Claims

1. Transporter construct comprising at least one sequence of the generic formula (I) (SEQ ID NO: 1):

$$D_lLLL_xD_m(LLL_yD_n)_a$$

wherein:	D	is a D-amino acid;
	L	is a L-amino acid;
	a	is 0 – 3;
	l, m and n	are independently from each other 1 or 2;
	x and y	are independently from each other 0, 1 or 2;

2. Transporter contruct according to claim 1, wherein the transporter construct comprises at least one sequence according to one of the following subformulas (Ia) to (Id) (SEQ ID NOs: 2 to 5):

(Ia): $D_lLLL_xD_m$;

(Ib): $D_lLLL_xD_mLLL_yD_n$;

(Ic): $D_lLLL_xD_mLLL_yD_nLLL_yD_n$; or

(Id): $D_lLLL_xD_mLLL_yD_nLLL_yD_nLLL_yD_n$.

3. Transporter contruct according to claims 1 or 2, wherein the transporter construct comprises at least one sequence according to the following subformula (Ie) (SEQ ID NO: 6):

$$DLLLD(LLLD)_a .$$

4. Transporter contruct according to any of claims 1, 2 or 3, wherein the transporter construct comprises at least one sequence according to the following subformula (If) (SEQ ID NO: 7):

$$DLLLDLLLD .$$

5. Transporter contruct according to any of claims 1 to 4, wherein the sequence according to generic formula (I) or according to any of subformulas (Ia), (Ib), (Ic), (Id), (Ie), or (If), is used with or is applied to a trafficking sequence derived from HIV-1 TAT protein (SEQ ID NO: 8), preferably derived from an amino acid sequence containing TAT residues 48-57 or 49 to 57 of HIV-1 TAT protein (SEQ ID NO: 8), or derived from HSV VP22 (*Herpes simplex*), from antennapedia carrier sequence (*Drosophila antennapedia*), FGF, lactoferrin, or is derived from a basic peptide having a length of 5 to 15 amino acids, preferably 10 to 12 amino acids and comprising at least 80 %, more preferably 85 % or even 90 % basic amino acids selected from arginine, lysine and/or histidine, or may be selected from arginine rich peptide sequences, including R_9, R_8, R_7, R_6, R_5, from VP22, from PTD-4 derived proteins or peptides, from RGD-K_{16}, from PEPT1/2 or PEPT1/2 derived proteins or peptides, from SynB3 or SynB3 derived proteins or peptides, from PC inhibitors, from P21 derived proteins or peptides, from JNKI derived proteins or peptides, or from a variant, fragment or derivative of one of these trafficking sequences.

6. Transporter contruct according to any of claims 1 to 5, wherein the sequence according to generic formula (I) or according to any of subformulas (Ia), (Ib), (Ic), (Id), (Ie), or (If), is used with or is applied to one of the following sequences or a reverse sequence thereof, or a variant or fragment of these sequences:

SEQUENCE/PEPTIDE NAME	SEQ ID NO	AA	SEQUENCE
TAT (1-86)	8	86	MEPVDPRLEP WKHPGSQPKT ACTNCYCKKC CFHCQVCFIT KALGISYGRK KRRQRRRPPQ GSQTHQVSLS KQPTSQSRGD PTGPKE
TAT (37-72)	9	36	CFITKALGIS YGRKKRRQRR RPPQGSQTHQ VSLSKQ
TAT (37-58)	10	22	CFITKALGIS YGRKKRRQRR RP
TAT (38-58)GGC	11	24	FITKALGISY GRKKRRQRRR PGGC
TAT CGG(47-58)	12	15	CGGYGRKKRR QRRRP
TAT (47-58)GGC	13	15	YGRKKRRQRR RPGGC
TAT (1-72) Mut Cys/Ala 72	14	56	MEPVDPRLEP WKHPGSQPKT AFITKALGIS YGRKKRRQRR RPPQGSQTHQ VSLSKQ
L-generic-TAT	15	17	XXXXRKKRRQRRRXXXX (NH_2- XXXXRKKRRQRRRXXXX -COOH)
L-generic-TAT (s)	16	11	NH_2-X_n^b-RKKRRQRRR-X_n^b-COOH
L-TAT (s1a)	17	10	GRKKRRQRRR (NH_2-GRKKRRQRRR-COOH)
L-TAT (s1b)	18	9	RKKRRQRRR (NH_2-GRKKRRQRRR-COOH)

L-TAT (s1c)	19	11	YDRKKRRQRRR
r_3-L-TAT	20	9	rKKRrQRRr
r_3-L-TATi	21	9	rRRQrRKKr
□A-r_3-L-TAT	22	9	□A-rKKRrQRRr
□A-r_3-L-TATi	23	9	□A-rRRQrRKKr
FITC-□A-r_3-L-TAT	24	9	FITC-□A-rKKRrQRRr
FITC-□A-r_3-L-TATi	25	9	FITC-□A-rRRQrRKKr
TAT(s2-1)	26	9	rAKRrQRRr
TAT(s2-2)	27	9	rKARrQRRr
TAT(s2-3)	28	9	rKKArQRRr
TAT(s2-4)	29	9	rKKRrARRr
TAT(s2-5)	30	9	rKKRrQARr
TAT(s2-6)	31	9	rKKRrQRAr
TAT(s2-7)	32	9	rDKRrQRRr
TAT(s2-8)	33	9	rKDRrQRRr
TAT(s2-9)	34	9	rKKDrQRRr
TAT(s2-10)	35	9	rKKRrDRRr
TAT(s2-11)	36	9	rKKRrQDRr
TAT(s2-12)	37	9	rKKRrQRDr
TAT(s2-13)	38	9	rEKRrQRRr
TAT(s2-14)	39	9	rKERrQRRr
TAT(s2-15)	40	9	rKKErQRRr
TAT(s2-16)	41	9	rKKRrERRr
TAT(s2-17)	42	9	rKKRrQERr
TAT(s2-18)	43	9	rKKRrQREr
TAT(s2-19)	44	9	rFKRrQRRr
TAT(s2-20)	45	9	rKFRrQRRr
TAT(s2-21)	46	9	rKKFrQRRr
TAT(s2-22)	47	9	rKKRrFRRr
TAT(s2-23)	48	9	rKKRrQFRr
TAT(s2-24)	49	9	rKKRrQRFr
TAT(s2-25)	50	9	rRKRrQRRr
TAT(s2-26)	51	9	rKRRrQRRr
TAT(s2-27)	52	9	rKKKrQRRr
TAT(s2-28)	53	9	rKKRrRRRr
TAT(s2-29)	54	9	rKKRrQKRr
TAT(s2-30)	55	9	rKKRrQRKr
TAT(s2-31)	56	9	rHKRrQRRr
TAT(s2-32)	57	9	rKHRrQRRr
TAT(s2-33)	58	9	rKKHrQRRr
TAT(s2-34)	59	9	rKKRrHRRr
TAT(s2-35)	60	9	rKKRrQHRr
TAT(s2-36)	61	9	rKKRrQRHr
TAT(s2-37)	62	9	rIKRrQRRr
TAT(s2-38)	63	9	rKIRrQRRr
TAT(s2-39)	64	9	rKKIrQRRr
TAT(s2-40)	65	9	rKKRrIRRr
TAT(s2-41)	66	9	rKKRrQIRr
TAT(s2-42)	67	9	rKKRrQRIr
TAT(s2-43)	68	9	rLKRrQRRr
TAT(s2-44)	69	9	rKLRrQRRr
TAT(s2-45)	70	9	rKKLrQRRr
TAT(s2-46)	71	9	rKKRrLRRr
TAT(s2-47)	72	9	rKKRrQLRr

TAT(s2-48)	73	9	rKKRrQRLr
TAT(s2-49)	74	9	rMKRrQRRr
TAT(s2-50)	75	9	rKMRrQRRr
TAT(s2-51)	76	9	rKKMrQRRr
TAT(s2-52)	77	9	rKKRrMRRr
TAT(s2-53)	78	9	rKKRrQMRr
TAT(s2-54)	79	9	rKKRrQRMr
TAT(s2-55)	80	9	rNKRrQRRr
TAT(s2-56)	81	9	rKNRrQRRr
TAT(s2-57)	82	9	rKKNrQRRr
TAT(s2-58)	83	9	rKKRrNRRr
TAT(s2-59)	84	9	rKKRrQNRr
TAT(s2-60)	85	9	rKKRrQRNr
TAT(s2-61)	86	9	rQKRrQRRr
TAT(s2-62)	87	9	rKQRrQRRr
TAT(s2-63)	88	9	rKKQrQRRr
TAT(s2-64)	89	9	rKKRrKRRr
TAT(s2-65)	90	9	rKKRrQQRr
TAT(s2-66)	91	9	rKKRrQRQr
TAT(s2-67)	92	9	rSKRrQRRr
TAT(s2-68)	93	9	rKSRrQRRr
TAT(s2-69)	94	9	rKKSrQRRr
TAT(s2-70)	95	9	rKKRrSRRr
TAT(s2-71)	96	9	rKKRrQSRr
TAT(s2-72)	97	9	rKKRrQRSr
TAT(s2-73)	98	9	rTKRrQRRr
TAT(s2-74)	99	9	rKTRrQRRr
TAT(s2-75)	100	9	rKKTrQRRr
TAT(s2-76)	101	9	rKKRrTRRr
TAT(s2-77)	102	9	rKKRrQTRr
TAT(s2-78)	103	9	rKKRrQRTr
TAT(s2-79)	104	9	rVKRrQRRr
TAT(s2-80)	105	9	rKVRrQRRr
TAT(s2-81)	106	9	rKKVrQRRr
TAT(s2-82)	107	9	rKKRrVRRr
TAT(s2-83)	108	9	rKKRrQVRr
TAT(s2-84)	109	9	rKKRrQRVr
TAT(s2-85)	110	9	rWKRrQRRr
TAT(s2-86)	111	9	rKWRrQRRr
TAT(s2-87)	112	9	rKKWrQRRr
TAT(s2-88)	113	9	rKKRrWRRr
TAT(s2-89)	114	9	rKKRrQWRr
TAT(s2-90)	115	9	rKKRrQRWr
TAT(s2-91)	116	9	rYKRrQRRr
TAT(s2-92)	117	9	rKYRrQRRr
TAT(s2-93)	118	9	rKKYrQRRr
TAT(s2-94)	119	9	rKKRrYRRr
TAT(s2-95)	120	9	rKKRrQYRr
TAT(s2-96)	121	9	rKKRrQRYr
r_3R_6	122	9	rRRRrRRRr
L-R_9	123	9	RRRRRRRRR
L-R_8	124	8	RRRRRRRR
L-R_7	125	7	RRRRRRR
L-R_6	126	6	RRRRRR

L-R_5	127	5	RRRRR
PTD-4	128	11	YARAAARQARA
PTD-4 (variant 1)	129	11	WARAAARQARA
PTD-4 (variant 2)	130	11	WARAQRAAARA
L-P1 Penetratin	131	16	RQVKVWFQNRRMKWKK
D-P1 Penetratin	132	16	KKWKMRRNQFWVKVQR
JNKI, bestfit	133	17	WKRAAARKARAMSLNLF
JNKI, bestfit (variant 1)	134	17	WKRAAARAARAMSLNLF
MDCK transcytose sequence	135	9	RYRGDLGRR
YKGL	136	4	YKGL
r_3 (generic)	252	9	rXXXrXXXr

7. Transporter contruct according to any of claims 1 to 6, wherein the transporter construct comprises at least one sequence according to rXXXrXXXr (SEQ ID NO: 252), wherein:

   r represents an D-enatiomeric arginine;

   X is any L-amino acid;

   and wherein each X may be selected individually and independently of any other X within SEQ ID NO: 252.

8. Transporter construct according to claim 8, wherein at least 4 out of said 6 X L-amino acids are individually selected from the group of L amino acids consisting of K or R.

9. Transporter contruct according to any of claims 1 to 8, wherein the transporter construct comprises the subformula (If) **DLLLDLLLD** (SEQ ID NO: 7) and wherein the transporter sequence is selected from the sequences:

SEQUENCE/PEPTIDE NAME	SEQ ID NO	AA	SEQUENCE
r_3-L-TAT	20	9	rKKRrQRRr
r_3-L-TATi	21	9	rRRQrRKKr
A-r_3-L-TAT	22	9	A-rKKRrQRRr
A-r_3-L-TATi	23	9	A-rRRQrRKKr
FITC- A-r_3-L-TAT	24	9	FITC- A-rKKRrQRRr
FITC- A-r_3-L-TATi	25	9	FITC- A-rRRQrRKKr
TAT(s2-1)	26	9	rAKRrQRRr
TAT(s2-2)	27	9	rKARrQRRr
TAT(s2-3)	28	9	rKKArQRRr
TAT(s2-4)	29	9	rKKRrARRr
TAT(s2-5)	30	9	rKKRrQARr
TAT(s2-6)	31	9	rKKRrQRAr

TAT(s2-7)	32	9	rDKRrQRRr
TAT(s2-8)	33	9	rKDRrQRRr
TAT(s2-9)	34	9	rKKDrQRRr
TAT(s2-10)	35	9	rKKRrDRRr
TAT(s2-11)	36	9	rKKRrQDRr
TAT(s2-12)	37	9	rKKRrQRDr
TAT(s2-13)	38	9	rEKRrQRRr
TAT(s2-14)	39	9	rKERrQRRr
TAT(s2-15)	40	9	rKKErQRRr
TAT(s2-16)	41	9	rKKRrERRr
TAT(s2-17)	42	9	rKKRrQERr
TAT(s2-18)	43	9	rKKRrQREr
TAT(s2-19)	44	9	rFKRrQRRr
TAT(s2-20)	45	9	rKFRrQRRr
TAT(s2-21)	46	9	rKKFrQRRr
TAT(s2-22)	47	9	rKKRrFRRr
TAT(s2-23)	48	9	rKKRrQFRr
TAT(s2-24)	49	9	rKKRrQRFr
TAT(s2-25)	50	9	rRKRrQRRr
TAT(s2-26)	51	9	rKRRrQRRr
TAT(s2-27)	52	9	rKKKrQRRr
TAT(s2-28)	53	9	rKKRrRRRr
TAT(s2-29)	54	9	rKKRrQKRr
TAT(s2-30)	55	9	rKKRrQRKr
TAT(s2-31)	56	9	rHKRrQRRr
TAT(s2-32)	57	9	rKHRrQRRr
TAT(s2-33)	58	9	rKKHrQRRr
TAT(s2-34)	59	9	rKKRrHRRr
TAT(s2-35)	60	9	rKKRrQHRr
TAT(s2-36)	61	9	rKKRrQRHr
TAT(s2-37)	62	9	rIKRrQRRr
TAT(s2-38)	63	9	rKIRrQRRr
TAT(s2-39)	64	9	rKKIrQRRr
TAT(s2-40)	65	9	rKKRrIRRr
TAT(s2-41)	66	9	rKKRrQIRr
TAT(s2-42)	67	9	rKKRrQRIr
TAT(s2-43)	68	9	rLKRrQRRr
TAT(s2-44)	69	9	rKLRrQRRr
TAT(s2-45)	70	9	rKKLrQRRr
TAT(s2-46)	71	9	rKKRrLRRr
TAT(s2-47)	72	9	rKKRrQLRr
TAT(s2-48)	73	9	rKKRrQRLr
TAT(s2-49)	74	9	rMKRrQRRr
TAT(s2-50)	75	9	rKMRrQRRr
TAT(s2-51)	76	9	rKKMrQRRr
TAT(s2-52)	77	9	rKKRrMRRr
TAT(s2-53)	78	9	rKKRrQMRr
TAT(s2-54)	79	9	rKKRrQRMr
TAT(s2-55)	80	9	rNKRrQRRr
TAT(s2-56)	81	9	rKNRrQRRr
TAT(s2-57)	82	9	rKKNrQRRr
TAT(s2-58)	83	9	rKKRrNRRr
TAT(s2-59)	84	9	rKKRrQNRr
TAT(s2-60)	85	9	rKKRrQRNr

TAT(s2-61)	86	9	rQKRrQRRr
TAT(s2-62)	87	9	rKQRrQRRr
TAT(s2-63)	88	9	rKKQrQRRr
TAT(s2-64)	89	9	rKKRrKRRr
TAT(s2-65)	90	9	rKKRrQQRr
TAT(s2-66)	91	9	rKKRrQRQr
TAT(s2-67)	92	9	rSKRrQRRr
TAT(s2-68)	93	9	rKSRrQRRr
TAT(s2-69)	94	9	rKKSrQRRr
TAT(s2-70)	95	9	rKKRrSRRr
TAT(s2-71)	96	9	rKKRrQSRr
TAT(s2-72)	97	9	rKKRrQRSr
TAT(s2-73)	98	9	rTKRrQRRr
TAT(s2-74)	99	9	rKTRrQRRr
TAT(s2-75)	100	9	rKKTrQRRr
TAT(s2-76)	101	9	rKKRrTRRr
TAT(s2-77)	102	9	rKKRrQTRr
TAT(s2-78)	103	9	rKKRrQRTr
TAT(s2-79)	104	9	rVKRrQRRr
TAT(s2-80)	105	9	rKVRrQRRr
TAT(s2-81)	106	9	rKKVrQRRr
TAT(s2-82)	107	9	rKKRrVRRr
TAT(s2-83)	108	9	rKKRrQVRr
TAT(s2-84)	109	9	rKKRrQRVr
TAT(s2-85)	110	9	rWKRrQRRr
TAT(s2-86)	111	9	rKWRrQRRr
TAT(s2-87)	112	9	rKKWrQRRr
TAT(s2-88)	113	9	rKKRrWRRr
TAT(s2-89)	114	9	rKKRrQWRr
TAT(s2-90)	115	9	rKKRrQRWr
TAT(s2-91)	116	9	rYKRrQRRr
TAT(s2-92)	117	9	rKYRrQRRr
TAT(s2-93)	118	9	rKKYrQRRr
TAT(s2-94)	119	9	rKKRrYRRr
TAT(s2-95)	120	9	rKKRrQYRr
TAT(s2-96)	121	9	rKKRrQRYr
r_3R_6	122	9	rRRRrRRRr
L-R_9	123	9	RRRRRRRRR

10. Transporter contruct according to any of claims 1 to 9, wherein the transporter construct comprises the subformula (If) **DLLLDLLLD** (SEQ ID NO: 7) and wherein the transporter sequence is used with or is applied to a trafficking sequence derived from HIV-1 TAT protein having a Tyrosine (Y) at position 2 of the TAT derived sequence, the sequence preferably selected from sequence TAT(s2-91) (SEQ ID NO: 116).

11. Transporter contruct according to any of claims 5 to 10, wherein the transporter sequence according to generic formula (I) or according to any of subformulas (Ia),

(Ib), (Ic), (Id), (Ie), or (If), is used with or is applied to a variant or a fragment of any of the trafficking sequences listed in claims 5 to 10, having at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80% or 85%, preferably at least 90%, more preferably at least 95% and most preferably at least 99% over the whole length of any of the trafficking sequences listed in claims 5 to 10.

12. Transporter cargo conjugate molecule, comprising
    a) a component (A), wherein component (A) comprises the transporter construct according to any of claims 1 to 11; and
    b) a component (B), comprising an effector molecule.

13. Transporter cargo conjugate molecule according to claim 12, wherein the effector molecule is selected from therapeutically active proteins and peptides, protein kinase inhibitors, inhibitors of the protein kinase c-Jun amino terminal kinase, antigens, antibodies, apoptotic factors, proteases implicated in pathological states, preferably peptidic protease inhibitors, BH3-domains or BH3-only proteins, nucleic acids encoding these proteins, siRNAs, antisense RNAs, cytotoxic agents, and small organic compounds including protease inhibitors.

14. Transporter cargo conjugate molecule according to claim 12 or 13, furthermore comprising at least one additional component (C), (D) and/or (E) different to component (B), wherein the at least one optional additional component (C), (D) and/or (E) is selected independently from each other from different effector molecules or their fragments or variants as defined for component (B).

15. Transporter cargo conjugate molecule according to any of claims 12 to 14, wherein components (A) and (B), and optional components (C), (D) and/or (E) are covalently linked with each other.

16. Transporter cargo conjugate molecule according to any of claims 12 to 15, wherein the at least one additional component (C), (D) and/or (E) is selected from a signal sequence or localisation sequence, which directs the inventive transporter cargo conjugate molecule to a particular intracellular target localization or to a particular cell type.

17. Transporter cargo conjugate molecule according to any of claims 12 to 16, wherein component (B) and/or the at least one additional components (C), (D) and/or (E) is (are) a protein or peptide sequence and is (are) composed of L-amino acids, D-amino acids or a mixture of both.

18. Transporter cargo conjugate molecule according to any of claims 12 to 17, wherein component (A) is positioned at the C-terminal end of the transporter cargo conjugate molecule, provided that component (B) is a protein or peptide sequence.

19. Transporter cargo conjugate molecule according to any of claims 12 to 18 for use as a medicament.

20. Pharmaceutical composition comprising a transporter cargo conjugate molecule according to any of claims 12 to 19 and optionally a pharmaceutically acceptable carrier and/or vehicle.

21. Use of a transporter construct according to any of claims 1 to 11 for the preparation of a transporter cargo conjugate molecule.

22. Use of a transporter construct according to claim 21, wherein the transporter cargo conjugate molecule is as defined according to any of claims 12 to 18.

23. Use of a transporter construct according to any of claims 1 to 11 or a transporter cargo conjugate molecule as defined according to any of claims 12 to 18 for the transport of a cargo molecule into cells or tissue of a patient to be treated, wherein the cargo is as defined according to any of claims 12 to 18.

24. Use according to claim 23 for the transport of a cargo molecule into white blood cells and/or neuronal cells, in particular of a patient to be treated.

25. Use of a transporter cargo conjugate molecule according to any of claims 12 to 18 for the preparation of a medicament for the prophylaxis, treatment and/or

amelioration of cancer or tumor diseases, including diseases caused by defective apoptosis, inflammatory diseases, infectious diseases, viral (infectious) diseases, diseases strongly related to JNK signalling, autoimmune disorders or diseases, cardiovascular diseases, neuronal or neurodegenerative diseases, diseases of the liver, diseases of the spine, diseases of the uterus, major depressive disorders, non-chronic or chronic inflammatory digestive diseases, hearing loss, diseases of the inner ear, or for use in tissue transplantation.

Claims

1. Transporter construct comprising at least one D-/L-pattern of the generic formula (I):

$$D_lLLL_xD_m(LLL_yD_n)_a$$

wherein:

D	is a D-amino acid;
L	is a L-amino acid;
a	is 0 – 3;
l, m and n	are independently from each other 1 or 2;
x and y	are independently from each other 0, 1 or 2;

in particular wherein the transporter construct comprises at least one D-/L-pattern according to one of the following subformulas (Ia) to (If):

(Ia): $D_lLLL_xD_m$;

(Ib): $D_lLLL_xD_mLLL_yD_n$;

(Ic): $D_lLLL_xD_mLLL_yD_nLLL_yD_n$;

(Id): $D_lLLL_xD_mLLL_yD_nLLL_yD_nLLL_yD_n$,

(Ie): $DLLLD(LLLD)_a$, or

(If): $DLLLDLLLD$, and

wherein the D-/L-pattern according to generic formula (I) or according to any of subformulas (Ia), (Ib), (Ic), (Id), (Ie), or (If), is applied to one of the following sequences:

SEQUENCE/PEPTIDE NAME	SEQ ID NO	AA	SEQUENCE
TAT (1-86)	8	86	MEPVDPRLEP WKHPGSQPKT ACTNCYCKKC CFHCQVCFIT KALGISYGRK KRRQRRRPPQ GSQTHQVSLS KQPTSQSRGD PTGPKE
TAT (37-72)	9	36	CFITKALGIS YGRKKRRQRR RPPQGSQTHQ VSLSKQ
TAT (37-58)	10	22	CFITKALGIS YGRKKRRQRR RP
TAT (38-58)GGC	11	24	FITKALGISY GRKKRRQRRR PGGC
TAT CGG(47-58)	12	15	CGGYGRKKRR QRRRP
TAT (47-58)GGC	13	15	YGRKKRRQRR RPGGC
TAT (1-72) Mut Cys/Ala 72	14	56	MEPVDPRLEP WKHPGSQPKT AFITKALGIS YGRKKRRQRR RPPQGSQTHQ VSLSKQ
L-generic-TAT	15	17	XXXXRKKRRQRRRXXXX (NH_2- XXXXRKKRRQRRRXXXX -COOH)
L-generic-TAT (s)	16	11	NH_2-X_n^b-RKKRRQRRR-X_n^b-COOH

L-TAT (s1a)	17	10	GRKKRRQRRR (NH_2-GRKKRRQRRR-COOH)
L-TAT (s1b)	18	9	RKKRRQRRR (NH_2-GRKKRRQRRR-COOH)
L-TAT (s1c)	19	11	YDRKKRRQRRR
r_3-L-TAT	20	9	rKKRrQRRr
r_3-L-TATi	21	9	rRRQrRKKr
βA-r_3-L-TAT	22	9	βA-rKKRrQRRr
βA-r_3-L-TATi	23	9	βA-rRRQrRKKr
FITC-βA-r_3-L-TAT	24	9	FITC-βA-rKKRrQRRr
FITC-βA-r_3-L-TATi	25	9	FITC-βA-rRRQrRKKr
TAT(s2-1)	26	9	rAKRrQRRr
TAT(s2-2)	27	9	rKARrQRRr
TAT(s2-3)	28	9	rKKArQRRr
TAT(s2-4)	29	9	rKKRrARRr
TAT(s2-5)	30	9	rKKRrQARr
TAT(s2-6)	31	9	rKKRrQRAr
TAT(s2-7)	32	9	rDKRrQRRr
TAT(s2-8)	33	9	rKDRrQRRr
TAT(s2-9)	34	9	rKKDrQRRr
TAT(s2-10)	35	9	rKKRrDRRr
TAT(s2-11)	36	9	rKKRrQDRr
TAT(s2-12)	37	9	rKKRrQRDr
TAT(s2-13)	38	9	rEKRrQRRr
TAT(s2-14)	39	9	rKERrQRRr
TAT(s2-15)	40	9	rKKErQRRr
TAT(s2-16)	41	9	rKKRrERRr
TAT(s2-17)	42	9	rKKRrQERr
TAT(s2-18)	43	9	rKKRrQREr
TAT(s2-19)	44	9	rFKRrQRRr
TAT(s2-20)	45	9	rKFRrQRRr
TAT(s2-21)	46	9	rKKFrQRRr
TAT(s2-22)	47	9	rKKRrFRRr
TAT(s2-23)	48	9	rKKRrQFRr
TAT(s2-24)	49	9	rKKRrQRFr
TAT(s2-25)	50	9	rRKRrQRRr
TAT(s2-26)	51	9	rKRRrQRRr
TAT(s2-27)	52	9	rKKKrQRRr
TAT(s2-28)	53	9	rKKRrRRRr
TAT(s2-29)	54	9	rKKRrQKRr
TAT(s2-30)	55	9	rKKRrQRKr
TAT(s2-31)	56	9	rHKRrQRRr
TAT(s2-32)	57	9	rKHRrQRRr
TAT(s2-33)	58	9	rKKHrQRRr
TAT(s2-34)	59	9	rKKRrHRRr
TAT(s2-35)	60	9	rKKRrQHRr
TAT(s2-36)	61	9	rKKRrQRHr
TAT(s2-37)	62	9	rIKRrQRRr
TAT(s2-38)	63	9	rKIRrQRRr
TAT(s2-39)	64	9	rKKIrQRRr
TAT(s2-40)	65	9	rKKRrIRRr
TAT(s2-41)	66	9	rKKRrQIRr
TAT(s2-42)	67	9	rKKRrQRIr
TAT(s2-43)	68	9	rLKRrQRRr
TAT(s2-44)	69	9	rKLRrQRRr
TAT(s2-45)	70	9	rKKLrQRRr
TAT(s2-46)	71	9	rKKRrLRRr
TAT(s2-47)	72	9	rKKRrQLRr
TAT(s2-48)	73	9	rKKRrQRLr
TAT(s2-49)	74	9	rMKRrQRRr

TAT(s2-50)	75	9	rKMRrQRRr
TAT(s2-51)	76	9	rKKMrQRRr
TAT(s2-52)	77	9	rKKRrMRRr
TAT(s2-53)	78	9	rKKRrQMRr
TAT(s2-54)	79	9	rKKRrQRMr
TAT(s2-55)	80	9	rNKRrQRRr
TAT(s2-56)	81	9	rKNRrQRRr
TAT(s2-57)	82	9	rKKNrQRRr
TAT(s2-58)	83	9	rKKRrNRRr
TAT(s2-59)	84	9	rKKRrQNRr
TAT(s2-60)	85	9	rKKRrQRNr
TAT(s2-61)	86	9	rQKRrQRRr
TAT(s2-62)	87	9	rKQRrQRRr
TAT(s2-63)	88	9	rKKQrQRRr
TAT(s2-64)	89	9	rKKRrKRRr
TAT(s2-65)	90	9	rKKRrQQRr
TAT(s2-66)	91	9	rKKRrQRQr
TAT(s2-67)	92	9	rSKRrQRRr
TAT(s2-68)	93	9	rKSRrQRRr
TAT(s2-69)	94	9	rKKSrQRRr
TAT(s2-70)	95	9	rKKRrSRRr
TAT(s2-71)	96	9	rKKRrQSRr
TAT(s2-72)	97	9	rKKRrQRSr
TAT(s2-73)	98	9	rTKRrQRRr
TAT(s2-74)	99	9	rKTRrQRRr
TAT(s2-75)	100	9	rKKTrQRRr
TAT(s2-76)	101	9	rKKRrTRRr
TAT(s2-77)	102	9	rKKRrQTRr
TAT(s2-78)	103	9	rKKRrQRTr
TAT(s2-79)	104	9	rVKRrQRRr
TAT(s2-80)	105	9	rKVRrQRRr
TAT(s2-81)	106	9	rKKVrQRRr
TAT(s2-82)	107	9	rKKRrVRRr
TAT(s2-83)	108	9	rKKRrQVRr
TAT(s2-84)	109	9	rKKRrQRVr
TAT(s2-85)	110	9	rWKRrQRRr
TAT(s2-86)	111	9	rKWRrQRRr
TAT(s2-87)	112	9	rKKWrQRRr
TAT(s2-88)	113	9	rKKRrWRRr
TAT(s2-89)	114	9	rKKRrQWRr
TAT(s2-90)	115	9	rKKRrQRWr
TAT(s2-91)	116	9	rYKRrQRRr
TAT(s2-92)	117	9	rKYRrQRRr
TAT(s2-93)	118	9	rKKYrQRRr
TAT(s2-94)	119	9	rKKRrYRRr
TAT(s2-95)	120	9	rKKRrQYRr
TAT(s2-96)	121	9	rKKRrQRYr
r_3R_6	122	9	rRRRrRRRr
L-R_9	123	9	RRRRRRRRR
L-R_8	124	8	RRRRRRRR
L-R_7	125	7	RRRRRRR
L-R_6	126	6	RRRRRR
L-R_5	127	5	RRRRR
PTD-4	128	11	YARAAARQARA
PTD-4 (variant 1)	129	11	WARAAARQARA
PTD-4 (variant 2)	130	11	WARAQRAAARA
L-P1 Penetratin	131	16	RQVKVWFQNRRMKWKK
D-P1 Penetratin	132	16	KKWKMRRNQFWVKVQR
JNKI, bestfit	133	17	WKRAAARKARAMSLNLF
JNKI, bestfit (variant 1)	134	17	WKRAAARAARAMSLNLF
MDCK transcytose	135	9	RYRGDLGRR

sequence			
YKGL	136	4	YKGL
r_3 (generic)	252	9	rXXXrXXXr

or a reverse sequence thereof, or a variant or fragment of these sequences, wherein a variant or fragment of these sequences retains the function to provide for translocation across biological membranes and consists of a peptide sequence having at least 80% sequence identity over the whole length to the respective native sequence.

2. Transporter construct according to claim 1, wherein the transporter construct comprises at least one sequence according to rXXXrXXXr, wherein:

r represents an D-enatiomeric arginine;

X is any L-amino acid;

and wherein each X may be selected individually and independently of any other X within rXXXrXXXr, in particular, wherein at least 4 out of said 6 X L-amino acids are individually selected from the group of L amino acids consisting of K or R.

3. Transporter construct according to any of claims 1 to 2, wherein the transporter construct comprises a sequence selected from the group of sequences:

SEQUENCE/PEPTIDE NAME	SEQ ID NO	AA	SEQUENCE
r_3-L-TAT	20	9	rKKRrQRRr
r_3-L-TATi	21	9	rRRQrRKKr
βA-r_3-L-TAT	22	9	βA-rKKRrQRRr
βA-r_3-L-TATi	23	9	βA-rRRQrRKKr
FITC-βA-r_3-L-TAT	24	9	FITC-βA-rKKRrQRRr
FITC-βA-r_3-L-TATi	25	9	FITC-βA-rRRQrRKKr
TAT(s2-1)	26	9	rAKRrQRRr
TAT(s2-2)	27	9	rKARrQRRr
TAT(s2-3)	28	9	rKKArQRRr
TAT(s2-4)	29	9	rKKRrARRr
TAT(s2-5)	30	9	rKKRrQARr
TAT(s2-6)	31	9	rKKRrQRAr
TAT(s2-7)	32	9	rDKRrQRRr
TAT(s2-8)	33	9	rKDRrQRRr
TAT(s2-9)	34	9	rKKDrQRRr
TAT(s2-10)	35	9	rKKRrDRRr
TAT(s2-11)	36	9	rKKRrQDRr
TAT(s2-12)	37	9	rKKRrQRDr
TAT(s2-13)	38	9	rEKRrQRRr
TAT(s2-14)	39	9	rKERrQRRr
TAT(s2-15)	40	9	rKKErQRRr
TAT(s2-16)	41	9	rKKRrERRr
TAT(s2-17)	42	9	rKKRrQERr
TAT(s2-18)	43	9	rKKRrQREr
TAT(s2-19)	44	9	rFKRrQRRr
TAT(s2-20)	45	9	rKFRrQRRr
TAT(s2-21)	46	9	rKKFrQRRr

TAT(s2-22)	47	9	rKKRrFRRr
TAT(s2-23)	48	9	rKKRrQFRr
TAT(s2-24)	49	9	rKKRrQRFr
TAT(s2-25)	50	9	rRKRrQRRr
TAT(s2-26)	51	9	rKRRrQRRr
TAT(s2-27)	52	9	rKKKrQRRr
TAT(s2-28)	53	9	rKKRrRRRr
TAT(s2-29)	54	9	rKKRrQKRr
TAT(s2-30)	55	9	rKKRrQRKr
TAT(s2-31)	56	9	rHKRrQRRr
TAT(s2-32)	57	9	rKHRrQRRr
TAT(s2-33)	58	9	rKKHrQRRr
TAT(s2-34)	59	9	rKKRrHRRr
TAT(s2-35)	60	9	rKKRrQHRr
TAT(s2-36)	61	9	rKKRrQRHr
TAT(s2-37)	62	9	rIKRrQRRr
TAT(s2-38)	63	9	rKIRrQRRr
TAT(s2-39)	64	9	rKKIrQRRr
TAT(s2-40)	65	9	rKKRrIRRr
TAT(s2-41)	66	9	rKKRrQIRr
TAT(s2-42)	67	9	rKKRrQRIr
TAT(s2-43)	68	9	rLKRrQRRr
TAT(s2-44)	69	9	rKLRrQRRr
TAT(s2-45)	70	9	rKKLrQRRr
TAT(s2-46)	71	9	rKKRrLRRr
TAT(s2-47)	72	9	rKKRrQLRr
TAT(s2-48)	73	9	rKKRrQRLr
TAT(s2-49)	74	9	rMKRrQRRr
TAT(s2-50)	75	9	rKMRrQRRr
TAT(s2-51)	76	9	rKKMrQRRr
TAT(s2-52)	77	9	rKKRrMRRr
TAT(s2-53)	78	9	rKKRrQMRr
TAT(s2-54)	79	9	rKKRrQRMr
TAT(s2-55)	80	9	rNKRrQRRr
TAT(s2-56)	81	9	rKNRrQRRr
TAT(s2-57)	82	9	rKKNrQRRr
TAT(s2-58)	83	9	rKKRrNRRr
TAT(s2-59)	84	9	rKKRrQNRr
TAT(s2-60)	85	9	rKKRrQRNr
TAT(s2-61)	86	9	rQKRrQRRr
TAT(s2-62)	87	9	rKQRrQRRr
TAT(s2-63)	88	9	rKKQrQRRr
TAT(s2-64)	89	9	rKKRrKRRr
TAT(s2-65)	90	9	rKKRrQQRr
TAT(s2-66)	91	9	rKKRrQRQr
TAT(s2-67)	92	9	rSKRrQRRr
TAT(s2-68)	93	9	rKSRrQRRr
TAT(s2-69)	94	9	rKKSrQRRr
TAT(s2-70)	95	9	rKKRrSRRr
TAT(s2-71)	96	9	rKKRrQSRr
TAT(s2-72)	97	9	rKKRrQRSr
TAT(s2-73)	98	9	rTKRrQRRr
TAT(s2-74)	99	9	rKTRrQRRr
TAT(s2-75)	100	9	rKKTrQRRr
TAT(s2-76)	101	9	rKKRrTRRr
TAT(s2-77)	102	9	rKKRrQTRr
TAT(s2-78)	103	9	rKKRrQRTr
TAT(s2-79)	104	9	rVKRrQRRr
TAT(s2-80)	105	9	rKVRrQRRr
TAT(s2-81)	106	9	rKKVrQRRr
TAT(s2-82)	107	9	rKKRrVRRr

TAT(s2-83)	108	9	rKKRrQVRr
TAT(s2-84)	109	9	rKKRrQRVr
TAT(s2-85)	110	9	rWKRrQRRr
TAT(s2-86)	111	9	rKWRrQRRr
TAT(s2-87)	112	9	rKKWrQRRr
TAT(s2-88)	113	9	rKKRrWRRr
TAT(s2-89)	114	9	rKKRrQWRr
TAT(s2-90)	115	9	rKKRrQRWr
TAT(s2-91)	116	9	rYKRrQRRr
TAT(s2-92)	117	9	rKYRrQRRr
TAT(s2-93)	118	9	rKKYrQRRr
TAT(s2-94)	119	9	rKKRrYRRr
TAT(s2-95)	120	9	rKKRrQYRr
TAT(s2-96)	121	9	rKKRrQRYr
r_3R_6	122	9	rRRRrRRRr

or a variant or fragment of these sequences, wherein a variant or fragment of these sequences retains the function to provide for translocation across biological membranes and consists of a peptide sequence having at least 80% sequence identity over the whole length to the respective native trafficking sequence.

4. Transporter construct according to any of claims 1 to 3, wherein the transporter construct comprises the subformula (If) **DLLLDLLLD** and wherein the subformula (If) is applied to a trafficking sequence derived from HIV-1 TAT protein having a Tyrosine (Y) at position 2 of the TAT derived sequence, the sequence preferably selected from sequence rYKRrQRRr (TAT(s2-91)).

5. Transporter construct according to claim 3, wherein the transporter construct comprises a sequence selected from the group consisting of rKKRrQRRr (r_3-L-TAT) and rRRQrRKKr (r_3-L-TATi).

6. Transporter construct according to any of claims 1 to 5, wherein the generic formula (I) or any of subformulas (Ia), (Ib), (Ic), (Id), (Ie), or (If), is applied to a variant or a fragment of any of the trafficking sequences listed in claims 1 to 4, having at least 80% or 85%, preferably at least 90%, more preferably at least 95% and most preferably at least 99% over the whole length of any of the trafficking sequences listed in claims 1 to 5.

7. Transporter cargo conjugate molecule, comprising

a) a component (A), wherein component (A) comprises the transporter construct according to any of claims 1 to 6; and

b) a component (B), comprising an effector molecule, in particular wherein the effector molecule is selected from therapeutically active proteins and peptides, protein kinase inhibitors, inhibitors of the protein kinase c-Jun amino terminal kinase, antigens, antibodies,

apoptotic factors, proteases implicated in pathological states, preferably peptidic protease inhibitors, BH3-domains or BH3-only proteins, nucleic acids encoding these proteins, siRNAs, antisense RNAs, cytotoxic agents, and small organic compounds including protease inhibitors.

8. Transporter cargo conjugate molecule according to claim 7, furthermore comprising at least one additional component (C), (D) and/or (E) different to component (B), wherein the at least one optional additional component (C), (D) and/or (E) is selected independently from each other from different effector molecules as defined for component (B).

9. Transporter cargo conjugate molecule according to any of claims 7 to 8, wherein:

a) components (A) and (B), and optional components (C), (D) and/or (E) are covalently linked with each other, and/or

b) wherein the at least one additional component (C), (D) and/or (E) is selected from a signal sequence or localisation sequence, which directs the inventive transporter cargo conjugate molecule to a particular intracellular target localization or to a particular cell type, and/or

c) wherein component (B) and/or the at least one additional components (C), (D) and/or (E) is (are) a protein or peptide sequence and is (are) composed of L-amino acids, D-amino acids or a mixture of both, and/or

d) wherein component (A) is positioned at the C-terminal end of the transporter cargo conjugate molecule, provided that component (B) is a protein or peptide sequence.

10. Transporter cargo conjugate molecule according to any of claims 7 to 9 for use as a medicament.

11. Pharmaceutical composition comprising a transporter cargo conjugate molecule according to any of claims 7 to 10 and optionally a pharmaceutically acceptable carrier and/or vehicle.

12. Use of a transporter construct according to any of claims 1 to 6 for the preparation of a transporter cargo conjugate molecule, in particular wherein the transporter cargo conjugate molecule is as defined according to any of claims 7 to 9.

13. Use of a transporter construct according to any of claims 1 to 6 or a transporter cargo conjugate molecule as defined according to any of claims 7 to 9 for preparation of a medicament for the transport of a cargo molecule into cells or tissue of a patient to be treated, in particular wherein the cargo is as defined according to any of claims 7 to 9.

14. Use according to claim 13 for the transport of a cargo molecule into white blood cells and/or neuronal cells, in particular of a patient to be treated.

15. Use of a transporter cargo conjugate molecule according to any of claims 7 to 9 for the preparation of a medicament for the prophylaxis, treatment and/or amelioration of cancer or tumor diseases, including diseases caused by defective apoptosis, inflammatory diseases, infectious diseases, viral (infectious) diseases, diseases strongly related to JNK signalling, autoimmune disorders or diseases, cardiovascular diseases, neuronal or neurodegenerative diseases, diseases of the liver, diseases of the spine, diseases of the uterus, major depressive disorders, non-chronic or chronic inflammatory digestive diseases, hearing loss, diseases of the inner ear, or for use in tissue transplantation.