Single-chain TRAIL-receptor agonist proteins

Related Applications

The instant application claims the benefit of priority to U.S. Provisional Patent Application No. 61/983,152, filed April 23, 2014, which is incorporated by reference herein in its entirety.

Field of the Invention

The present invention provides specific TRAIL receptor agonist proteins comprising three soluble TRAIL domains and an Fc fragment, nucleic acid molecules encoding the TRAIL receptor agonist proteins, and uses thereof. The TRAIL receptor agonist proteins are substantially non-aggregating and suitable for therapeutic, diagnostic and/or research applications.

Background of the Invention

It is known that trimerization of TNF superfamily (TNFSF) cytokines is required for efficient receptor binding and activation. Trimeric complexes of TNF superfamily cytokines, however, are difficult to prepare from recombinant monomeric units.

WO 01/49866 and WO 02/09055 disclose recombinant fusion proteins comprising a TNF cytokine and a multimerization component, particularly a protein from the C1q protein family or a collectin. A disadvantage of these fusion proteins is, however, that the trimerization domain usually has a large molecular weight and/or that the trimerization is rather inefficient.

Schneider et al. (J Exp Med 187 (1989), 1205-1213) describe that trimers of TNF cytokines are stabilized by N-terminally positioned stabilization motifs. In CD95L, the stabilization of the receptor binding domain trimer is presumably caused by N-terminal amino acid domains which are located near the cytoplasmic membrane.

Shiraishi et al. (Biochem Biophys Res Commun 322 (2004), 197-202) describe that the receptor binding domain of CD95L may be stabilized by N-terminally positioned artificial α-helical coiled-coil (leucine zipper) motifs. It was found, however, that the orientation of the polypeptide chains to each other, *e.g.* parallel or antiparallel orientation, can hardly be predicted. Further, the optimal number of heptad-repeats in the coiled-coil zipper motif are difficult to determine. In addition, coiled-coil structures have the tendency to form macromolecular aggregates after alteration of pH and/or ionic strength.

WO 01/25277 relates to single-chain oligomeric polypeptides which bind to an extracellular ligand binding domain of a cellular receptor, wherein the polypeptide comprises at least three receptor binding sites of which at least one is capable of binding to a ligand binding domain of the cellular receptor and at least one is incapable of effectively binding to a ligand binding domain of the cellular receptor, whereby the single-chain oligomeric polypeptides are capable of binding to the receptor, but incapable of activating the receptor. For example, the monomers are derived from cytokine ligands of the TNF family, particularly from TNF-α.

WO 2005/103077 discloses single-chain fusion polypeptides comprising at least three monomers of a TNF family ligand member and at least two peptide linkers that link the monomers of the TNF ligand family members to one another. Recent experiments, however, have shown that these single-chain fusion polypeptides show undesired aggregation.

WO 2010/010051 discloses single-chain fusion polypeptides comprising three soluble TNF family cytokine domains and at least two peptide linkers. The described fusion polypeptides are substantially non-aggregating.

Moreover, previous work, including that of Papadopoulos et al. (Cancer Chemother Pharmacol, 2015, DOI 10.1007/s00280-015-2712-0), has demonstrated that TRAIL receptor superclustering can result in toxicity.

Accordingly, there is a need in the art for novel TRAIL receptor agonists that exhibit high biological activity, high stability, low toxicity, and allow for efficient recombinant manufacturing.

Summary

In a first aspect, there is provided a nucleic acid molecule comprising SEQ ID NO:16. In a second aspect, there is provided a nucleic acid molecule comprising nucleotides 19 to 2298 of SEQ ID NO:16. In a third aspect, there is provided a nucleic acid molecule comprising nucleotides 79 to 2298 of SEQ ID NO:16.

The present disclosure provides specific TRAIL receptor agonist proteins that exhibit low proteolytic degradation, long half-life, and low TRAIL receptor superclustering *in vivo* (along with concomitant toxicity).

The TRAIL receptor agonist proteins of the instant disclosure generally comprise:(i) a first soluble TRAIL cytokine domain; (ii) a first peptide linker; (iii) a second soluble TRAIL domain; (iv) a second peptide linker; (v) a third soluble TRAIL domain; and (vi) an antibody Fc fragment.

In one embodiment, the present disclosure provides a single-chain fusion polypeptide comprising: (i) a first soluble TRAIL domain, (ii) a first peptide linker, (iii) a second soluble TRAIL domain, (iv) a second peptide linker, (v) a third soluble TRAIL domain, and (vi) an antibody Fc fragment. In one embodiment, the antibody Fc fragment (vi) is located N terminal to the first TRAIL domain (i) and/or C-terminal to the third TRAIL domain (v). In another embodiment the antibody Fc fragment is located C-terminally to the third TRAIL domain (v). In one embodiment, the polypeptide is substantially non aggregating. In another embodiment, the second and/or third soluble TRAIL domain is an N-terminally shortened domain which optionally comprises amino acid sequence mutations.

In one embodiment, at least one of the soluble TRAIL domains, particularly at least one of the soluble TRAIL domains (iii) and (v), is a soluble TRAIL domain with an N-terminal sequence which starts between amino acid Gln120 and Val122 of human TRAIL and wherein Arg121 may be replaced by a neutral amino acid, *e.g.*, Ser or Gly. In another embodiment, at least one of the soluble TRAIL domains, particularly at least one of the soluble TRAIL domains (iii) and (v), is a soluble TRAIL domain with an N-terminal sequence selected from (a) Arg121 – Val122 – Ala123 and (b)

(Gly/Ser)121 – Val122 – Ala123. In one embodiment, the soluble TRAIL domain ends with amino acid Gly281 of human TRAIL and/or optionally comprises a mutation at positions R130, G160, H168, R170, H177, Y189, R191 , Q193, E195, N199, K201, Y213, T214, S215, H264, I266, D267 or D269 or at two or more of said positions. In one embodiment, the soluble TRAIL domain (i) consists of amino acids Gln120 – Gly281 of human TRAIL according to SEQ ID NO: 1 and the soluble TRAIL domains (iii) and (v) consist of amino acids Arg121 – Gly281 of human TRAIL according to SEQ ID NO: 1.

In one embodiment, the first and second peptide linkers (ii) and (iv) independently have a length of 3-8 amino acids, particularly a length of 3, 4, 5, 6, 7, or 8 amino acids, and preferably are glycine/serine linkers, optionally comprising an asparagine residue which may be glycosylated. In one embodiment, the first and the second peptide linkers (ii) and (iv) consist of the amino acid sequence according to SEQ ID NO: 2. In another embodiment, the polypeptide additionally comprises an N-terminal signal peptide domain, *e.g.*, of SEQ ID NO: 12, which may comprise a protease cleavage site, and/or which additionally comprises a C-terminal element which may comprise and/or connect to a recognition/purification domain, *e.g.*, a Strep-tag according to SEQ ID NO: 13.

In one embodiment, the antibody Fc fragment (vi) is fused to the soluble TRAIL domain (i) and/or (v) via a hinge-linker, preferably of SEQ ID NO: 11. In another embodiment, the antibody Fc fragment (vi) consists of the amino acid sequence as shown in SEQ ID NO: 10 or 17. In one embodiment, the polypeptide comprises the amino acid sequence of SEQ ID NO: 14, 15 or 18.

In another embodiment, the present disclosure provides a TRAIL receptor agonist protein comprising a polypeptide having the amino acid sequence set forth in SEQ ID NO: 19, 20 or 21.

In another embodiment, the present disclosure provides a TRAIL receptor agonist protein comprising a polypeptide having the amino acid sequence set forth in SEQ ID NO: 26, 27, 28, 29, or 30.

In another embodiment, the present disclosure provides a TRAIL receptor agonist protein comprising two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19. In one embodiment, the two polypeptides are covalently linked through three interchain disulfide bonds formed between cysteine residues 513, 519, and 522 of each polypeptide.

In one embodiment, one or more of the asparagine residues at positions 168 and 337 of the polypeptide(s) are N-glycosylated. In another embodiment, the asparagine residues at positions 168 and 337 of the polypeptide(s) are both N-glycosylated.

In another embodiment, the polypeptide(s) are further post-translationally modified. In another embodiment, the post-translational modification comprises the N-terminal glutamine modified to pyroglutamate.

In another embodiment, the present disclosure provides a pharmaceutical composition comprising a TRAIL receptor agonist protein disclosed herein and one or more pharmaceutically acceptable carriers, diluents, excipients, and/or adjuvants.
In another embodiment, the present disclosure provides a nucleic acid molecule encoding the TRAIL receptor agonist protein. In another embodiment, the present disclosure provides an expression vector comprising the nucleic acid molecule. In a fourth aspect, there is provided an expression vector comprising the nucleic acid molecule according to the second or third aspect. In another embodiment, the present disclosure provides a cell comprising the nucleic acid molecule. In a fifth aspect, there is provided a cell comprising the nucleic acid molecule according to the second or third aspect. In a further embodiment, the cell is a eukaryotic cell. In another embodiment, the cell is a mammalian cell. In another embodiment, the cell is a Chinese Hamster Ovary (CHO) cell. In other embodiments, the cell is selected from the group consisting of CHO-DBX11, CHO-DG44, CHO-S, and CHO-K1 cells. In other embodiments, the cell is selected from the group consisting of Vero, BHK, HeLa, COS, MDCK, HEK-293, NIH-3T3, W138, BT483, Hs578T, HTB2, BT20, T47D, NS0, CRL7030, HsS78Bst, PER.C6, SP2/0-Agl4, and hybridoma cells.

In another embodiment, the present disclosure provides a method of treating a subject having a TRAIL-associated disease or disorder, the method comprising administering to the subject an effective amount of the TRAIL receptor agonist protein. In one

embodiment, the TRAIL receptor agonist protein is administered alone. In another embodiment, the TRAIL receptor agonist protein is administered before, concurrently, or after the administration of a second agent. In another embodiment, the disease or disorder is selected from the group consisting of: tumors, infectious diseases, inflammatory diseases, metabolic diseases, autoimmune disorders, degenerative diseases, apoptosis-associated diseases, and transplant rejections. In one embodiment, the tumors are solid tumors. In one embodiment, the tumors arise from the group of cancers consisting of sarcoma, esophageal cancer, and gastric cancer. In another embodiment, the tumors arise from Ewing's sarcoma or fibrosarcoma, In another embodiment, the tumors arise from the group of cancers consisting of Non-Small Cell Lung Carcinoma (NSCLC), pancreatic cancer, colorectal cancer, breast cancer, ovarian cancer, head and neck cancers, and Small Cell Lung Cancer (SCLC). In another embodiment, the tumors are lymphatic tumors. In one embodiment, the tumors are hematologic tumors. In another embodiment, the tumors arise from non-Hodgkin's lymphoma, leukemia, acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), B cell lymphoma, Burkitt's lymphoma, chronic myelocytic leukemia (CML), chronic lymphocytic leukemia (CLL), or hairy cell leukemia. In another embodiment, the autoimmune disorders are rheumatoid diseases, arthritic diseases, or rheumatoid and arthritic diseases. In a further embodiment, the disease or disorder is rheumatoid arthritis. In another embodiment, the degenerative disease is a neurodegenerative disease. In a further embodiment, the neurodegenerative disease is multiple sclerosis.

In one embodiment, the second agent is a chemotherapeutic, radiotherapeutic, or biological agent. In one embodiment, the second agent is selected from the group consisting of Duvelisib, Ibrutinib, Navitoclax, and Venetoclax, In another embodiment, the second agent is an apoptotic agent. In one embodiment, the apoptotic second agent is selected from the group consisting of Bortezomib, Azacitidine, Dasatinib, and Gefitinib. In a particular embodiment, the pharmaceutical compositions disclosed herein are administered to a patient by intravenous or subcutaneous administration. In other embodiments, the disclosed pharmaceutical compositions are administered to a patient by oral, parenteral, intramuscular, intrarticular, intrabronchial, intraabdominal, intracapsular, intracartilaginous, intracavitary, intracelial,

intracerebellar, intracerebroventricular, intracolic, intracervical, intragastric, intrahepatic, intramyocardial, intraosteal, intrapelvic, intrapericardiac, intraperitoneal, intrapleural, intraprostatic, intrapulmonary, intrarectal, intrarenal, intraretinal, intraspinal, intrasynovial, intrathoracic, intrauterine, intravesical, bolus, vaginal, rectal, buccal, sublingual, intranasal, or transdermal administration.

In one embodiment, the TRAIL receptor agonist protein is administered as a single bolus. In another embodiment, TRAIL receptor agonist protein may be administered over several divided doses. The TRAIL receptor agonist protein can be administered at about 0.1-100 mg/kg. In one embodiment, the TRAIL receptor agonist protein can be administered at a dosage selected from the group consisting of: about 0.1-0.5, 0.1-1, 0.1-10, 0.1-20, 0.1-50, 0.1-75, 1-10, 1-15, 1-7.5, 1.25-15, 1.25-7.5, 2.5-7.5, 2.5-15, 5-15, 5-7.5,1-20, 1-50, 7-75, 1-100, 5-10, 5-15, 5-20, 5-25, 5-50, 5-75, 10-20, 10-50, 10-75, and 10-100 mg/kg. In other embodiments, the TRAIL receptor agonist protein is present in pharmaceutical compositions at about 0.1-100 mg/ml. In one embodiment, the TRAIL receptor agonist protein is present in pharmaceutical compositions at an amount selected from the group consisting of: about 0.1-0.5, 0.1-1, 0.1-10, 0.1-20, 0.1-50, 0.1-75, 1-10, 1-20, 1-50, 1-75, 1-100, 5-10, 5-15, 5-20, 5-25, 5-50, 5-75, 10-20, 10-50, 10-75, or 10-100 mg/ml. In other embodiments, a therapeutically effective amount of TRAIL receptor agonist protein is administered to a subject. In another embodiment, a prophylactically effective amount of TRAIL receptor agonist protein is administered to a subject.

Description of the Figures

Figure 1 Domain structure of a single-chain fusion polypeptide comprising three TRAIL domains. I., II., III. Soluble TRAIL domains.

Figure 2 Schematic picture representing the general structure of TRAIL.
■ ■ ■ Cell membrane, N-terminus located within the cell,
1. anti-parallel β-fold of receptor-binding domain (RBD),
2. interface of RBD and cell membrane,
3. protease cleavage site.

Figure 3 Schematic picture representing the structure of the native TRAIL trimer. Cylindric structures represent RBDs. N-termini connect RBDs with the cell membrane.

Figure 4 Schematic picture representing the structure of three soluble domains comprising the receptor-binding domain of a TRAIL. I., II., III. soluble TRAIL domains.

Figure 5 Trimerization of the soluble domains comprising the RBD of TRAIL, characterized in that the N- and C-termini of the three soluble domains form a surface.

Figure 6 Schematic picture representing the structure of the single-chain TRAIL comprising all or a part of the stalk-region illustrating the requirement of longer linkers to compensate for the distance to the N-terminus of the next soluble domain.

Figure 7 scFv-TRAIL fusion protein known from the art.

Figure 8 Fc-TRAIL fusion protein known from the art.

Figure 9A Single-chain fusion polypeptide comprising an additional Fab antibody fragment.

Figure 9B Single-chain fusion polypeptide comprising an additional scFv antibody fragment.

Figure 10 Dimerization of two N-terminally fused scFc fusion polypeptides via disulfide bridges.

Figure 11 Dimerization of two C-terminally fused scFc fusion polypeptides via disulfide bridges.

Figure 12 Dimerization of single-chain fusion polypeptides via a linker.

Figure 13 Single-chain fusion polypeptide comprising an additional Fab antibody fragment further fused to a second fusion polypeptide or to a scFv fusion polypeptide.

Figure 14 Dimerization of two scFab fusion polypeptides via disulfide bridges.

Figure 15 N-terminally fused scFc fusion polypeptides further comprising a Fv and/or Fab antibody fragment.

Figure 16 C-terminally fused scFc fusion polypeptides further comprising a Fv and/or Fab antibody fragment.

Figure 17A The exemplary TRAIL receptor agonist protein as shown with the N-terminal signal peptide domain is set forth in SEQ ID NO: 14. The mature protein (which does not include the N-terminal signal peptide domain) is set forth in SEQ ID NO: 19.

Figure 17B Schematic picture representing the overall structure and annotated sequence of an exemplary TRAIL receptor agonist protein.

Figure 18 Assay setup of the ELISA for the quantitation of the TRAIL-receptor agonists containing an FC-domain.

Figure 19 A TRAIL receptor agonist protein comprising two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19 induces cell death in human tumor cell lines *in vitro*. SKM-1, Colo205 or Jurkat cells were treated with increasing concentrations the TRAIL receptor agonist protein for 24 hours and cell viability assessed.

Figures 20(A-C) A TRAIL receptor agonist protein comprising two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19 synergizes with anti-tumorigenic agents *in vitro*. SU-DHL-4 cells were incubated with increasing concentrations of the TRAIL receptor agonist protein in the presence or absence of the indicated concentrations of venetoclax (Figure 20A) or navitoclax (Figure 20B) for 24 hours. Alternatively, (Figure 20C) NCI-H596 cells were treated with increasing concentrations of the TRAIL receptor agonist protein in the presence or absence of the indicated concentrations of docetaxel (DTX) for 72 hours. Cell viability was assessed and synergy determined by Bliss sum.

Figure 21 Effect of TRAIL receptor agonist protein comprising two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19 on tumor growth in the Colo205 colorectal carcinoma xenograft model.

Figure 22 Effect of TRAIL receptor agonist protein comprising two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19 on tumor growth in the SKM-1 acute myeloid leukemia xenograft model.

Figure 23 Effect of TRAIL receptor agonist protein comprising two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19 on tumor growth in the H460LM non-small cell lung xenograft model.

Figures 24(A-G) Effect of TRAIL receptor agonist protein comprising two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19 on tumor growth in PDX models. Diamonds, TRAIL receptor agonist protein-treated; Squares, untreated. Tumor volumes are shown for (A) CTG-0069, (B) CTG-0167, (C) CTG-0293, (D) CTG-0785, (E) CTG-0714, (F) CTG-0136, and (G) CTG-0485.

Detailed Description of the Invention

According to the present invention, it was found that fusing a single-chain TRAIL receptor-binding domain to an Fc domain results in a hexavalent TRAIL receptor agonist providing high biological activity combined with good stability. Accordingly, a single-chain fusion polypeptide comprising at least three soluble TRAIL domains connected by two peptide linkers and N‑terminally and/or C-terminally an antibody Fc fragment, is provided.

Preferably, the single-chain fusion polypeptide is non-aggregating. The term "non-aggregating" refers to a monomer content of the preparation of ≥ 50%, preferably ≥ 70% and more preferably ≥ 90%. The ratio of monomer content to aggregate content may be determined by examining the amount of aggregate formation using size-exclusion chromatography (SEC). The stability concerning aggregation may be determined by SEC after defined time periods, *e.g.* from a few to several days, to weeks and months under different storage conditions, *e.g.* at 4°C or 25°C. For the fusion protein, in order to be classified as substantially non -aggregating, it is preferred that the monomer content is as defined above after a time period of several days, *e.g.* 10 days, more preferably after several weeks, *e.g.* 2, 3 or 4 weeks, and most preferably after several months, *e.g.* 2 or 3 months of storage at 4°C, or 25°C.

The single-chain fusion polypeptide may comprise additional domains which may be located at the N- and/or C-termini thereof. Examples for additional fusion domains are *e.g.* an N-terminal signal peptide domain which may comprise a protease cleave site or a C-terminal element which may comprise and/or connect to a recognition/purification domain. According to a preferred embodiment, the fusion polypeptide comprises a Strep-tag at its C-terminus that is fused via a linker. An exemplary Strep-tag including a short serine linker is shown in SEQ ID NO: 13.

The TRAIL receptor agonist protein of the present invention comprises three soluble domains derived from TRAIL. Preferably, those soluble domains are derived from a mammalian, particularly human TRAIL including allelic variants and/or derivatives thereof. The soluble domains comprise the extracellular portion of TRAIL including

the receptor binding domain without membrane located domains. Like other proteins of the TNF superfamily, TRAIL is anchored to the membrane via an N -terminal portion of 15-30 amino acids, the so-called stalk-region. The stalk region contributes to trimerization and provides a certain distance to the cell membrane. However, the stalk region is not part of the receptor binding domain (RBD).

Importantly, the RBD is characterized by a particular localization of its N- and C-terminal amino acids. Said amino acids are immediately adjacent and are located centrally to the axis of the trimer. The first N-terminal amino acids of the RBD form an anti-parallel beta-strand with the C-terminal amino acids of the RBD (Figs. 2 and 3).

Thus, the anti-parallel beta-strand of the RBD forms an interface with the cell membrane, which is connected to and anchored within the cell membrane via the amino acids of the stalk region. It is highly preferred that the soluble TRAIL domains of the TRAIL receptor agonist protein comprise a receptor binding domain of the TRAIL lacking any amino acids from the stalk region (Figs. 4 and 5). Otherwise, a long linker connecting the C-terminus of one of the soluble domains with the N -terminus of the next soluble domain would be required to compensate for the N-terminal stalk-region of the next soluble domain (Figure 6), which might result in instability and/or formation of aggregates.

A further advantage of such soluble domains is that the N- and C-terminal amino acids of the RBD are not accessible for any anti-drug antibodies. Preferably, the single-chain fusion polypeptide is capable of forming an ordered trimeric structure comprising at least one functional binding site for the respective TRAIL receptor.

The TRAIL receptor agonist protein comprises three functional TRAIL receptor binding sites, *i.e.* amino acid sequences capable of forming a complex with a TRAIL receptor. Thus, the soluble domains are capable of binding to the corresponding TRAIL receptor. In one embodiment, at least one of the soluble domains is capable of receptor activation, whereby apoptotic and/or proliferative activity may be affected. In a further embodiment, one or more of the soluble domains are selected as not being capable of receptor activation.

The soluble TRAIL domain may be derived from human TRAIL as shown in SEQ ID NO: 1. Preferably, the soluble TRAIL domains are derived from human TRAIL, particularly starting from amino acids 120-122 and comprise particularly amino acids 120-281, 121-281 or 122-281 of SEQ ID NO: 1. Optionally, amino acid Arg121 of SEQ ID NO: 1 may be replaced by a non-charged amino acid, *e.g.* Ser or Gly.

Table 1: Sequence of Human TRAIL Protein

SEQ ID NO	Sequence
1	MAMMEVQGGPSLGQTCVLIVIFTVLLQSLCVAVTYVYFTNELK QMQDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQ LRQLVRKMILRTSEETISTVQEKQQNISPLVRERGPQRVAAHI TGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLH LRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIY KYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKEND RIFVSVTNEHLIDMDHEASFFGAFLVG

As indicated above, the soluble TRAIL domains may comprise the wild-type sequences as indicated in SEQ ID NO: 1. It should be noted, however, that it is possible to introduce mutations in one or more of these soluble domains, *e.g.* mutations which alter (*e.g.* increase or decrease) the binding properties of the soluble domains. In one embodiment, soluble domains may be selected which cannot bind to the corresponding cytokine receptor.

In a further preferred embodiment of the invention, the soluble TRAIL domain (i) comprises a mutant of TRAIL or a receptor binding domain thereof which binds and/or activates TRAIL-receptor 1 (TRAILR1) and/or TRAIL-receptor 2 (TRAILR2). The binding and/or activity of the mutant may be, *e.g.*, determined by the assays as described in van der Sloot et al. (PNAS, 2006, 103:8634-8639), Kelley et al. (J. Biol. Chem., 2005, 280:2205-2215), or MacFarlane et al. (Cancer Res., 2005, 65: 11265-11270).

The mutant may be generated by any technique and is known by the skilled person, *e.g.*, the techniques described in van der Sloot et al. (PNAS, 2006, 103:8634-8639), Kelley et al. (J. Biol. Chem., 2005, 280:2205-2215), or MacFarlane et al. (Cancer Res., 2005, 65: 11265-11270) and may comprise any type of structural mutations, *e.g.*, substitution, deletion, duplication and/or insertion of an amino acid. A preferred embodiment is the generation of substitutions. The substitution may affect at least one amino acid of TRAIL or a receptor binding domain thereof as described herein. In a preferred embodiment, the substitution may affect at least one of the amino acids of TRAIL, *e.g.*, human TRAIL (*e.g.*, SEQ ID NO: 1). Preferred substitutions in this regard affect at least one of the following amino acids of human TRAIL of SEQ ID NO: 1: R130, G160, Y189, R191, Q193, E195, N199, K201, Y213, T214, S215, H264, 1266, D267, D269. Preferred amino acid substitutions of human TRAIL of SEQ ID NO:1 are at least one of the following substitutions: R130E, G160M, Y189A, Y189Q, R191K, Q193S, Q193R, E195R, N199V, N199R, K201R, Y213W, T214R, S215D, H264R, I266L, D267Q, D269H, D269R, or D269K.

The amino acid substitution(s) may affect the binding and/or activity of TRAIL, *e.g.*, human TRAIL, to or on either the TRAILR1 or the TRAILR2. Alternatively, the amino acid substitution(s) may affect the binding and/or activity of TRAIL, *e.g.*, human TRAIL, to or on both, the TRAILR1 and the TRAILR2. The binding and/or activity of the TRAILR1 and/or TRAILR2 may be affected positively, *i.e.*, stronger, more selective or more specific binding and/or more activation of the receptor. Alternatively, the binding and/or activity of the TRAILR1 and/or TRAILR2 may be affected negatively, *i.e.*, weaker, less selective or less specific binding and/or less or no activation of the receptor.

Examples of mutants of TRAIL with amino acid substitution(s) of the invention that affect binding and/or activation of both TRAILR1 and TRAILR2 may be found, *e.g.*, in Table 1 of MacFarlane et al. (cf. above) and may comprise a human TRAIL mutant with the following two amino acid substitutions of SEQ ID NO: 1 Y213W and S215D or with the following single amino acid substitution: Y189A.

Examples of mutants of TRAIL with amino acid substitution(s) of the invention that affect binding and/or activation of TRAILR1 may be found, *e.g.*, in Table 1 of MacFarlane et al. (cf. above) and may comprise a human TRAIL mutant with the following four amino acid substitutions of SEQ ID NO: 1 N 199V, K201R, Y213W and S215D or with the following five amino acid substitutions: Q193S, N199V, K201R, Y213W and S215D, or may be found in Table 2 of Kelley et al. (cf. above) and may comprise a human TRAIL mutant with the following six amino acid substitutions: Y213W, S215D, Y189A, Q193S, N199V, and K201R, or with Y213W, S215D, Y189A, Q193S, N199R, and K201R.

Examples of mutants of TRAIL with amino acid substitution(s) of the invention that affect binding and/or activation of TRAILR2 may be found, *e.g.*, in Table 1 of MacFarlane et al. (cf. above) or in Table 2 of Kelley et al. (cf. above) and may comprise a human TRAIL mutant with the following six amino acid substitutions of SEQ ID NO: 1: Y189Q, R191 K, Q193R, H264R, I266L, and D267Q , or may be found in Table 2 of van der Sloot et al. (cf. above) and may comprise a human TRAIL mutant with the following single amino acid substitution: D269H, or with the following two amino acid substitutions: D269H and E195R or D269H and T214R.

Thus one preferred embodiment is a TRAIL receptor agonist protein as described herein wherein at least one of the soluble domains comprises a mutant of TRAIL or of a receptor binding domain thereof which binds and/or activates TRAILR1 and/or TRAILR2.

Further examples of mutants of TRAIL, which show reduced TRAIL induced receptor aggregation are H168 (S, T, Q), R170 (E, S, T, Q) and H177 (S, T).

One preferred embodiment of a TRAIL receptor agonist protein comprising a mutant of TRAIL or of a receptor binding domain as described herein is a TRAIL receptor agonist protein wherein component (i) comprises at least one amino acid substitution, particularly as indicated below.

Such an amino acid substitution affects at least one of the following amino acid positions of human TRAIL (SEQ ID NO: 1): R130, G160, H168, R170, H177, Y189, R191 , Q193, E195, N199, K201 , Y213, T214, S215, H264, 1266, D267, D269.

Such an amino acid substitution is at least one of the following: R13OE, G16OM, H168 (S, T, Q), R170 (E, S, T, Q), H177 (SJ)1 Y189A, Y189Q, R191K, Q193S, Q193R, E195R, N199V, N199R, K201R, Y213W, T214R, S215D, H264R, I266L, D267Q, D269H, D269R, or D269K.

A preferred TRAIL-R2 selective domain comprises amino acid substitutions Y189Q, R191K, Q193R, H264R, I266L and D267Q.

A preferred TRAIL-R1 selective domain comprises amino acid substitutions Y189A, Q193S, N199V, K201R, Y213W and S215D.

The single-chain fusion molecule of the present invention comprises three soluble TRAIL domains, namely components (i), (iii) and (v). The stability of a single-chain TRAIL fusion polypeptide against aggregation is enhanced, if the second and/or third soluble TRAIL domain is an N-terminally shortened domain which optionally comprises amino acid sequence mutations. Thus, preferably, both the second and the third soluble TRAIL domain are N-terminally shortened domains which optionally comprise amino acid sequence mutations in the N-terminal regions, preferably within the first five amino acids of the N-terminus of the soluble TRAIL domain. These mutations may comprise replacement of charged, *e.g.* acidic or basic amino acids, by neutral amino acids, particularly serine or glycine.

In contrast thereto, the selection of the first soluble TRAIL domain is not as critical. Here, a soluble domain having a full-length N-terminal sequence may be used. It should be noted, however, that also the first soluble TRAIL domain may have an N-terminally shortened and optionally mutated sequence.

In a further preferred embodiment of the present invention, the soluble TRAIL domains (i), (iii) and (v) are soluble human TRAIL domains. The first soluble TRAIL

domain (i) may be selected from native, shortened and/or mutated sequences. Thus, the first soluble TRAIL domain (i) has an N-terminal sequence which may start between amino acid GIu116 and Val122 of human TRAIL, and wherein Arg121 may be replaced by a neutral amino acid, *e.g.* by Ser or GIy. The second and third soluble TRAIL domains (iii) and (v) have a shortened N-terminal sequence which preferably starts between amino acid Gln120 and Val122 of human TRAIL and wherein Arg121 may be replaced by another amino acid, *e.g.* Ser or Gly.

Preferably, the N-terminal sequence of the soluble TRAIL domains (iii) and (v) is selected from:
(a) Arg121 - Val122 - Ala123 and
(b) (Gly/Ser) 121.

The soluble TRAIL domain preferably ends with amino acid Gly281 of human TRAIL. In certain embodiments, the TRAIL domain may comprise internal mutations as described above.

Components (ii) and (iv) of the TRAIL receptor agonist protein are peptide linker elements located between components (i) and (iii) or (iii) and (v), respectively. The flexible linker elements have a length of 3-8 amino acids, particularly a length of 3, 4, 5, 6, 7, or 8 amino acids. The linker elements are preferably glycine/serine linkers, *i.e.* peptide linkers substantially consisting of the amino acids glycine and serine. In cases in which the soluble cytokine domain terminates with S or G (C-terminus), *e.g.* human TRAIL, the linker starts after S or G. In cases in which the soluble cytokine domain starts with S or G (N-terminus), the linker ends before this S or G.

It should be noted that linker (ii) and linker (iv) do not need to be of the same length. In order to decrease potential immunogenicity, it may be preferred to use shorter linkers. In addition it turned out that shorter linkers lead to single chain molecules with reduced tendency to form aggregates. Whereas linkers that are substantially longer than the ones disclosed here may exhibit unfavorable aggregations properties.

If desired, the linker may comprise an asparagine residue which may form a glycosylate site Asn-Xaa-Ser. In certain embodiments, one of the linkers, *e.g.* linker (ii) or linker (iv) comprises a glycosylation site. In other embodiments, both linkers (iv) comprise glycosylation sites. In order to increase the solubility of the sc TRAIL proteins and/or in order to reduce the potential immunogenicity, it may be preferred that linker (ii) or linker (iv) or both comprise a glycosylation site.

Preferred linker sequences are selected from GSGSGSGS (SEQ ID NO: 3), GSGSGNGS (SEQ ID NO: 2), GGSGSGSG (SEQ ID N0: 4), GGSGSG (SEQ ID NO: 5), GGSG (SEQ ID NO: 6), GGSGNGSG (SEQ ID NO: 7), GGNGSGSG (SEQ ID NO: 8), GGNGSG (SEQ ID NO: 9), and GSGS (SEQ ID NO: 23).

According to a most preferred embodiment, the linker sequences are each GSGSGNGS according to SEQ ID NO: 2. Example linker sequences are shown in Table 2.

Table 2: Example Linker Sequences

SEQ ID NO	Sequence
2	GSGSGNGS
3	GSGSGSGS
4	GGSGSGSG
5	GGSGSG
6	GGSG
7	GGSGNGSG
8	GGNGSGSG
9	GGNGSG
22	GSGSGS
23	GSGS
24	GSG

The TRAIL receptor agonist protein additionally comprises an antibody Fc fragment domain which may be located N-terminal to the first TRAIL domain (i) and/or C-terminal to the third TRAIL domain (v). Preferably, the antibody Fc fragment domain comprises or consists of an amino acid sequence as shown in SEQ ID NO: 10. Alternatively, the Fc fragment domain comprises or consists of an amino acid sequence as shown in SEQ ID NO: 17. Example Fc fragment domains are shown in Table 3.

Table 3: Example Fc Fragment Domains

SEQ ID NO	Sequence
10	PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTVLHQDW LNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK
17	PAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPE VKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW LNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQK SLSLSPGK

The total number of glycosites and the individual position of the carbohydrates in three dimensions impacts the in-vivo stability of TRAIL receptor agonist proteins. Further, carbohydrate recognition depends on local density of the terminal saccharides, the branching of the carbohydrate tree and the relative position of the carbohydrates matter.

Depletion of CH2-domain carbohydrates is necessary in order to avoid Fc-receptor based crosslinking *in vivo* and potential TRAIL-receptor superclustering-based toxicity. Further, partially degraded carbohydrates reduce the *in vivo* half-life of TRAIL

receptor agonist proteins through lectin-driven mechanisms. By reducing the total number of glycosylation sites on the molecule, the resulting compound is less accessible to these mechanisms, increasing half-life. Accordingly, in one embodiment, the overall number of glycosites on the TRAIL receptor agonist proteins of the instant invention was reduced through the depletion of CH2 glycosites, resulting in TRAIL receptor agonist proteins comprising N297S equivalent mutations (according to the EU numbering system) creating aglycosl-CH2 domains.

CH2-glycosites present on the inner surface areas normally shield the subdomain from proteases during “open Fc-conformation transits” wherein hinge-interchain disulfide bonds are reduced and the covalent interchain linkage is disrupted. This enables CH2-dissociation and exposure of the inner surface area towards proteases. TRAIL receptor agonist proteins comprising an N297S equivalent mutation (according to the EU numbering system) creating an aglycosl-CH2 are therefore likely to be less proteolytically stable that equivalent structures with wild-type CH2 glycosylation. This would impact the compound’s stability during USP/DSP/storage, where host cell proteases are present and have long-term access to the structure. Accordingly, in certain embodiments, the TRAIL receptor agonist lacks CH2 glycosites, but comprises glycosites in the linker sequences of each polypeptide chain (e.g., GSGSGNGS according to SEQ ID NO: 2). In certain exemplary embodiments, the TRAIL receptor agonist comprises two glycosites per polypeptide chain, for a total of four glycosites,

According to a preferred embodiment of the invention, the antibody Fc fragment domain is fused via a hinge‑linker element. The hinge-linker element has a length of 10-30 amino acids, particularly a length of 15-25 amino acids, *e.g.* 22 amino acids. The hinge-linker element preferably comprises the hinge-region sequence of an immunoglobulin, herein referred to as “Ig hinge-region”. The term “Ig hinge‑region” means any polypeptide comprising an amino acid sequence that shares sequence identity or similarity with a portion of a naturally occurring Ig hinge-region sequence which includes the cysteine residues at which the disulfide bonds link the two heavy chains of the immunoglobulin.

Derivatives and analogues of the hinge-region can be obtained by mutations. A derivative or analogue as referred to herein is a polypeptide comprising an amino acid sequence that shares sequence identity or similarity with the full length sequence of the wild type (or naturally occurring protein) except that it has one or more amino acid sequence differences attributable to a deletion, insertion and/or substitution. According to the present invention, however, the term “hinge-linker” is not limited to those linkers comprising an Ig hinge-region or a derivative thereof, but any linkers long enough to allow the domains attached by the hinge-linker element to attain a biologically active confirmation.

The number of molecules with open Fc-conformation in an individual TRAIL receptor agonist protein depends on the number of interchain-disulfide bonds present in the hinge region. Accordingly, in one embodiment a third cysteine was introduced into the hinge region of the TRAIL receptor agonist proteins of the instant invention in order to ameliorate the effect of depleting the CH2-glycosites.

Further, the TRAIL receptor agonist proteins of the invention additionally comprise mutation of the upper-hinge lysine to a glycine to reduce proteolytic processing at this site.

A particularly preferred hinge-linker element comprises or consists of the amino acid sequence as shown in SEQ ID NO: 11 (Table 4).

The TRAIL receptor agonist protein may additionally comprise an N-terminal signal peptide domain, which allows processing, *e.g.* extracellular secretion, in a suitable host cell. Preferably, the N-terminal signal peptide domain comprises a protease cleavage site, *e.g.* a signal peptidase cleavage site and thus may be removed after or during expression to obtain the mature protein. A particularly preferred N-terminal signal peptide domain comprises the amino acid sequence as shown in SEQ ID NO: 12 (Table 4).

Further, the TRAIL receptor agonist protein may additionally comprise a C-terminal element, having a length of *e.g.* 1-50, preferably 10-30 amino acids which may

include or connect to a recognition/purification domain, *e.g.* a FLAG domain, a Strep-tag or Strep-tag II domain and/or a poly-His domain. According to a particularly preferred embodiment, the fusion polypeptide comprises a Strep-tag fused to the C-terminus via a short serine linker as shown in SEQ ID NO: 13 (Table 4).

An exemplary hinge-linker element, N-terminal signal peptide domain, and short serine linker are shown in Table 4.

Table 4: Exemplary domains and linkers

SEQ ID NO	Sequence
11	GPGSSSSSSSGSCDKTHTCPPC
12	METDTLLVFVLLVWVPAGNG
13	SSSSSSAWSHPQFEK
25	GPGSSSSSSGSCDKTHTCPPC

According to a particularly preferred embodiment of the invention, the fusion polypeptide comprises three soluble TRAIL domains fused by peptide linker elements of SEQ ID NO: 2. The first soluble TRAIL domain (i) consists of amino acids 120-281 of human TRAIL according to SEQ ID NO: 1 and the soluble TRAIL domains (iii) and (v) consist of amino acids 121-281 of human TRAIL according to SEQ ID NO: 1. Additionally, the fusion polypeptide comprises an antibody Fc fragment domain according to SEQ ID NO: 10 that is fused C-terminally to the soluble TRAIL domain (v) via a hinge-linker according to SEQ ID NO: 11. The inventors surprisingly found that this particular fusion polypeptide provides improved biological activity and is particularly stable. The amino acid sequence of an exemplary embodiment of a TRAIL receptor agonist protein of the invention is set forth in SEQ ID NO: 19.

Further, the fusion polypeptide may comprise an N-terminal signal peptide domain *e.g.* according to SEQ ID NO: 12. A specific example of a TRAIL receptor agonist protein of the invention is shown in SEQ ID NO: 14.

According to another preferred embodiment, the fusion polypeptide may additionally comprise a C-terminal Strep-tag that is fused to the polypeptide of the invention via a short serine linker as shown in SEQ ID NO: 13. According to this aspect of the invention, the Fc fragment preferably consists of the amino acid sequence as shown in SEQ ID NO: 10 or 17. Further, the Fc fragment may consist of a shorter Fc fragment, for example including amino acids 1‑217 of SEQ ID NO: 10. Particularly preferred examples of fusion polypeptides comprising a C-terminal Strep-tag are shown in SEQ ID NOs: 15 and 18.

The exemplary TRAIL receptor agonist proteins as shown in SEQ ID NOs: 14, 15 and 18 each comprise an N-terminal signal peptide domain. The signal peptide domain includes amino acids 1-20. In each case, the mature protein starts with amino acid 21. Mature exemplary TRAIL receptor agonist proteins of the instant invention are set forth in SEQ ID NO: 19, 20, 21, 26, 27, 28, 29, and 30. Exemplary TRAIL receptor agonist proteins described above are shown in Table 5.

The TRAIL receptor agonist as set forth in SEQ ID NO: 19 has a reduced total number of glycosylation sites (the N297S mutation in the CH2 region providing an aglycosylated CH2 domain), an increased number of inter-chain disulfide bonds in the hinge region, and the mutation of an upper-hinge lysine to a glycine. These alterations provide a decrease in potential degradation and TRAIL receptor superclustering (along with concomitant toxicity) while increasing the half-life of the molecule. In some embodiments, the N-terminal glutamine is modified to pyroglutamate (Liu *et al.* 2011, J. Biol. Chem. 286:11211-11217).

Table 5: Exemplary TRAIL Receptor Agonist Proteins

SEQ ID NO	Sequence
14	METDTLLVFVLLVWVPAGNGQRVAAHITGTRGRSNTLSSPNSKNEK ALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRF QEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVGGSGS GNGSRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGH

	SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQ YIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRI FVSVTNEHLIDMDHEASFFGAFLVGGSGSGNGSRVAAHITGTRGRS NTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSA RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS FFGAFLVGGPGSSSSSSSGSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
15	METDTLLVFVLLVWVPAGNGQRVAAHITGTRGRSNTLSSPNSKNEK ALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRF QEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVGGSGS GNGSRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGH SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQ YIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRI FVSVTNEHLIDMDHEASFFGAFLVGGSGSGNGSRVAAHITGTRGRS NTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSA RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS FFGAFLVGGPGSSSSSSSGSCDKTHTCPPCPAPELLGGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYSSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGSSSSSSAWSHPQFEK
18	METDTLLVFVLLVWVPAGNGQRVAAHITGTRGRSNTLSSPNSKNEK ALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRF QEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYG LYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVGGSGS GNGSRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGH SFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQ

	YIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRI FVSVTNEHLIDMDHEASFFGAFLVGGSGSGNGSRVAAHITGTRGRS NTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEK GFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSA RNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS FFGAFLVGGPGSSSSSSSGSCDKTHTCPPCPAPPVAGPSVFLFPP KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEW ESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCS VMHEALHNHYTQKSLSLSPGK
19	QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK YTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVS VTNEHLIDMDHEASFFGAFLVGGSGSGNGSRVAAHITGTRGRSNTL SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNS CWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG AFLVGGSGSGNGSRVAAHITGTRGRSNTLSSPNSKNEKALGRKINS WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENT KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGG IFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVGGPGSSSSSSGS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG K
20	QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK YTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVS VTNEHLIDMDHEASFFGAFLVGGSGSGNGSRVAAHITGTRGRSNTL SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNS CWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG AFLVGGSGSGNGSRVAAHITGTRGRSNTLSSPNSKNEKALGRKINS

	WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENT KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGG IFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVGGPGSSSSSSSGS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTVLH QDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRE EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG SSSSSSAWSHPQFEK
21	QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK YTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVS VTNEHLIDMDHEASFFGAFLVGGSGSGNGSRVAAHITGTRGRSNTL SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNS CWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG AFLVGGSGSGNGSRVAAHITGTRGRSNTLSSPNSKNEKALGRKINS WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENT KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGG IFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVGGPGSSSSSSSGS CDKTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDV SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSREE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDG SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
26	QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK YTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVS VTNEHLIDMDHEASFFGAFLVGGSGSGNGSRVAAHITGTRGRSNTL SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNS CWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG AFLVGGSGSGNGSRVAAHITGTRGRSNTLSSPNSKNEKALGRKINS WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENT KNDKQMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGG IFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVGGPGSSSSSSGSD

	KTHTCPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQD WLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSREEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSSS SSSAWSHPQFEK
27	QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK YTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVS VTNEHLIDMDHEASFFGAFLVGGSGSGNGSRVAAHITGTRGRSNTL SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNS CWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG AFLVGGSGSRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESS RSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDK QMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELK ENDRIFVSVTNEHLIDMDHEASFFGAFLVGGPGSSSSSSSGSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSSSSS SAWSHPQFEK
28	QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK YTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVS VTNEHLIDMDHEASFFGAFLVGGSGSGSRVAAHITGTRGRSNTLSS PNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIY SQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCW SKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFL VGGSGSGSRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESS RSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDK QMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELK ENDRIFVSVTNEHLIDMDHEASFFGAFLVGGPGSSSSSSSGSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTVLHQDWL

	NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGSSSSS SAWSHPQFEK
29	QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK YTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVS VTNEHLIDMDHEASFFGAFLVGGSGSGNGSRVAAHITGTRGRSNTL SSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFY YIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNS CWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFG AFLVGGSGSRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESS RSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDK QMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELK ENDRIFVSVTNEHLIDMDHEASFFGAFLVGGPGSSSSSSSGSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
30	QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLS NLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYK YTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVS VTNEHLIDMDHEASFFGAFLVGGSGSGSRVAAHITGTRGRSNTLSS PNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIY SQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPDPILLMKSARNSCW SKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFL VGGSGSGSRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESS RSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDK QMVQYIYKYTSYPDPILLMKSARNSCWSKDAEYGLYSIYQGGIFELK ENDRIFVSVTNEHLIDMDHEASFFGAFLVGGPGSSSSSSSGSCDKT HTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHE DPEVKFNWYVDGVEVHNAKTKPREEQYSSTYRVVSVLTVLHQDWL NGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

A further aspect of the present invention relates to a nucleic acid molecule encoding a TRAIL receptor agonist protein as described herein. The nucleic acid molecule may be a DNA molecule, *e.g.* a double-stranded or single- stranded DNA molecule, or an RNA molecule. The nucleic acid molecule may encode the TRAIL receptor agonist protein or a precursor thereof, *e.g.* a pro- or pre-proform of the TRAIL receptor agonist protein which may comprise a signal sequence or other heterologous amino acid portions for secretion or purification which are preferably located at the N- and/or C-terminus of the TRAIL receptor agonist protein. The heterologous amino acid portions may be linked to the first and/or second domain via a protease cleavage site, *e.g.* a Factor X3, thrombin or IgA protease cleavage site. A specific example of a nucleic acid sequence of the invention is shown in Table 6 as SEQ ID NO: 16. This nucleic acid molecule encodes the fusion polypeptide of SEQ ID NO: 14.

Table 6: Nucleic Acid Sequence of Exemplary TRAIL Receptor Agonist Protein

SEQ ID NO	Sequence
16	gatatcggtaccgccaccatggaaaccgacaccctgctggtgttcgtgctgctcgtgtgggtgcc agccggcaatggacagagagtggccgctcatatcaccggcacccggggcagatctaacacc ctgtccagccccaactccaagaacgagaaggccctgggccggaagatcaactcctgggagt cctccagatccggccactcctttctgtccaacctgcacctgagaaacggcgagctggtcatcca cgagaagggcttctactacatctactcccagacctacttcaggtttcaggaagagatcaaagag aacacaaagaacgacaagcagatggtgcagtatatctacaagtacacctcctaccccgaccc catcctgctgatgaagtccgcccggaactcctgctggtccaaggatgctgagtacggcctgtac agcatctaccagggcggcatcttcgagctgaaagagaacgaccggatcttcgtgtccgtgacc aacgagcacctgatcgacatggaccacgaggccagctttttcggcgcctttctcgtgggcggat ccggaagcggaaacggcagtagagtggctgcccacattaccggaaccagaggccggtcca acaccctgagcagccctaacagcaaaaatgagaaagctctcgggcgcaagatcaacagct gggaatctagcagaagcggccacagctttctgagcaatctgcatctgcggaacggcgaactc gtgattcatgagaaggggttttattatatctatagccagacatactttcgattccaggaggaaatca aggaaaacaccaaaaatgataaacagatggtccagtacatttataagtataccagctaccctg atcctatcctcctcatgaagtctgccagaaactcttgttggagcaaggacgccgagtatggactg tactctatctatcaggggggatctttgaactcaaagaaaacgatcgcatctttgtcagcgtcacc aatgagcatctcattgatatggatcatgaagctagtttcttcggggcattcctcgtgggaggctccg gctctggcaacggatctagagtcgccgcacacatcacagggaccagaggcagaagcaata ccctgtcctccccaaatagtaaaaacgaaaaggcactcggccgcaaaattaattcctgggag

	agcagcagatccgggcacagttttctgtctaatctccatctgaggaatggggagctggtgattca cgaaaaaggattttactacatttacagtcagacttactttcgttttcaggaagagattaaggaaaat accaaaaacgacaagcagatggtccagtacatctataaatacacctcttatcctgacccaattct gctcatgaagagtgcccgcaacagctgctggtctaaagacgccgaatacgggctgtattccatt taccaggggggaatttttgagctgaaggaaaatgatcggatttttgtctctgtcacaaacgaaca cctcatcgatatggatcacgaagcctctttctttggcgccttcctggtcggaggccctggctcgagt tccagctcctcttctggctcctgcgacaagacccacacctgtccccttgtcctgcccctgaactg ctgggcggaccttccgtgttcctgttccccccaaagcccaaggacaccctgatgatctcccgga cccccgaagtgacctgcgtggtggtggatgtgtctcacgaggaccctgaagtgaagttcaattg gtacgtggacggcgtggaagtgcacaacgccaagaccaagcccagagaggaacagtactc ctccacctaccgggtggtgtctgtgctgaccgtgctgcaccaggactggctgaacggcaaaga gtacaagtgcaaggtgtccaacaaggccctgcctgcccccatcgaaaagaccatctccaagg ccaagggccagccccgggaaccccaggtgtacacactgccccctagccgggaagagatga ccaagaaccaggtgtccctgacctgcctggtcaagggcttttacccctccgacattgccgtgga atgggagtccaacggccagcctgagaacaactacaagaccacccccccctgtgctggactcc gacggctcattcttcctgtactccaagctgacagtggacaagtcccggtggcagcagggcaac gtgttctcctgctccgtgatgcacgaggccctgcacaaccactacacccagaagtccctgtccct gagccccggcaaatgatagaagcttgatatc

The nucleic acid molecule may be operatively linked to an expression control sequence, *e.g.* an expression control sequence which allows expression of the nucleic acid molecule in a desired host cell. The nucleic acid molecule may be located on a vector, *e.g.* a plasmid, a bacteriophage, a viral vector, a chromosomal integration vector, etc. Examples of suitable expression control sequences and vectors are described for example by Sambrook et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, and Ausubel et al. (1989), Current Protocols in Molecular Biology, John Wiley & Sons or more recent editions thereof.

Various expression vector/host cell systems may be used to express the nucleic acid sequences encoding the TRAIL receptor agonist proteins of the present invention. Suitable host cells include, but are not limited to, prokaryotic cells such as bacteria, *e.g. E.coli*, eukaryotic host cells such as yeast cells, insect cells, plant cells or animal cells, preferably mammalian cells and, more preferably, human cells. Further, the invention relates to a non-human organism transformed or transfected with a nucleic

acid molecule as described above. Such transgenic organisms may be generated by known methods of genetic transfer including homologous recombination.

A further aspect of the present invention relates to a pharmaceutical or diagnostic composition comprising as the active agent at least one TRAIL receptor agonist protein, a respective nucleic acid encoding therefore, or a transformed or transfected cell, all as described herein.

The term “TRAIL-associated disease or disorder” as used herein is any disease or disorder which may be ameliorated by addition of a TRAIL receptor agonist. At least one TRAIL receptor agonist protein, respective nucleic acid encoding therefore, or transformed or transfected cell, all as described herein may be used in therapy, *e.g.*, in the prophylaxis and/or treatment of disorders caused by, associated with and/or accompanied by dysfunction of TRAIL, particularly proliferative disorders, such as tumors, *e.g.* solid or lymphatic tumors; infectious diseases; inflammatory diseases; metabolic diseases; autoimmune disorders, *e.g.* rheumatoid and/or arthritic diseases; degenerative diseases, *e.g.* neurodegenerative diseases such as multiple sclerosis; apoptosis-associated diseases or transplant rejections.

The term "dysfunction of TRAIL" as used herein is to be understood as any function or expression of TRAIL that deviates from the normal function or expression of TRAIL, *e.g.*, overexpression of the TRAIL gene or protein, reduced or abolished expression of the TRAIL gene or protein compared to the normal physiological expression level of TRAIL, increased activity of TRAIL, reduced or abolished activity of TRAIL, increased binding of TRAIL to any binding partners, *e.g.*, to a receptor, particularly a TRAIL receptor or another cytokine molecule, reduced or abolished binding to any binding partner, *e.g.* to a receptor, particularly a TRAIL receptor or another cytokine molecule, compared to the normal physiological activity or binding of TRAIL.

In various embodiments, a method is provided for diagnosing and/or treating a human subject suffering from a disorder which can be diagnosed and/or treated by targeting TRAIL receptors comprising administering to the human subject a TRAIL receptor agonist protein disclosed herein such that the effect on the activity of the

target, or targets, in the human subject is agonistic, one or more symptoms is alleviated, and/or treatment is achieved. The TRAIL receptor agonist proteins provided herein can be used to diagnose and/or treat humans suffering from primary and metastatic cancers, including carcinomas of breast, colon, rectum, lung (*e.g.*, small cell lung cancer "SCLC" and non- small cell lung cancer "NSCLC"), oropharynx, hypopharynx, esophagus, stomach, pancreas, liver, gallbladder and bile ducts, small intestine, urinary tract (including kidney, bladder and urothelium), female genital tract (including cervix, uterus, and ovaries as well as choriocarcinoma and gestational trophoblastic disease), male genital tract (including prostate, seminal vesicles, testes and germ cell tumors), endocrine glands (including the thyroid, adrenal, and pituitary glands), and skin, as well as hemangiomas, melanomas, sarcomas (including those arising from bone and soft tissues as well as Kaposi’s sarcoma), tumors of the brain, nerves, eyes, and meninges (including astrocytomas, gliomas, glioblastomas, retinoblastomas, neuromas, neuroblastomas, Schwannomas, and meningiomas), tumors arising from hematopoietic malignancies, acute leukemia, acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), B cell lymphoma, Burkitt's lymphoma, chronic myelocytic leukemia (CML), chronic lymphocytic leukemia (CLL), hairy cell leukemia, Hodgkin’s and non-Hodgkin’s lymphomas, DLBCL, follicular lymphomas, hematopoietic malignancies, Kaposi's sarcoma, malignant lymphoma, malignant histiocytosis, malignant melanoma, multiple myeloma, paraneoplastic syndrome/hypercalcemia of malignancy, or solid tumors.

A pharmaceutical composition comprising a TRAIL receptor agonist protein disclosed herein and a pharmaceutically acceptable carrier is provided. In some embodiments, the pharmaceutical composition comprises at least one additional therapeutic agent for treating a disorder. For example, the additional agent may be a therapeutic agent, a chemotherapeutic agent; an imaging agent, a cytotoxic agent, an angiogenesis inhibitor, a kinase inhibitor (including but not limited to a KDR and a TIE-2 inhibitor), a co-stimulation molecule modulator or an immune checkpoint inhibitor (including but not limited to anti-B7.1, anti-B7.2, anti-B7.3, anti-B7.4, anti-CD28, anti-B7RP1, CTLA4-Ig, anti-CTLA-4, anti-PD-1, anti-PD-L1, anti-PD-L2, anti-ICOS, anti-LAG-3, anti-Tim3, anti-VISTA, anti-HVEM, anti-BTLA, LIGHT fusion protein, anti-CD137, anti-CD137L, anti-OX40, anti-OX40L, anti-CD70, anti-CD27, anti-GAL9, anti-A2AR, anti-KIR, anti-IDO-1, anti-CD20), a dendritic cell/antigen-presenting cell modulator

(including but not limited to anti-CD40 antibody, anti-CD40 L, anti-DC-SIGN, anti-Dectin-1, anti-CD301, anti-CD303, anti-CD123, anti-CD207, anti-DNGR1, anti-CD205, anti-DCIR, anti-CD206, anti-ILT7), a modulator for Toll-like receptors (including but not limited to anti-TLR-1, anti-TLR-2, anti-TLR-3, anti-TLR-4, anti-TLR-4, anti-TLR-5, anti-TLR-6, anti-TLR-7, anti-TLR-8, anti-TLR-9), an adhesion molecule blocker (including but not limited to an anti-LFA-1 antibody, an anti-E/L selectin antibody, a small molecule inhibitor), an anti-cytokine antibody or functional fragment thereof (including but not limited to an anti-IL-18, an anti-TNF, or an anti-IL-6/cytokine receptor antibody), a bispecific redirected T cell or NK cell cytotoxicity (including but not limited to a BiTE®), a chimeric T cell receptor (CAR-T) based therapy, a T cell receptor (TCR)-based therapy, a therapeutic cancer vaccine, methotrexate, cyclosporin, rapamycin, FK506, a detectable label or reporter, a TNF antagonist, an anti-rheumatic, a muscle relaxant, a narcotic, a non-steroid anti-inflammatory drug (NSAID), an analgesic, an anesthetic, a sedative, a local anesthetic, a neuromuscular blocker, an antimicrobial, an antipsoriatic, a corticosteriod, an anabolic steroid, an erythropoietin, an immunization, an immunoglobulin, an immunosuppressive, a growth hormone, a hormone replacement drug, a radiopharmaceutical, an antidepressant, an antipsychotic, a stimulant, an asthma medication, a beta agonist, an inhaled steroid, an epinephrine or analog, a cytokine, or a cytokine antagonist.

In an embodiment, a method of treating a cancer or in the prevention or inhibition of metastases from the tumors described herein, the TRAIL receptor agonist protein(s) can be used alone or in combination with one or more additional agents, *e.g.*, a chemotherapeutic, radiotherapy, or biological agent. In some embodiments, the agent can include the following:13-cis-Retinoic Acid; 2-CdA; 2-Chlorodeoxyadenosine; 5-Azacitidine; 5-Fluorouracil; 5-FU; 6-Mercaptopurine; 6-MP; 6-TG; 6-Thioguanine; Abraxane; Accutane®; Actinomycin-D; Adriamycin®; Adrucil®; Afinitor®; Agrylin®; Ala-Cort®; Aldesleukin; Alemtuzumab; ALIMTA; Alitretinoin; Alkaban-AQ®; Alkeran®; All-transretinoic Acid; Alpha Interferon; Altretamine; Amethopterin; Amifostine; Aminoglutethimide; Anagrelide; Anandron®; Anastrozole; Arabinosylcytosine; Ara-C Aranesp®; Aredia®; Arimidex®; Aromasin®; Arranon®; Arsenic Trioxide; Arzerra™; Asparaginase; ATRA; Avastin®; Azacitidine; BCG; BCNU; Bendamustine; Bevacizumab; Bexarotene; BEXXAR®; Bicalutamide; BiCNU; Blenoxane®; Bleomycin; Bortezomib; Busulfan; Busulfex®; C225; Calcium

Leucovorin; Campath®; Camptosar®; Camptothecin-11; Capecitabine Carac™; Carboplatin; Carmustine; Carmustine Wafer; Casodex®; CC-5013; CCI-779; CCNU; CDDP; CeeNU; Cerubidine®; Cetuximab; Chlorambucil; Cisplatin; Citrovorum Factor; Cladribine; Cortisone; Cosmegen®; CPT-11; Cyclophosphamide; Cytadren®; Cytarabine; Cytarabine Liposomal; Cytosar-U®; Cytoxan®; Dacarbazine; Dacogen; Dactinomycin; Darbepoetin Alfa; Dasatinib; Daunomycin; Daunorubicin; Daunorubicin Hydrochloride; Daunorubicin Liposomal; DaunoXome®; Decadron; Decitabine; Delta-Cortef®; Deltasone®; Denileukin; Diftitox; DepoCyt™; Dexamethasone; Dexamethasone Acetate; Dexamethasone Sodium Phosphate; Dexasone; Dexrazoxane; DHAD; DIC; Diodex; Docetaxel; Doxil®; Doxorubicin; Doxorubicin Liposomal; Droxia™; DTIC; DTIC-Dome®; Duralone®; Duvelisib; Efudex®; Eligard™; Ellence™; Eloxatin™; Elspar®; Emcyt®; Epirubicin; Epoetin Alfa; Erbitux; Erlotinib; Erwinia L-asparaginase; Estramustine; Ethyol Etopophos®; Etoposide; Etoposide Phosphate; Eulexin®; Everolimus; Evista®; Exemestane; Fareston®; Faslodex®; Femara®; Filgrastim; Floxuridine; Fludara®; Fludarabine; Fluoroplex®; Fluorouracil; Fluorouracil (cream); Fluoxymesterone; Flutamide; Folinic Acid; FUDR®; Fulvestrant; Gefitinib; Gemcitabine; Gemtuzumab ozogamicin; Gemzar; Gleevec™; Gliadel® Wafer; GM-CSF; Goserelin; Granulocyte-Colony Stimulating Factor (G-CSF); Granulocyte Macrophage Colony Stimulating Factor (G-MCSF); Halotestin®; Herceptin®; Hexadrol; Hexalen®; Hexamethylmelamine; HMM; Hycamtin®; Hydrea®; Hydrocort Acetate®; Hydrocortisone; Hydrocortisone Sodium Phosphate; Hydrocortisone Sodium Succinate; Hydrocortone Phosphate; Hydroxyurea; Ibrutinib; Ibritumomab; Ibritumomab Tiuxetan; Idamycin®; Idarubicin Ifex®; Interferon-alpha; Interferon-alpha-2b (PEG Conjugate); Ifosfamide; Interleukin-11 (IL-11); Interleukin-2 (IL-2); Imatinib mesylate; Imidazole Carboxamide; Intron A®; ipilimumab, Iressa®; Irinotecan; Isotretinoin; Ixabepilone; Ixempra™; KADCYCLA®; Kidrolase (t) Lanacort®; Lapatinib; L-asparaginase; LCR; Lenalidomide; Letrozole; Leucovorin; Leukeran; Leukine™; Leuprolide; Leurocristine; Leustatin™; Lirilumab; Liposomal Ara-C; Liquid Pred®; Lomustine; L-PAM; L-Sarcolysin; Lupron®; Lupron Depot®; Matulane®; Maxidex; Mechlorethamine; Mechlorethamine Hydrochloride; Medralone®; Medrol®; Megace®; Megestrol; Megestrol Acetate; MEK inhibitors; Melphalan; Mercaptopurine; Mesna; Mesnex™; Methotrexate; Methotrexate Sodium; Methylprednisolone; Meticorten®; Mitomycin; Mitomycin-C; Mitoxantrone M-

Prednisol®; MTC; MTX; Mustargen®; Mustine; Mutamycin®; Myleran®; Mylocel™; Mylotarg®; Navitoclax; Navelbine®; Nelarabine; Neosar®; Neulasta™; Neumega®; Neupogen®; Nexavar®; Nilandron®; Nilotinib; Nilutamide; Nipent®; Nitrogen Mustard Novaldex®; Nivolumab; Novantrone®; Nplate; Octreotide; Octreotide acetate; Ofatumumab; Oncospar®; Oncovin®; Ontak®; Onxal™; Oprelvekin; Orapred®; Orasone®; Oxaliplatin; Paclitaxel; Paclitaxel Protein-bound; Pamidronate; Panitumumab; Panretin®; Paraplatin®; Pazopanib; Pediapred®; PEG Interferon; Pegaspargase; Pegfilgrastim; PEG-INTRON™; PEG-L-asparaginase; PEMETREXED; Pembrolizumab; Pentostatin; Pertuzumab; Phenylalanine Mustard; Pidilizumab; Platinol®; Platinol-AQ®; Prednisolone; Prednisone; Prelone®; Procarbazine; PROCRIT®; Proleukin®; Prolifeprospan 20 with Carmustine Implant; Purinethol®; BRAF inhibitors; Raloxifene; Revlimid®; Rheumatrex®; Rituxan®; Rituximab; Roferon-A®; Romiplostim; Rubex®; Rubidomycin hydrochloride; Sandostatin®; Sandostatin LAR®; Sargramostim; Solu-Cortef®; Solu-Medrol®; Sorafenib; SPRYCEL™; STI-571; STIVAGRA™, Streptozocin; SU11248; Sunitinib; Sutent®; Tamoxifen Tarceva®; Targretin®; Tasigna®; Taxol®; Taxotere®; Temodar®; Temozolomide Temsirolimus; Teniposide; TESPA; Thalidomide; Thalomid®; TheraCys®; Thioguanine; Thioguanine Tabloid®; Thiophosphoamide; Thioplex®; Thiotepa; TICE®; Toposar®; Topotecan; Toremifene; Torisel®; Tositumomab; Trastuzumab; Treanda®; Tremelimumab; Tretinoin; Trexall™; Trisenox®; TSPA; TYKERB®; Urelumab; VCR; Vectibix™; Velban®; Velcade®; Venetoclax; VePesid®; Vesanoid®; Viadur™; Vidaza®; Vinblastine; Vinblastine Sulfate; Vincasar Pfs®; Vincristine; Vinorelbine; Vinorelbine tartrate; VLB; VM-26; Vorinostat; Votrient; VP-16; Vumon®; Xeloda®; Zanosar®; Zevalin™; Zinecard®; Zoladex®; Zoledronic acid; Zolinza; or Zometa®, and/or any other agent not specifically listed here that target similar pathways.

When two or more substances or principles are to be used as part of a combined treatment regimen, they can be administered via the same route of administration or via different routes of administration, at essentially the same time or at different times (*e.g.* essentially simultaneously, consecutively, or according to an alternating regime). When the substances or principles are to be administered simultaneously via the same route of administration, they may be administered as different

pharmaceutical formulations or compositions or part of a combined pharmaceutical formulation or composition, as will be clear to the skilled person.

Also, when two or more active substances or principles are to be used as part of a combined treatment regimen, each of the substances or principles may be administered in the same amount and according to the same regimen as used when the compound or principle is used on its own, and such combined use may or may not lead to a synergistic effect. However, when the combined use of the two or more active substances or principles leads to a synergistic effect, it may also be possible to reduce the amount of one, more than one, or all of the substances or principles to be administered, while still achieving the desired therapeutic action. This may, *e.g.*, be useful for avoiding, limiting or reducing any unwanted side-effects that are associated with the use of one or more of the substances or principles when they are used in their usual amounts, while still obtaining the desired pharmaceutical or therapeutic effect.

The effectiveness of the treatment regimen used according to the invention may be determined and/or followed in any manner known per se for the disease or disorder involved, as will be clear to the clinician. The clinician will also be able, where appropriate and on a case-by-case basis, to change or modify a particular treatment regimen, so as to achieve the desired therapeutic effect, to avoid, limit or reduce unwanted side-effects, and/or to achieve an appropriate balance between achieving the desired therapeutic effect on the one hand and avoiding, limiting or reducing undesired side effects on the other hand.

Generally, the treatment regimen will be followed until the desired therapeutic effect is achieved and/or for as long as the desired therapeutic effect is to be maintained. Again, this can be determined by the clinician.

In various embodiments, pharmaceutical compositions comprising one or more TRAIL receptor agonist proteins, either alone or in combination with prophylactic agents, therapeutic agents, and/or pharmaceutically acceptable carriers are provided herein. In various embodiments, nonlimiting examples of the uses of the pharmaceutical compositions disclosed herein include diagnosing, detecting, and/or monitoring a disorder, preventing, treating, managing, and/or ameliorating a disorder or one or more symptoms thereof, and/or in research. The formulation of

pharmaceutical compositions, either alone or in combination with prophylactic agents, therapeutic agents, and/or pharmaceutically acceptable carriers, are known to one skilled in the art (US Patent Publication No. 20090311253 A1).

In various embodiments, a pharmaceutical formulation can comprise one or more amino acid, one or more polysaccharide and/or polysorbate, and a TRAIL receptor agonist protein present at a concentration of between about 0.1 and 100 mg/ml, inclusive of endpoints (*e.g.*, 0.1-10, 1-10, .01-50, 1-50, 1-100, 10-100, 25-100, 25-50, or 50-100 mg/ml), where the formulation is at a pH between about 5.0 and 7.0, inclusive of endpoints (*e.g.*, a pH of about 5.0-6.0, 5.5-6.0, 5.0-6.5, 5.5-6.5, or 6.0-7.0). In an embodiment, at least one amino acid in the formulation is histidine and is present at a concentration of about 10-20 mM, 10-15mM, 15-20mM, or about 15mM. In an embodiment, at least one polysaccharide in the formulation is sucrose and is present at a concentration of about 0-8.0% weight/volume (w/v). In an embodiment, the polysorbate in the formulation is polysorbate 80 and is at a concentration of about 0-0.06% w/v. In an embodiment, at least one amino acid in the formulation is arginine and is present at a concentration of about 0-1.5% w/v (*e.g.*, 0.5-1.5, 1.0-1.5, or 0.5-1.0 w/v). In an embodiment, the TRAIL receptor agonist protein is present in the formulation at a concentration of about 0.1-100 mg/ml, (*e.g.*, about 1-100 mg/ml, or about 1-15 mg/ml, or about 1-7.5 mg/ml, or about 2.5-7.5 mg/ml, or about 5-7.5 mg/ml, or about 25-100 mg/ml, or about 20-60 mg/ml, or about 25-50 mg/ml, or about 25 mg/ml, or about 50 mg/ml, or about 0.1-60 mg/ml, or about about 0.1-25 mg/ml, or about 1.0-60 mg/ml, or about 0.5-60 mg/ml, or about 0.1-2.0 mg/ml, or about 0.5-2.0 mg/ml, or about 1-5 mg/ml, or about 1-7.5 mg/ml, or about 1-15 mg/ml, or about 0.5 mg/ml, or about 1.0 mg/m).

As used herein, the phrase "effective amount" means an amount of TRAIL agonist protein that results in a detectable improvement (*e.g.*, at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, or more from baseline) in one or more parameters associated with a dysfunction of TRAIL or with a TRAIL-associated disease or disorder.

In various embodiments, the pharmaceutical formulation is an aqueous formulation, a lyophilized formulation, or a lyophilized and rehydrated formulation. In an

embodiment, the hydrating solution is dextrose and/or saline (*e.g.*, dextrose at a concentration of about 5% w/v and/or the saline at a concentration of about 0.9% w/v). In an embodiment, the pharmaceutical formulation comprises about 15 mM histidine, about 0.03% (w/v) polysorbate 80, about 4% (w/v) sucrose, and about 0.1-25 mg/ml of the TRAIL receptor agonist protein, or about 1-15 mg/ml of TRAIL receptor agonist protein, and is at a pH of about 6. In an embodiment, the formulation further comprises at least one additional agent.

In various embodiments, a formulation is used containing about 25 mg/ml TRAIL receptor agonist protein, about 15 mM histidine, 0.03% polysorbate 80 (weight/volume, w/v), 4.0% sucrose (w/v), and a pH of about 6.0. In some embodiments, the formulation does not comprise arginine. In some embodiments, the formulation exhibits unexpectedly improved freeze-thaw stability, liquid formulation stability, and/or lyophilized formulation stability, as compared to other formulations comprising other components or concentrations.

Methods of administering a therapeutic agent provided herein include, but are not limited to, oral administration, parenteral administration (*e.g.*, intradermal, intramuscular, intraperitoneal, intravenous and subcutaneous), epidural administration, intratumoral administration, mucosal administration (*e.g.*, intranasal and oral routes) and pulmonary administration (*e.g.*, aerosolized compounds administered with an inhaler or nebulizer). The formulation of pharmaceutical compositions for specific routes of administration, and the materials and techniques necessary for the various methods of administration are available and known to one skilled in the art (US Patent Publication No. 20090311253 A1).

In various embodiments, dosage regimens may be adjusted to provide for an optimum desired response (*e.g.*, a therapeutic or prophylactic response). For example, a single bolus may be administered, several divided doses may be administered over time or the dose may be proportionally reduced or increased as indicated by the exigencies of the therapeutic situation. In some embodiments, parenteral compositions are formulated in dosage unit form for ease of administration and uniformity of dosage. The term “dosage unit form” refers to physically discrete

units suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier.

[0164] An exemplary, non-limiting range for a therapeutically or prophylactically effective amount of a TRAIL receptor agonist protein provided herein is about 0.1-100 mg/kg, (*e.g.*, about 0.1-0.5, 0.1-1, 0.1-10, 0.1-20, 0.1-50, 0.1-75, 1-10, 1-15, 1-7.5, 1.25-15, 1.25-7.5, 2.5-7.5, 2.5-15, 5-15, 5-7.5,1-20, 1-50, 7-75, 1-100, 5-10, 5-15, 5-20, 5-25, 5-50, 5-75, 10-20, 10-50, 10-75, or 10-100 mg/kg, or any concentration in between). In some embodiments, the TRAIL receptor agonist protein is present in a pharmaceutical composition at a therapeutically effective concentration, *e.g.*, a concentration of about 0.1-100 mg/ml (*e.g.*, about 0.1-0.5, 0.1-1, 0.1-10, 0.1-20, 0.1-50, 0.1-75, 1-10, 1-20, 1-50, 1-75, 1-100, 5-10, 5-15, 5-20, 5-25, 5-50, 5-75, 10-20, 10-50, 10-75, or 10-100 mg/ml, or any concentration in between). Note that dosage values may vary with the type and/or severity of the condition to be alleviated. It is to be further understood that for any particular subject, specific dosage regimens may be adjusted over time according to the individual need and/or the professional judgment of the person administering or supervising the administration of the compositions, and that dosage ranges set forth herein are exemplary only and are not intended to limit the scope or practice of the claimed composition.

Examples

1. Manufacture of a TRAIL receptor agonist protein (sc TRAIL wt)

1.1 Polypeptide structure

A) Amino acids Met1 – Gly20
Ig-Kappa-signal peptide, assumed signal peptidase cleavage site after amino acid GIy 20.

B) Amino acids Gln21 – Gly182
First soluble cytokine domain of the human TRAIL ligand (TRAIL, amino acid 120 - 281 of SEQ ID NO: 1).

C) Amino acids GIy 183 – Ser 190
First peptide linker element of SEQ ID NO: 2.

D) Amino acids Arg191 – Gly351
Second soluble cytokine domain of the human TRAIL ligand (TRAIL, amino acids 121 - 281 of SEQ ID NO: 1).

E) Amino acids GIy352 – Ser359.
Second peptide linker element of SEQ ID NO: 2.

F) Amino acids Arg360 – Gly520
Third soluble cytokine domain of the human TRAIL ligand (TRAIL, amino acids 121-281 of SEQ ID NO: 1).

G) Amino acids Gly521 – Cys542
Hinge-linker element of SEQ ID NO: 11.

H) Amino acids Pro543 - Lys760
Antibody Fc fragment domain of SEQ ID NO: 10.

The above TRAIL receptor agonist protein is shown in SEQ ID NO: 14.

The indicated linkers may be replaced by other preferred linkers, *e.g.* as shown in SEQ ID NOs: 3-9.

It should be noted that the first and second peptide linkers do not need to be identical.

The signal peptide sequence (A) may be replaced by any other suitable, *e.g.* mammalian signal peptide sequence.

1.2 Gene cassette encoding the polypeptide

The synthetic gene may be optimized in view of its codon usage for the expression in suitable host cells, *e.g.* insect cells or mammalian cells. A preferred nucleic acid sequence is shown in SEQ ID NO: 16.

2. Expression and Purification

Cloning, expression and purification of fusion polypeptides

The aforementioned fusion proteins were expressed recombinantly in two different eukaryotic host cells:
For initial analysis of aforementioned TRAIL receptor agonist fusion proteins, Hek293T cells grown in DMEM + GlutaMAX (GibCo) supplemented with 10% FBS, 100 units/ml Penicillin and 100 [mu]g/ml Streptomycin were transiently transfected with a plasmid containing an expression cassette for a fusion polypeptide and an appropriate selection marker, *e.g.* a functional expression cassette comprising a blasticidine, puromycin or hygromycin resistence gene. In those cases, where a plurality of polypeptide chains is necessary to achieve the final product, the expression cassettes were either combined on one plasmid or positioned on different plasmids during the transfection. Cell culture supernatant containing recombinant fusion polypeptide was harvested three days post transfection and clarified by centrifugation at 300 x g followed by filtration through a 0.22 µm sterile filter.

For larger scale expression of TRAIL receptor agonist fusion proteins to be used *in vivo*, synthetic DNA cassettes encoding the aforementioned proteins were inserted into eukaryotic expression vectors comprising appropriate selection markers (*e.g.* a functional expression cassette comprising a blasticidin, puromycin or hygromycin resistence gene) and genetic elements suitable to enhance the number of transcriptionally active insertion sites within the host cells genome. The sequence verified expression vectors were introduced by electroporation into suspension adapted Chinese Hamster Ovary cells (CHO-S, Invitrogen). Appropriate selection pressure was applied three days post-transfection to the transfected cells. Surviving cells carrying the vector derived resistance gene(s) were recovered by subsequent

cultivation under selection pressure. Upon stable growth of the selected cell pools in chemically defined medium (PowerCHO2-CD, Lonza) at 37°C and 7% CO2 atmosphere in an orbital shaker incubator (100 rpm, 50mm shaking throw), the individual supernatants were analysed by ELISA-assays detecting the aforementioned proteins and the cell pools with the highest specific productivity were expanded in shake flasks prior to protein production (orbital shaker, 100 rpm, shaking throw 50mm).

For lab-scale protein production, individual cell pools were cultured for 7-12 days in chemically defined medium (PowerCHO2-CD, Lonza) at 37°C and 7% CO2 atmosphere in a Wave bioreactor 20/50 EHT (GE-Healthcare). The basal medium was PowerCHO2-CD supplemented with 4mM Glutamax. Wave culture started with a viable cell concentration of 0.3 to 0.4 x 10e6 cells/ml and the following settings (for a five- or ten liter bag): shaking frequency 18rpm, shaking ankle 7°, gas current 0.2-0.3 L/min, 7% CO2, 36.5°C. During the Wave run, the cell culture were fed twice with PowerFeed A (Lonza), usually on day 2 (20% feed) and day 5 (30% feed). After the second feed, shaking frequency was increased to 22rpm, as well as the shaking ankle to 8°.

The bioreactor was usually harvested in between day 7 to day 12 when the cell viability dropped below 80%. First, the culture supernatant was clarified using a manual depth filtration system (Millipore Millistak Pod, MC0HC 0.054m^2). For Strep-tagged proteins, Avidin was added to a final concentration of 0.5mg/L. Finally, the culture supernatant containing the TRAIL receptor agonist fusion protein was sterile filtered using a bottle top filter (0.22µm, PES, Corning) and stored at 2-8°C until further processing.

For affinity purification Streptactin Sepharose was packed to a column (gel bed 1 ml), equilibrated with 15 ml buffer W (100 mM Tris-HCI, 150 mM NaCI, pH 8.0) or PBS pH 7.4 and the cell culture supernatant was applied to the column with a flow rate of 4 ml/min. Subsequently, the column was washed with 15 ml buffer W and bound polypeptide was eluted stepwise by addition of 7 x 1 ml buffer E (100 mM Tris HCI,

150 mM NaCl, 2.5 mM Desthiobiotin, pH 8.0). Alternately, PBS pH 7.4 containing 2.5 mM Desthiobiotin can be used for this step.

Alternately to the Streptactin Sepharose based method, the affinity purification was performed employing a column with immobilized Protein-A as affinity ligand and a Akta chromatography system (GE-Healthcare). A solid phase material with high affinity for the FC-domain of the fusion protein was chosen: MABSelect Sure™ (GE Healthcare). Briefly, the clarified cell culture supernatant was loaded on a HiTrap MabSelectSure column (CV=5ml) equilibrated in wash-buffer-1 (20 mM Pi, 95 mM NaCl, pH7.2) not exceeding a load of 10mg fusion protein per ml column-bed. The column was washed with ten column-volumes (10CV) of aforementioned equilibration buffer followed by four column-volumes (4CV) of wash-buffer-2 (20mM Pi, 95mM NaCl, pH 8.0) to deplete host-cell protein and host-cell DNA. The column was then eluted with elution buffer (20mM Pi, 95mM NaCl, pH 3.5) and the eluate was collected in up to ten fractions with each fraction having a volume equal to column-bed volume (5ml). Each fraction was neutralized with an equal volume of aforementioned wash-buffer-2. The linear velocity was set to 150cm/h and kept constant during the aforementioned affinity chromatography method.
The protein amount of the eluate fractions was quantitated and peak fractions were concentrated by ultrafiltration and further purified by size exclusion chromatography (SEC).

SEC was performed on Superdex 200 10/300 GL or HiLoad 26/60 columns using an Akta chromatography system (GE-Healthcare). The columns were equilibrated with phosphate buffered saline and the concentrated, affinity-purified polypeptide was loaded onto the SEC column with the sample volume not exceeding 2 % (v/v) of the column-volume. In the case of Superdex200 10/300 GL columns (GE Healthcare), a flow rate of 0.5ml per minute was applied. In the case of HiLoad 26/60 Superdex200 columns, a flow rate of 2.5 ml per minute was applied. The elution profile of the polypeptide was monitored by absorbance at 280 nm

For determination of the apparent molecular weight of purified fusion polypeptide under native conditions a Superdex 200 column was loaded with standard proteins of

known molecular weight. Based on the elution volume of the standard proteins a calibration curve was plotted and the apparent molecular weight of purified fusion polypeptide was determined. The FC-domain comprising TRAIL receptor agonist fusion proteins typically eluted from the Supoerdex200 columns with an apparent molecular weight for the homodimer of approx. 160-180 kDa.

3. Apoptosis Assay

A cellular assay with a Jurkat A3 permanent T-cell line was used to determine the apoptosis inducing activity of the TRAIL-receptor agonist fusion proteins. Jurkat cells were grown in flasks with RPMI 1640-medium + GlutaMAX (GibCo) supplemented with 10% FBS, 100 units/ml Penicillin and 100 µg/ml Streptomycin. Prior to the assay, 100,000 cells were seeded per well into a 96-well microtiterplate. The addition of different concentrations of fusion peptides to the wells was followed by a 3 hour incubation at 37°C. Cells were lysed by adding lysis buffer (250 mM HEPES, 50 mM MgCl2, 10 mM EGTA, 5% Triton-X-100, 100 mM DTT, 10 mM AEBSF, pH 7.5) and plates were put on ice for 30 minutes to 2 hours. Apoptosis is paralleled by an increased activity of caspases, *e.g.* Caspase-3. Hence, cleavage of the specific caspase substrate Ac-DEVD-AFC (Biomol) was used to determine the extent of apoptosis. In fact, Caspase activity correlates with the percentage of apoptotic cells determined morphologically after staining the cells with propidium iodide and Hoechst-33342. For the caspase activity assay, 20 µl cell lysate was transferred to a black 96-well microtiterplate. After the addition of 80 µl buffer containing 50 mM HEPES, 1% Sucrose, 0.1% CHAPS, 50 µM Ac-DEVD-AFC, and 25 mM DTT, pH 7.5, the plate was transferred to a Tecan Infinite 500 microtiterplate reader and the increase in fluorescence intensity was monitored (excitation wavelength 400 nm, emission wavelength 505 nm).

3.1 Cell death assay

For the determination of cell death in HT1080 fibrosarcoma cells 15,000 cells were plated in 96-well plates overnight in RPM1 1640-medium + GlutaMAX (GibCo) supplemented with 10 % FBS (Biochrom). Cells were coincubated with cycloheximide

(Sigma) at a final concentration of 2.5 g/ml. Cell death was quantified by staining with buffer KV (0.5% crystal violet, 20% methanol). After staining, the wells were washed with water and air-dried. The dye was eluted with methanol and optical density at 595 nm was measured with an ELISA reader.

4. Stability/Aggregation Test

4.1 Principle of the aggregation analysis (Definition for soluble protein)

The content of monomers (defined trimeric assembly of TRAIL receptor binding modules) and aggregates is determined by analytical SEC as described in Example 2. For this particular purpose the analysis is performed in buffers containing physiological salt concentrations at physiological pH (*e.g.* 0.9% NaCI, pH 7.4; PBS pH 7.4). A typical aggregation analysis is done on a Superdex200 column (GE Healthcare). This column separates proteins in the range between 10 to 800 kDa.

For determination of the apparent molecular weight of purified fusion polypeptide under native conditions a Superdex 200 column is loaded with standard proteins of known molecular weight. Based on the elution volume of the standard proteins a calibration curve is plotted and the apparent molecular weight of purified fusion polypeptide is calculated based on the elution volume.

SEC analysis of soluble, non-aggregated proteins, *e.g.* trimeric TRAIL, typically shows a distinct single protein peak at a defined elution volume. This elution volume corresponds to the apparent native molecular weight of the particular protein and approximately complies to the theoretical molecular weight calculated on the basis of the primary amino acid sequence.

If protein aggregation occurs the SEC analysis shows additional protein peaks with lower retention volumes. For TRAIL, the aggregation of soluble proteins occurs in a characteristic manner. The proteins tend to form oligomers of the "trimers", forming nonamers (3 x 3) and 27mers (3 x 9). These oligomers serve as aggregation seeds and a high content of oligomers potentially leads to aggregation of the protein.

Oligomers of large molecular weight and aggregates elute in the void volume of the Superdex200 column and cannot be analysed by SEC with respect to their native molecular weight.

Due to the induction of (complete) aggregation, purified preparations of TRAIL-SF fusion proteins should preferably contain only defined trimeric proteins and only a very low amount of oligomerised protein. The degree of aggregation/oligomerisation of a particular TRAIL-SF protein preparation is determined on basis of the SEC analysis by calculating the peak areas of the OD280 diagram for the defined trimeric and the oligomer/aggregate fraction, respectively. Based on the total peak area the percentage of defined trimeric protein is calculated as follows:

(% Trimer content = [Peak area trimer] / [Total peak area] x 100)

The definition for soluble protein as used in this text, describes a protein preparation of purified TRAIL protein in a buffer of physiological salt concentrations at physiological pH that contains a defined soluble protein (trimeric assembly of TRAIL domains) content of > 90% within a typical protein concentration range from 0.2 to 10.0 mg/ml.

5. Half-Life Determination

Molecules A-D are each made up of two polypeptides covalently linked by interchain disulfide bonds. The number of glycosites and hinge cysteines (resulting in interchain disulfide bonds between proteins) were tested in order to determine the effect that altering these characteristics has on the half-life of these compounds.

Female NMRI mice were treated with 1.2 mg/kg bw and/or with 4 mg/kg bw of the specified compounds as a single intravenous bolus injection. Whole blood was collected before application (predose), and up to 168 hours after test item administration. Serum was prepared and samples were stored at –80 °C until determination of serum concentrations. Pharmacokinetic parameters were calculated using the mean serum concentrations and the pharmacokinetic evaluation program

PK Solutions Version 2.0 for non-compartmental pharmacokinetic data analysis (Summit Research Services, Montrose, CO). PK Solutions is an automated, Excel-based application, which computes pharmacokinetic parameters from concentration-time data obtained from analysis of *e.g.* biological samples following intravenous or extra-vascular routes of administration. PK Solutions calculates results without presuming any specific compartmental model.

Quantitation of the test items in serum was performed with an ELISA-assay detecting the individual TRAIL-receptor agonists shown in Table 7 independent of a Strep-Tag being part of the molecules. The general layout is shown in Figure 18. The results are summarized in Table 7.

Molecule A (made up of two polypeptides of SEQ ID NO:26) has two hinge cysteines (forming two interchain disulfide bonds) and an N residue at position 297 of the Fc region (according to the EU index), resulting in wild-type CH2 glycosylation. Molecule A also has glycosites at positions 168 and 337. Molecule B (made up of two polypeptides of SEQ ID NO: 19) has three hinge cysteines (forming three interchain disulfide bonds) (at positions 513, 519, and 522) and an N297S mutation at position 297 of the Fc region (according to the EU index), resulting in aglycosylation of the CH2 domain. Molecule B also has glycosites at positions 168 and 337. Molecule C (made up of two polypeptides of SEQ ID NO: 27) has three hinge cysteines (forming three interchain disulfide bonds) and an N297S mutation at position 297 of the Fc region (according to the EU index), resulting in aglycosylation of the CH2 domain. Further, there is a glycosite at position 168 (linker 1), but not at position 337 (linker 2). Molecule D (made up of two polypeptides of SEQ ID NO:28) has three hinge cysteines (forming three interchain disulfide bonds) and an N297S mutation at position 297 of the Fc region (according to the EU index), resulting in aglycosylation of the CH2 domain. Further, the glycosites on both linker 1 and linker 2 (positions 168 and 337, respectively) have been depleted in Molecule D.

The *in vivo* stability (as judged by compound half-life) of Molecule B (both linkers glycosylated, CH2 glycosites depleted, and the addition of a third hinge cysteine) was enhanced when compared to Molecule A. Further, the depletion of all glycosites in

from the compound (Molecule D) resulted in reduced *in vivo* stability and low productivity during transient expression. Molecule C (first linker glycosylated, second linker aglycosylated, CH2 glycosites depleted) demonstrated an intermediate *in vivo* stability when compared to Molecules B and D (see results in Table 7).

Table 7: Results of Compound Half-life Testing in NMRI-mice

Molecule	Number of glycosylation sites	Number of hinge cysteines	Terminal Half-life 4mg/kg i.v.(hour)	Terminal Half-life 1.2 mg/kg i.v.(hour)
A	6	2	23.1	17.7
B	4	3	33.94	28.28
C	2	3	21.03	-
D	0	3	8.81	-

These experimental results demonstrate that combining linker glycosylation (in both linkers 1 and 2) with a third interchain disulfide bond (through the addition of a hinge cysteine) and the deglycosylation of the CH2 domain in the Fc region results in greater *in vivo* stability in the molecules of the instant invention.

6. *In vitro* demonstration of efficacy

6.1 TRAIL receptor agonist protein of SEQ ID NO: 19 inhibits human hematologic and solid tumor cell survival *in vitro*

Tumor cells were seeded at 10,000 cells/well in 96-well plates in the recommended media containing 10% FBS and treated with a TRAIL receptor agonist protein made up of two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19 for 24 hours at 37^{o}C in a humidified, 5% CO_2 atmosphere. Cell viability was subsequently assessed using CellTiter-Glo® reagent as described by the manufacturer's instructions (Promega; Madison, WI). IC_{50} values were determined by non-linear regression analysis of the concentration response data normalized to non-treated control cells. Examples of resulting concentration response curves for Colo205, Jurkat and SKM-1 cells that demonstrate a loss in cell viability in response to TRAIL receptor agonist protein made up of two polypeptides having the amino acid

sequence set forth in SEQ ID NO: 19 treatment are shown in Figure 19. Table 8 shows the results of hematologic (A; (n=40; Non-Hodgkin's Lymphoma, NHL; Acute Myeloid Lymphoma, AML; Acute Lymphoblastic Leukemia, ALL) and solid tumor (B; (n=44; Non-Small Cell Lung Carcinoma, NSCLC; Pancreatic; Colorectal Cancer, CRC; Breast Cancer, BrCa; Ovarian, Fibrosarcoma; Head and Neck, H&N; Small Cell Lung Cancer, SCLC) cell lines treated with a TRAIL receptor agonist protein made up of two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19 for 24 hours and viability assessed by CellTiter-Glo®. Resulting IC_{50}s for TRAIL receptor agonist protein made up of two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19-mediated effects on tumor cell viability are presented.

Table 8

Potency of TRAIL receptor agonist protein of SEQ ID NO: 19 in human tumor cancer cell lines *in vitro*

Tumor cell line	Tumor Type	SEQ ID NO:19 IC_{50} (ng/ml)
A		
SU-DHL-8	NHL	1.36
NUDHL-1	NHL	6.50
OCI-Ly8	NHL	7.49
ULA	NHL	8.44
OCI-Ly2	NHL	18.98
OCI-LY19	NHL	26.34
WSU-NHL	NHL	31.60
OCI-Ly7	NHL	63.76
SU-DHL-5	NHL	82.07
OCI-Ly18	NHL	196.20
OCI-Ly1	NHL	416.95
SU-DHL-16	NHL	545.55
SU-DHL-2	NHL	1000.00

WSU-DLCL2	NHL	1000.00
Toledo	NHL	1000.00
OCI-LY3	NHL	1000.00
RL	NHL	1000.00
SU-DHL-4	NHL	1000.00
U2932	NHL	1000.00
HT	NHL	1000.00
RC-K8	NHL	1000.00
SKM-1	AML	0.95
PL-21	AML	10.67
EOL-1	AML	18.31
HL-60	AML	76.62
OCI-AML2	AML	124.32
UKE-1	AML	205.35
MV4-11	AML	312.55
SET-2	AML	384.80
MOLM-13	AML	722.10
OCI-AML5	AML	1032.60
Kasumi-1	AML	1000.00
KG-1	AML	1000.00
OCI-AML3	AML	1000.00
SHI-1	AML	1000.00
SKNO-1	AML	1000.00
TF-1	AML	1000.00
THP-1	AML	1000.00
HEL	AML	1000.00
Jurkat	ALL	3.08
B		
NCI-H847	NSCLC	14.53
NCI-H647	NSCLC	24.75
NCI-H2444	NSCLC	27.75
NCI-H2170	NSCLC	30.16
NCI-H460	NSCLC	36.85

NCI-H838	NSCLC	44.48
NCI-H1792	NSCLC	61.09
NCI-H2347	NSCLC	81.06
NCI-H1373	NSCLC	125.15
NCI-H522	NSCLC	259.87
NCI-H2110	NSCLC	314.20
NCI-H596	NSCLC	397.80
HCC4006	NSCLC	407.24
NCI-H2122	NSCLC	480.55
NCI-H1299	NSCLC	716.00
NCI-H1975	NSCLC	741.50
HCC827	NSCLC	2824.50
NCI-H727	NSCLC	3178.00
NCI-H1944	NSCLC	4068.75
NCI-H1299	NSCLC	4214.87
Calu-6	NSCLC	4757.00
NCI-H1693	NSCLC	5000.00
HCC2935	NSCLC	5000.00
A549	NSCLC	5000.00
NCI-H1395	NSCLC	5000.00
NCI-H2172	NSCLC	5000.00
Calu-1	NSCLC	5000.00
NCI-H441	NSCLC	5000.00
NCI-H23	NSCLC	5000.00
NCI-H661	NSCLC	5000.00
NCI-H1650-GFP	NSCLC	>3
BxPC3	Pancreatic	16.00
Capan-1	Pancreatic	393.00
MIA PaCa-2	Pancreatic	158.00
PANC-1	Pancreatic	>1000
SW48	CRC	6.10
Colo205	CRC	1.30

SW480	CRC	132.00
HCT 116-GFP	CRC	337.00
HCC38	BrCa	3.00
HCC1569	BrCa	219.00
MCF7	BrCa	>3000
MDA-MB-231	BRCa	235.00
HeyA8-GFP	Ovarian	141.00
Fadu-GFP	H&N	>3
HT-1080	Fibrosarcoma	377.00
NCI-H211	SCLC	72.58

6.2 TRAIL receptor agonist protein of SEQ ID NO: 19 synergizes with anti-tumorigenic agents to induce tumor cell death

Tumor cells were seeded at 10,000 cells/well in 96-well plates in the recommended media containing 10% FBS and co-treated with a TRAIL receptor agonist protein made up of two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19 and venetoclax (ABT-199), navitoclax (ABT-263) or docetaxel (DTX) for 24hrs at 37^{o}C in a humidified, 5% CO_2 atmosphere. Cell viability was subsequently assessed using CellTiter-Glo® reagent as described by the manufacturer's instructions. The Bliss independence model (Wong *et al.,* 2012; Mol. Cancer Ther. 11:1026-1035; Bernebaum, 1981 Adv. Cancer Res. 35:269-335; Borisy *et al.,* 2003 Proc. Natl. Acad. Sci. USA 100:7977-7982) was employed to assess combination activity, with negative integers indicating antagonism, a value of zero indicating additive activity, and positive integers indicating synergy. Bliss scores were calculated for each combination in the dose matrix and totaled to give a "Bliss sum" value. An example of synergistic tumor cell death induced by co-treating human tumor cells with a TRAIL receptor agonist protein made up of two polypeptides having the amino acid sequence set forth in SEQ ID NO:19 and venetoclax, navitoclax or DTX, with the associated Bliss sum is shown in Figures 20(A-C). Bliss sums determined for these combinations in a number of tumor cell lines are depicted in Table 9.

Table 9

Bliss synergy assessment of cell killing by TRAIL receptor agonist protein of SEQ ID NO:19 in combination with DTX in NSCLC cell lines (A) and venetoclax or navitoclax in NHL & AML cell lines (B) *in vitro*.

Tumor Cell line	**Bliss Sum (SEQ ID NO:19 + DTX)**	**Tumor Cell line**	**Bliss Sum (SEQ ID NO:19+ venitoclax)**	**Bliss Sum (SEQ ID NO:19 + navitoclax)**
LG0552	748.2	WSU-DLCL2	1292	560
NCI-H522	549.1	SU-DHL-4	898	617
NCI-H647	452	OCI-AML3	831.9	456.4
NCI-H727	429.4	OCI-AML5	777.8	174.5
NCI-H1373	387.1	U2932	736.2	636.1
NCI-H596	261	PL-21	600.8	244.9
HCC2935	224.2	ULA	343.8	79.4
NCI-H2347	154	OCI-Ly18	309.8	8.3
NCI-H2444	135	MV4;11	301.1	351
A549	118.1	RL	286.1	446.7
NCI-H23	70.6	MOLM-13	270.6	264.8
NCI-H847	64.2	SKM-1	222.9	88.1
HCC4006	15.75	OCI-Ly1	218.8	69.1
NCI-H2170	-97.1	SU-DHL-16	217.5	142.5
LG0567	-105.2	OCI-AMl2	160.2	145.5
HCC2935	-183	OCI-Ly8	154.9	177
HCC827	-292.8	THP-1	152.7	43.1
NCI-H661	-344.5	OCI-Ly3	146.5	-242.2
NCI-H441	-362	OCI-Ly2	145	127.2
NCI-H1395	-512	OCI-Ly19	114.9	37.3
NCI-H1944	-565	SKNO-1	104.7	-138.9
NCI-H1693	-584	UKE-1	80.5	28.9
Calu-6	-628.7	WSU-NHK	79.8	84
LG0481	-803	EOL-1	69.7	-6.3
NCI-H2172	-1404	SU-DHL-2	53.5	-31.8

Toledo	51.4	-68.2
HEL	21.5	-92.4
NuDHL-1	-28.4	18.7
TF-1	-100.6	-50.2
RC-K8	-131	-68
HT	-173	12.1
HL-60	-176	-112.7
SHI-1	-208.4	-122.6
SU-DHL-8	-210.6	-37
SU-DHL-5	-233.8	-280.6
SET-2	-248.4	71.2
KG-1	-260	-20.3
Kasumi-1	-356.4	-241.2

7. TRAIL receptor agonist protein of SEQ ID NO:19 treatment inhibits tumor growth *in vivo*

The effect of a TRAIL receptor agonist protein made up of two polypeptides having the amino acid sequence set forth in SEQ ID NO:19 on tumor growth was evaluated in subcutaneous Colo205 (colorectal), SKM-1 (acute myeloid leukemia), and H460LM (non-small cell lung) xenograft tumors implanted in SCID female mice (Charles Rivers Laboratories; Wilmington, MA). Briefly, human cancer cells were inoculated subcutaneously into the right hind flank of female SCID mice on study day 0. Administration of TRAIL receptor agonist protein of SEQ ID NO:19 (0.3, 1, or 3 mkd dosed IV, QDx5 or IP, Q2Dx5 as indicated) was initiated at the time of size match. Tumor volume was measured for the duration of the experiment until the mean tumor volume in each group reached an endpoint of >2000 mm^3 for Colo205 and SKM-1 or >2500 mm^3 for H460LM. Results are shown in Figures 21-23. Administration of a TRAIL receptor agonist protein made up of two polypeptides having the amino acid sequence set forth in SEQ ID NO:19 induced significant tumor growth inhibition in the Colo205, SKM-1, and H460LM xenograft tumor models.

The effect of of a TRAIL receptor agonist protein made up of two polypeptides having the amino acid sequence set forth in SEQ ID NO:19 on tumor growth was also

evaluated in patient-derived xenograft models CTG-0069 (colorectal), CTG-0167 (NSCLC), CTG-0293 (pancreatic), CTG-0714 (sarcoma), CTG-0136 (esophageal), CTG-485 (gastric), and CTG-0785 (Ewing's sarcoma) implanted in NSG female mice (Champions Oncology; Hackensack, NJ). Briefly, tumor fragments were propagated subcutaneously into the right hind flank of female NSG mice on study day 0. Administration of a TRAIL receptor agonist protein made up of two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19 (3 mkd dosed IP, Q2Dx5) was initiated at the time of size match. Tumor volume was measured for the duration of the experiment until the mean tumor volume in each group reached an endpoint of >2000 mm^3 or 60 days. Results are shown in Figures 24(A-G). Administration of a TRAIL receptor agonist protein made up of two polypeptides having the amino acid sequence set forth in SEQ ID NO: 19 induced significant tumor growth inhibition in the CTG-0069 (colorectal), CTG-0167 (NSCLC), CTG-0293 (pancreatic), CTG-0714 (sarcoma), CTG-0136 (esophageal), CTG-485 (gastric), and CTG-0785 (Ewing's sarcoma) PDX models.

Claims

1. A nucleic acid molecule comprising SEQ ID NO:16.

2. A nucleic acid molecule comprising nucleotides 19 to 2298 of SEQ ID NO:16.

3. A nucleic acid molecule comprising nucleotides 79 to 2298 of SEQ ID NO:16.

4. An expression vector comprising the nucleic acid molecule according to Claims 2 or 3.

5. A cell comprising the nucleic acid molecule according to Claims 2 or 3.

6. The cell according to Claim 5, which is a eukaryotic cell.

7. The cell according to Claim 6, wherein the cell is a mammalian cell.

8. The cell according to Claim 7, wherein the cell is a Chinese Hamster Ovary (CHO) cell.