

## Claims

1. A polypeptide having the structure of formula (I)

$$A-L_1-B-L_2-C \quad (I)$$

wherein

A is an N-terminal amino acid stretch of an adenovirus penton base protein c:

B is an amino acid stretch of an adenovirus penton base protein;

C is a C-terminal amino acid stretch of an adenovirus penton base;

wherein B is an amino acid stretch located between A and C in the sequence of said adenovirus penton base;

wherein A, B and C form the jellyroll fold domain of said adenovirus penton base protein;

L<sub>1</sub> and L<sub>2</sub> are independently from one another selected from the group consisting of an oligopeptide, a polypeptide, a protein, and a protein complex;

wherein said oligopeptide, polypeptide, protein and protein complex, respectively, are either essentially non-adenoviral or, if adenoviral, A-L<sub>1</sub>-B-L<sub>2</sub>-C form a penton base chimera wherein A, B and C form the jellyroll fold domain of an adenovirus penton base of one adenovirus subtype and L<sub>1</sub> and L<sub>2</sub> form the crown domain of an adenovirus penton base of an adenovirus subtype different from the adenovirus subtype of the jellyroll fold domain.

2. The polypeptide of claim 1, wherein amino acid stretch A comprises beta sheets 1, 2 and 3 of the jellyroll fold domain of said adenovirus.

3. The polypeptide of claim 1 or 2, wherein amino acid stretch B comprises beta sheets 4 and 5 of the jellyroll fold domain of said adenovirus.

4. The polypeptide according to any one of the preceding claims, wherein amino acid stretch C comprises beta sheets 6, 7 and 8 of the jellyroll fold domain of adenovirus.

5. The polypeptide according to any one of the preceding claims, wherein amino acid stretches A, B, and C have an amino acid sequence each independently selected from the group consisting of penton bases of human adenovirus serotype 2, human adenovirus serotype 3, human adenovirus serotype 4, human adenovirus serotype 5, human adenovirus serotype 7, human adenovirus serotype 11, human adenovirus

serotype 12, human adenovirus serotype 17, human adenovirus serotype 25, human adenovirus serotype 35, human adenovirus serotype 37, human adenovirus serotype 41, gorilla adenovirus, chimpanzee adenovirus, simian adenovirus serotype 18, simian adenovirus serotype 20, simian adenovirus serotype 49, rhesus adenovirus serotype 51, rhesus adenovirus serotype 52, and rhesus adenovirus serotype 53.

6. The polypeptide of claim 5, wherein amino acid stretch A has the following consensus sequence (SEQ ID NO: 21):

(U)<sub>1-47</sub> PTX<sub>1</sub>GRNSIRY SX<sub>2</sub>X<sub>3</sub>X<sub>4</sub>PX<sub>5</sub>X<sub>6</sub>DTT X<sub>7</sub>X<sub>3</sub>YLVDNKSA DIASLNYQND  
HSNFX<sub>5</sub>TTVX<sub>9</sub>Q NNDX<sub>10</sub>X<sub>11</sub>PX<sub>12</sub>EAX<sub>13</sub> TQTINX<sub>14</sub>DX<sub>15</sub>RS RWGX<sub>16</sub>X<sub>17</sub>LKTIX<sub>18</sub>  
X<sub>19</sub>TZ<sub>1</sub>Z<sub>2</sub>Z<sub>3</sub>Z<sub>4</sub>Z<sub>5</sub>Z<sub>6</sub>Z<sub>7</sub>Z<sub>8</sub> Z<sub>9</sub>Z<sub>10</sub>Z<sub>11</sub>Z<sub>12</sub>Z<sub>13</sub>Z<sub>14</sub>Z<sub>15</sub>

wherein: amino acid stretch A ends on the C-terminal side before Z<sub>1</sub> at residue T or at an amino acid from Z<sub>1</sub> to Z<sub>15</sub>

U is any or no amino acid

X<sub>1</sub> is E or G

X<sub>2</sub> is E or S

X<sub>3</sub> is L or V

X<sub>4</sub> is A or S

X<sub>5</sub> is L or Q

X<sub>6</sub> is Y or E

X<sub>7</sub> is R or K

X<sub>8</sub> is V or L

X<sub>9</sub> is V or I

X<sub>10</sub> is F or Y

X<sub>11</sub> is T or S

X<sub>12</sub> is A or T or I or G

X<sub>13</sub> is S or G

X<sub>14</sub> is F or L

X<sub>15</sub> is E or D

X<sub>16</sub> is A or G

X<sub>17</sub> is D or Q

X<sub>18</sub> is L or M

X<sub>19</sub> is H or R

Z<sub>1</sub> , if present, is N

Z<sub>2</sub> , if present, is M

- 5                   Z<sub>3</sub>       , if present, is P  
                     Z<sub>4</sub>       , if present, is N  
                     Z<sub>5</sub>       , if present, is V or I  
                     Z<sub>6</sub>       , if present, is N  
                     Z<sub>7</sub>       , if present, is E or D  
                     Z<sub>8</sub>       , if present, is Y or F  
                     Z<sub>9</sub>       , if present, is M  
                     Z<sub>10</sub>      , if present, is F or S or Y  
 10                  Z<sub>11</sub>      , if present, is T or S  
                     Z<sub>12</sub>      , if present, is S or N  
                     Z<sub>13</sub>      , if present, is K  
                     Z<sub>14</sub>      , if present, is F  
                     Z<sub>16</sub>      , if present, is K
- 15    7.       The polypeptide of claim 6, wherein amino acid stretch A is selected from the group consisting of the following sequences:  
               from an amino acid selected from positions 1 to 48, to an amino acid selected from positions 129 to 144 of UniProt Acc. No. Q2Y0H9;  
               from an amino acid selected from positions 1 to 48, to an amino acid selected from  
 20       positions 129 to 144 of UniProt Acc. No. P03276;  
               from an amino acid selected from positions 1 to 44, to an amino acid selected from positions 125 to 140 of UniProt Acc. No. Q2KSF3;  
               from an amino acid selected from positions 1 to 48, to an amino acid selected from positions 129 to 144 of UniProt Acc. No. P12538;  
 25       from an amino acid selected from positions 1 to 48, to an amino acid selected from positions 129 to 144 of UniProt Acc. No. Q9JFT6;  
               from an amino acid selected from positions 1 to 48, to an amino acid selected from positions 129 to 144 of UniProt Acc. No. D2DM93;  
               from an amino acid selected from positions 1 to 38, to an amino acid selected from  
 30       positions 119 to 134 of UniProt Acc. No. P36716;  
               from an amino acid selected from positions 1 to 35, to an amino acid selected from positions 116 to 131 of UniProt Acc. No. F1DT65;  
               from an amino acid selected from positions 1 to 43, to an amino acid selected from positions 124 to 139 of UniProt Acc. No. M0QUK0;  
 35       from an amino acid selected from positions 1 to 49, to an amino acid selected from positions 130 to 145 of UniProt Acc. No. Q7T941;

from an amino acid selected from positions 1 to 35, to an amino acid selected from positions 116 to 131 of UniProt Acc. No. Q912J1;

from an amino acid selected from positions 1 to 46, to an amino acid selected from positions 127 to 142 of UniProt Acc. No. F8WQN4;

5 from an amino acid selected from positions 1 to 49, to an amino acid selected from positions 130 to 145 of UniProt Acc. No. E5L3Q9;

from an amino acid selected from positions 1 to 44, to an amino acid selected from positions 125 to 140 of UniProt Acc. No. G9G849;

10 from an amino acid selected from positions 1 to 46, to an amino acid selected from positions 127 to 142 of UniProt Acc. No. H8PFZ9;

from an amino acid selected from positions 1 to 45, to an amino acid selected from positions 126 to 141 of UniProt Acc. No. F6KSU4;

from an amino acid selected from positions 1 to 46, to an amino acid selected from positions 127 to 142 of UniProt Acc. No. F2WTK5;

15 from an amino acid selected from positions 1 to 43, to an amino acid selected from positions 124 to 139 of UniProt Acc. No. A0A0A1EWW1;

from an amino acid selected from positions 1 to 43, to an amino acid selected from positions 124 to 139 of UniProt Acc. No. A0A0A1EWX7; and

20 from an amino acid selected from positions 1 to 44, to an amino acid selected from positions 125 to 140 of UniProt Acc. No. A0A0A1EWZ7.

8. The polypeptide according to any one of claims 5 to 7, wherein amino acid stretch B of above general formula (I) has the following sequence (SEQ ID NO: 22):

25  $Z_{17}Z_{18}Z_{19}Z_{20}Z_{21}Z_{22}Z_{23}Z_{24}Z_{25}Z_{26} Z_{27}QVYWSLPDX_{20} MX_{21}DPVTFRST$   
 $X_{22}QX_{23}X_{24}NX_{25}PVVGX_{26} ELZ_{28}Z_{29}Z_{30}$

wherein: amino acid stretch B begins on the N-terminal side at an amino acid from  $Z_{17}$  to  $Z_{27}$  or at amino acid Q after  $Z_{27}$ ;

30 amino acid stretch B ends on the C-terminal side before  $Z_{28}$  at amino acid L or at an amino acid from  $Z_{28}$  to  $Z_{30}$ ;

$Z_{17}$  , if present, is L or S

$Z_{18}$  , if present, is T or P or C

$Z_{19}$  , if present, is T or P

35  $Z_{20}$  , if present, is P or S or A or R

$Z_{21}$  , if present, is N or D

$Z_{22}$  , if present, is G or V

$Z_{23}$  , if present, is H or T

5                   Z<sub>24</sub>       , if present, is C  
                     Z<sub>25</sub>       , if present, is G  
                     Z<sub>26</sub>       , if present, is A or V or S  
                     Z<sub>27</sub>       , if present, is E or Q  
                     X<sub>20</sub>       is L or M  
                     X<sub>21</sub>       is Q or K  
                     X<sub>22</sub>       is Q or R or S  
                     X<sub>23</sub>       is V or I  
 10                  X<sub>24</sub>       is S or N  
                     X<sub>25</sub>       is Y or F  
                     X<sub>26</sub>       is A or V  
                     Z<sub>28</sub>       , if present, is M or L  
                     Z<sub>29</sub>       , if present, is P  
                     Z<sub>30</sub>       , if present, is V or F

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9. The polypeptide of claim 8, wherein amino acid stretch B is selected from the group consisting of the following sequences:

from an amino acid selected from positions 398 to 409, to an amino acid selected  
 from positions 440 to 443 of UniProt Acc. No. Q2Y0H9;  
 20   from an amino acid selected from positions 425 to 436, to an amino acid selected  
      from positions 467 to 470 of UniProt Acc. No. P03276;  
      from an amino acid selected from positions 379 to 390, to an amino acid selected  
      from positions 421 to 444 of UniProt Acc. No. Q2KSF3;  
      from an amino acid selected from positions 425 to 436, to an amino acid selected  
 25   from positions 467 to 470 of UniProt Acc. No. P12538;  
      from an amino acid selected from positions 398 to 409, to an amino acid selected  
      from positions 440 to 443 of UniProt Acc. No. Q9JFT6;  
      from an amino acid selected from positions 415 to 426, to an amino acid selected  
      from positions 457 to 460 of UniProt Acc. No. D2DM93;  
 30   from an amino acid selected from positions 351 to 362, to an amino acid selected  
      from positions 393 to 397 of UniProt Acc. No. P36716;  
      from an amino acid selected from positions 370 to 381, to an amino acid selected  
      from positions 413 to 416 of UniProt Acc. No. F1DT65;  
      from an amino acid selected from positions 388 to 399, to an amino acid selected  
 35   from positions 440 to 443 of UniProt Acc. No. M0QUK0;  
      from an amino acid selected from positions 445 to 456, to an amino acid selected  
      from positions 497 to 500 of UniProt Acc. No. Q7T941;

from an amino acid selected from positions 372 to 383, to an amino acid selected from positions 414 to 417 of UniProt Acc. No. Q912J1;

from an amino acid selected from positions 362 to 373, to an amino acid selected from positions 404 to 407 of [Please insert UniProt Acc. No. F8WQN4;

5 from an amino acid selected from positions 416 to 427, to an amino acid selected from positions 458 to 461 of UniProt Acc. No. E5L3Q9;

from an amino acid selected from positions 372 to 383, to an amino acid selected from positions 420 to 423 of UniProt Acc. No. G9G849;

10 from an amino acid selected from positions 353 to 364, to an amino acid selected from positions 395 to 398 of UniProt Acc. No. H8PFZ9;

from an amino acid selected from positions 358 to 369, to an amino acid selected from positions 400 to 403 of UniProt Acc. No. F6KSU4;

from an amino acid selected from positions 356 to 367, to an amino acid selected from positions 398 to 401 of UniProt Acc. No. F2WTK5;

15 from an amino acid selected from positions 352 to 363, to an amino acid selected from positions 394 to 397 of UniProt Acc. No. A0A0A1EWW1;

from an amino acid selected from positions 350 to 361, to an amino acid selected from positions 392 to 395 of UniProt Acc. No. A0A0A1EWX7; and

20 from an amino acid selected from positions 351 to 362, to an amino acid selected from positions 393 to 396 of UniProt Acc. No. A0A0A1EWZ7.

10. The polypeptide according to any one of claims 5 to 9, wherein amino acid stretch C of above general formula (I) has the following sequence (SEQ ID NO: 23):

25 Z<sub>31</sub>Z<sub>32</sub>Z<sub>33</sub>ALTDHGT LPLRSSIX<sub>27</sub>GV QRVTX<sub>28</sub>TDARR RTCPYVYKA  
LGIVX<sub>30</sub>PX<sub>31</sub>VLS SRTF

wherein: amino acid stretch C begins on the N-terminal side at an amino acid from Z<sub>31</sub> to Z<sub>33</sub> or at amino acid A after Z<sub>33</sub>;

30 Z<sub>31</sub> , if present, is N

Z<sub>32</sub> , if present, is V

Z<sub>33</sub> , if present, is P

X<sub>27</sub> is R or S or G

X<sub>28</sub> is V or I

35 X<sub>29</sub> is Y or H

X<sub>30</sub> is A or S

X<sub>31</sub> is R or K

11. The polypeptide of claim 10, wherein the amino acid stretch C is selected from the group consisting of the following sequences:

from an amino acid selected from positions 492 to 495, to the C-terminal amino acid of UniProt Acc. No. Q2Y0H9;

from an amino acid selected from positions 519 to 522, to the C-terminal amino acid of UniProt Acc. No. P03276;

from an amino acid selected from positions 466 to 469, to the C-terminal amino acid of UniProt Acc. No. Q2KSF3;

from an amino acid selected from positions 492 to 495, to the C-terminal amino acid of UniProt Acc. No. P12538;

from an amino acid selected from positions 465 to 468, to the C-terminal amino acid of UniProt Acc. No. Q9JFT6;

from an amino acid selected from positions 482 to 485, to the C-terminal amino acid of UniProt Acc. No. D2DM93;

from an amino acid selected from positions 419 to 422, to the C-terminal amino acid of UniProt Acc. No. P36716;

from an amino acid selected from positions 438 to 441, to the C-terminal amino acid of [Please insert UniProt Acc. No. F1DT65;

from an amino acid selected from positions 455 to 458, to the C-terminal amino acid of UniProt Acc. No. M0QUK0;

from an amino acid selected from positions 522 to 525, to the C-terminal amino acid of UniProt Acc. No. Q7T941;

from an amino acid selected from positions 439 to 442, to the C-terminal amino acid of UniProt Acc. No. Q912J1;

from an amino acid selected from positions 429 to 432, to the C-terminal amino acid of UniProt Acc. No. F8WQN4;

from an amino acid selected from positions 483 to 486, to the C-terminal amino acid of UniProt Acc. No. E5L3Q9;

from an amino acid selected from positions 445 to 448, to the C-terminal amino acid of UniProt Acc. No. G9G849;

from an amino acid selected from positions 420 to 423, to the C-terminal amino acid of UniProt Acc. No. H8PFZ9;

from an amino acid selected from positions 425 to 428, to the C-terminal amino acid of UniProt Acc. No. F6KSU4;

from an amino acid selected from positions 423 to 426, to the C-terminal amino acid of UniProt Acc. No. F2WTK5;

from an amino acid selected from positions 419 to 422, to the C-terminal amino acid of UniProt Acc. No. A0A0A1EWW1;

from an amino acid selected from positions 417 to 420, to the C-terminal amino acid of UniProt Acc. No. A0A0A1EWX7; and

from an amino acid selected from positions 418 to 421, to the C-terminal amino acid of UniProt Acc. No. A0A0A1EWZ7.

12. The polypeptide according to any one of the preceding claims wherein amino acid stretch A has the sequence of positions 1 to 132 of UniProt Acc. No. Q2Y0H9, amino acid stretch B has the sequence of positions 407 to 442 of UniProt Acc. No. Q2Y0H9, and amino acid stretch C has the sequence of positions 493 to 544 of UniProt Acc. No. Q2Y0H9.

13. The polypeptide according to any one of the preceding claims wherein  $L_1$  and/or  $L_2$  is an oligopeptide having a sequence of 4 to 40 amino acids being selected from amino acids G and S.

14. The polypeptide of claim 13 wherein  $L_1$  and/or  $L_2$  is independently selected from the group consisting of GGGS (SEQ ID NO: 24) and GGSGGS (SEQ ID NO: 25).

15. The polypeptide according to any one of claims 1 to 12 wherein  $L_1$  is an adenoviral sequence comprising an RGD loop of an adenovirus penton base having a different serotype compared to the serotype of the adenovirus(es) from which said amino acid stretches A, B and C are derived and/or  $L_2$  is an adenoviral sequence comprising a variable loop of an adenovirus penton base having a different serotype compared to the serotype of the adenovirus from which said amino acid stretches A, B and C are derived.

16. The polypeptide of claim 15 wherein  $L_1$  is a big fragment of a crown domain of an adenovirus penton base having a different serotype compared to the serotype of the adenovirus(es) from which said amino acid stretches A, B and C are derived and  $L_2$  is a small fragment of a crown domain of an adenovirus penton base having a different serotype compared to the serotype of the adenovirus(es) from which said amino acid stretches A, B and C are derived.

17. The polypeptide of claim 16 wherein the big and the small fragment are derived from a penton base protein of the same adenovirus.

18. The polypeptide of claim 16 wherein the big and the small fragment are derived from a penton base protein of different adenoviruses.
19. The polypeptide according to any one of claims 15 to 18 wherein one or more non-adenoviral sequences are inserted into the RGD loop and/or variable loop of the crown domain of the adenovirus penton base chimera.
20. The polypeptide according to any one of the preceding claims wherein L<sub>1</sub> and/or L<sub>2</sub> comprise an antigen.
21. The polypeptide of claim 20 wherein the antigen is selected from the group consisting of an antigen of an infectious agent and a tumour antigen.
22. The polypeptide according to any one of the preceding claims wherein a nucleic acid, a drug, label and/or binding partner of a biological binding pair is/are coupled to L<sub>1</sub> and/or L<sub>2</sub>.
23. A nucleic acid encoding the polypeptide according to any one of the preceding claims.
24. A nucleic acid comprising a sequence having the following general formula (II)
- $$5'-a-is_1-l_1-is_2-b-is_3-l_2-is_4-c-3' \quad (II)$$
- wherein
- a is a nucleotide sequence encoding A of general formula (I);
- b is a nucleotide sequence encoding B of general formula (I);
- c is a nucleotide sequence encoding C of general formula (I);
- l<sub>1</sub>, l<sub>2</sub> are each a nucleotide sequence; and
- is<sub>1</sub> to is<sub>4</sub> are each independently a nucleotide sequence comprising at least one insertion site.
25. The nucleic acid of claim 24 wherein is<sub>1</sub> to is<sub>4</sub> are selected from the group consisting of recognition sequences of restriction enzymes, and recognition sequences of homing endonucleases.
26. The nucleic acid of claim 25 wherein is<sub>1</sub> comprises an EcoRI site, is<sub>2</sub> comprises a RsrII site, is<sub>3</sub> comprises a SacI site, and is<sub>4</sub> comprises a XbaI site.

27. A vector comprising a nucleic acid according to any one of claims 23 to 26.
28. The vector of claim 27 comprising a nucleic claim according to any one of claims 23 to 26 within an expression cassette.
29. A recombinant host cell comprising the nucleic acid according to any one of claims 23 to 26 or the vector of claim 27 or 28.
30. A pentameric complex of the polypeptide according to any one of claims 1 to 22.
31. A virus-like particle (VLP) comprising 12 pentameric complexes of claim 30.
32. The polypeptide according to any one of claims 1 to 22, the nucleic acid of claim 23, the vector of claim 27 or 28, the host cell of claim 29, or the VLP of claim 31 for use as a medicament.
33. A pharmaceutical composition comprising the polypeptide according to any one of claims 1 to 22, the nucleic acid of claim 23, the vector of claim 27 or 28, the host cell of claim 29, or the VLP of claim 31 together with at least one pharmaceutically acceptable carrier, excipient and/or diluent.
34. A method for producing the polypeptide according to any one of claims 1 to 22 comprising the step of cultivating the recombinant host cell of claim 29, wherein the host cell comprises a vector of claim 28 which comprises a nucleic of claim 23, under conditions allowing the expression of said polypeptide.
35. A method for producing the VLP of claim 31 comprising the step of incubating a solution of the polypeptide according to any one of claims 1 to 22 under conditions allowing the assembly of the polypeptide into a VLP.
36. The polypeptide according to any one of claims 1 to 22, the nucleic acid of claim 23, the vector of claim 27 or 28, the host cell of claim 29, or the VLP of claim 31 for use in the treatment and/or prevention of an infectious disease, an immune disease, tumour or cancer.