CLAIMS

1. A mutant IL-2 derived from human IL-2 with the sequence SEQ ID NO: 1 or from a variant thereof, comprising at least one non-endogenous transglutaminase motif as compared to SEQ ID NO: 1 or variant thereof, wherein said motif is inserted by:

- insertion of a Q residue at one or more of the following positions by reference to SEQ ID NO: 1: H16, L18, L19, N26, K32, N33, T41, F42, T51, L53, Q57, H79, E95, E100, E110 and S130, and/or
- insertion of a motif at the N-terminus or C-terminus, wherein said motif comprises a sequence selected from the group comprising or consisting of LQS and TQG,

optionally wherein the mutant IL-2 comprises, by reference to SEQ ID NO: 1, (i) a substitution of the cysteine residue 125 with any other amino acid residue, preferably a serine residue (*i.e.*, a C125S mutation), (ii) a substitution of the glutamine 74 residue with any other amino acid residue, preferably a glutamate residue (*i.e.,* a Q74E mutation), or (iii) both a substitution of the cysteine residue 125 with any other amino acid residue, preferably a serine residue (*i.e.*, a C125S mutation) and a substitution of the glutamine 74 residue with any other amino acid residue, preferably a glutamate residue (*i.e.,* a Q74E mutation).

2. The mutant IL-2 according to claim **1**, wherein said at least one non-endogenous transglutaminase motif is inserted by insertion of a Q residue at one or more of the following positions by reference to SEQ ID NO: 1: H16, L18, L19, N26, K32, N33, T41, F42, Q57, H79, E95, E100, S130.

3. The mutant IL-2 according to claim **1** or claim **2**, wherein said at least one non-endogenous transglutaminase motif comprises or consists of a sequence selected from the group comprising or consisting of X_1LQ wherein X_1 is A, L, H, I or V; NX_2Q wherein X_2 is Y, H or F; YRQ, LTQ; AQX_3 wherein X_3 is A or E, TEQ, LFQ; GSQ and VIQ , preferably comprising or consisting of X_1LQ wherein X_1 is L, H, I or V; NX_2Q wherein X_2 is Y, H or F; YRQ, LTQR (SEQ ID NO: 2); LFQ; GSQ and VIQ.

4. The mutant IL-2 according to any one of claims **1** to **3**, wherein said at least one non-endogenous transglutaminase motif comprises or consists of:

- a sequence selected from the group comprising or consisting of LEHLLQD (SEQ ID NO: 3), LEHLQSD (SEQ ID NO: 4), LLQLLLD (SEQ ID NO: 5), MILQGIN (SEQ ID NO: 6), MLLQGIN (SEQ ID NO: 7), NNYQNP (SEQ ID NO: 8), NNHQNP (SEQ ID NO: 9), LLQFKF (SEQ ID NO: 10), LLQAKF (SEQ ID NO: 11), MLTQRF (SEQ ID NO: 12), LLQC (SEQ ID NO: 13), KNFQLRPRD (SEQ ID NO: 14), KLFQLRPRD (SEQ ID NO: 15), KLLQLRPRD (SEQ ID NO: 16), VLQ, LLQ, GSQTT (SEQ ID NO: 17), GSQST (SEQ ID NO: 18), VIQ, NNYRQP (SEQ ID NO: 102), NRYRQP (SEQ ID NO: 103), MLTQGF (SEQ ID NO: 104), LAQELK (SEQ ID NO: 105), LAQALK (SEQ ID NO: 106), KATEQK (SEQ ID NO: 107), EYALQ (SEQ ID NO: 108) and DYALQ (SEQ ID NO: 109), preferably comprising or consisting of LEHLLQD (SEQ ID NO: 3), LEHLQSD (SEQ ID NO: 4), LLQLLLD (SEQ ID NO: 5), MILQGIN (SEQ ID NO: 6), MLLQGIN (SEQ ID NO: 7), NNYQNP (SEQ ID NO: 8), NNHQNP (SEQ ID NO: 9), LLQFKF (SEQ ID NO: 10), LLQAKF (SEQ ID NO: 11), MLTQRF (SEQ ID NO: 12), LLQC (SEQ ID NO: 13), KNFQLRPRD (SEQ ID NO: 14), KLFQLRPRD (SEQ ID NO: 15), KLLQLRPRD (SEQ ID NO: 16), VLQ, LLQ, GSQTT (SEQ ID NO: 17), GSQST (SEQ ID NO: 18), VIQ, NNYRQP (SEQ ID NO: 102) and NRYRQP (SEQ ID NO: 103), and/or
- a sequence selected from the group comprising or consisting of LQSPGAPTSSSTKKTQ (SEQ ID NO: 40), TQGAPTSSSTKKTQ (SEQ ID NO: 41), LQSPTSSSTKKTQ (SEQ ID NO: 42), TQGASSSTKKTQ (SEQ ID NO: 43), TQGASSTKKTQ (SEQ ID NO: 44), and TQGASTKKTQ (SEQ ID NO: 45), preferably wherein said sequence is added at the N-terminus, and/or
- a sequence selected from the group comprising or consisting of GGTQGA (SEQ ID NO: 46), GGLQSP (SEQ ID NO: 47), GLQSP (SEQ ID NO: 48), LQSP (SEQ ID NO: 49) and QGA, preferably wherein said sequence is added at the C-terminus.

5. The mutant IL-2 according to any one of claims **1** to **4**, wherein said at least one non-endogenous transglutaminase motif is inserted by:

- insertion of a Q residue at one or more of the following positions by reference to SEQ ID NO: 1: N33, T41, F42, H79, E100, and /or
- insertion of a motif at the N-terminus or C-terminus, wherein said motif comprises or consists of a sequence selected from the group comprising or consisting of LQS and TQG.

6. The mutant IL-2 according to any one of claims **1** to **5**, wherein said at least one non-endogenous transglutaminase motif comprises or consists of:

- a sequence selected from the group comprising or consisting of LLQFKF (SEQ ID NO: 10), LLQAKF (SEQ ID NO: 11), MLTQRF (SEQ ID NO: 12), KLFQLRPRD (SEQ ID NO: 15), KLLQLRPRD (SEQ ID NO: 16), GSQST (SEQ ID NO: 18), NNYRQP (SEQ ID NO: 102) and NRYRQP (SEQ ID NO: 103), and/or
- a sequence selected from the group comprising or consisting of LQS and TQG, preferably wherein said sequence is added at the C-terminus or at the N-terminus.

7. The mutant IL-2 according to any one of claims **1** to **6**, wherein said at least one non-endogenous transglutaminase motif comprises or consists of:

- a sequence selected from the group comprising or consisting of LLQFKF (SEQ ID NO: 10), LLQAKF (SEQ ID NO: 11), MLTQRF (SEQ ID NO: 12), KLFQLRPRD (SEQ ID NO: 15), KLLQLRPRD (SEQ ID NO: 16), GSQST (SEQ ID NO: 18), NNYRQP (SEQ ID NO: 102) and NRYRQP (SEQ ID NO: 103) , and/or
- a sequence selected from the group comprising or consisting of LQSPGAPTSSSTKKTQ (SEQ ID NO: 40), LQSPTSSSTKKTQ (SEQ ID NO: 42), and TQGASSTKKTQ (SEQ ID NO: 44), preferably wherein said sequence is added at the N-terminus, and/or

- a sequence selected from the group comprising or consisting of GGLQSP (SEQ ID NO: 47), GLQSP (SEQ ID NO: 48), LQSP (SEQ ID NO: 49) and QGA, preferably wherein said sequence is added at the C-terminus.

8. The mutant IL-2 according to any one of claims **1** to **7**, wherein the mutant comprises or consists of a sequence selected from the group comprising or consisting of SEQ ID NO: 30, SEQ ID NO: 20, SEQ ID NO: 19, SEQ ID NO: 21 to SEQ ID NO: 29, SEQ ID NO: 31 to SEQ ID NO: 39, SEQ ID NO: 51 to SEQ ID NO: 63, SEQ ID NO: 110 to SEQ ID NO: 117, more preferably comprising or consisting of SEQ ID NO: 19 to SEQ ID NO: 39, SEQ ID NO: 51 to SEQ ID NO: 63 and SEQ ID NOs: 110 and 111.

9. The mutant IL-2 according to any one of claims **1** to **8**, wherein the mutant comprises or consists of a sequence selected from the group comprising or consisting of SEQ ID NO: 26 to SEQ ID NO: 28, SEQ ID NO: 30 to SEQ ID NO: 34, SEQ ID NO: 38, SEQ ID NO: SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, and SEQ ID NO: 58 to SEQ ID NO: 63 and SEQ ID NOs: 110 and 111.

10. The mutant IL-2 according to any one of claims **1** to **9**, wherein the mutant IL-2 further comprises a substitution of the F42 residue by reference to SEQ ID NO: 1 into any other amino acid, more preferably a substitution of the F42 residue into an alanine residue.

11. A fusion protein comprising a mutant IL-2 according to any one of claims **1** to **10**, and further comprising at least one masking moiety, wherein the at least one masking moiety is linked to a Q residue of the at least one non-endogenous transglutaminase motif of the mutant IL-2 with a cleavable linker.

12. The fusion protein according to claim **11**, wherein the masking moiety is a polyethylene glycol (PEG), preferably a linear or a branched PEG.

13. The fusion protein according to any one of claims **11** to **12**, wherein the fusion protein further comprises an antibody or antigen-binding fragment thereof or an

antibody mimetic, preferably wherein the antibody or antigen-binding fragment thereof or antibody mimetic is linked to the mutant IL-2 with a linker.

14. The mutant IL-2 or the fusion protein according to any one of claims **1** to **13**, for use as a medicament.

15. Use of the mutant IL-2 or the fusion protein according to any one of claims **1** to **13**, in the manufacture of a medicament for the treatment of a cancer or an inflammatory disease.