Claims

1. A T cell engager (TCE) masking molecule comprising:

(i) a binding peptide that binds to an anti-CD3 epsilon (CD3ε) paratope of a CD3ε binding domain of a TCE, wherein the anti-CD3ε paratope is directed against an epitope located within CD3ε, wherein CD3ε comprises the amino acid sequence of SEQ ID NO: 257, and wherein the binding peptide and comprises at the N-terminus at least the sequence of X1DGX2EE (SEQ ID NO: 261), wherein X1 is Q, pE, or S, and wherein X2 is N, E, S, T, V, or I;

(ii) a linker covalently linked to the C-terminus of the binding peptide; and

(iii) a half-life extending polymer covalently linked to the linker.

2. The TCE masking molecule of claim 1, wherein the anti-CD3ε paratope binds to an epitope comprising (i.) at least one amino acid residue of K67 or S77 of SEQ ID NO:257; or (ii.) at least the amino acid residues K67, N68, I69, G70, S71, D72, E73, D74, H75, L76, and S77 of SEQ ID NO: 257.

3. The TCE masking molecule of claim 1, wherein the anti-CD3ε paratope is directed to a CD3ε epitope consisting of the amino acid sequence of SEQ ID NO: 258 or consisting of the amino acid sequence of SEQ ID NO: 259.

4. The TCE masking molecule of any one of the preceding claims, wherein the binding peptide binds to an anti-CD3ε paratope and comprises at the N-terminus at least the sequence of X1X2X3X4EX5X6X7 (SEQ ID NO: 393), wherein X1 is Q, pyroglutamic acid (pE), or S, and wherein X2 is D, and wherein X3 is G, and wherein X4 is N, E, S, T, V, or I, and wherein X5 is E, and wherein X6 is A, C, D, E, F, G, H, I, K, L , M , N,P, Q, R, S, T, V, W, or Y, and wherein X7 is A, C, D, E, F, G, H, I, K, L , M , N,P, Q, R, S, T, V, W, or Y.

5. The TCE masking molecule of any one of the preceding claims, wherein the binding peptide binds to an anti-CD3ε paratope and comprises at the N-terminus at least the sequence of pEX1X2X3EX4LK (SEQ ID NO: 396), wherein X1 is D, and wherein X2 is G, and wherein X3 is N, E, S, T, V, or I, and wherein X4 is E.

6. The TCE masking molecule of any one of the preceding claims, wherein the anti-CD3ε binding peptide comprises a palindrome.

7. The TCE masking molecule of any one of the preceding claims, wherein the palindrome has a K at the position between the mirrored amino acids.

8. The TCE masking molecule of any one of the preceding claims, wherein the binding peptide binds to an anti-CD3ε paratope and comprises at the N-terminus at least the amino acid sequence of any one of SEQ ID NO: 263 to 284, 286 to 293, 295 to 303, 308 to 338, 385 to 388, 397 to 419 and 431.

9. The TCE masking molecule of any one of the preceding claims, wherein the binding peptide binds to an anti-CD3ε paratope and comprises at the C-terminus a cysteine.

10. The TCE masking molecule of any one of the preceding claims, wherein the binding peptide at its C-terminus further comprises the amino acids G and C or G and K.

11. The TCE masking molecule of any one of claims 1 to 8, wherein the binding peptide binds to an anti-CD3ε paratope and comprises the sequence of pEX1X2X3EX4X5X6GX7 (SEQ ID NO: 433), wherein X1 is D, and wherein X2 is G, and wherein X3 is N, E, S, T, V, or I, and wherein X4 is E, , and wherein X5 is A, C, D, E, F, G, H, I, K, L , M , N, P, Q, R, S, T, V, W, or Y, and wherein X6 is A, C, D, E, F, G, H, I, K, L , M , N,P, Q, R, S, T, V, W, or Y, and wherein X7 is C or K.

12. The TCE masking molecule of any one of claims 1 to 8 and 14, wherein the binding peptide binds to an anti-CD3ε paratope and comprises the sequence of pEX1X2X3EELKGX4 (SEQ ID NO: 434), wherein X1 is D, and wherein X2 is G, , and wherein X3 is N, E, S, T, V, or I, preferably N or E, and wherein X4 is C or K.

13. The TCE masking molecule of any one of claims 1 to 8 and 14 to 15, wherein the binding peptide binds to an anti-CD3ε paratope and comprises the sequence of pEX1GX2EELKGX3 (SEQ ID NO: 435), wherein X1 is Dand wherein X2 is N, E, S, T, V, or I, preferably N or E, and wherein X3 is C or K.

14. The TCE masking molecule of any one of claims 1 to 8 and 14 to 16, wherein the binding peptide binds to an anti-CD3ε paratope and comprises the sequence of pEDGX1EELKGX2 (SEQ ID NO: 436), wherein X1 is N, , E, S, T, V, or I, preferably N or E, and wherein X2 is C or K.

15. The TCE masking molecule of any one of the preceding claims, wherein the binding peptide binds to an anti-CD3ε paratope and comprises the sequence of SEQ ID NO: 297, 300, 303, 304, 305, 306, 307, 384 or 389.

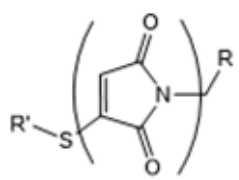
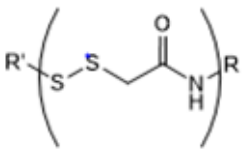
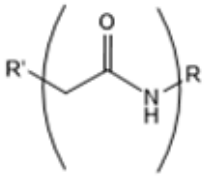
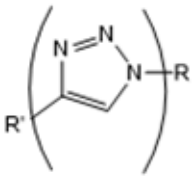
16. The TCE masking molecule of any one of the preceding claims, wherein the linker is

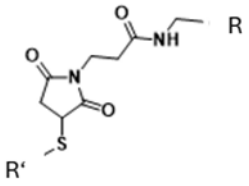
(a) a disulfide linker comprising disulfide (R-S-S-R'), wherein R is a half-life extending polymer and R' is a binding peptide;

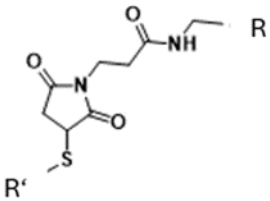
(b) a free thiol containing linear or branched PEGs, an OPSS derivative, a maleimide, a nor-bornene, an acrylimide, an acrylate, a vinyl sulfone, or an amine; or

(c) a carboxyl linker comprising an amine, an amide, or an epsilon derivatized acetyl bromide.

17. The TCE masking molecule of any one of the preceding claims, wherein the linker is selected from any one of the following moieties:

:  ,  ,  , and  , or wherein the linker is selected from a maleimide – thiosuccinimide linker having the formula

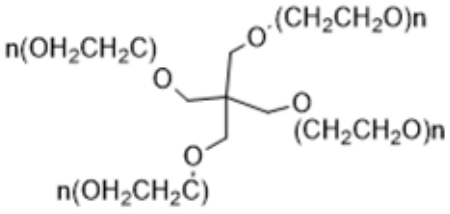
 when the C-terminal amino acid of the binding peptide is K; and

an acetamide – thioether having the formula  when the C-terminal amino acid of the binding peptide is C, and a disulfide having the formula R'-S-S-R when the C-terminal amino acid of the binding peptide is C,

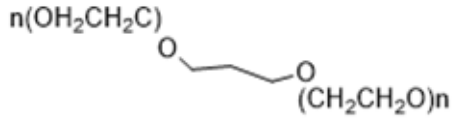
wherein R is a half-life extending polymer and R' is a binding peptide.

18. The TCE masking molecule of any one of the preceding claims, wherein the half-life extending polymer is mono-methoxy polyethylene glycol (mPEG), linear, 2-arm, 4-arm, 8-arm polyethylene glycol (PEG).; PLGA; peptide acrylate, polyglycerols, polyoxazolines, polyvinylpyrrolidone, polyacrylamides, poly(N-acryloylmorpholine), poly(N,N-dimethylacrylamide), poly(2-hydroxypropylmethacrylamide), polysarcosine, poly(2-hydroxyethylmethacrylamide), hyaluronic acids, sialic acid, poly[(organo)phosphazenes], or heparin.

19. The TCE masking molecule of any one of the preceding claims, wherein the half-life extending polymer is:

(i.)  ,

wherein n equals an integer of 20 to 200, preferably 20 to 169, more preferably 20, 103 or 113



(ii.) wherein n equals an integer of 40 to 400, preferably about 40 or about 208, or

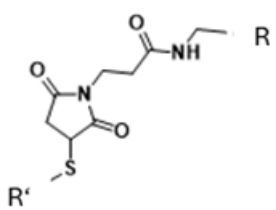
(iii.) 

, wherein n equals a number of 80 to 700, preferably 80 to 675, more preferably about 83, about 166 or about 417 .

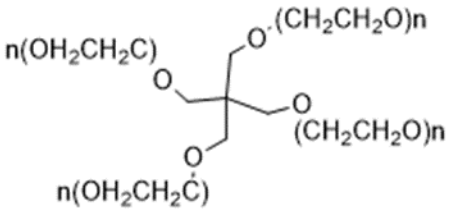
20. The TCE masking molecule of any of the preceding claims, wherein the half-life extending polymer is a non-branched linear, or a branched 2-arm, 4-arm, or 8-arm PEG, preferably linear or 4-arm, with a molecular weight of 2 kDa to 60 kDa, preferably 4 kDa to 30 kDa or 10 kDa to 30 kDa, or more preferably about 5 or about 20 kDa.

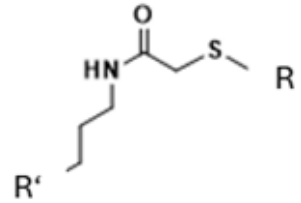
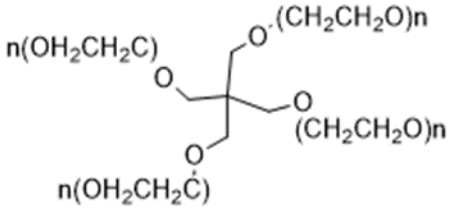
21. The TCE masking molecule of any one of the preceding claims, wherein the half-life extending polymer is a branched polymer, preferably a 2-arm, 4-arm or 8-arm PEG with a molecular weight of 2 kDa to 60 kDa to which more than one binding peptide is linked via a linker each, preferably 2, 4 or 8 binding peptides to one half-life extending polymer.

22. The TCE masking molecule of any one of claims 1 to 5, 11 to 14, and 16 to 21, comprising the sequence of pEX1X2X3EELKGX4 (SEQ ID NO: 434), wherein X1 is D, H or N, and wherein X2 is G, F or Y, preferably G or F, and wherein X3 is N, H, Q, R, E, S, T, V, C, D, F, K L, M, W, Y or I, preferably N, E, H, Q or R, most preferably N or E, and

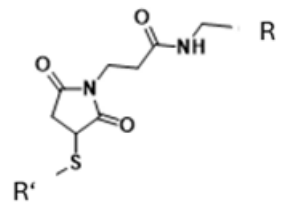
(a.) wherein and wherein X4 is C; a linker chosen from maleimide – thiosuccinimide linker having the formula 

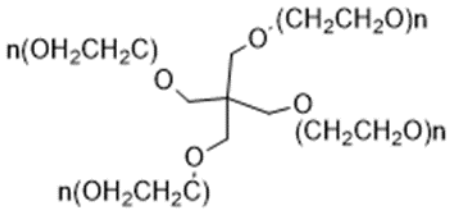
and a disulfide having the formula R'-S-S-R; and a half-life

extending polymer that is a PEG of the following formula 

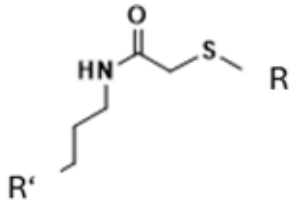
or  having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa; or (b.) wherein and wherein X4 is K; an acetamide – thioether having the formula  ; and a half-life extending polymer that is a PEG of the following formula  or  having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa.

23. The TCE masking molecule of any one of claims 1 to 5, 11 to 14, and 16 to 22 comprising the sequence of pEX1GX2EELKGX3 (SEQ ID NO: 435), wherein X1 is D, H or N, and wherein X2 is N, H, Q, R, E, S, T, V, C, D, F, K L, M, W, Y or I, preferably E, N, H, Q or R, most preferably N or E, and

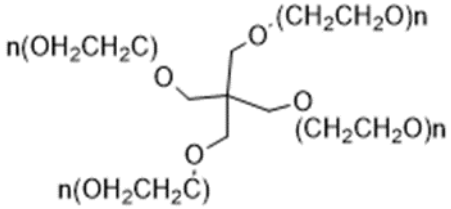
(a.) wherein and wherein X3 is C; a linker chosen from maleimide – thiosuccinimide linker having the formula  and a disulfide having the formula R'-S-S-R; and a half-life

extending polymer that is a PEG of the following formula  or

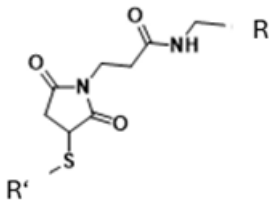
 having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa; or (b.) wherein and wherein X3 is K; an acetamide – thioether having the formula

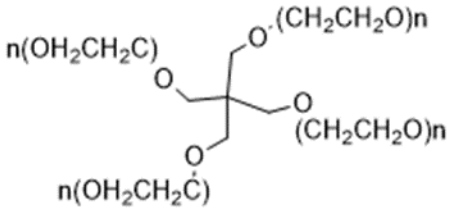


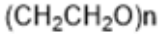
; and a half-life extending polymer that is a PEG of the following formula

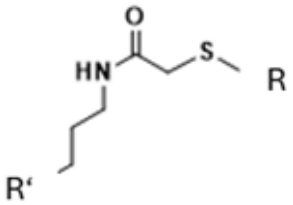
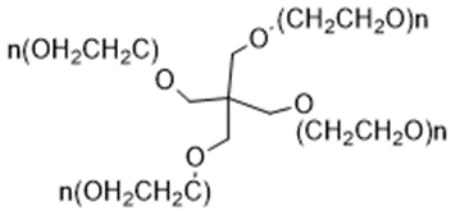
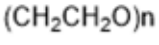
 or  having a molecular weight of 5 kDa to 20 kDa, preferably about 5 kDa or about 10 kDa, or about 20 kDa.

24. The TCE masking molecule of any one of claims 1 to 5, 11 to 14 and 16 to 23 comprising the sequence of pEDGX1EELKGX2 (SEQ ID NO: 436), wherein X1 is N or E, and wherein (a.) X2 is C; a linker chosen from maleimide – thiosuccinimide linker having the formula



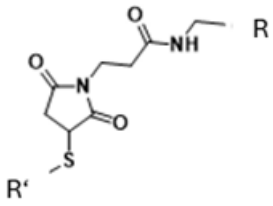
and a disulfide having the formula R'-S-S-R; and a half-life extending polymer that is a PEG of the following formula  or

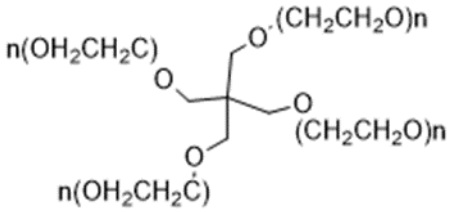
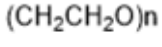
 having a molecular weight of about 5 kDa or about 20 kDa; or (b) the sequence of

pEDGX1EELKGX2 (SEQ ID NO: 436), wherein X1 is N or E, and wherein X2 is K; an acetamide – thioether having the formula  ; and a half-life extending polymer that is a PEG of the following formula  or  having a molecular weight of 5 kDa to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa.

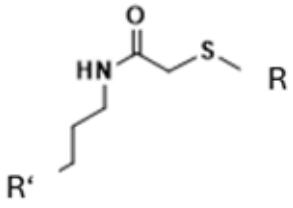
25. The TCE masking molecule of any one of claims 1 to 5, 11 to 14 and 16 to 24, comprising

(a) the amino acid sequence of SEQ ID NO 304, 306, 384 or 389, and

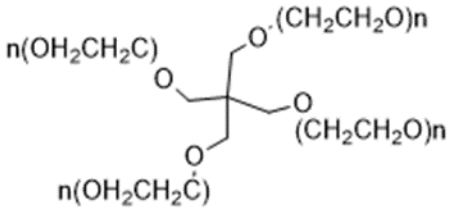
a linker chosen from maleimide – thiosuccinimide linker having the formula  and a disulfide having the formula R'-S-S-R;

and a half-life extending polymer that is a PEG of the following formula  or  having a molecular weight of 5 kDa to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa or

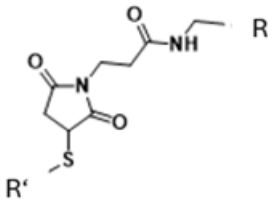
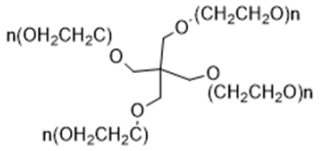
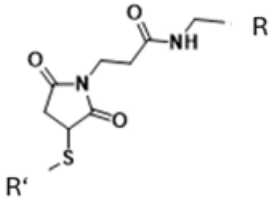
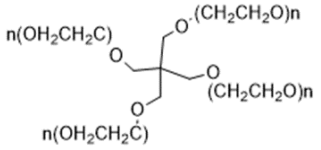
(b) the amino acid sequence of SEQ ID 305 or 307;

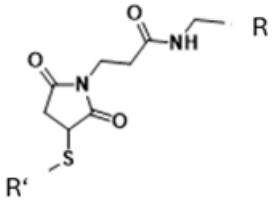
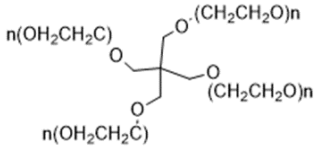
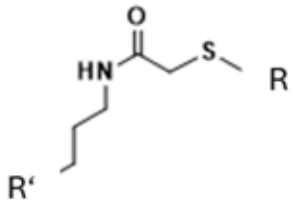
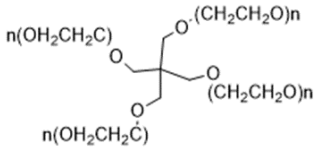
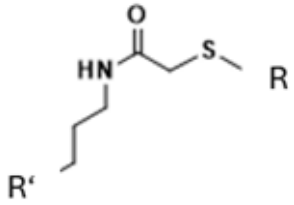
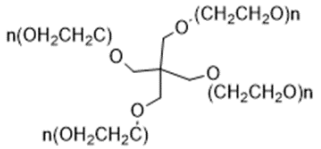
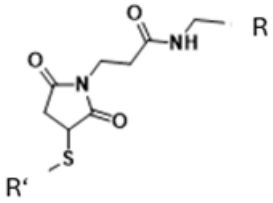
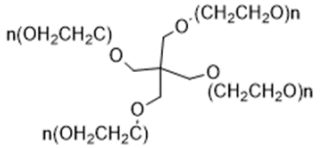
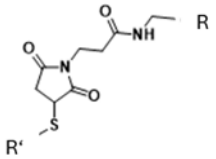
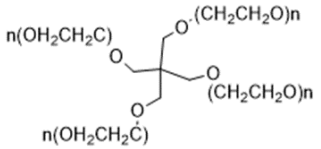
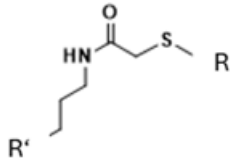
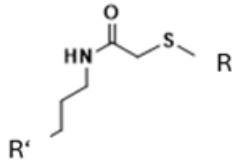
an acetamide – thioether having the formula 

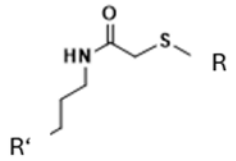
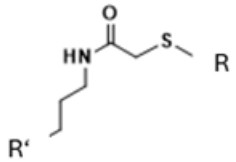
and a half-life extending polymer that is a PEG of the following formula

 or  having a molecular weight of 5 kDa to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa.

26. The TCE masking molecule of any one of the preceding claims comprising any of the combinations (a.) to (k.) of a binding peptide, a linker and a half-life extending PEG polymer, wherein R' stands for the binding peptide and R stands for the half-life extending PEG polymer.

	Peptide seq	**Linker**	**PEG configuration**
(a.)	pEDGNEELKGC (SEQ ID NO 304)	 Thiosuccinimide	 4 arm, 20 kDa
(b.)	pEDGNEELKGC (SEQ ID NO 304)	 Thiosuccinimide	 4 arm, 20 kDa

(c.)	pEDGEEELKGC (SEQ ID NO 306)	 Thiosuccinimide	 4 arm, 20 kDa
(d.)	pEDGNEELKGK (SEQ ID NO 305)	 Thioether	 4 arm, 20 kDA
(e.)	pEDGEEELKGK (SEQ ID NO 307)	 Thioether	 4 arm, 20 kDA
(f.)	pEDGNEELKGC (SEQ ID NO 306)	 Thiosuccinimide	 4 arm, 5 kDa
(g.)	pEDGEEELKGC (SEQ ID NO 306)	 Thiosuccinimide	 4 arm, 5 kDa
(h.)	pEDGNEELKGK (SEQ ID NO 305)	 Thioether	$(CH_2CH_2O)n$ Linear, 20 kDa
(i.)	pEDGEEELKGK (SEQ ID NO 307)		$(CH_2CH_2O)n$ Linear, 20 kDa

		Thioether	
(j.)	pEDGNEELKGK (SEQ ID NO 305)	 Thioether	$(CH_2CH_2O)n$ Linear, 10 kDa
(k.)	pEDGEEELKGK (SEQ ID NO 307)	 Thioether	$(CH_2CH_2O)n$ Linear, 10 kDa

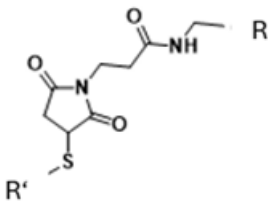
27. Use of a T cell engager (TCE) masking molecule in the manufacture of a medicament for reducing the severity of cytokine release syndrome in a human subject undergoing treatment with a TCE, wherein the TCE masking molecule comprises:

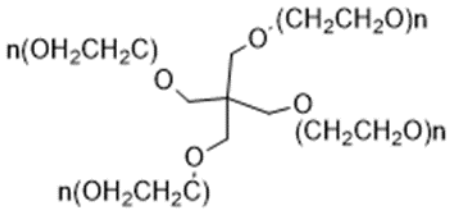
(i.) a binding peptide that binds an anti-CD3ε paratope of a CD3ε binding domain of a TCE, wherein the anti-CD3ε paratope is directed against an epitope located within CD3ε, and wherein CD3ε comprises the amino acid sequence of SEQ ID NO: 257;

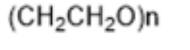
(ii.) a linker, wherein the linker is covalently linked to the C-terminus of the binding peptide; and

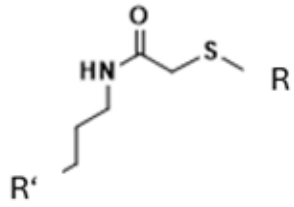
(iii.) at least one half-life extending polymer of preferably at least 2 kDa, wherein the polymer is covalently linked to the linker;

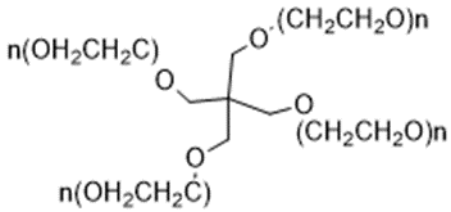
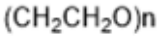
wherein the TCE masking molecule comprises:

a binding peptide which binds to an anti-CD3ε paratope and comprises the sequence of pEX1X2X3EELKGX4 (SEQ ID NO: 434), wherein X1 is D, H or N, and wherein X2 is G, F or Y, preferably G or F, and wherein X3 is N, H, Q, R, E, S, T, V, C, D, F, K L, M, W, Y or I, preferably N, E, H, Q or R, and (a.) wherein and wherein X4 is C; a linker chosen from maleimide – thiosuccinimide linker having the formula  and a disulfide having the formula R'-S-S-R; and a half-life

extending polymer that is a PEG of the following formula  or

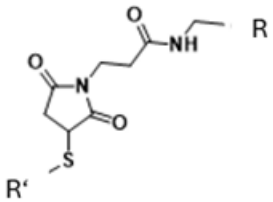
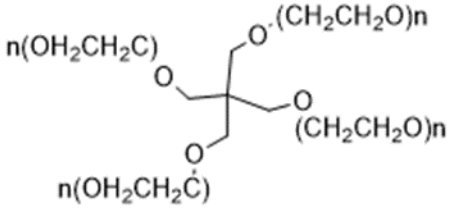
 having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa; or (b.) wherein and wherein X4 is K; an acetamide – thioether having the formula

 ; and a half-life extending polymer that is a PEG of the following formula

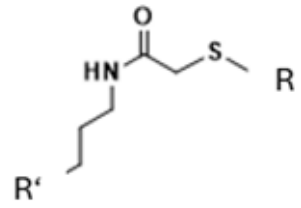
 or  having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa, wherein R' stands for the binding peptide and R stands for the half-life extending PEG polymer.

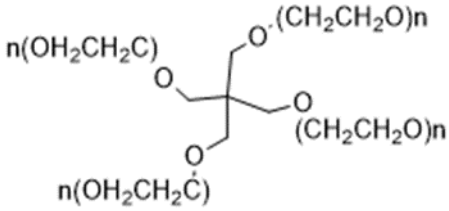
28. The use of claim 27, wherein the T cell engager masking molecule comprises:

a binding peptide which binds to an anti-CD3ε paratope and comprises the sequence of pEX1GX2EELKGX3 (SEQ ID NO: 435), wherein X1 is D, H or N, and wherein X2 is N, H, Q, R, E, S, T, V, C, D, F, K L, M, W, Y or I, preferably N, H, Q or R, and (a.) wherein and wherein X3 is C; a linker chosen from maleimide – thiosuccinimide linker having the formula

 and a disulfide having the formula R'-S-S-R; and a half-life extending polymer that is a PEG of the following formula  or

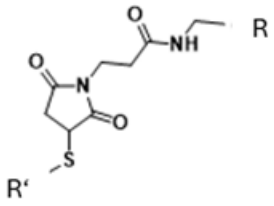

having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa; or (b.) wherein and wherein X3 is K; an acetamide – thioether having the

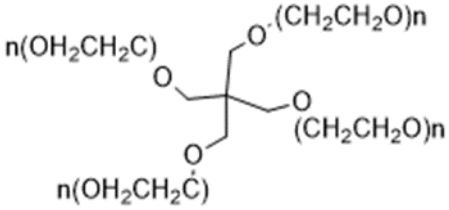

formula ; and a half-life extending polymer that is a PEG of the following


formula or 
having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa, wherein R' stands for the binding peptide and R stands for the half-life extending PEG polymer.

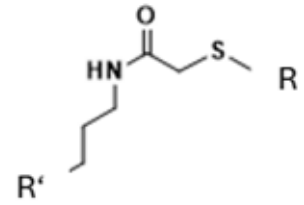
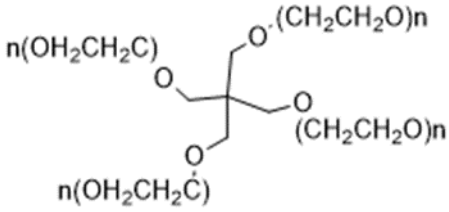
29. The use of any one of claims 27 or 28, wherein the T cell engager masking molecule comprises:

a binding peptide which binds to an anti-CD3ε paratope and comprises the sequence of pEDGX1EELKGX2 (SEQ ID NO: 436), wherein X1 is D, H or N, and wherein X1 is N, H, Q, R, E, S, T, V, C, D, F, K L, M, W, Y or I, preferably N, E, H, Q or R, most preferably N or E, and (a.) wherein and wherein X2 is C; a linker chosen from maleimide – thiosuccinimide linker having the


formula and a disulfide having the formula R'-S-S-R; and a half-life


extending polymer that is a PEG of the following formula

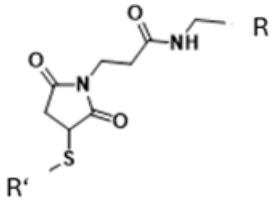

or having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa; or (b.) wherein and wherein X2 is K; an acetamide – thioether having the

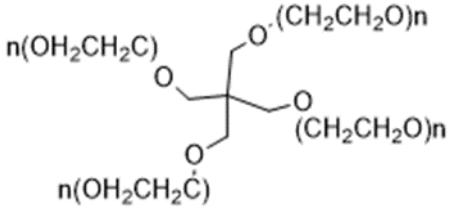
formula  ; and a half-life extending polymer that is a PEG of the following formula  or  having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa, wherein R' stands for the binding peptide and R stands for the half-life extending PEG polymer.

30. The use of any one of claims 27 to 29, wherein the T cell engager masking molecule comprises:

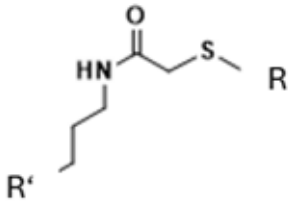
or preferably consists of

(a) the amino acid sequence of SEQ ID NO 304, 306, 384 or 389, and

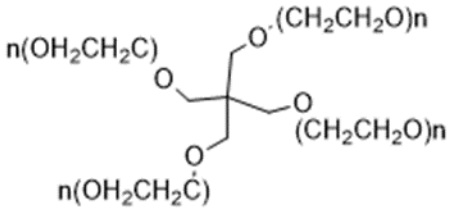
a linker chosen from maleimide – thiosuccinimide linker having the formula  and a disulfide having the formula R'-S-S-R;

and a half-life extending polymer that is a PEG of the following formula  or  having a molecular weight of 5 kDa to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa; or

(b) the amino acid sequence of SEQ ID NO 305 or 307;

an acetamide – thioether having the formula 

and a half-life extending polymer that is a PEG of the following formula



or 

having a molecular weight of 5 kDa to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa, wherein R' stands for the binding peptide and R stands for the half-life extending PEG polymer.

31. The use of any one of Claims 27 to 30, wherein the immunotherapy comprises that a T cell engager is to be administered.

32. The use of any one of claims 27-31, wherein the molar ratio of the TCE masking molecule to the T cell engager is in the range of 1000 to 1, or 250:1 to 10:1, or 100:1 to 25:1.

33. The use of any of claims 27 to 32, wherein the TCE masking molecule is to be administered before, during or after administration of a TCE.

34. The use of any one of claim 27 to 33, wherein the TCE is:

(i) A TCE comprising at least a first, a second, and a third domain in an amino to carboxyl order, wherein:

the first domain binds to a target cell surface antigen, wherein the antigen is preferably a tumor antigen;

the second domain binds to an epitope of CD3ε; and

the third domain comprises two polypeptide monomers, each comprising a hinge, a CH2, and a CH3 domain, wherein the two polypeptide monomers are fused to each other via a peptide linker,

and wherein the third domain comprises in an amino to carboxyl order: hinge-CH2-CH3-linker-hinge-CH2-CH3;

(ii) A TCE comprising:

a first binding domain, wherein the first binding domain comprises an scFv, scFab, or Fab which binds to a first target cell surface antigen (TAA1);

a second binding domain wherein the second binding domain comprises an scFv, scFab, or Fab which binds to an extracellular epitope on the human CD3ε chain;

a spacer, wherein said spacer is a single chain fragment crystallizable (scFc), human serum albumin (HSA), programmed death receptor 1 (PD1), or a hetero fragment crystallizable (hetero FC);

a third binding domain wherein the third binding domain comprises an scFv, scFab, or Fab which binds to a second target cell surface antigen (TAA2); and

a fourth binding domain wherein the fourth binding domain comprises an scFv, scFab, or Fab which binds to an epitope ofCD3ε,

wherein the first binding domain binds to the first target cell surface antigen and the third binding domain binds to the second target cell surface antigen simultaneously, wherein the first target cell surface antigen and the second target cell surface antigen are on the same target cell,

wherein the TCE is preferably a single polypeptide chain,

wherein the first target cell surface antigen and the second target cell surface antigen are not identical, and

wherein the first binding domain and the second binding domain form a first bispecific entity and the third and the fourth binding domain form a second bispecific entity, and

wherein the spacer entity is positioned between the first and the second bispecific entities;

(iii) an IgG-based bispecific antibody; or(iv) a heterodimeric antibody.

35. The use of claim 33, wherein the TCE under (i.) of claim 33 is a single chain molecule.

36. The use of claim 34 or 35, wherein a glycosylation site at Kabat position 314 of the CH2 domains in the third domain of the TCE under (i.) and (ii.) of claim 39 is removed by a N314X substitution, wherein X is any amino acid excluding Q.

37. The use of any one of claims 34 to 36, wherein each of the polypeptide monomers of the third domain comprises an amino acid sequence that is at least 90% identical to an amino acid sequence selected from the group consisting of: SEQ ID NOs: 437 to 444, or comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 437 to 444.

38. The use of any one of claims 34 to 37, wherein the CH2 domain comprises an intra domain cysteine disulfide bridge.

39. The use of any one of claims 34 to 38, wherein the tumor antigen is CDH19, CDH3, MSLN, DLL3, FLT3, EGFRvIII, BCMA, PSMA, CD33, CD19, CD20, CLDN18.2, CLDN6, MUC17, EpCAM, STEAP1, or CD70.

40. The use of any one of claims 34-39, wherein the TCE under (i.) in claim 34 comprises in an amino to carboxyl order:

(a) a first domain;

(b) a peptide linker having an amino acid sequence of any one of SEQ ID NOs: 187-189;

(c) a second domain;

(d) a peptide linker having an amino acid sequence of any one of SEQ ID NOs: 187, 188, 189, 195, 196, 197 and 198;

(e) a first peptide monomer of the third domain having an amino acid sequence of any of SEQ ID NOs 437 to 444;

(f) a peptide linker having an amino acid sequence of any one of SEQ ID NOs: 191, 192, 193 and 194; and

(g) a second peptide monomer of the third domain having an amino acid sequence of any of SEQ ID NOs 437 to 444.

41. The use of any of claims 34 to 40, wherein the first and/or third binding domain of the TCE under (ii.) in claim 39 comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from the group consisting of:

(a) CDR-H1 as depicted in SEQ ID NO: 4, CDR-H2 as depicted in SEQ ID NO: 5, CDR-H3 as depicted in SEQ ID NO: 6, CDR-L1 as depicted in SEQ ID NO: 1, CDR-L2 as depicted in SEQ ID NO: 2 and CDR-L3 as depicted in SEQ ID NO: 3;

(b) CDR-H1 as depicted in SEQ ID NO: 29, CDR-H2 as depicted in SEQ ID NO: 30, CDR-H3 as depicted in SEQ ID NO: 31, CDR-L1 as depicted in SEQ ID NO: 34, CDR-L2 as depicted in SEQ ID NO: 35 and CDR-L3 as depicted in SEQ ID NO: 36;

(c) CDR-H1 as depicted in SEQ ID NO: 42, CDR-H2 as depicted in SEQ ID NO: 43, CDR-H3 as depicted in SEQ ID NO: 44, CDR-L1 as depicted in SEQ ID NO: 45, CDR-L2 as depicted in SEQ ID NO: 46 and CDR-L3 as depicted in SEQ ID NO: 47;

(d) CDR-H1 as depicted in SEQ ID NO: 53, CDR-H2 as depicted in SEQ ID NO: 54, CDR-H3 as depicted in SEQ ID NO: 55, CDR-L1 as depicted in SEQ ID NO: 56, CDR-L2 as depicted in SEQ ID NO: 57 and CDR-L3 as depicted in SEQ ID NO: 58;

(e) CDR-H1 as depicted in SEQ ID NO: 65, CDR-H2 as depicted in SEQ ID NO: 66, CDR-H3 as depicted in SEQ ID NO: 67, CDR-L1 as depicted in SEQ ID NO: 68, CDR-L2 as depicted in SEQ ID NO: 69 and CDR-L3 as depicted in SEQ ID NO: 70;

(f) CDR-H1 as depicted in SEQ ID NO: 83, CDR-H2 as depicted in SEQ ID NO: 84, CDR-H3 as depicted in SEQ ID NO: 85, CDR-L1 as depicted in SEQ ID NO: 86, CDR-L2 as depicted in SEQ ID NO: 87 and CDR-L3 as depicted in SEQ ID NO: 88;

(g) CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 96, CDR-L1 as depicted in SEQ ID NO: 97, CDR-L2 as depicted in SEQ ID NO: 98 and CDR-L3 as depicted in SEQ ID NO: 99;

(h) CDR-H1 as depicted in SEQ ID NO: 105, CDR-H2 as depicted in SEQ ID NO: 106, CDR-H3 as depicted in SEQ ID NO: 107, CDR-L1 as depicted in SEQ ID NO: 109, CDR-L2 as depicted in SEQ ID NO: 110 and CDR-L3 as depicted in SEQ ID NO: 111;

(i) CDR-H1 as depicted in SEQ ID NO: 115, CDR-H2 as depicted in SEQ ID NO: 116, CDR-H3 as depicted in SEQ ID NO: 117, CDR-L1 as depicted in SEQ ID NO: 118, CDR-L2 as depicted in SEQ ID NO: 119 and CDR-L3 as depicted in SEQ ID NO: 120;

(j) CDR-H1 as depicted in SEQ ID NO: 126, CDR-H2 as depicted in SEQ ID NO: 127, CDR-H3 as depicted in SEQ ID NO: 128, CDR-L1 as depicted in SEQ ID NO: 129, CDR-L2 as depicted in SEQ ID NO: 130 and CDR-L3 as depicted in SEQ ID NO: 131;

(k) CDR-H1 as depicted in SEQ ID NO: 137, CDR-H2 as depicted in SEQ ID NO: 138, CDR-H3 as depicted in SEQ ID NO: 139, CDR-L1 as depicted in SEQ ID NO: 140, CDR-L2 as depicted in SEQ ID NO: 141 and CDR-L3 as depicted in SEQ ID NO: 142;

(l) CDR-H1 as depicted in SEQ ID NO: 152, CDR-H2 as depicted in SEQ ID NO: 153, CDR-H3 as depicted in SEQ ID NO: 154, CDR-L1 as depicted in SEQ ID NO: 155, CDR-L2 as depicted in SEQ ID NO: 156 and CDR-L3 as depicted in SEQ ID NO: 157;

(m) CDR-H1 as depicted in SEQ ID NO: 167, CDR-H2 as depicted in SEQ ID NO: 168, CDR-H3 as depicted in SEQ ID NO: 169, CDR-L1 as depicted in SEQ ID NO: 170, CDR-L2 as depicted in SEQ ID NO: 171 and CDR-L3 as depicted in SEQ ID NO: 172,;

(n) CDR-H1 as depicted in SEQ ID NO: 203, CDR-H2 as depicted in SEQ ID NO: 204, CDR-H3 as depicted in SEQ ID NO: 205, CDR-L1 as depicted in SEQ ID NO: 206, CDR-L2 as depicted in SEQ ID NO: 207 and CDR-L3 as depicted in SEQ ID NO: 208;

(o) CDR-H1 as depicted in SEQ ID NO: 214, CDR-H2 as depicted in SEQ ID NO: 215, CDR-H3 as depicted in SEQ ID NO: 216, CDR-L1 as depicted in SEQ ID NO: 217, CDR-L2 as depicted in SEQ ID NO: 218 and CDR-L3 as depicted in SEQ ID NO: 219;

(p) CDR-H1 as depicted in SEQ ID NO: 226, CDR-H2 as depicted in SEQ ID NO: 227, CDR-H3 as depicted in SEQ ID NO: 228, CDR-L1 as depicted in SEQ ID NO: 229, CDR-L2 as depicted in SEQ ID NO: 230 and CDR-L3 as depicted in SEQ ID NO: 231;

(q) CDR-H1 as depicted in SEQ ID NO: 238, CDR-H2 as depicted in SEQ ID NO: 239, CDR-H3 as depicted in SEQ ID NO: 240, CDR-L1 as depicted in SEQ ID NO: 241, CDR-L2 as depicted in SEQ ID NO: 242 and CDR-L3 as depicted in SEQ ID NO: 243; and

(r) CDR-H1 as depicted in SEQ ID NO: 420, CDR-H2 as depicted in SEQ ID NO: 421, CDR-H3 as depicted in SEQ ID NO: 422, CDR-L1 as depicted in SEQ ID NO: 423, CDR-L2 as depicted in SEQ ID NO: 424 and CDR-L3 as depicted in SEQ ID NO: 425.

42. The use of any one of claims 34 to 41, wherein the TCE comprises the amino acid sequence of SEQ ID NO: 17, 52, 63, 81, 93, 104, 114, 125, 136, 147, 162, 177, 213,226, 238, 248, 255 or 430, preferably 104 or 255.

43. The use of claim 34, wherein the heterodimeric antibody comprises:

(a) a first monomer comprising a first heavy chain comprising:

(i) a first variable heavy domain;

(ii) a first constant heavy chain comprising a first CH1 domain and a first Fc domain; (iii) a scFv that binds CD3ε and comprises a scFv variable light domain, an scFv linker, and a scFv variable heavy domain

wherein the scFv is covalently attached between the C-terminus of the CH1 domain and the N-terminus of the first Fc domain using domain linker(s);

(b) a second monomer comprising a second heavy chain comprising a second variable

heavy domain and a second constant heavy chain comprising a second Fc domain; and

(c) a common light chain comprising a variable light domain and a constant light domain,

wherein the first variable heavy domain and the variable light domain bind human STEAP1, and

wherein the second variable heavy domain and the variable light domain bind human STEAP1, and wherein

(1) the first monomer comprises the amino acid sequence of SEQ ID NO: 375, the second monomer comprises the sequence of SEQ ID NO: 374, and the common light chain

comprises the sequence of SEQ ID NO:373;

(2) the first monomer comprises the amino acid sequence of SEQ ID NO: 380, the second

monomer comprises the sequence of SEQ ID NO:376, and the common light chain

comprises the sequence of SEQ ID NO:373; or

(3) the first monomer comprises the amino acid sequence of SEQ ID NO: 379, the second

monomer comprises the sequence of SEQ ID NO: 378, and the common light chain

comprises the sequence of SEQ ID NO: 377.

44. The TCE masking molecule or the use of any of the preceding claims, wherein the CD3ε binding domain has 80, 90, 95 or 99% sequence identity with the sequence of SEQ ID NO 26, 381, 382 or 383 or has the sequence of SEQ ID NO 26, 381, 382 or 383

45. Use of a T cell engager (TCE) masking molecule in the manufacture of a medicament for reducing the severity of cytokine release in a human subject undergoing treatment with a TCE, wherein the TCE masking molecule comprises:

(i.) a binding peptide that binds to an anti-CD3ε paratope of a CD3ε binding domain of a TCE, wherein the anti-CD3ε paratope is directed against an epitope located within CD3ε, and wherein CD3ε comprises the amino acid sequence of SEQ ID NO: 257;

(ii) a linker covalently linked to the C-terminus of the binding peptide; and

(iii) a half-life extending polymer covalently linked to the linker.

46. Use of a T cell engager (TCE) masking molecule in the manufacture of a medicament for attenuating in vivo exposure of a TCE after administration of the TCE, wherein the administration is preferably via the i.v. or s.c. route, wherein the TCE masking molecule comprises:

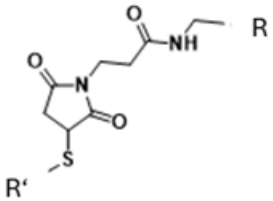
(i.) a binding peptide that binds to an anti-CD3ε paratope of a CD3ε binding domain of a TCE, wherein the anti-CD3ε paratope is directed against an epitope located within CD3ε, and wherein CD3ε comprises the amino acid sequence of SEQ ID NO: 257,

(ii) a linker covalently linked to the C-terminus of the binding peptide; and

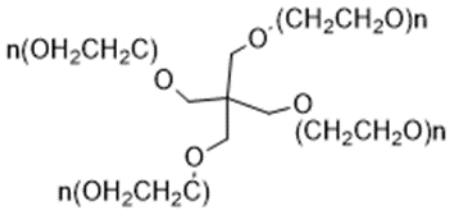
(iii) a half-life extending polymer covalently linked to the linker, wherein the binding peptide binds to an anti-CD3ε paratope with a Kd which is at least 1.5-fold lower than the Kd for the amino acid sequence of SEQ ID NO: 262 binding to an anti-CD3ε paratope, preferably, at least 2-fold lower, more preferably 3-fold, lower, and wherein the TCE masking molecule is to be administered at a molar excess of 10 to 1000, or 25 to 250 with respect to the TCE.

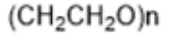
47. The use of claim 46, wherein the TCE masking molecule is to be administered before, during or after the administration of the TCE.

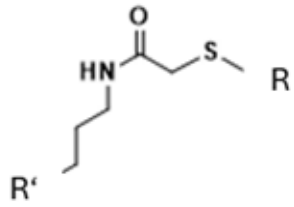
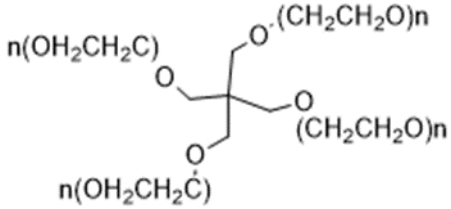
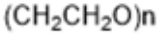
48. The use of claim 46 or 47, wherein the T cell engager masking molecule comprises:

a binding peptide which binds to an anti-CD3ε paratope and comprises the sequence of pEX1X2X3EELKGX4 (SEQ ID NO: 434), wherein X1 is D, H or N, and wherein X2 is G, F or Y, preferably G or F, and wherein X3 is N, H, Q, R, E, S, T, V, C, D, F, K L, M, W, Y or I, preferably N, E, H, Q or R, and (a.) wherein and wherein X4 is C; a linker chosen from maleimide – thiosuccinimide linker having the formula 

and a disulfide having the formula R'-S-S-R; and a half-life

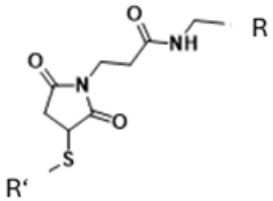
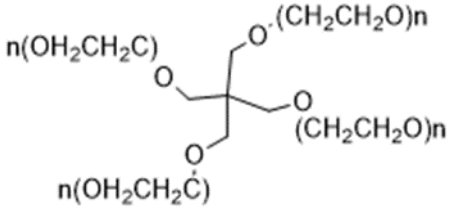
extending polymer that is a PEG of the following formula  or

 having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa; or (b.) wherein and wherein X4 is K; an acetamide – thioether having the formula

 ; and a half-life extending polymer that is a PEG of the following formula  or  having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa, wherein R' stands for the binding peptide and R stands for the half-life extending PEG polymer.

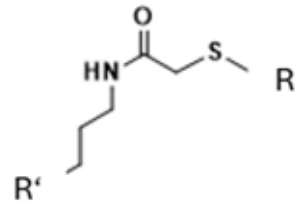
49. The use of claims 46 to 48, wherein the T cell engager masking molecule comprises:

a binding peptide which binds to an anti-CD3ε paratope and comprises the sequence of pEX1GX2EELKGX3 (SEQ ID NO: 435), wherein X1 is D, H or N, and wherein X2 is N, H, Q, R, E, S, T, V, C, D, F, K L, M, W, Y or I, preferably N, H, Q or R, and (a.) wherein and wherein X3 is C; a linker chosen from maleimide – thiosuccinimide linker having the formula

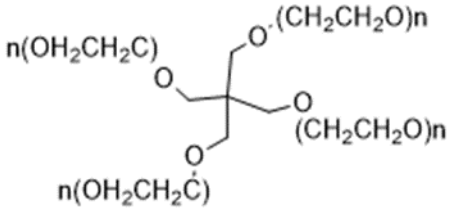
 and a disulfide having the formula R'-S-S-R; and a half-life extending polymer that is a PEG of the following formula  or



having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa; or (b.) wherein and wherein X3 is K; an acetamide – thioether having the

formula 

; and a half-life extending polymer that is a PEG of the following

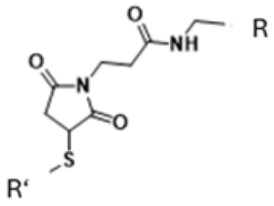
formula 

or 

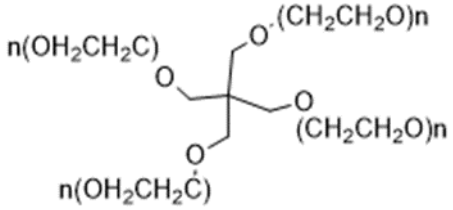
having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa, wherein R' stands for the binding peptide and R stands for the half-life extending PEG polymer.

50. The use of claims 46 to 49, wherein the T cell engager masking molecule comprises:

a binding peptide which binds to an anti-CD3ε paratope and comprises the sequence of pEDGX1EELKGX2 (SEQ ID NO: 436), wherein X1 is D, H or N, and wherein X1 is N, H, Q, R, E, S, T, V, C, D, F, K L, M, W, Y or I, preferably N, E, H, Q or R, most preferably N or E, and (a.) wherein and wherein X2 is C; a linker chosen from maleimide – thiosuccinimide linker having the

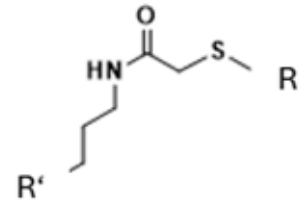
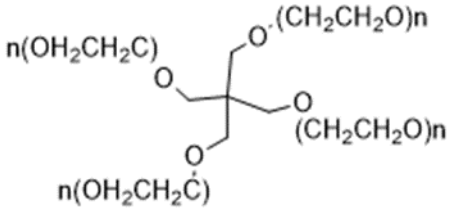
formula 

and a disulfide having the formula R'-S-S-R; and a half-life

extending polymer that is a PEG of the following formula 

or 

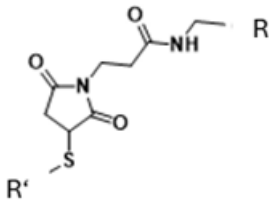
having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa; or (b.) wherein and wherein X2 is K; an acetamide – thioether having the

formula  ; and a half-life extending polymer that is a PEG of the following formula  or  having a molecular weight of 5 to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa, wherein R' stands for the binding peptide and R stands for the half-life extending PEG polymer.

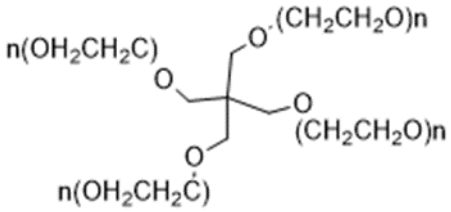
51. The use of claims 46 to 50, wherein the T cell engager masking molecule comprises:

(a) the amino acid sequence of SEQ ID NO 304, 306, 384 or 389, and

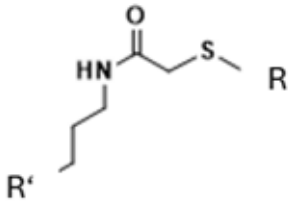
a linker chosen from maleimide – thiosuccinimide linker having the formula

 and a disulfide having the formula R'-S-S-R;

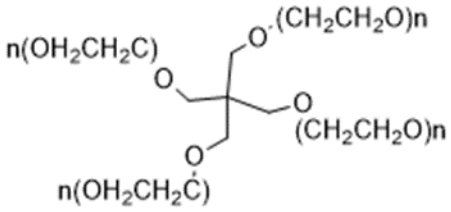
and a half-life extending polymer that is a PEG of the following formula

 or  having a molecular weight of 5 kDa to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa; or

(b) the amino acid sequence of SEQ ID NO 305 or 307;

an acetamide – thioether having the formula 

and a half-life extending polymer that is a PEG of the following formula



or 

having a molecular weight of 5 kDa to 20 kDa, preferably about 5 kDa or about 10 kDa or about 20 kDa, wherein R’ stands for the binding peptide and R stands for the half-life extending PEG polymer.

52. The use of any one of Claims 46 to 51, wherein the immunotherapy comprises that a T cell engager is to be administered.

53. The use of any one of claims 46-52, wherein the molar ratio of the TCE masking molecule to the TCE is in the range of 1000 to 1, or 250:1 to 10:1, or 100:1 to 25:1.

54. The use of any of claims 56 to 53, wherein the TCE masking molecule is to be administered before, during or after administration of a TCE.

55. The use of any one of claim 46 to 53, wherein the TCE is:

(i) A TCE comprising at least a first, a second, and a third domain in an amino to carboxyl order, wherein:

the first domain binds to a target cell surface antigen, wherein the antigen is preferably a tumor antigen;

the second domain binds to an epitope of CD3ε; and

the third domain comprises two polypeptide monomers, each comprising a hinge, a CH2, and a CH3 domain, wherein the two polypeptide monomers are fused to each other via a peptide linker, and wherein the third domain comprises in an amino to carboxyl order: hinge-CH2-CH3-linker-hinge-CH2-CH3;

(ii) A TCE comprising:

a first binding domain, wherein the first binding domain comprises an scFv, scFab, or Fab which binds to a first target cell surface antigen (TAA1);

a second binding domain wherein the second binding domain comprises an scFv, scFab, or Fab which binds to an extracellular epitope on the human CD3ε chain;

a spacer, wherein said spacer is a single chain fragment crystallizable (scFc), human serum albumin (HSA), programmed death receptor 1 (PD1), or a hetero fragment crystallizable (hetero FC);

a third binding domain wherein the third binding domain comprises an scFv, scFab, or Fab which binds to a second target cell surface antigen (TAA2); and

a fourth binding domain wherein the fourth binding domain comprises an scFv, scFab, or Fab which binds to an epitope ofCD3ε,

wherein the first binding domain binds to the first target cell surface antigen and the third binding domain binds to the second target cell surface antigen simultaneously, wherein the first target cell surface antigen and the second target cell surface antigen are on the same target cell,

wherein the TCE is a preferably a single polypeptide chain;

wherein the first target cell surface antigen and the second target cell surface antigen are not identical, and

wherein the first binding domain and the second binding domain form a first bispecific entity and the third and the fourth binding domain form a second bispecific entity, and

wherein

the spacer entity is positioned between the first and the second bispecific entities;

(iii) an IgG-based bispecific antibody; or

(iv) a heterodimeric antibody.

56. The use of claim 55, wherein the TCE under (i.) of claim 55 is a single chain molecule.

57. The use of claim 55 or 56, wherein a glycosylation site at Kabat position 314 of the CH2 domains in the third domain of the TCE is removed by a N314X substitution, wherein X is any amino acid excluding Q.

58. The use of any one of claims 55 to 57, wherein each of the polypeptide monomers of the third domain comprises an amino acid sequence that is at least 90% identical to an amino acid sequence selected from the group consisting of: SEQ ID NOs: 437 to 444, or comprises the amino acid sequence selected from the group consisting of SEQ ID NOs: 437 to 444.

59. The use of any one of claims 55 to 58, wherein the CH2 domain comprises an intra domain cysteine disulfide bridge.

60. The use of any one of claims 55 to 59, wherein the tumor antigen is CDH19, CDH3, MSLN, DLL3, FLT3, EGFRvIII, BCMA, PSMA, CD33, CD19, CD20, CLDN18.2, CLDN6, MUC17, EpCAM, STEAP1, or CD70.

61. The use of any one of claims 55 to 60, wherein the TCE under (i.) in claim 54 comprises in an amino to carboxyl order:

(a) a first domain;

(b) a peptide linker having an amino acid sequence of any one of SEQ ID NOs: 187-189;

(c) a second domain;

(d) a peptide linker having an amino acid sequence of any one of SEQ ID NOs: 187, 188, 189, 195, 196, 197 and 198;

(e) a first peptide monomer of the third domain having an amino acid sequence of any of SEQ ID NOs 437 to 444;

(f) a peptide linker having an amino acid sequence of any one of SEQ ID NOs: 191, 192, 193 and 194; and

(g) a second peptide monomer of the third domain having an amino acid sequence of any of SEQ ID NOs 437 to 444.

62. The use of any of claims 55 to 61, wherein the first and/or third binding domain of the TCE under (ii.) in claim 39 comprises a VH region comprising CDR-H1, CDR-H2 and CDR-H3 and a VL region comprising CDR-L1, CDR-L2 and CDR-L3 selected from the group consisting of:

(a) CDR-H1 as depicted in SEQ ID NO: 4, CDR-H2 as depicted in SEQ ID NO: 5, CDR-H3 as depicted in SEQ ID NO: 6, CDR-L1 as depicted in SEQ ID NO: 1, CDR-L2 as depicted in SEQ ID NO: 2 and CDR-L3 as depicted in SEQ ID NO: 3;

(b) CDR-H1 as depicted in SEQ ID NO: 29, CDR-H2 as depicted in SEQ ID NO: 30, CDR-H3 as depicted in SEQ ID NO: 31, CDR-L1 as depicted in SEQ ID NO: 34, CDR-L2 as depicted in SEQ ID NO: 35 and CDR-L3 as depicted in SEQ ID NO: 36;

(c) CDR-H1 as depicted in SEQ ID NO: 42, CDR-H2 as depicted in SEQ ID NO: 43, CDR-H3 as depicted in SEQ ID NO: 44, CDR-L1 as depicted in SEQ ID NO: 45, CDR-L2 as depicted in SEQ ID NO: 46 and CDR-L3 as depicted in SEQ ID NO: 47;

(d) CDR-H1 as depicted in SEQ ID NO: 53, CDR-H2 as depicted in SEQ ID NO: 54, CDR-H3 as depicted in SEQ ID NO: 55, CDR-L1 as depicted in SEQ ID NO: 56, CDR-L2 as depicted in SEQ ID NO: 57 and CDR-L3 as depicted in SEQ ID NO: 58;

(e) CDR-H1 as depicted in SEQ ID NO: 65, CDR-H2 as depicted in SEQ ID NO: 66, CDR-H3 as depicted in SEQ ID NO: 67, CDR-L1 as depicted in SEQ ID NO: 68, CDR-L2 as depicted in SEQ ID NO: 69 and CDR-L3 as depicted in SEQ ID NO: 70;

(f) CDR-H1 as depicted in SEQ ID NO: 83, CDR-H2 as depicted in SEQ ID NO: 84, CDR-H3 as depicted in SEQ ID NO: 85, CDR-L1 as depicted in SEQ ID NO: 86, CDR-L2 as depicted in SEQ ID NO: 87 and CDR-L3 as depicted in SEQ ID NO: 88;

(g) CDR-H1 as depicted in SEQ ID NO: 94, CDR-H2 as depicted in SEQ ID NO: 95, CDR-H3 as depicted in SEQ ID NO: 96, CDR-L1 as depicted in SEQ ID NO: 97, CDR-L2 as depicted in SEQ ID NO: 98 and CDR-L3 as depicted in SEQ ID NO: 99;

(h) CDR-H1 as depicted in SEQ ID NO: 105, CDR-H2 as depicted in SEQ ID NO: 106, CDR-H3 as depicted in SEQ ID NO: 107, CDR-L1 as depicted in SEQ ID NO: 109, CDR-L2 as depicted in SEQ ID NO: 110 and CDR-L3 as depicted in SEQ ID NO: 111;

(i) CDR-H1 as depicted in SEQ ID NO: 115, CDR-H2 as depicted in SEQ ID NO: 116, CDR-H3 as depicted in SEQ ID NO: 117, CDR-L1 as depicted in SEQ ID NO: 118, CDR-L2 as depicted in SEQ ID NO: 119 and CDR-L3 as depicted in SEQ ID NO: 120;

(j) CDR-H1 as depicted in SEQ ID NO: 126, CDR-H2 as depicted in SEQ ID NO: 127, CDR-H3 as depicted in SEQ ID NO: 128, CDR-L1 as depicted in SEQ ID NO: 129, CDR-L2 as depicted in SEQ ID NO: 130 and CDR-L3 as depicted in SEQ ID NO: 131;

(k) CDR-H1 as depicted in SEQ ID NO: 137, CDR-H2 as depicted in SEQ ID NO: 138, CDR-H3 as depicted in SEQ ID NO: 139, CDR-L1 as depicted in SEQ ID NO: 140, CDR-L2 as depicted in SEQ ID NO: 141 and CDR-L3 as depicted in SEQ ID NO: 142;

(l) CDR-H1 as depicted in SEQ ID NO: 152, CDR-H2 as depicted in SEQ ID NO: 153, CDR-H3 as depicted in SEQ ID NO: 154, CDR-L1 as depicted in SEQ ID NO: 155, CDR-L2 as depicted in SEQ ID NO: 156 and CDR-L3 as depicted in SEQ ID NO: 157;

(m) CDR-H1 as depicted in SEQ ID NO: 167, CDR-H2 as depicted in SEQ ID NO: 168, CDR-H3 as depicted in SEQ ID NO: 169, CDR-L1 as depicted in SEQ ID NO: 170, CDR-L2 as depicted in SEQ ID NO: 171 and CDR-L3 as depicted in SEQ ID NO: 172;

(n) CDR-H1 as depicted in SEQ ID NO: 203, CDR-H2 as depicted in SEQ ID NO: 204, CDR-H3 as depicted in SEQ ID NO: 205, CDR-L1 as depicted in SEQ ID NO: 206, CDR-L2 as depicted in SEQ ID NO: 207 and CDR-L3 as depicted in SEQ ID NO: 208;

(o) CDR-H1 as depicted in SEQ ID NO: 214, CDR-H2 as depicted in SEQ ID NO: 215, CDR-H3 as depicted in SEQ ID NO: 216, CDR-L1 as depicted in SEQ ID NO: 217, CDR-L2 as depicted in SEQ ID NO: 218 and CDR-L3 as depicted in SEQ ID NO: 219;

(p) CDR-H1 as depicted in SEQ ID NO: 226, CDR-H2 as depicted in SEQ ID NO: 227, CDR-H3 as depicted in SEQ ID NO: 228, CDR-L1 as depicted in SEQ ID NO: 229, CDR-L2 as depicted in SEQ ID NO: 230 and CDR-L3 as depicted in SEQ ID NO: 231;

(q) CDR-H1 as depicted in SEQ ID NO: 238, CDR-H2 as depicted in SEQ ID NO: 239, CDR-H3 as depicted in SEQ ID NO: 240, CDR-L1 as depicted in SEQ ID NO: 241, CDR-L2 as depicted in SEQ ID NO: 242 and CDR-L3 as depicted in SEQ ID NO: 243; and

(r) CDR-H1 as depicted in SEQ ID NO: 420, CDR-H2 as depicted in SEQ ID NO: 421, CDR-H3 as depicted in SEQ ID NO: 422, CDR-L1 as depicted in SEQ ID NO: 423, CDR-L2 as depicted in SEQ ID NO: 424 and CDR-L3 as depicted in SEQ ID NO: 425.

63. The use of any one of claims 55 to 62, wherein the TCE comprises the amino acid sequence of SEQ ID NO: 17, 52, 63, 81, 93, 104, 114, 125, 136, 147, 162, 177, 213,226, 238, 248, 255 or 430, preferably 104 or 255.

64. The use of claim 55, wherein the heterodimeric antibody comprises:

(a) a first monomer comprising a first heavy chain comprising:

(i) a first variable heavy domain;

(ii) a first constant heavy chain comprising a first CH1 domain and a first Fc domain; (iii) a scFv that binds CD3ε and comprises a scFv variable light domain, an scFv linker, and a scFv variable heavy domain

wherein the scFv is covalently attached between the C-terminus of the CH1 domain and the N-terminus of the first Fc domain using domain linker(s);

(b) a second monomer comprising a second heavy chain comprising a second variable

heavy domain and a second constant heavy chain comprising a second Fc domain; and

(c) a common light chain comprising a variable light domain and a constant light domain,

wherein the first variable heavy domain and the variable light domain bind human STEAP1, and

wherein the second variable heavy domain and the variable light domain bind human STEAP1, and wherein

(1) the first monomer comprises the amino acid sequence of SEQ ID NO: 375, the second monomer comprises the sequence of SEQ ID NO: 374, and the common light chain

comprises the sequence of SEQ ID NO:373;

(2) the first monomer comprises the amino acid sequence of SEQ ID NO: 380, the second

monomer comprises the sequence of SEQ ID NO:376, and the common light chain

comprises the sequence of SEQ ID NO:373; or

(3) the first monomer comprises the amino acid sequence of SEQ ID NO: 379, the second

monomer comprises the sequence of SEQ ID NO: 378, and the common light chain

comprises the sequence of SEQ ID NO: 377.

65. The TCE masking molecule or the use of any of the preceding claims, wherein the CD3ε binding domain has 80, 90, 95 or 99% sequence identity with the sequence of SEQ ID NO 26, 381, 382 or 383 or has the sequence of SEQ ID NO 26, 381, 382 or 383.

66. Use of a T cell engager (TCE) masking molecule in the manufacture of a medicament for the attenuation of in vivo exposure of a TCE after administration of the TCE molecule, wherein the administration is preferably via the i.v. or s.c. route, wherein the TCE masking molecule comprises:

(i.) a binding peptide that binds to an anti-CD3ε paratope of a CD3ε binding domain of a TCE, wherein the anti-CD3ε paratope is directed against an epitope located within CD3ε, and wherein CD3ε comprises the amino acid sequence of SEQ ID NO: 257;

(ii) a linker covalently linked to the C-terminus of the binding peptide; and

(iii) a half-life extending polymer covalently linked to the linker,

wherein the binding peptide binds to an anti-CD3ε paratope with a Kd which is at least 1.5-fold lower than the Kd for the amino acid sequence of SEQ ID NO: 262 binding to an anti-CD3ε paratope, preferably, at least 2-fold lower, more preferably 3-fold lower, and wherein the TCE masking molecule is to be administered before, during or after the administration of the TCE at a molar excess of 10 to 1000, or 25 to 250 with respect to the TCE.