Claims

1. An isolated engineered polypeptide comprising the amino acid stretches essentially corresponding to a first and a second fragment of the penton base protein of an adenovirus wherein the first fragment of the polypeptide is present between the first and second amino acid stretches forming the jellyroll fold domain in the full length penton base protein and wherein the second fragment of the polypeptide is present between the second and third fragments forming the jellyroll fold domain in the full length penton base protein, respectively, wherein the isolated engineered polypeptide lacks the amino acid stretches forming the jellyroll fold domain of the adenovirus penton base protein, wherein optionally the first and/or second fragments of the polypeptide contain(s) one or more heterologous modification(s).

2. The polypeptide of claim 1 having the structure of the following general formula (I):

N-A-L-B-C (I)

wherein

A represents an amino acid stretch corresponding to the N-terminal amino acid stretch of the adenovirus penton base protein present between the first and the second amino acid stretch forming the jellyroll fold domain of the adenovirus penton base protein;

B represents an amino acid stretch corresponding to the C-terminal amino acid stretch of the adenovirus penton base protein inserted between the second and the third amino acid stretch forming the jellyroll fold domain of the adenovirus penton base protein;

L represents a chemical group selected from the group consisting of an amino acid, an oligopeptide and a polypeptide;

N may or may not be present, and, if present, represents a chemical group consisting of an amino acid, an oligopeptide and a polypeptide;

C: may or may not be present, and, if present, represents a chemical group consisting of an amino acid, an oligopeptide and a polypeptide;

wherein, optionally, fragment A and/or B contain(s) one or more heterologous modifications.

3. The polypeptide according to any one of claims 2 wherein the fragment A comprises an amino acid sequence selected from the group consisting of the amino acid sequences according to the following table and amino acid sequences having an identity of at least 85 %, more preferred at least 90 %, even more preferred 95 %, particularly preferred at least 98 %, most preferred at least 99 %, with the respective amino acid sequence shown in the following table:

Sequence based on penton base protomer of	Sequence according to UniProt Acc. No.	SEQ ID NO:	N-terminal amino acid selected from positions	C-terminal amino acid selected from positions
hAd3	Q2Y0H9	1	130 to 137	399 to 405
hAd2	P03276	2	130 to 137	426 to 432
hAd4	Q2KSF3	3	126 to 133	380 to 386
hAd5	P12538	4	130 to 137	426 to 432
hAd7	Q9JFT6	5	130 to 137	399 to 405
hAd11	D2DM93	6	130 to 137	416 to 422
hAd12	P36716	7	120 to 127	352 to 358
hAd17	F1DT65	8	117 to 124	371 to 377
hAd25	M0QUK0	9	125 to 133	389 to 395
hAd35	Q7T941	10	131 to 138	446 to 452
hAd37	Q912J1	11	117 to 124	373 to 379
hAd41	F8WQN4	12	128 to 135	362 to 368
gorAd	E5L3Q9	13	131 to 138	417 to 423
ChimpAd	G9G849	14	126 to 133	373 to 379
sAd18	H8PFZ9	15	128 to 135	354 to 360
sAd20	F6KSU4	16	127 to 134	359 to 365
sAd49	F2WTK5	17	128 to 135	357 to 363
rhAd51	A0A0A1EWW1	18	125 to 132	353 to 359
rhAd52	A0A0A1EWX7	19	125 to 132	351 to 357
rhAd53	A0A0A1EWZ7	20	126 to 133	352 to 358

wherein, optionally, fragment A contains one or more heterologous modifications.

4. The polypeptide of claim 2 or 3 wherein the fragment B comprises an amino acid sequence selected from the group consisting of the amino acid sequences according to the following table and amino acid sequences having an identity of at least 85 %, more preferred at least 90 %, even more preferred 95 %, particularly preferred at

least 98 %, most preferred at least 99 %, with the respective amino acid sequence shown in the following table:

Sequence based on penton base protomer of	Sequence according to UniProt Acc. No.	SEQ ID NO:	N-terminal amino acid selected from positions	C-terminal amino acid selected from positions
hAd3	Q2Y0H9	1	441 to 444	491 to 494
hAd2	P03276	2	468 to 471	518 to 521
hAd4	Q2KSF3	3	422 to 445	465 to 468
hAd5	P12538	4	468 to 471	491 to 494
hAd7	Q9JFT6	5	441 to 444	464 to 467
hAd11	D2DM93	6	458 to 461	481 to 484
hAd12	P36716	7	394 to 398	418 to 421
hAd17	F1DT65	8	414 to 417	438 to 441
hAd25	M0QUK0	9	441 to 444	454 to 457
hAd35	Q7T941	10	498 to 501	521 to 524
hAd37	Q912J1	11	415 to 418	438 to 441
hAd41	F8WQN4	12	405 to 408	438 to 441
gorAd	E5L3Q9	13	459 to 462	482 to 485
ChimpAd	G9G849	14	421 to 424	444 to 457
sAd18	H8PFZ9	15	396 to 399	419 to 422
sAd20	F6KSU4	16	401 to 404	424 to 427
sAd49	F2WTK5	17	399 to 402	422 to 425
rhAd51	A0A0A1EWW1	18	395 to 398	418 to 421
rhAd52	A0A0A1EWX7	19	393 to 396	416 to 419
rhAd53	A0A0A1EWZ7	20	394 to 397	417 to 420

wherein, optionally, fragment B contains one or more heterologous modifications.

5. The polypeptide according to any one of claims 2 to 4 characterized in that fragment A and/or B contain(s) one or more heterologous modifications wherein said one or more heterologous modifications is/are contained in the following sites:

- the RGD loop region of fragment A; and/or
- the V-loop of fragment A; and/or
- the floor region having the sequence (from N- to C-terminal) X_1-X_2-X_3-X_4-X_5-X_6-D-X_7-X_8-X_9-S-Y-N-X_{10}-X_{11}-X_{12}-X_{13}-X_{14}-X_{15}-X_{16} (SEQ ID NO: 21) of fragment A, wherein

X_1 is I or L, and is preferably I;

X_2 is selected from the group consisting of K, Q and E, and is preferably Q;
X_3 is P or A, and is preferably P;
X_4 is selected from the group consisting of L, V and I, and is preferably L
X_5 is selected from the group consisting of T, E, A, K and L, and is preferably E;
X_6 is selected from the group consisting of E, K, T and Q, and is preferably K;
X_7 is selected from the group consisting of S, P and D, and is preferably S;
X_8 is selected from the group consisting of K, T and S, and is preferably K;
X_9 is selected from the group consisting of K, S, N, G and D, and is preferably S;
X_{10} is L or V, and is preferably V;
X_{11} is I or L, and is preferably I;
X_{12} is selected from the group consisting of S, E and P, and is preferably E;
X_{13} is no amino acid (i.e. not present) or is N, and is preferably no amino acid;
X_{14} is D or G, and is preferably D;
X_{15} is selected from the group consisting of S, K, Q and T, and is preferably K; and
X_{16} is selected from the group consisting of T, N, I, K and M, and is preferably I;
and/or
- the sequence (from N- to C-terminal) T-H-V-F-X_{17}-R-F-P (SEQ ID NO: 22) of fragment B wherein X_{17} is D or N, and is preferably N.

6. The polypeptide of claim 5 wherein the N-terminus of the RGD loop region of fragment A is defined by the following sequence (from N-terminal to C-terminal):
X_{18}-X_{19}-X_{20}-X_{21}-X_{22}-X_{23}-X_{24}-X_{25}-X_{26} (SEQ ID NO: 23) wherein
X_{18} is selected from the group consisting of D, E and N, and is preferably D;
X_{19} is selected from the group consisting of V, L, and I, and is preferably V;
X_{20} is any amino acid, preferably selected from the group consisting of A, D, E, K, S, and T, and is more preferably T;
X_{21} is any amino acid, preferably selected from the group consisting of A, D, E, and K, and is more preferably A;
X_{22} is selected from the group consisting of F, Y, and W, and is preferably Y;
X_{23} is selected from the group consisting of A, D, E, N, and Q, is preferably E or Q, and is more preferably E;
X_{24} is any amino acid, preferably selected from the group consisting of A, D, E, N, and K, and is more preferably E;
X_{25} is selected from the group consisting of S or T, and is preferably S; and
X_{26} is any amino acid and constitutes the N-terminal amino acid of the RGD loop region

7. The polypeptide of claim 5 or 6 wherein the C-terminus of the RGD loop region of fragment A is defined by the following sequence (from N-terminal to C-terminal):
X_{27}-X_{28}-X_{29}-X_{30}-X_{31}-X_{32}-X_{33}-X_{34} (SEQ ID NO: 24)
Wherein
X_{27} is any amino acid and constitutes the C-terminal amino acid of the second RGD loop;
X_{28} is selected from the group consisting of I, L and V, and is preferably I;
X_{29} is selected from the group consisting of D, E, K, N, Q, and V, is preferably Q or K, and is more preferably Q;
X_{30} is selected from the group consisting of C, G and P, and is preferably P;
X_{31} is selected from the group consisting of I, L and V, is preferably L or V and is more preferably L;
X_{32} is selected from the group consisting of D, E, S and T, is preferably E or T and is more preferably E;
X_{33} is selected from the group consisting of D, E, , S and T, is preferably E, or T, and is more preferably K; and
X_{34} is selected from the group consisting of D and E, and is preferably D;

8. The polypeptide according to any one of claims 5 to 7 wherein the N-terminus of the V loop of fragment A is defined by the following sequence (from N-terminal to C-terminal):
X_{35}-X_{36}-X_{37}-X_{38}-X_{39}-X_{40}-X_{41}-X_{42} (SEQ ID NO: 25)
wherein
X_{35} is selected from the group consisting of F, Y, and W, and is preferably F;
X_{36} is selected from the group consisting of H, K and R, and is preferably K;
X_{37} is selected from the group consisting of A, V, I, and L, and is preferably A;
X_{38} is selected from the group consisting of H, K, and R, and is preferably R;
X_{39} is selected from the group consisting of A, V, I, and L, and is preferably V;
X_{40} is selected from the group consisting of A, V, I, L and M, and is preferably M;
X_{41} is selected from the group consisting of A, V, I, and L, and is preferably V; and
X_{42} is any amino acid and constitutes the N-terminal amino acid of the V loop.

9. The polypeptide according to any one of claims 5 to 8 wherein the C-terminus of the V loop of fragment A is defined by the following sequence (from N-terminal to C-terminal):
X_{43}-X_{44}-X_{45}-X_{46}-X_{47}-X_{48}-X_{49} (SEQ ID NO: 26)
wherein

X_{43} is any amino acid and constitutes the C-terminal amino acid of the V loop;
X_{44} is selected from the group consisting of F, Y, and W, and is preferably Y;
X_{45} is selected from the group consisting of D, E, S and T, is preferably E or T and is more preferably E;
X_{46} is selected from the group consisting of F, Y, and W, and is preferably W;
X_{47} is selected from the group consisting of A, F, V, Y, and W, is preferably F or V and is more preferably F;
X_{48} is selected from the group consisting of D, E, S and T, is preferably D or E and is more preferably E; and
X_{49} is selected from the group consisting of F, Y, and W, and is preferably F.

10. The polypeptide according to any one of claims 2 to 9 wherein the heterologous modification is selected from the group consisting of one or more single amino acid mutations in comparison to the wildtype sequence of fragment A and/or B, one or more replacements of wildtype amino acid stretches by one or more heterologous amino acids and/or amino acid stretches one or more insertions of heterologous amino acid stretches, one or more deletions of one or more amino acids and one or more amino acid modifications as well as any combination(s) thereof.

11. The polypeptide according to any one of claims 2 to 10, wherein the heterologous modification provides a target specific binding entity.

12. The polypeptide of claim 11, wherein the target specific binding entity is selected from the group consisting of antigens, epitopes, CDRs, antibodies, antibody fragments such as an antigen binding (Fab) fragment, a Fab' fragment, a F(ab')2fragment, a heavy chain antibody, a single-domain antibody (sdAb), a single-chain fragment variable (scFv), a fragment variable (Fv), a VH domain, a VL domain, a single domain antibody, a nanobody, an IgNAR (immunoglobulin new antigen receptor), a di-scFv, a bispecific T-cell engager (BITEs), a dual affinity re-targeting (DART) molecule, a triple body, a diabody, a single-chain diabody, a paratope, an alternative scaffold protein, and a fusion protein thereof, a toxin and a venom.

13. The polypeptide according to any one of claims 1 to 3 having one of the following amino acid sequences (from N- terminal to C-terminal):

MSYYHHHHHHDYDIPTTENLYFQGAMGSGIQPNVNEYMFSNKFKARVMVSRKAPEGVTVNDTY
DHKEDILKYEWFEFILPEGNFSATMTIDLMNNAIIDNYLEIGRQNGVLESDIGVKFDTRNFRL
GWDPETKLIMPGVYTYEAFHPDIVLLPGCGVDFTESRLSNLLGIRKRHPFQEGFKIMYEDLEG
GNIPALLDVTAYEESKKDTTTETTTKKELKIQPLEKDSKSRSYNVLEDKINTAYRSWYLSYNY

GNPEKGIRSWTLLTTSDVTCGANGDSGNPVFSKSFYNEQAVYSQQLRQATSLTHVFNRFPENQ
ILIRPPAPTITTVSENVP
(SEQ ID NO: 27)

GAMGSGIQPNVNEYMFSNKFKARVMVSRKAPEGVTVNDTYDHKEDILKYEWFEFILPEGNFSA
TMTIDLMNNAIIDNYLEIGRQNGVLESDIGVKFDTRNFRLGWDPETKLIMPGVYTYEAFHPDI
VLLPGCGVDFTESRLSNLLGIRKRHPFQEGFKIMYEDLEGGNIPALLDVTAYEESKKDTTTET
TTKKELKIQPLEKDSKSRSYNVLEDKINTAYRSWYLSYNYGNPEKGIRSWTLLTTSDVTCGAN
GDSGNPVFSKSFYNEQAVYSQQLRQATSLTHVFNRFPENQILIRPPAPTITTVSENVP
(SEQ ID NO: 32)

MSYYHHHHHHDYDIPTTENLYFQGTIMHTNMPNVNEFMYSNKFKARVMVSRKAPEGVTVNDTY
DHKEDILEYEWVEFELPEGNFSVTMTIDLMNNAIIDNYLAVGRQNGVLESDIGVKFDTRNFRL
GWDPVTELVMPGVYTNEAFHPDIVLLPGCGVDFTESRLSNLLGIRKRQPFQEGFQIMYEDLEG
GNIPALLDVDAYEKSKKDTTTETTTKKELKIQPVEKDSKDRSYNVLPDKINTAYRSWYLAYNY
GDPEKGVRSWTLLTTSDVTCGVEQAELLPVYSKSFFNEQAVYSQQLRAFTSLTHVFNRFPENQ
ILVRPPAPTITTVSENVP
(SEQ ID NO: 28)

QGTIMHTNMPNVNEFMYSNKFKARVMVSRKAPEGVTVNDTYDHKEDILEYEWVEFELPEGNFS
VTMTIDLMNNAIIDNYLAVGRQNGVLESDIGVKFDTRNFRLGWDPVTELVMPGVYTNEAFHPD
IVLLPGCGVDFTESRLSNLLGIRKRQPFQEGFQIMYEDLEGGNIPALLDVDAYEKSKKDTTTE
TTTKKELKIQPVEKDSKDRSYNVLPDKINTAYRSWYLAYNYGDPEKGVRSWTLLTTSDVTCGV
EQAELLPVYSKSFFNEQAVYSQQLRAFTSLTHVFNRFPENQILVRPPAPTITTVSENVP
(SEQ ID NO: 33)

14. A nucleic acid encoding a polypeptide according to any one of the preceding claims.

15. A vector comprising the nucleic acid of claim 14.

16. The vector of claim 15 containing the nucleic acid of claim 14 within an expression cassette.

17. A recombinant host cell comprising the nucleic acid of claim 14 or the vector of claim 15 or 16.

18. A method for the production of a polypeptide according to any one of claims 1 to 13 comprising the step of culturing the host cell of claim 17 containing the vector of claim 16 under conditions allowing the expression of said polypeptide.

19. The method of claim 18 further comprising the step of purifying the polypeptide from the cultured host cells.

20. The polypeptide according to any one of claims 1 to 13 for use as a medicament, preferably for use in the treatment and/or prevention of an infectious disease, an immune disease, tumour or cancer.

21. A pharmaceutical composition comprising a polypeptide according to any one of claims 1 to 13, optionally together with at least one pharmaceutically acceptable carrier, excipient and/or diluent.

22. A method of identifying a binding sequence to a target molecule comprising the steps of:

(i) preparing a library of vectors each containing a nucleotide sequence encoding a polypeptide having a candidate binding sequence in an expression cassette, each polypeptide encoded by said nucleotide sequence comprising a candidate binding sequence as a heterologous modification in one or more of RGD loop region and/or V loop and/or floor region and/or B loop as defined in any one of claims 5 to 9, wherein the candidate binding sequence encoded by the nucleotide sequence in each vector is different such that the vectors contain a randomized library of nucleotide sequences encoding randomized candidate binding sequences; or

(ii) expressing the polypeptides encoded by the nucleotide sequences from the library of vectors of step (i) in a host cell or a cell-free system, preferably cell free system;

(iii) contacting the polypeptides expressed in step (ii), optionally after purification from the host cells or the cell-free system, preferably cell free system, with the target molecule; and

(iv) detecting which polypeptide(s) have/has bound to the target molecule.

23. The method of claim 22 further comprising the step of determining the dissociation constant(s) (K_d) of the polypeptide(s) bound to the target molecule.