or variants and derivatives thereof; provided however, that when the truncated sTNFR polypeptide comprises the amino acid residues 15-122, 16-122, 17-122, 18-122, 19-122, 20-122, 21-122, 22-122, 23-122, 24-122, 25-122, 26-122, 27-122, 28-122, 29-122, 30-122, 31-122, or 32-122 of SEQ ID NO: 16, the polypeptide does not further comprise amino acid residues 123-179 of SEQ ID NO: 16, or a portion thereof;
and optionally further comprising an amino-terminal methionine.

**REMARKS**

**Claim Status.** Claims 1 to 31 are pending in the application. Claims 1 and 3 are amended hereby. No claim has been added or canceled.

**Support for Amendments.** In order to bring the instant application into compliance with 37 C.F.R. § 1.822(e), Applicants amended the specification and claims in a Preliminary Amendment filed January 29, 2002. Applicants noticed in preparing the instant response that the amendments of January 29, 2002 resulted in the inadvertent omission of certain contiguous fragments, particularly those extending only to residue 103 at the C-terminus and those beginning at residue 19 at the N-terminus. Such fragments are clearly supported in the specification prior to the amendment of January 29, 2002 (see, e.g., page 6, line 8 et seq.). Applicants seek entry of the above-described amendments solely to correct these inadvertent omissions and contend that no new matter has been added by these amendments.

**Election under Restriction Requirement.** Applicants elect to prosecute claims 1-12, 22-25, 28, and 31, designated as Group A by the Examiner. The Action states that the claims of Group A are drawn to truncated sTNFR polypeptides. Applicants further elect to prosecute the claims that are drawn to the sTNFR polypeptide of SEQ ID NO: 2, with traverse. Applicants also elect the species of truncated sTNFR polypeptide comprising amino acid residues 1-105 of SEQ ID NO: 2, further comprising an amino-terminal methionine (i.e., the species of truncated...
sTNFR polypeptide comprising the amino acid sequence of SEQ ID NO: 8). The Action states that the specific truncations of the polypeptide of SEQ ID NO: 2 that are listed in claim 1 constitute patently distinct species of the claimed invention. The basis for Applicants’ traversal of the requirement is as follows.

Applicants respectfully submit that there will be no undue hardship on the Office in performing a search with respect to the sTNFR-I polypeptides of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, and SEQ ID NO: 14. The truncated sTNFR-I polypeptides of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, and SEQ ID NO: 14 share 100% sequence identity with residues 19-104 of the sTNFR-I polypeptide of SEQ ID NO: 2 (see Exhibit A, which contains a sequence alignment performed using the application MacVector 7.1.1 (Accelrys, Cambridge, UK; http://www.accelrys.com) at the default settings). The relationship of the truncated sTNFR-I polypeptides of SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, and SEQ ID NO: 14 to the sTNFR-I polypeptide of SEQ ID NO: 2 is shown in Table I.

<table>
<thead>
<tr>
<th>SEQ ID NO:</th>
<th>Construct</th>
<th>Relationship to SEQ ID NO: 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>4</td>
<td>sTNFR-I 2.6D/C105</td>
<td>residues 1-105 of SEQ ID NO: 2, further comprising an amino-terminal methionine, and having a Cys substitution at position 105</td>
</tr>
<tr>
<td>6</td>
<td>sTNFR-I 2.6D/C106</td>
<td>residues 1-108 of SEQ ID NO: 2, further comprising an amino-terminal methionine</td>
</tr>
<tr>
<td>8</td>
<td>sTNFR-I 2.6D/N105</td>
<td>residues 1-105 of SEQ ID NO: 2, further comprising an amino-terminal methionine</td>
</tr>
<tr>
<td>10</td>
<td>sTNFR-I 2.3D/d8</td>
<td>residues 19-105 of SEQ ID NO: 2, further comprising an amino-terminal methionine</td>
</tr>
<tr>
<td>12</td>
<td>sTNFR-I 2.3D/d18</td>
<td>residues 9-105 of SEQ ID NO: 2, further comprising an amino-terminal methionine</td>
</tr>
<tr>
<td>14</td>
<td>sTNFR-I 2.3D/d15</td>
<td>residues 16-105 of SEQ ID NO: 2, further comprising an amino-terminal methionine, and having a Ser substitution at position 18</td>
</tr>
</tbody>
</table>

As indicated in Table I, the truncated sTNFR-I polypeptides of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, and SEQ ID NO: 14 comprise species
of the genus of truncated sTNFR polypeptides of claim 1 (i.e., the polypeptides of SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, and SEQ ID NO: 12 are fragments of SEQ ID NO: 2, and the polypeptides of SEQ ID NO: 4 and SEQ ID NO: 14 are fragments of SEQ ID NO: 2 having a single amino acid substitution). As the polypeptides of SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, and SEQ ID NO: 14 comprise species of the specific truncations of the polypeptide of SEQ ID NO: 2 that are listed in claim 1, Applicants respectfully request reconsideration of the restriction requirement of section 3 of the instant Action.

Applicants enclose a petition for a one-month extension of time. The Commissioner is authorized to charge any additional fees or credit any overpayment to Deposit Account No. 13-2490.

Conclusion. If Examiner O'Hara believes it to be helpful, she is invited to contact the undersigned representative by telephone at (312) 913-0001. In light of the foregoing amendments and remarks, the Applicants respectfully request entry of all amendments, removal of all requirements, and allowance of all claims.

Respectfully submitted,
McDonnell Boehnen Hulbert & Berghoff

Dated: November 12, 2002

By: Donald L. Zuhn, Ph.D.
Reg. No. 48,710
EXHIBIT A

ClustalW (v1.4) multiple sequence alignment

7 Sequences Aligned
Alignment Score = 14527
Gaps Inserted = 0
Conserved Identities = 66

SEQ02  1  DSVCPQSKYIHPQNSICCTKHGTYLYNDCPGPGQDTDCRECESG9F  49
SEQ04  1  MDSVCPQSKYIHPQNSICCTKHGTYLYNDCPGPGQDTDCRECESGSF  50
SEQ06  1  MDSVCPQSKYIHPQNSICCTKHGTYLYNDCPGPGQDTDCRECESGSF  50
SEQ08  1  MDSVCPQSKYIHPQNSICCTKHGTYLYNDCPGPGQDTDCRECESGSF  50
SEQ10  1  MCTKCHGTYLYNDCPGPGQDTDCRECESGSF  32
SEQ12  1  MYIHPQNSICCTKCHGTYLYNDCPGPGQDTDCRECESGSF  42
SEQ14  1  MSICSTKCHGTYLYNDCPGPGQDTDCRECESGSF  35

******************************
SEQ02  50  TASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGRKNNQYRHYSNE  99
SEQ04  51  TASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGRKNNQYRHYSNE  100
SEQ06  51  TASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGRKNNQYRHYSNE  100
SEQ08  51  TASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGRKNNQYRHYSNE  100
SEQ10  33  TASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGRKNNQYRHYSNE  82
SEQ12  43  TASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGRKNNQYRHYSNE  92
SEQ14  36  TASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGRKNNQYRHYSNE  85

******************************
SEQ02  100  LFQCFNCSLCLMGTVMLSCQEKQKNTVCCTCHAOGFLENECVGCNCCKKL  149
SEQ04  101  LFQCFPC  106
SEQ06  101  LFQCFNCSL  109
SEQ08  101  LFQCFN  106
SEQ10  83  LFQCFNCSL  91
SEQ12  93  LFQCFNCSL  101
SEQ14  66  LFQCFNCSL  94

*****
SEQ02  150  ECTKLCLPQRIN  161
SEQ04  107  106
SEQ06  110  109
SEQ08  107  106
SEQ10  92  91
SEQ12  102  101
SEQ14  95  94

Received from <> at 11/12/02 8:28:46 PM [Eastern Standard Time]
AMENDMENTS TO THE SPECIFICATION

Marked Up Version of Specification under 37 C.F.R. 1.121(b)(1)(iii)

Please amend the specification at page 6, line 8 to page 7, line 5 to read as follows:


Please amend the specification at page 7, line 13 to page 8, line 24 to read as follows:

The truncated sTNFRs of the present invention also include polypeptides comprising amino acid residues 1-122, 1-121, 1-120, 1-119, 1-118, 1-117, 1-116, 1-115, 2-122, 2-121, 2-120, 2-119, 2-118, 2-117, 2-116, 2-115, 3-122, 3-121, 3-120, 3-119, 3-118, 3-117, 3-116, 3-115, 4-122, 4-121, 4-120, 4-119, 4-118, 4-117, 4-116, 4-115, 5-122, 5-121, 5-120, 5-119, 5-118, 5-

Please amend the specification at page 14, line 1 to page 16, line 12 to read as follows:

As used herein, the term "truncated sTNFR(s)" includes one or more biologically active synthetic or recombinant molecules comprising amino acid residues 1-110, 1-109, 1-108, 1-107, 1-106, 1-105, 1-104, 1-103, 2-116, 2-109, 2-108, 2-107, 2-106, 2-105, 2-104, 2-103, 3-110, 3-

Please amend the specification at page 17, line 18 to page 19, line 24 to read as follows:

18-103, 19-110, 19-109, 19-108, 19-107, 19-106, 19-105, 19-104, or 19-103 of SEQ ID NO: 2; or variants thereof, provided however, that when the truncated sTNFR polypeptide comprises amino acid residues 3-110, 4-110, 5-110, 6-110, 7-110, 8-110, 9-110, 10-110, 11-110, 12-110, 13-110, 14-110, 15-110, 16-110, 17-110, or 18-110, or 19-110 of SEQ ID NO: 2, the polypeptide does not further comprise amino acid residues 111-161 of SEQ ID NO: 2, or a portion thereof.

24-122, 25-122, 26-122, 27-122, 28-122, 29-122, 30-122, or 31-122 of SEQ ID NO: 16, the polypeptide does not further comprise amino acid residues 123-179 of SEQ ID NO: 16, or a portion thereof.
AMENDMENTS TO THE CLAIMS

Marked Up Versions of Amended Claims under 37 C.F.R. 1.121(e)(1)(ii)


3. (Twice Amended) A truncated sTNFR polypeptide comprising amino acid residues 1-122, 1-121, 1-120, 1-119, 1-118, 1-117, 1-116, 1-115, 2-122, 2-121, 2-120, 2-119, 2-118, 2-117, 2-116, 2-115, 3-122, 3-121, 3-120, 3-119, 3-118, 3-117, 3-116, 3-115, 4-122, 4-121, 4-120, 4-119, 4-118, 4-117, 4-116, 4-115, 5-122, 5-121, 5-120, 5-119, 5-118, 5-117, 5-116, 5-115, 6-122, 6-121, 6-120, 6-119, 6-118, 6-117, 6-116, 6-115, 7-122, 7-121, 7-120, 7-119, 7-118, 7-117, 7-116, 7-115, 8-122, 8-121, 8-120, 8-119, 8-118, 8-117, 8-116, 8-115, 9-122, 9-121, 9-120, 9-119, 9-118, 9-117, 9-116, 9-115, 10-122, 10-121, 10-120, 10-119, 10-118, 10-117, 10-116, 10-115.
Fax transmittal

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Pages, with cover: 22
Re: Application Serial No. 09/882,735

Date: November 12, 2002
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McDonnell Bohannan Hubert & Borghoff
Law Offices