFRARAKEQLAALK
42-58                                                        LAALKKHHENEISHHAK
                                                             H
                                                             HH
                                                             HHE
                                                             HHEN
                                                             HHENE
                                                             HHENEI
                                                             HHENEIS
                                                             HHENEISH
                                                             HHENEISHH
                                                             HHENEISHHA
                                                             HHENEISHHAK
                                                             HHENEISHHAKE
                                                             HHENEISHHAKEI
                                                             HHENEISHHAKEIE
                                                             HHENEISHHAKEIER
                                                             HHENEISHHAKEIERL
                                                             HHENEISHHAKEIERLQ
                                                             HHENEISHHAKEIERLQK
                                                             HHENEISHHAKEIERLQKE
                                                             HHENEISHHAKEIERLQKEI
                                                             HHENEISHHAKEIERLQKEIE
                                                             HHENEISHHAKEIERLQKEIER
                                                             HHENEISHHAKEIERLQKEITER
                                                             HHENEISHHAKEIERLQKEITERH
                                                             HHENEISHHAKEIERLQKEITERHK
                                                             HHENEISHHAKEIERLQKEITERHKQ
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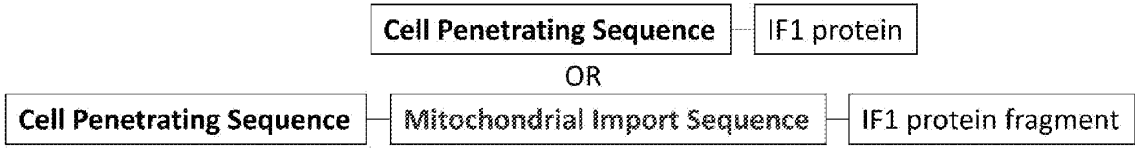
FIGURE 10J


Human IF1 protein, and some non-limiting IF1 sub-sequence embodiments of the invention, wherein all IF1 (all species) sub-sequences are componentry to this invention
1 14 49
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
Without mitochondrial import sequence GSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
1-60 GSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEI
1-56 GSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHH
1-47 GSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKK
10-84 RGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
10-47 RGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKK
10-46 RGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALK
14-47 SIREAGGAFGKREQAEEERYFRAQSREQLAALKK
15-47 (control serine absent) IREAGGAFGKREQAEEERYFRAQSREQLAALKK
14-47 (S14A and E26A substitution) AIREAGGAFGKRAQAEEERYFRAQSREQLAALKK
22-46 FGKREQAEEERYFRAQSREQLAALK
42-58 LAALKKHHEEEIVHHKK
H
HH
HHE
HHEE
HHEEE
HHEEEI
HHEEEIV
HHEEEIVH
HHEEEIVHH
HHEEEIVHHK
HHEEEIVHHKK
HHEEEIVHHKKE
HHEEEIVHHKKEI
HHEEEIVHHKKEIE
HHEEEIVHHKKEIER
HHEEEIVHHKKEIERL

FIGURE 10K

Mitochondrial Import Sequence
IF1 protein fragment
Firstly, human IF1 protein, and then some IF1 sub-sequences joined to the mitochondrial import sequence (MAVTALAARTWLGVWGVRTMQARGF) of human IF1
-23 1 14 49
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEI
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHH
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKK
MAVTALAARTWLGVWGVRTMQARGFRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKK
MAVTALAARTWLGVWGVRTMQARGFRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALK
MAVTALAARTWLGVWGVRTMQARGFSIREAGGAFGKREQAEEERYFRAQSREQLAALKK
MAVTALAARTWLGVWGVRTMQARGFIREAGGAFGKREQAEEERYFRAQSREQLAALKK
MAVTALAARTWLGVWGVRTMQARGFAIREAGGAFGKRAQAEEERYFRAQSREQLAALKK
MAVTALAARTWLGVWGVRTMQARGFFGKREQAEEERYFRAQSREQLAALK
MAVTALAARTWLGVWGVRTMQARGFLAALKKHHEEEIVHHKK
MAVTALAARTWLGVWGVRTMQARGFHEEEIV
MAVTALAARTWLGVWGVRTMQARGFHHEEEIVHHKK
MAVTALAARTWLGVWGVRTMQARGFHHEEEIVHHKKE
MAVTALAARTWLGVWGVRTMQARGFHHEEEIVHHKKEIER
MAVTALAARTWLGVWGVRTMQARGFHHEEEIVHHKKEIERL

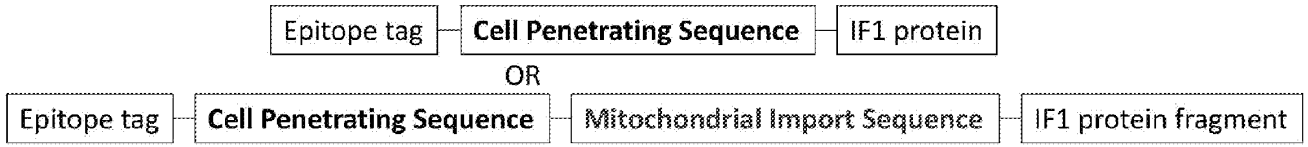
FIGURE 10L



Human IF1 protein joined to HIV-1 Tat cell penetrating sequence (**YGRKKRRQRRR**) by an optional glycine (G, increases flexibility between domains), and below that, some IF1 sub-sequences joined to a mitochondrial import sequence (MAVTALAARTWLGVWGVRTMQARGF) joined to the HIV-1 Tat sequence by an optional G {*underlined = optional*}

YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK**HH**EEEIV**H**HKKEIERLQKEIERHKQKIKMLKHDD
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK**HH**EEEIV**H**HKKEI
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK**HH**EEEIV**H**H
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGFRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK**HH**EEEIV**H**HKKEIERLQKEIERHKQKIKMLKHDD
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGFRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGFRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALK
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**I**REAGGAFGKR**E**QAEEERYFRAQSREQLAALKK
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGFFGKR**E**QAEEERYFRAQSREQLAALK
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGFLAALKK**HH**EEEIV**H**HKK
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**H**
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**E
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EE
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEE
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEEI
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**H**
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HH**
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HK**
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HK**
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHKK**
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHKKE**
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHKKEI**
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHKKEIE**
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHKKEIER**
YGRKKRRQRRRG MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHKKEIERL**

FIGURE 10M



Human IF1 protein joined to HIV-1 Tat Cell Penetrating Sequence (**YGRKKRRQRRR**) joined to an affinity/epitope tag (HHHHHH, HHHHHHDYKDDDDK) , wherein the Tat sequence is flanked by optional glycines (confers flexibility between domains), and below that, some IF1 sub-sequences joined to a Mitochondrial Import Sequence (**MAVTALAARTWLGVWGVRTMQARGF**) joined to the Tat sequence joined to an epitope tag, wherein the Tat sequence is flanked, on either side, by optional glycines (*underlined residue = optional*)

HHHHHH**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK**HH**EEEIV**H**HKKEIERLQKEIERHKQKIKMLKHDD
HHHHHH**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK**HH**EEEIV**H**HKKEI
HHHHHH**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK**HH**EEEIV**HH**
HHHHHH**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGFRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK**HH**EEEIV**H**HKKEIERLQKEIERHKQKIKMLKHDD
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGFRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGFRGAG**S**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALK
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARG**FS**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARG**F**IREAGGAFGKR**E**QAEEERYFRAQSREQLAALKK
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARG**FA**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGFFGKR**E**QAEEERYFRAQSREQLAALK
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGFLAALKK**HH**EEEIV**H**HKK
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**H**
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**E
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EE
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EEE
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EEEI
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**H**
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HH**
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHK**
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHKK**
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHKKE**
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHKKEI**
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHKKEIE**
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHKKEIER**
HHHHHHDYKDDDDK**G**YGRKKRRQRRR**G**MAVTALAARTWLGVWGVRTMQARGF**HH**EEEIV**HHKKEIERL**

FIGURE 10N

```
# Some non-limiting human IF1 sub-sequence embodiments, wherein all IF1 sub-sequences (all species) are componentry to this invention.
HHEEEIVHHKK                    # Some non-limiting IF1 sub-sequence embodiments joined to an illustrative (non-limiting)
HH                             mitochondrial import sequence.
  HE                           MAVTALAAATWLGVWGVRTMQARGFHH
    EE                         MAVTALAAATWLGVWGVRTMQARGFHE
      EE             HHEEEIVHHKK MAVTALAAATWLGVWGVRTMQARGFEE
        EI           HHEEEI    MAVTALAAATWLGVWGVRTMQARGFEE
          IV         HEEEIV    MAVTALAAATWLGVWGVRTMQARGFEI
            VH       EEEIVH    MAVTALAAATWLGVWGVRTMQARGFIV
              HH     EEIVHH    MAVTALAAATWLGVWGVRTMQARGFVH
                HK   EIVHHK    MAVTALAAATWLGVWGVRTMQARGFEIVHHK
                  KK   IVHHKK  MAVTALAAATWLGVWGVRTMQARGFIVHHKK
HHE                  HHEEEIV   MAVTALAAATWLGVWGVRTMQARGFHHEEEIV
  HEE                HEEEIVH   MAVTALAAATWLGVWGVRTMQARGFHHEEEIVH
    EEE              EEEIVHH   MAVTALAAATWLGVWGVRTMQARGFEEEIVHH
      EEI            EEIVHHK   MAVTALAAATWLGVWGVRTMQARGFEEEIVHHK
        EIV          EIVHHKK   MAVTALAAATWLGVWGVRTMQARGFEIVHHKK
          IVH        HHEEEIVH  MAVTALAAATWLGVWGVRTMQARGFHHEEEIVH
            VHH      HEEEIVHH  MAVTALAAATWLGVWGVRTMQARGFHEEEIVHH
              HHK    EEEIVHHK  MAVTALAAATWLGVWGVRTMQARGFEEEIVHHK
                HKK  EEIVHHKK  MAVTALAAATWLGVWGVRTMQARGFEIVHHKK
HHEE                 HHEEEIVHH MAVTALAAATWLGVWGVRTMQARGFHHEEEIVHH
  HEEE               HEEEIVHHK MAVTALAAATWLGVWGVRTMQARGFHEEEIVHHK
    EEEI             EEEIVHHKK MAVTALAAATWLGVWGVRTMQARGFEEEIVHHKK
      EEIV           HHEEEIVHK MAVTALAAATWLGVWGVRTMQARGFEEEIVHHK
        EIVH         HEEEIVHKK MAVTALAAATWLGVWGVRTMQARGFEIVHHKK
          IVHH       HHEEEIVHKK MAVTALAAATWLGVWGVRTMQARGFIVHHKK
            VHHK     HHEEEIVHHKK MAVTALAAATWLGVWGVRTMQARGFVHHKK
              HHKK                MAVTALAAATWLGVWGVRTMQARGFVHHKK
HHEEE                            MAVTALAAATWLGVWGVRTMQARGFHHKK
  HEEEI                          MAVTALAAATWLGVWGVRTMQARGFHHEEE
    EEEIV                        MAVTALAAATWLGVWGVRTMQARGFHEEEI
      EEIVH                      MAVTALAAATWLGVWGVRTMQARGFEEEIV
        EIVHH                    MAVTALAAATWLGVWGVRTMQARGFEEEIVH
          IVHHK                  MAVTALAAATWLGVWGVRTMQARGFEIVHHK
            VHHKK                MAVTALAAATWLGVWGVRTMQARGFIVHHKK
                                 MAVTALAAATWLGVWGVRTMQARGFVHHKK
```

FIGURE 10O

Some non-limiting IF1 sub-sequence embodiments joined to an illustrative (non-limiting) mitochondrial import sequence (MIS, MAVTALAARTWLGVWGVRTMQARGF) joined to an illustrative (non-limiting) Cell Penetrating (CPP) sequence, the HIV-1 Tat sequence, by an optional G (*underlined = optional*), wherein the 3 modules can be in the sequence in a different order than shown and/or wherein one or more of the 3 sequence motifs (IF1 sub-sequence, MIS, Tat) can be in the opposite direction than shown.

YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHE
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEE
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEE
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEI
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFIV
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFVH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFKK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHHE
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHEE
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEE
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEI
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEIV
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFIVH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFVHH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHHK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHKK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHHEE
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHEEE
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEEI
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEIV
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEIVH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFIVHH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFVHHK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHHKK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHHEEE
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHEEEI
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEEIV
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEIVH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEIVHH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFIVHHK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFVHHKK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHHEEEI
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHEEEIV
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEEIVH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEIVHH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEIVHHK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFIVHHKK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHHEEEIV
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHEEEIVH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEEIVHH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEIVHHK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEIVHHKK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHHEEEIVH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHEEEIVHH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEEIVHHK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEIVHHKK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHHEEEIVHH
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHEEEIVHHK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFEEEIVHHKK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHHEEEIVHHK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHEEEIVHHKK
YGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFHHEEEIVHHKK

FIGURE 10P

a) Human (122.5) MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLRHKQKIKMLKHDD

b) Bowhead whale (211) MA**A**TALAARTR**F**GVW**S**VW**A**MQGRGFGS**E**S**A**D**N**LGS**S**AG**A**IRDAGGAFGKK**E**QAEEERYFRA**R**A**K**EQLAALKKHHEN**E**I**S**HH**V**KEIEH**L**QKEIERHKQ**S**IKK**L**KHDDD

c) Fin whale (114) MA**A**TALAARTR**F**GVW**S**VW**A**MQGRGFGS**E**S**A**D**N**LGS**S**AG**A**VRDAGGAFGKK**E**QAEEERYFRA**R**A**K**EQLAALKKHHEN**E**I**S**HH**V**KEIEH**L**QKEIERHKQ**S**IKK**L**KHDDD

d) Blue whale (110) MA**A**VELVAWMQ**L**RVWS**V**WVMQ**L**GLGFGS**E**PA**D**N**L**GS**S**EA**T**VWN**A**GVDFRKR**E**QAKGERYLRA**R**A**K**EQLAALKKHHEN**E**I**S**HH**V**KEIEH**L**QKEIERHKQ**S**IKK**L**KHDDD

e) Humpback whale (95) MA**A**TALAARTR**F**GVW**S**VW**A**MQGRGFGS**E**S**A**D**N**LRS**S**AG**A**VRDAGGAFGKK**E**QAEEERYFRA**R**A**K**EQLAALKKHHEN**E**I**S**HH**E**KEIEH**L**QKEIERHKQ**S**IKK**L**KHDDD

f) Killer whale (90) MA**A**TALAARTR**F**GVW**S**VW**A**MQGRGFGS**E**S**A**D**N**LGS**T**AG**A**VRDAGGAFGKK**E**QAEEERYFRA**R**A**K**EQLAALKKHHEN**E**I**S**HH**M**KEIEH**L**QKEIERHKQ**S**IKK**L**KHDDD

g) Sperm whale (77) MA**A**TALAARTR**F**GVW**S**VW**A**MQGRGFGS**E**S**A**D**N**LGS**S**EA**T**VWN**A**GVDFRKR**E**QAKGQRYLRA**C**A**K**EQLAALKKHHEN**E**I**S**HH**V**KEIEC**L**QKEMEEHKQ**L**VKK**L**KHHDDD

h) Gray whale (77) MQGS**E**P**A**D**N**LG**S**SEA**T**VWN**A**GVDFRKR**E**QAKGQRYLRA**R**A**K**EQLAALKKHHEN**E**I**S**HH**V**KEIEH**L**QKEIERHKQ**S**IKK**L**KHDDD

i) Cuvier's beaked whale (62) MA**A**TALAARTR**F**GVW**S**VW**A**MQGRGFGS**E**S**A**D**N**LGS**S**AG**A**IRDAGGAFGKR**E**QAEEERYFRA**R**A**K**EQLAALKKHHEN**E**I**S**HH**V**KEIEH**L**QKEIERHKQ**S**IKK**L**KQDDD

j) Long-finned pilot whale (60) MA**A**TALAARTR**F**GVW**S**VW**A**MQ**G**RGFGS**E**S**A**D**N**LGS**S**AG**A**VRDAGGAFGKK**E**QAEEERYFRA**R**A**K**EQLAALKKHHEN**E**I**S**HH**M**KEIEH**L**QKEIERHKQ**S**IKK**L**KRDDD

k) Minke whale (50) MA**A**TALAARTR**F**GVW**S**VW**A**MQ**G**RGFGS**E**S**A**D**N**LGS**S**AG**A**VRDAGGAFGKK**E**QAEEERYFRA**R**A**K**EQLAALKKHHEN**E**I**S**HH**V**KEIEH**L**QKEIERHKQ**S**IKK**L**KRDDD

l) Narwhal (50) MA**A**TALAARTR**F**GVW**S**VW**A**MQ**G**RGFGS**E**S**A**D**N**LGS**S**AG**A**VRDAGGAFGKR**E**QAEEERYFRA**R**A**K**EQLAALKKHHEN**E**I**S**HH**M**KEIEH**L**QKEIERHKQ**S**IKK**L**KHND

m) Beluga Whale (40) MA**A**TALAARTR**F**GVW**S**VW**A**MQ**G**RGFGS**E**S**A**D**N**LGS**S**AG**A**VRDAGGAFGKR**E**QAEEERYFRA**R**A**K**EQLAALKKHHEN**E**I**S**HH**M**KEIEH**L**QKEIERHKQ**S**IKK**L**KNDDD

n) Bottlenose dolphin (51.6) MA**A**TALAARTR**F**GVW**S**VW**A**MQ**G**RGFGS**E**S**A**D**N**LGS**S**AG**A**VRDAGGAFGKK**E**QAEEERYFRA**R**A**K**EQLAALKKHHEN**E**I**S**HH**M**KEIEH**L**QKEIERHKQ**S**IKK**L**KRDDD

o) Yangtze river dolphin (24) MA**A**TALAARTR**F**GVW**S**VW**A**MQ**G**RGFGS**E**S**A**D**N**LGS**S**AG**A**VRDAGGAFGKR**E**QAEEERYFRA**R**A**K**EQLTALKKHHEN**E**I**S**HH**M**KEIEH**L**QKEIERHKQ**S**IKK**L**KHDDD

p)Galápagos tortoise(177) **MAVAGLRGEGLRAALGMQQRGWSSGSDQLGELGSGAGKGGGGGGSIREAGGAFGKREQAAHEERYFREKEREQLASLREYHEEEIDHHKKEIQRLQKEIDRHKNKIKKLKGDDD

q)EasternBoxTurtle (138) **MAAAGLRGGLRGALVMQQRGWSSGSGSDQLGELGSGAGKGGGGGGSIREAGGAFGKRQAAHEERYFRDKEREQLASLREHHEEEIDHHKKEIQRLQKEIERHKYKIKKLKGDDD

r)GreenSeaTurtle (75) **MAAAGLRGGLRGALALQQRGWSSGSGSGSDQLGELGSGAGKGGGGGGSIREAGGAFGKRQAAHEERYFREKEAEQLASLRKHHEEEIDHHKKEIERLQKEIERHKYKIKKLKNDD

s)WestPaintedTurtle (61) **MAAAGLRGGLRGALVMQQRGWSSGSGSDQLGELGSGAGKGGGGGGSIREAGGAFGKRQAAHEERYFRDKEREQLASLREHHEEEIDHHKKEIQRLQKEIERHKIKIKKLKGDDD

t)Red earedTerrapin (41) **MAAAGLRGGLRGALVMQQRGWSSGSGSDQLGELGSGAGKGGGGGGSIREAGGAFGKRQAAHEERYFRDKEREQLASLREHHEEEIDHHKKEIQRLQKEIERHKIKIKKLKGDDD

u) Alligator (77) **MAAGVLRSGLRGALFMQQRGWSSGSGADQLGELGKGAGKGGGGGGSIREAGGAFGKRQVAEEERYFREAEREKLANLRKHHEEEIYHHKKEIERLQKEIERHKSKIKKLKGDD

v)KomodoDragon(62) **MAAVGAAIRSGLRGAVAFPSQQRAWSSGSDQLGELGKGAGKGGGGGTIREAGGAFGKRQVAEEERYFREAEREKLANLRKHHEEEIYHHKKEIERLQKEIERHKSKIKKLKGDD

w) Crocodile (57) **MAAGVLRGGLRGAFLMQQQRGWSSGSGSGADQLGELGKGAGKGGGGGGSIREAGGAFGKRQAAEEERYFREREREQLAALRKHHEEEIDHHKKQIEVLQKEIERHKYKIKKLKNDDD

z) Kakapo (60) **MAAAAAARGGLRGALVLQQQRWSSGSGSGADQLGELGKGAGKGGGGGGCAIREAGGAFGKKQAAEEERYFREKEREQLSALRKHHEEEIDHHQKEIERLQKEIERHKYKIKKLKDDN

y) Sablefish (114) **MSRFLLRADIERCVASQIRMASDQLGELGKGAGKGGGGGGSVRSAGGAFGKREVAEEERYFRQKEKEQMEALRKHHVEEIEHHKKEIERLQKEIDRHKGKIRKLKNHDD

x) European eel (88) **MSRLLKSNLRGFLITQIRMSSDQLGELGKGAGKGGGGGGSSVREAGGALGKRQAAEEERYFKRKEQEQLAALRRHHEEEIDHHKKEIERLQKEIDRHKGKIRKLKKHDD

aa) West Indian manatee (69) MAVTALAARV**R**LY**S**LGA**F**AMQAQGF**S**SDQSEDL**D**RAGSIREAGGAF**A**KREA**A**AEEERYFRAQ**A**KEQLAALKKY**H**EEEIVHSKKEIERLQKEIERHKQKIKKLKKHDD

bb) African bush elephant (65) MATTALAARV**R**L**C**ALGVRVT**V**QAQGFSSDQ**P**HDLDRGAGA**I**REAGGAFA**K**REA**A**AEEERYFRAQ**A**KEQLAALKKY**H**EEEITH**T**KKEIERLQ**N**EIERHKQKIKKLKKHDD

cc) Gorilla (60.1) MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAT**L**KKHHEEEIVHHKKEIERLRHKQKIKMLKDD

dd) White-faced capuchin (54) MAVTALAARTWLGVWGVRTMQARSFGSDQSENLDRGAGSIREAGGAFGKREQAEEERYFRA**Q**T**R**EQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKILKHDD

ee) Bolivian squirrel monkey (30) MAVTALAARTWLGVWGVRTMQARSFGSDQSEN**L**DRGAGSIREAGGAFGKREQAEEERYFRA**Q**T**R**EQLAALKKHHE**D**EIVHHKKEIERLQKEIERHKQKIK**I**LKHDD

ff) Common marmoset (23) MAVTALAARTWLGVWGVRTMQARSFGSDQSEN**L**DRGAGSIREAGGAFGKREQAEEERYFRA**Q**A**R**EQLAALKKHHE**D**EIVHHKKEIERLQKEIERHKQKIKILK**D**DD

gi) Philippine tarsier (16) MAVSALVARTWLGMWGVRA**R**QTRGFGSDQSENVDRSSGSIREAGGAFGKREQAEEERYFRA**Q**TREQLAALKKHHED**E**IGHHKKEIERLQKEIERHKQKIKT**L**KHDD

hi) Naked mole rat (31) MAGTALASRARLGVWGVRAMQTRGFSSDKDHESSGSIRDAGGAFGKREQAEEERFFRQKTKEQLEALKKHHEDEIVHHKKAIEMVEKEIERHKQKIKQLKHDD

ii) Damaraland mole-rat (15.5) MAGTALASRARLGVRGVRAMQTRGFSSDKDHESSGAGSIRDAGGAFGKREQAEEERFFRQKTKEQL**D**ALKKHHEDEIYHHKKAIE**Q**VEKEIERHKQKIKQLK**H**H**E**

jj) Mouse (4) **MAGSALAVRAR**F**GVWGMK**V**LQTRGFVS**DS**SDSMDTG**AGSIREAGGAFGKRE**K**AED**RY**FRE**K**TKEQLA**A**LR**K**HHEDEIDHHSK**E**IERLQ**K**QIERHK**K**IQQLK**NNH**

FIGURE 10Q

a) Human (122.5) MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLRKEQKIRMLKHDD
b) Bowhead whale (211) MAATALAAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRAPAKEQLAALKKHKENEISHHVKEIEHLQKEIERLRKEQSIKKLKHDDD
c) Fin whale (114) MAATALAAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAVRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHKENEISHHVKEIEHLQKEIERLRKEQSIKKLKHDDD
d) Blue whale (110) MAAVELVAWMQLRVWSVWVMQGLGFGSEPADNLGSSEAAVWNACVDFRKREQAKGERYLRARAKEQLAALKKHKENEISHHVKEIEHLQKEIERLRKEQSIKKLKHDDD
e) Humpback whale (95) MAATALAARTRFGVWSVWAMQGRGFGSESADNLRSSAGAVRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHKENEISHHEKEIEHLQKEIERLRKEQSIKKLKHDDD
f) Killer whale (90) MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSTAGAVRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHKENEISHHMKEIEHLQKEIERLRKEQSIKKLKHDDD
g) Sperm whale (77) MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAVRDAGGAFGKREQAEEERYFRARAKEQLAALKKHKENEISHHVKEIEHLQKEIERLRKEQSIKKLKHDDD
h) Gray whale (77) MQGSEPADNLGSSEAAVWNACVDFRKREQAKGQRYLRACAKEQLAALKKHKENEISHHVKEIECLQKEMEEKKQLVKKLKHHDDD
i) Cuvier's beaked whale (62) MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKREQAEEERYFRARAKEQLAALKKHKENEISHHVKEIEHLQKEIERLRKEQSIKKLKQDDD
j) Long-finned pilot whale (60) MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAVRDAGGAFGKKEQAEEERYFRAPAKEQLAALKKHKENEISHHMKEIEHLQKEIERLRKEQSIKKLKRDDD
k) Minke whale (50) MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAVRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHKENEISHHVKEIEHLQKEIERLRKEQSIKKLKRDDD
l) Narwhal (50) MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAVRDAGGAFGKREQAEEERYFRARAKEQLAALKKHKENEISHHMKEIEHLQKEIERLRKEQSIKKLKRNDD
m) Beluga Whale (40) MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAVRDAGGAFGKREQAEEERYFRARAKEQLAALKKHKENEISHHMKEIEHLQKEIERLRKEQSIKKLKHDDD
n) Bottlenose dolphin (51.6) MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAVRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHKENEISHHMKEIEHLQKEIERLRKEQSIKKLKRDDD
o) Yangtze river dolphin (24) MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAVRDAGGAFGKREQAEEERYFRARAKEQLTALKKHKENEISHHMKEIEHLQKEIERLRKEQSIKKLKHDDD
p)Galápagos tortoise(177) MAVAGLRGGLRAALGMQQRGWSSGSDQLGELGSGAGKGGGGGGAIREAGGAFGKRQAAHEERYFREKEREQLASLREYKEEEIDHHKKEIQRLQKEIDRLRKNKIKKLKGDDDD
q)EasternBoxTurtle (138) MAAAGLRGGLRGALVMQQRGWSSGSGSDQLGELGSGAGKGGGGGGAIREAGGAFGKRQAAHEERYFRDKEREQLASLREHKEEEIDHHKKEIQRLQKEIDRLRKNKIKKLKGDDD
r)GreenSeaTurtle (75) MAAAGLRGGLRGALALQQRGWSSGSGSGSDQLGELGSGAGKGGGGGGAIREAGGAFGKRQAAHEERYFREKEAEQLASLRKHKEEEIDHHKKEIERLQKEIERLRKYKIKKLKNDD
s)WestPaintedTurtle (61) MAAAGLRGGLRGALVMQQRGWSSGSGSGSDQLGELGSGAGKGGGGGGAIREAGGAFGKRQAAHEERYFRDKEREQLASLREHKEEEIDHHKKEIQRLQKEIERLRKEKIKIKKLKGDDDD
t)Red-earedTerrapin (41) MAAAGLRGGLRGALVMQQRGWSSGSGSDQLGELGSGAGKGGGGGGAIREAGGAFGKRQAAHEERYFRDKEREQLASLREHKEEEIDHHKKEIQRLQKEIERLRKIKIKKLKGDDD
u) Alligator (77) MAAGVLRSGLRGAFLMQQQRGWSSGSGADQLGELGKGAGKGGGGGGAIREAGGAFGKRQVAEEERYFREKERPQLAALRKHKEEEIDHHKKQIELLQKEIERGKYKIKKLKNDDDDD
v)KomodoDragon(62) MAAVGAALRSGLRGAVAEFSQQRAWSSGSDQLGELGKGAGKGGGGGGAIREAGGAFGKRQVAEEERYFREAERKELANLRKHKEEEIYHHKKEIERLRQKEIERHKSKIKKLGDDD
w) Crocodile (57) MAAGVLRGGLRGAFLMQQQRWSSGSGSGADQLGELGKGAGKGGGGGGAIREAGGAFGKRQAAEEERYFRERERQLAALRKHKEEEIDHHKKQIEVLQKEIERNKYKIKKLKNDDD
z) Kakapo (60) MAAAAAARGGLRGALVLQQQRWSSGSGADQLGELGKGAGKGGGGGGAIREAGGAFGKKQAAEEERYFREKEREQLGALRKHKEEEIDHHQKEIERLQKEIERNKYKIKKLKDDN
y) Sablefish (114) MSRTLIRADIRRCVASQIRMASDQLGELGKGAGKGGGGGGAVRSAGGAFGKRIVAEEERYFRQKEKEQMPALRKHKVEEIEHHKKEIERLQKEIERLRKGKIRKLNHDD
x) European eel (88) MSRLIKSNLRGFLITQIRMSSDQLGELGKGAGKGGGGGGAVREAGGALGKRQAAEEERYFRKKEQEQLAALRKHKEEEIDHHKKEIERLQREIDRHKGKIRKLKHDD
aa) West Indian manatee (69) MAVTALAARVRLYSLGARAMQAQGFSSDQSEDLDRRAGAIREAGGAFAKREAAEEERYFRAQAKEQLAALKKYKEEEIVHSKKEIERLQKEIERHKQKIKKLKHDD
bb) African bush elephant (65) MATTALAARVRLCALGVRVTVQAQGFSSDQPHDLDRGAGAIREAGGAFAKREAAEEERYFRAQAKEQLAALKKYKEEEITHTKKEIERLQNEIERHKQKIKKLKHDD
cc) Gorilla (60.1) MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLATLKKHKEEEIVHMKKEIERLQKEIERHKQKIKMLKHDD
dd) White-faced capuchin (54) MAVTALAARTWLGVWGVRTMQARSFGSDQSENLDRGAGAIREAGGAFGKREQAEEERYFRAQTREQLAALKKHKEEEIVHHKKEIERLQREIERHKQKIKILKHDD
ee) Bolivian squirrel monkey (30) MAVTALAARTWLGVWGVRTMQARSFGSDQSENLDRGAGAIREAGGAFGKREQAEEERYFRAQTREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKILKHDD
ff) Common marmoset (23) MAVTALAARTWLGVWGVRTMQARSFGSDQSENLDRGAGAIREAGGAFGKREQAEEERYFRAQARELAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKILKDDD
gg) Philippine tarsier (16) MAVSALVARTWLGMWGVRARQTRGFGSDQSENVDKSSGAIREAGGAFGKREQAEEERYFRAQTREQLAALKKHKEEERLQEHHKKEIERLQKEIERHKQKIKTLKHDD
hh) Naked mole rat (31) MAGTALASRARLGVWGVRAMQTRGFSSDKDHESSSGAIRDAGGAFGKREQAEEERFTRQKTKEQLEALKKHKEDEIYHHKKAIEHMEKEIERHKQKIKQLKHDD
ii) Damaraland mole-rat (15.5) MAGTALASRARLGVRGVRAMQTRGFSSDKDHHESSAGAIRDAGGAFGKREQAEEERFTRQKTKEQLDALKKHKEDEIYHHKKAIEQMEKEIERHKQKIKQLKHHE
jj) Mouse (4) MAGSALAVRARFGVWGMKVLQTRGFVSDSSDSMDTGAGAIREAGGAFGKREKAEEDRYFREKTKEQLAALRKHKEDEIDHHSKEIERLQKQIERHKKKIQQLKNNH

FIGURE 10R

Top sequence is IF1 protein of ***Bowhead whale.***
In other protein sequence embodiments of this figure (not shown), for each sequence below, the mitochondrial import sequence (underlined) is substituted for that of another species, optionally for that of human IF1 (MAVTALAARTWLGVWGVRTMQARGF) or mouse IF1 (MAGSALAVRARFGVWGMKVLQTRGF), preferably from the species that the protein is being administered to (optionally via expression therein).
In further protein sequence embodiments of this figure (not shown), a sequence of this figure is concatenated at its N-terminal end with a Cell Penetrating Peptide sequence (CPP) of the art, optionally the HiV-1 Tat sequence (YGRKKRRQRRR), optionally flanked on one or both sides by a G residue, preferably a human derived CPP such as (without limitation) R7, optionally which is in turn concatenated to an affinity/epitope sequence of the art (e.g. HHHHHHDYKDDDDK)

MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**Q**QAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK**AK**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKH**K**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKK**AK**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKKH**K**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD**D**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD**D**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**Q**QAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD**D**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK**AK**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD**D**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKH**K**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD**D**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKK**AK**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD**D**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKKH**K**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD**D**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD**D**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD**D**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD**DD**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD**DD**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**Q**QAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD**DD**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK**AK**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD**DD**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKH**K**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD**DD**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKK**AK**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD**DD**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKKH**K**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD**DD**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD**DD**
MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD**DD**

FIGURE 10S

a) Human (122.5) MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

b) Bowhead whale (211) MAATALAARTRFGVWSVWAMQGRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKKLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQSIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIEHLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHVKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEISHHKKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIDHHKKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHENEIVHHKKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRARAKEQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKKEQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIRDAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVGRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQAENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHKENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHKENEIDHHVKEIEHLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHKENEIDHHVKEIEHLQKEIERHKQSIKKLKHDDDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKAQAEEERYFRARAKEQLAALKKHKENEIDHHVKEIEHLQKEIERHKQSIKKLKHDDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKKLKHDDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKKLKHDDDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKKLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKKLKHDDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKKLKHDDDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQAENVGRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQAENVGRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQAENVGRGAGAIREAGGAFGKRAQAEEERYFRAQSREQLAALKKHKEEEIVHHKKEIERLQKEIERHKQKIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSDQAENVGRGAGAIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEEIVAHKKEIERLQKEIERHKQKIKKLKHDDD

FIGURE 10T

Bowhead whale IF1 + human/mouse IF1 mitochondrial targeting sequences respectively, thereafter H49K variants thereof, thereafter CPP fusion proteins thereof, thereafter affinity/epitope tagged thereof; 14-47 and 42-58 sub-sequences thereof; further variants

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
MAGSALAVRARFGVWGMKVLQTRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
MAGSALAVRARFGVWGMKVLQTRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
GYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
GYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
GYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
GYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
DYKDDDDKGYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
DYKDDDDKGYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
DYKDDDDKGYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
DYKDDDDKGYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
AIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK
LAALKKHHENEISHHVK
MAVTALAARTWLGVWGVRTMQARGFAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK
MAGSALAVRARFGVWGMKVLQTRGFAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK
MAVTALAARTWLGVWGVRTMQARGFLAALKKHHENEISHHVK
MAGSALAVRARFGVWGMKVLQTRGFLAALKKHHENEISHHVK
GYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK
GYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK
GYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFLAALKKHHENEISHHVK
GYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFLAALKKHHENEISHHVK
DYKDDDDKGYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK
DYKDDDDKGYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK
DYKDDDDKGYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFLAALKKHHENEISHHVK
DYKDDDDKGYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFLAALKKHHENEISHHVK
MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD
MAGSALAVRARFGVWGMKVLQTRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD
GYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD
GYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD
DYKDDDDKGYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD
DYKDDDDKGYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFGSESADNLGSSAGAIRDAGGAFGKK**A**QAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD
MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD
GYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD
DYKDDDDKGYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRARAKEQLAALKK**AK**ENEIS**A**HVKEIEHLQKEIERHKQSIKKLKHDDD

FIGURE 10U

Blue whale IF1 + human/mouse IF1 mitochondrial targeting sequences respectively, thereafter H49K+T14A variants thereof, thereafter CPP fusion proteins thereof, thereafter affinity/epitope tagged thereof; 14-47 sub-sequence thereof; further variants

MAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEATVWNAGVDFRKREQAKGERYLRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
MAGSALAVRARFGVWGMKVLQTRGFGSEPADNLGSSEATVWNAGVDFRKREQAKGERYLRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
MAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEA**A**VWNAGVDFRKREQAKGERYLRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
MAGSALAVRARFGVWGMKVLQTRGFGSEPADNLGSSEA**A**VWNAGVDFRKREQAKGERYLRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
GYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEATVWNAGVDFRKREQAKGERYLRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
GYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFGSEPADNLGSSEATVWNAGVDFRKREQAKGERYLRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
GYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEA**A**VWNAGVDFRKREQAKGERYLRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
GYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFGSEPADNLGSSEA**A**VWNAGVDFRKREQAKGERYLRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
DYKDDDDKGYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEATVWNAGVDFRKREQAKGERYLRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
DYKDDDDKGYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFGSEPADNLGSSEATVWNAGVDFRKREQAKGERYLRARAKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
DYKDDDDKGYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEA**A**VWNAGVDFRKREQAKGERYLRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
DYKDDDDKGYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFGSEPADNLGSSEA**A**VWNAGVDFRKREQAKGERYLRARAKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD
TVWNAGVDFRKREQAKGERYLRARAKEQLAALKK
AVWNAGVDFRKREQAKGERYLRARAKEQLAALKK
AVWNAGVDFRKREQAKGERYLRARAKEQLAALK
AVWNAGVDFRKREQAKGERYLRARAKEQLAAL
AVWNAGVDFRKREQAKGERYLRARAKEQLAA
MAVTALAARTWLGVWGVRTMQARGFTVWNAGVDFRKREQAKGERYLRARAKEQLAALKK
MAGSALAVRARFGVWGMKVLQTRGFTVWNAGVDFRKREQAKGERYLRARAKEQLAALKK
GYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFTVWNAGVDFRKREQAKGERYLRARAKEQLAALKK
GYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFTVWNAGVDFRKREQAKGERYLRARAKEQLAALKK
DYKDDDDKGYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFTVWNAGVDFRKREQAKGERYLRARAKEQLAALKK
DYKDDDDKGYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFTVWNAGVDFRKREQAKGERYLRARAKEQLAALKK
MAVTALAARTWLGVWGVRTMQARGFAVWNAGVDFRKREQAKGERYLRARAKEQLAALKK
MAGSALAVRARFGVWGMKVLQTRGFAVWNAGVDFRKREQAKGERYLRARAKEQLAALKK
GYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFA**V**WNAGVDFRKREQAKGERYLRARAKEQLAALKK
GYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFA**V**WNAGVDFRKREQAKGERYLRARAKEQLAALKK
DYKDDDDKGYGRKKRRQRRRGMAVTALAARTWLGVWGVRTMQARGFA**V**WNAGVDFRKREQAKGERYLRARAKEQLAALKK
DYKDDDDKGYGRKKRRQRRRGMAGSALAVRARFGVWGMKVLQTRGFA**V**WNAGVDFRKREQAKGERYLRARAKEQLAALKK

FIGURE 10V

Human IF1 + human/mouse IF1 mitochondrial targeting sequences respectively, thereafter H49K & S14A variants thereof, thereafter CPP fusion proteins thereof, thereafter affinity/epitope tagged thereof; 14-47 sub-sequence thereof; further variants thereof; 42-58 sub-sequence thereof; further variants thereof

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
MAGSALAVRARFGVWGMKVLQTRGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKKH**K**EEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
MAGSALAVRARFGVWGMKVLQTRGFGSDQSENVDRGAG**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKKH**K**EEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
RRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
RRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
RRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKKH**K**EEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
RRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFGSDQSENVDRGAG**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKKH**K**EEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
HHHHHHDYKDDDDKRRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
HHHHHHDYKDDDDKRRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
HHHHHHDYKDDDDKRRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKKH**K**EEEIVHHKKEIERLQKEIERHKQKIKMLKHDD
HHHHHHDYKDDDDKRRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFGSDQSENVDRGAG**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKKH**K**EEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

SIREAGGAFGKREQAEEERYFRAQSREQLAALKK
AIREAGGAFGKREQAEEERYFRAQSREQLAALKK
AIREAGGAFGKREQAEEERYFRAQSREQLAALK
AIREAGGAFGKREQAEEERYFRAQSREQLAAL
MAVTALAARTWLGVWGVRTMQARGFSIREAGGAFGKREQAEEERYFRAQSREQLAALKK
MAGSALAVRARFGVWGMKVLQTRGFSIREAGGAFGKREQAEEERYFRAQSREQLAALKK
RRRRRRRGMAVTALAARTWLGVWGVRTMQARGFSIREAGGAFGKREQAEEERYFRAQSREQLAALKK
RRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFSIREAGGAFGKREQAEEERYFRAQSREQLAALKK
HHHHHHDYKDDDDKRRRRRRRGMAVTALAARTWLGVWGVRTMQARGFSIREAGGAFGKREQAEEERYFRAQSREQLAALKK
HHHHHHDYKDDDDKRRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFSIREAGGAFGKREQAEEERYFRAQSREQLAALKK
MAVTALAARTWLGVWGVRTMQARGFA**_**IREAGGAFGKREQAEEERYFRAQSREQLAALKK
MAGSALAVRARFGVWGMKVLQTRGFA**_**IREAGGAFGKREQAEEERYFRAQSREQLAALKK
RRRRRRRGMAVTALAARTWLGVWGVRTMQARGF**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKK
RRRRRRRGMAGSALAVRARFGVWGMKVLQTRGF**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKK
HHHHHHDYKDDDDKRRRRRRRGMAVTALAARTWLGVWGVRTMQARGF**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKK
HHHHHHDYKDDDDKRRRRRRRGMAGSALAVRARFGVWGMKVLQTRGF**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKK

LAALKKHHEEEIVHHKK
MAVTALAARTWLGVWGVRTMQARGFLAALKKHHEEEIVHHKK
MAGSALAVRARFGVWGMKVLQTRGFLAALKKHHEEEIVHHKK
RRRRRRRGMAVTALAARTWLGVWGVRTMQARGFLAALKKHHEEEIVHHKK
RRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFLAALKKHHEEEIVHHKK
HHHHHHDYKDDDDKRRRRRRRGMAVTALAARTWLGVWGVRTMQARGFLAALKKHHEEEIVHHKK
HHHHHHDYKDDDDKRRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFLAALKKHHEEEIVHHKK

FIGURE 10W

Blue whale IF1 variants + human/mouse IF1 mitochondrial targeting sequences respectively, thereafter CPP fusion proteins thereof, thereafter affinity/epitope tagged thereof

MAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEA**A**VWNAGVDFRKREQAKGERYLRARAKEQLAALKKHKENEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

MAGSALAVRARFGVWGMKVLQTRGFGSEPADNLGSSEA**A**VWNAGVDFRKREQAKGERYLRARAKEQLAALKKHKENEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEA**A**VWNAGVDFRKR**A**QAKGERYLRARAKEQLAALKKHKENEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

MAGSALAVRARFGVWGMKVLQTRGFGSEPADNLGSSEA**A**VWNAGVDFRKR**A**QAKGERYLRARAKEQLAALKKHKENEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

RRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEA**A**VWNAGVDFRKREQAKGERYLRARAKEQLAALKKHK**E**NEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

RRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFGSEPADNLGSSEA**A**VWNAGVDFRKREQAKGERYLRARAKEQLAALKKHK**E**NEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

RRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEA**A**VWNAGVDFRKR**A**QAKGERYLRARAKEQLAALKKHK**E**NEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

RRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFGSEPADNLGSSEA**A**VWNAGVDFRKR**A**QAKGERYLRARAKEQLAALKKHK**E**NEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

HHHHHHDYKDDDDKRRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEA**A**VWNAGVDFRKREQAKGERYLRARAKEQLAALKKHK**E**NEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

HHHHHHDYKDDDDKRRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFGSEPADNLGSSEA**A**VWNAGVDFRKR**A**QAKGERYLRARAKEQLAALKKHK**E**NEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

HHHHHHDYKDDDDKRRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEA**A**VWNAGVDFRKR**A**QAKGERYLRARAKEQLAALKKHK**E**NEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

HHHHHHDYKDDDDKRRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFGSEPADNLGSSEA**A**VWNAGVDFRKR**A**QAKGERYLRARAKEQLAALKKHK**E**NEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEA**A**VWNAGVDFRKR**A**QAKGERYLRARAKEQLAALKKHK**E**NEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

RRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEA**A**VWNAGVDFRKR**A**QAKGERYLRARAKEQLAALKKHK**E**NEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

HHHHHHDYKDDDDKRRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSEPADNLGSSEA**A**VWNAGVDFRKR**A**QAKGERYLRARAKEQLAALKKHK**E**NEISA**H**VKEIEHLQKEIERHKQSIKKLKHDDD

Human IF1 variants + human/mouse IF1 mitochondrial targeting sequences respectively, thereafter CPP fusion proteins thereof, thereafter affinity/epitope tagged thereof

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKKHK**E**EEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

MAGSALAVRARFGVWGMKVLQTRGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKKHK**E**EEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIK**KL**KHDD**D**

MAGSALAVRARFGVWGMKVLQTRGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIK**KL**KHDD**D**

RRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

RRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

RRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIK**KL**KHDD**D**

RRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIK**KL**KHDD**D**

HHHHHHDYKDDDDKRRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

HHHHHHDYKDDDDKRRRRRRRGMAGSALAVRARFGVWGMKVLQTRGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

HHHHHHDYKDDDDKRRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

MAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

RRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

HHHHHHDYKDDDDKRRRRRRRGMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

FIGURE 10X

"-" is a disulphide bond; Human IF1 variants, CPP fusion proteins thereof, affinity/epitope tag thereof

RRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

RRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

RRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

HHHHHHDYKDDDDKRRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHEEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

HHHHHHDYKDDDDKRRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

HHHHHHDYKDDDDKRRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

HHHHHHDYKDDDDKRRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGF**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKK

HHHHHHDYKDDDDKRRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGF**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKK

RRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEIVHHKK

HHHHHHDYKDDDDKRRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFSIREAGGAFGKREQAEEERYFRAQSREQLAALKK

RRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAGSIREAGGAFGKREQAEEERYFRAQSREQLAALKK

RRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKKHKEEIVHHKKEIERLQKEIERHKQKIKMLKHDD

RRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKKHKEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

RRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKI**KL**KHDD**D**

RRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

HHHHHHDYKDDDDKRRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**K**EEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

HHHHHHDYKDDDDKRRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKI**K**LKHDDD

HHHHHHDYKDDDDKRRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKR**A**QAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

HHHHHHDYKDDDDKRRRRRRRC-CMAVTALAARTWLGVWGVRTMQARGFGSDQSENVDRGAG**A**IREAGGAFGKREQAEEERYFRAQSREQLAALKK**AK**EEEIV**A**HKKEIERLQKEIERHKQKIKMLKHDD

"|" is a disulphide bond; Bowhead whale IF1 variants,
with human mitochondrial import sequence, CPP fusion proteins thereof

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRA**C**AKEQLAALKKHHENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRA**C**AKEQLAALKKHHENEISHHVKEIECLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRA**C**AKEQLAALKKHHENEISHHVKEIECLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRA**C**AKEQLAALKKHHENEISHHVKEIECLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRA**C**AKEQLAALKKH**K**ENEISHHVKEIEHLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRA**C**AKEQLAALKKH**K**ENEISHHVKEIECLQKEIERHKQSIKKLKHDDD

MAVTALAARTWLGVWGVRTMQARGFGSESADNLGSSAGAIRDAGGAFGKKEQAEEERYFRA**C**AKEQLAALKKH**K**ENEISHHVKEIECLQKEIERHKQSIKKLKHDDD

FIGURE 10Y

Non-limiting examples of
Peptide inhibitors of F_1F_0 ATP hydrolysis

a)	*Melittin*	GQRKRKIWSILAPLGTTLVKLVAGIG
b)	*Presequence of subunit IV of yeast cytochrome c oxidase*	LLYRSSCLTRTAPKFFRISQRLSLM
c)	*Δ11,12*	LLYRSSCLTRTAPFFRISQRLSLM
d)	*Syn-A2*	LLYRSLLRLSLRSLLRLSLRSLM
e)	*Syn-C*	LLYRSLRLRLLSLSRLRLLSSLM
f)	*Bovine F_1 β subunit residues 394-413*	FVKRERATEDFFVRQREKEQLRRLK
g)	*Bovine F_1 β subunit residues 384-403*	FEKREKAQEDLYIRQHEKEQLEALK
h)	*Bovine F_1 β subunit residues 404-423*	DELSEEDKLFVSRARKIQRF

Corresponding F1 β subunit sequences of other species are also componentry to this invention.
Sequences shown in N to C direction by convention (in the literature some of these sequences are reported C to N).
Non-limiting invention embodiments:

Mitochondrial Import Sequence — Peptide inhibitor of F_1F_0 ATP hydrolysis

OR

Cell Penetrating Sequence — Peptide inhibitor of F_1F_0 ATP hydrolysis

OR

Cell Penetrating Sequence — **Mitochondrial Import Sequence** — Peptide inhibitor of F_1F_0 ATP hydrolysis

OR

Epitope tag — **Cell Penetrating Sequence** — Peptide inhibitor of F_1F_0 ATP hydrolysis

OR

Epitope tag — **Cell Penetrating Sequence** — **Mitochondrial Import Sequence** — Peptide inhibitor of F_1F_0 ATP hydrolysis

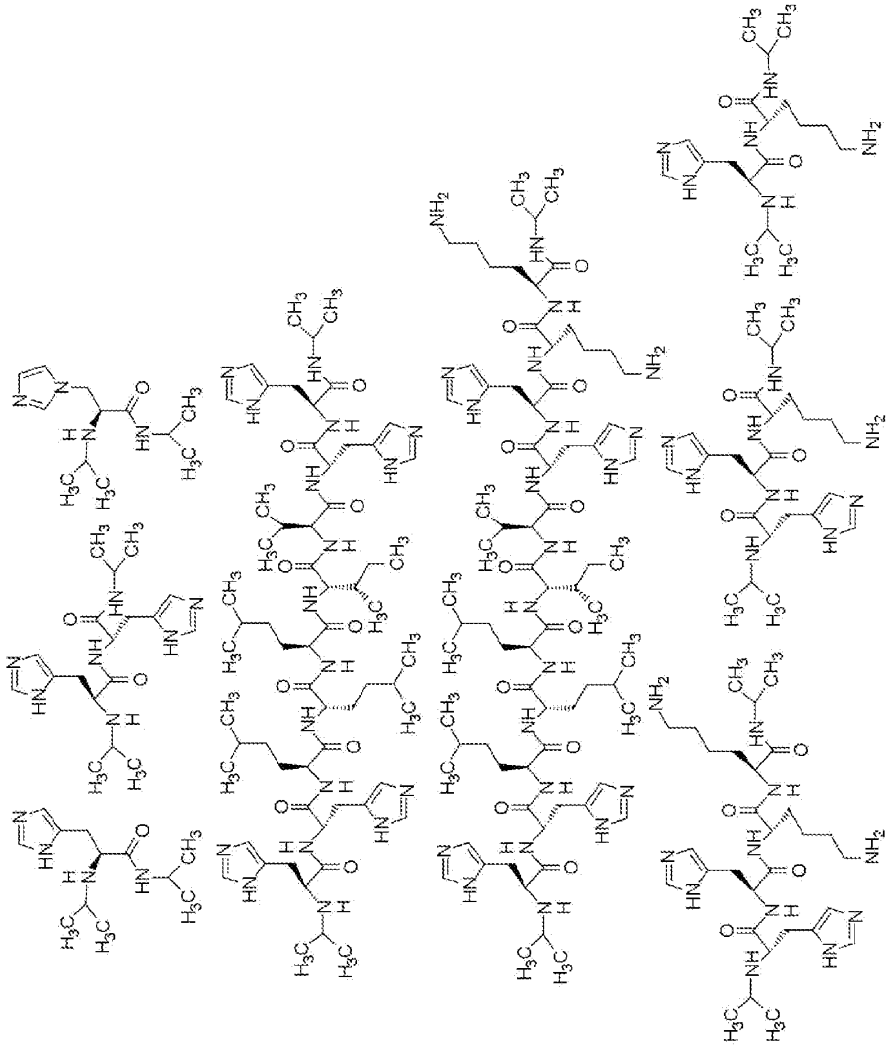


FIGURE 10Z