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[Continued on next page]

- (54) Title: ANTI-ROR1 ANTIBODIES, ROR1 X CD3 BISPECIFIC ANTIBODIES, AND METHODS OF USING THE SAME

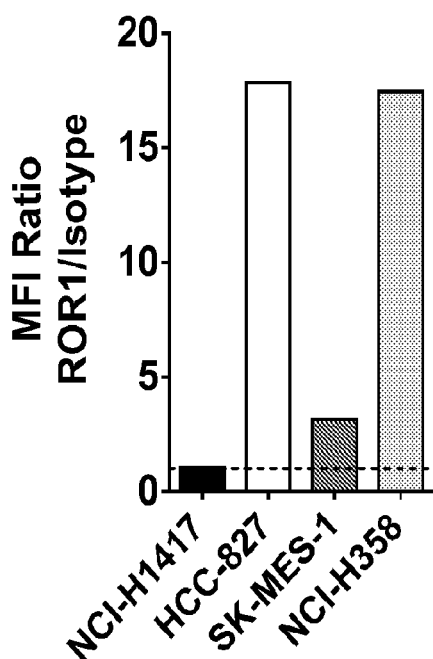


FIG. 1

- (57) Abstract: Provided herein are isolated antibodies that immunospecifically bind to ROR1, bispecific antibodies comprising an antigen-binding site that immunospecifically binds to ROR1 and an antigen-binding site that immunospecifically binds to CD3, and methods of using the same.



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ANTI-ROR1 ANTIBODIES, ROR1 X CD3 BISPECIFIC ANTIBODIES, AND METHODS OF
USING THE SAME

TECHNICAL FIELD

[0001] Provided herein are isolated antibodies that immunospecifically bind to ROR1, bispecific antibodies comprising an antigen-binding site that immunospecifically binds to ROR1 and an antigen-binding site that immunospecifically binds to CD3, and methods of using the same.

BACKGROUND

[0002] Receptor Tyrosine Kinase-Like Orphan Receptor 1 (ROR1) is a 106-kDa member of the receptor tyrosine kinase family. Structurally, the extracellular domain of the ROR1 receptor is composed of three distinct domains: a membrane-distal Immunoglobulin-Like Domain; a membrane-proximal Kringle Domain; and an intervening Frizzled Domain. Studies on ROR1-deficient mice suggest that this receptor plays a role in lung development during embryogenesis, but its expression in the adult is severely restricted, with expression limited to low-level expression in the lung and pancreas, as well as adipocytic and B cell lineages. While ROR1 expression is tightly regulated in normal adult tissues, high levels have been noted in both hematological and solid tumors. ROR1 is normally expressed during early development, but becomes activated by tumor specific mechanisms and may contribute to disease progression in the adult.

[0003] The ligands of ROR1 are believed to be wnt5a and NKX1-2. Wnt5a has been shown to bind to the Frizzled Domain in the extracellular part of ROR1 and, in transfected cells, has been shown to modulate NF- κ B activation and proliferation of normal and lung tumor cell lines. Binding of NKX1-2 to ROR1 has been shown to play a role in the survival of lung cancer cell lines through both kinase-dependent and kinase-independent mechanisms. ROR1 has been shown to interact with EGFR through the Kringle domain, and this interaction modulates signaling pathways that control apoptosis in lung cancer cell lines. While ROR1 expression does correlate with a worse prognosis in ovarian cancer, no link between ROR1 expression and clinical stage or reduced survival has been shown for lung cancer. Furthermore, although ROR1 siRNA knockdown of lung tumor cell lines leads to reduced viability *in vitro*, there is no evidence that targeting of ROR1 on primary lung cancer cells results in increased cell death.

SUMMARY

[0004] Disclosed herein are isolated antibodies, or antigen-binding fragments thereof, that immunospecifically bind to ROR1, the antibodies or antigen-binding fragments thereof comprising:

- a. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:3, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:4, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- b. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:11, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:12, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- c. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:15, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:16, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- d. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:18, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:20, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- e. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:24, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain

- CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- f. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:26, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:27, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:28, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:30, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:31, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:32;
- g. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:34, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:35, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:37, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:38;
- h. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:40, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:42, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:44;
- i. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:46, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:47, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:48, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:50, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:52;
- j. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:56, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60;

- k. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:62, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60;
- l. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:64, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:65, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- m. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:67, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:68, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:69, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- n. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:71, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:72, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- o. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:74, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:75, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:77, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:78;
- p. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:80, a light

chain CDR1 comprising the amino acid sequence of SEQ ID NO:82, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:83; or

- q. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:85, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:86, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:88, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:89;

wherein the CDRs are defined according to Kabat.

[0005] Further provided are isolated antibodies, or antigen-binding fragments thereof, that immunospecifically bind to ROR1, the antibodies or antigen-binding fragments thereof comprising:

- a. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:1 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- b. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:9 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- c. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:13 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- d. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:17 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- e. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:21 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;

- f. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:25 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:29;
- g. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:33 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:36;
- h. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:39 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:41;
- i. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:45 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:49;
- j. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:53 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:57;
- k. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:61 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:57;
- l. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:63 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- m. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:66 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;

- n. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:70 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- o. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:73 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:76;
- p. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:79 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:81; or
- q. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:84 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:87.

[0006] Isolated antibodies, or antigen-binding fragments thereof, that bind to an epitope on ROR1 comprising T324, V325, S326, V327, T328, S330, G331, R332, Q333, P336, N338, S339, Y341, H359, S360, Y361, L377, D378, and D387 are disclosed.

[0007] Further provided are nucleic acid molecules encoding the disclosed isolated antibodies or antigen-binding fragments thereof, vectors comprising the nucleic acid molecules, and cells expressing the isolated antibodies, or antigen-binding fragments thereof.

[0008] Disclosed are isolated antibodies, or antigen-binding fragments thereof, that compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising:

- a. a heavy chain comprising the amino acid sequence of SEQ ID NO:1 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- b. a heavy chain comprising the amino acid sequence of SEQ ID NO:9 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- c. a heavy chain comprising the amino acid sequence of SEQ ID NO:13 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- d. a heavy chain comprising the amino acid sequence of SEQ ID NO:17 and a light chain comprising the amino acid sequence of SEQ ID NO:5;

- e. a heavy chain comprising the amino acid sequence of SEQ ID NO:21 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- f. a heavy chain comprising the amino acid sequence of SEQ ID NO:25 and a light chain comprising the amino acid sequence of SEQ ID NO:29;
- g. a heavy chain comprising the amino acid sequence of SEQ ID NO:33 and a light chain comprising the amino acid sequence of SEQ ID NO:36;
- h. a heavy chain comprising the amino acid sequence of SEQ ID NO:39 and a light chain comprising the amino acid sequence of SEQ ID NO:41;
- i. a heavy chain comprising the amino acid sequence of SEQ ID NO:45 and a light chain comprising the amino acid sequence of SEQ ID NO:49;
- j. a heavy chain comprising the amino acid sequence of SEQ ID NO:53 and a light chain comprising the amino acid sequence of SEQ ID NO:57;
- k. a heavy chain comprising the amino acid sequence of SEQ ID NO:61 and a light chain comprising the amino acid sequence of SEQ ID NO:57;
- l. a heavy chain comprising the amino acid sequence of SEQ ID NO:63 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- m. a heavy chain comprising the amino acid sequence of SEQ ID NO:66 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- n. a heavy chain comprising the amino acid sequence of SEQ ID NO:70 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- o. a heavy chain comprising the amino acid sequence of SEQ ID NO:73 and a light chain comprising the amino acid sequence of SEQ ID NO:76;
- p. a heavy chain comprising the amino acid sequence of SEQ ID NO:79 and a light chain comprising the amino acid sequence of SEQ ID NO:81; or
- q. a heavy chain comprising the amino acid sequence of SEQ ID NO:84 and a light chain comprising the amino acid sequence of SEQ ID NO:87.

[0009] Isolated antibodies, or antigen-binding fragments thereof, that compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, wherein the reference antibody or antigen-binding fragment binds to an epitope on ROR1 comprising T324, V325, S326, V327, T328, S330, G331, R332, Q333, P336, N338, S339, Y341, H359, S360, Y361, L377, D378, and D387 are provided herein.

[0010] Disclosed are isolated ROR1 x CD3 bispecific antibodies and bispecific antigen-binding fragments thereof. In some embodiments, the isolated ROR1 x CD3 bispecific

antibodies or bispecific antigen-binding fragments thereof comprise: a) a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site comprising a heavy chain CDR1, CDR2, and CDR3 and a light chain CDR1, CDR2, and CDR3; and b) a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site comprising a heavy chain CDR1, CDR2, and CDR3 and a light chain CDR1, CDR2, and CDR3. Suitable first antigen-binding sites that immunospecifically bind ROR1 include those comprising:

- a. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:3, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:4, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- b. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:11, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:12, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- c. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:15, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:16, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- d. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:18, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:20, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- e. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:24, a light

- chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- f. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:26, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:27, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:28, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:30, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:31, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:32;
- g. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:34, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:35, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:37, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:38;
- h. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:40, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:42, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:44;
- i. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:46, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:47, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:48, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:50, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:52;
- j. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:56, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60;

- k. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:62, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60;
- l. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:64, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:65, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- m. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:67, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:68, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:69, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- n. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:71, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:72, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- o. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:74, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:75, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:77, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:78;
- p. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:80, a light

- chain CDR1 comprising the amino acid sequence of SEQ ID NO:82, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:83; or
- q. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:85, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:86, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:88, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:89;

wherein the CDRs are defined according to Kabat.

[0011] In the ROR1 x CD3 bispecific antibodies, or bispecific antigen-binding fragments thereof, the second antigen-binding site that immunospecifically bind CD3 can have a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0012] In some embodiments, the isolated ROR1 x CD3 bispecific antibodies, or bispecific antigen-binding fragments thereof, can comprise: a first heavy chain (HC1); a second heavy chain (HC2); a first light chain (LC1); and a second light chain (LC2), wherein the HC1 and the LC1 form a first antigen-binding site that immunospecifically binds ROR1, and the HC2 and the LC2 form a second antigen-binding site that immunospecifically binds CD3. In some aspects, the ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof, comprise a HC1 and LC1 wherein:

- a. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:3, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:4, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;

- b. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:11, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:12, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- c. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:15, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:16, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- d. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:18, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:20, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- e. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:24, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- f. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:26, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:27, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:28, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:30, a light chain CDR2 comprising the amino acid sequence of

- SEQ ID NO:31, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:32;
- g. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:34, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:35, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:37, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:38;
- h. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:40, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:42, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:44;
- i. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:46, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:47, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:48, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:50, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:52;
- j. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:56, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60;
- k. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID

- NO:62, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60;
- l. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:64, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:65, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - m. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:67, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:68, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:69, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - n. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:71, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:72, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - o. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:74, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:75, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:77, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:78;

- p. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:80, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:82, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:83; or
- q. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:85, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:86, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:88, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:89;

wherein the CDRs are defined according to Kabat.

[0013] In some aspects, the ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof comprise an HC1 and LC1 wherein

- a. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:1 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- b. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:9 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- c. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:13 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- d. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:17 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;

- e. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:21 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- f. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:25 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:29;
- g. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:33 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:36;
- h. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:39 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:41;
- i. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:45 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:49;
- j. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:53 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:57;
- k. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:61 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:57;
- l. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:63 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;

- m. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:66 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- n. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:70 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- o. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:73 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:76;
- p. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:79 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:81; or
- q. the HC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:84 and the LC1 comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:87.

[0014] In some embodiments, the HC2 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat. In some embodiments, the HC2 comprises an amino acid sequence that is at least 90% identical to SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90% identical to SEQ ID NO:91.

[0015] Also disclosed are nucleic acid molecules encoding the disclosed ROR1 x CD3 bispecific antibodies and bispecific antigen-binding fragments thereof, vectors comprising the nucleic acid molecules, and cells expressing the ROR1 x CD3 bispecific antibodies and bispecific antigen-binding fragments thereof.

[0016] Provided are methods of treating a subject having cancer, the methods comprising administering to the subject a therapeutically effective amount of any of the disclosed the ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof.

[0017] Further disclosed is the use of an effective amount of any of the disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof in the treatment of cancer, and the use of any of the disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof in the manufacture of a composition for the treatment of cancer.

BRIEF DESCRIPTION OF THE DRAWINGS

[0018] The summary, as well as the following detailed description, is further understood when read in conjunction with the appended drawings. For the purpose of illustrating the disclosed isolated antibodies, isolated bispecific antibodies, and methods, there are shown in the drawings exemplary embodiments of the isolated antibodies, isolated bispecific antibodies, and methods; however, the isolated antibodies, isolated bispecific antibodies, and methods are not limited to the specific embodiments disclosed. In the drawings:

[0019] **FIG. 1** illustrates the expression of cell-surface ROR1 in various lung tumor cell lines: small cell lung cancer (NCI-H1417); NSCLC adenocarcinoma (HCC-827); NSCLC squamous cell carcinoma (SK-MES-1); and bronchioalveolar carcinoma (NCI-H358). Flow cytometry expression analysis was performed using 0.5 μ l 2A2 anti-ROR1 clone (Biolegend cat# 357806). MFI values were normalized using binding of an mIgG1 isotype control antibody (Biolegend cat# 400120) at the same concentration to calculate the fold-change over background. Single replicates were run for each sample.

[0020] **FIG. 2A, FIG. 2B, and FIG. 2C** illustrate the binning of the 24 anti-ROR1 antibodies that were advanced to expression and purification as IgG4 PAA molecules. **(A)** Ig Domain binders. **(B)** Frizzled Domain binders. **(C)** Kringle Domain binders.

[0021] **FIG. 3** illustrates cross competition data for the Kringle domain binders for human ROR1. In this experiment 1 μ M competing mAb displaced the signal from the labeled RR1B69 molecule.

[0022] **FIG. 4A, FIG. 4B, and FIG. 4C** illustrate the binding affinity of the anti-ROR1 antibodies evaluated by flow cytometry to HCC827 cells. **(A)** Ig Domain binders. **(B)** Frizzled Domain binders. **(C)** Kringle Domain binders.

[0023] **FIG. 5A, FIG. 5B, and FIG. 5C** illustrate *in vitro* target cell killing data for the specified ROR1xCD3 bispecific antibodies. The data suggests that the Kringle domain binders were most effective in target cell killing. **(A)** Ig Domain binders. **(B)** Frizzled Domain binders. **(C)** Kringle Domain binders.

[0024] **FIG. 6A, FIG. 6B, and FIG. 6C** illustrate the DiscoverX® T cell mediated cytotoxicity assay carried out with the specified ROR1 x CD3 bispecific antibodies. In this experiment, modified SK-MES-1 cells were used. The data suggests that the Kringle domain binders were most effective in target cell killing. **(A)** Ig Domain binders. **(B)** Frizzled Domain binders. **(C)** Kringle Domain binders.

[0025] **FIG. 7A and FIG. 7B** illustrate the binding profiles of ROR1 x CD3 bispecific antibody, RCDB5, and its parental anti-ROR1 antibody, RR1B67, as obtained by Biacore (top left and bottom left panels, respectively) using recombinant ROR1 and via MSD-CAT (top right and bottom right panels, respectively) using HEK293 cells engineered to overexpress ROR1. The data shown here is an example for one of 3 or more experiments.

[0026] **FIG. 8** illustrates the admixture *in vivo* study in athymic nude mice. The data suggested a dose dependent effect in a solid tumor model.

[0027] **FIG. 9A and FIG. 9B** illustrate the anti-ROR1 parental RR1B67 and ROR1 x CD3 bispecific antibody RCDB5 binding to FcγRIIIa. **(A)** n=1; **(B)** n=2.

[0028] **FIG. 10A and FIG. 10B** illustrate anti-ROR1 parental RR1B67 and ROR1 x CD3 bispecific antibody RCDB5 binding to FcγRIIIa. **(A)** n=1; **(B)** n=2.

[0029] **FIG. 11A, FIG. 11B, FIG. 11C, and FIG. 11D** illustrate the RR1B67 epitope location and interactions with human ROR1 based on the crystal structure for the RR1B67 Fab / ROR1 kringle **(A)** Overall structure of RR1B67 Fab bound to the membrane-proximal kringle domain of human ROR1. A schematic representation of the extracellular domains (ECD) of ROR1 is shown for reference. **(B)** Overview of the RR1B67 epitope location on the ROR1 kringle domain. The three disulfide bonds and single glycosylation site on the human ROR1 kringle domain are also shown. **(C)** Interaction map showing direct contacts between ROR1 and RR1B67. Van der Waals interactions are shown as dashed lines and hydrogen bonds as solid lines with arrows pointing to the backbone atoms. **(D)** Close view of the interface between ROR1 and the RR1B67 light and heavy chains. Hydrogen bonds are shown as dashed lines

[0030] **FIG. 12** illustrates the epitope and paratope residues of RR1B67. The CDR regions (Kabat definition) and Ig-like, frizzled and kringle domains are underlined. The epitope

and paratope residues are shaded. Only the sequences for the extracellular region of human ROR1 and the RR1B67 Fab are shown.

[0031] FIG. 13A, 13B, and 13C illustrate the redirected T cell killing of lung tumor cells activated by ROR1 x CD3 bispecific antibodies RCDB5 and a prior art antibody, published in WO2014167022A1, Example 3C, Bispecific (Fab)₂x(Fab) antibody bivalent for ROR1 and monovalent for CD3, with Fc, for brevity termed “Engmab” antibody. (A) Percent of live lung tumor cells out of total number of plated cells after treatments with either RCDB5 or Engmab antibodies. (B) Total number of surviving tumor cells per well at the highest antibody concentration used (6.67 nM). (C) Activation of T (effector) cells, as indicated by the percent of CD25⁺ T cells, at different antibody concentrations.

[0032] FIG. 14A and 14B illustrate ROR1 expression in heme cancer cell lines. (A) ROR1 expression presented as mean fluorescence intensity (MFI) in MCL/CLL – black bar, B lymphoma – grey bar and MM– dashed bar by flow cytometry. Corresponding Fluorescence Minus One (FMO) staining - white bar, served as negative control. (B) Representative ROR1 expression in MAVER-1 cell line (open histogram) and FMO - (filled histogram).

[0033] FIG. 15 illustrates ROR1 receptor density (number of ROR1 molecules per cell) in MCL cell lines by flow cytometry.

[0034] FIG. 16A, 16B, 16C, 16D, and 16E illustrate ROR1 expression on primary cryopreserved CLL and MCL samples by flow cytometry. (A) % of tumor cells in lymphoid gate. Tumor cells were defined as % CD19⁺CD5⁺ live cells. (B) % of ROR1⁺ cells of CD19⁺CD5⁺ tumor cells. (C) ROR1 MFI measured on ROR1⁺ population. (D) Representative ROR1 expression on CLL, donor ID 110029386. (E) Representative ROR1 expression on MCL, donor ID 120137190 tumor cells. Open histogram - ROR1, filled histogram - FMO control.

[0035] FIG. 17A-F illustrate ROR1xCD3-mediated killing of MCL lines in whole blood cytotoxicity assay *in vitro*. (A), (B), and (C) show % cytotoxicity (100%- % Live CFSE⁺ cells) in MAVER-1, JeKo-1, and Z-138 cells, respectively. (D), (E), and (F) show T cell activation (% CD25 expression on CD4⁺ and CD8⁺ lymphocytes) in MAVER-1, JeKo-1, and Z-138 cells, respectively. D1 – donor 10347; D2 – donor 10207.

[0036] FIG. 18A-D illustrate ROR1xCD3-mediated killing of MCL lines in cytotoxicity assay *in vitro* using PBMC as effector cells. (A) % Cytotoxicity (100%- % Live CFSE⁺ cells) in MAVER-1 cells. (B) % Cytotoxicity (100%- % Live CFSE⁺ cells) in Z-138 cells. (C) T cell activation (% CD25 expression on CD4⁺ and CD8⁺ lymphocytes) in MAVER-1

cells. (D) T cell activation (% CD25 expression on CD4+ and CD8+ lymphocytes) in Z-138 cells. D1 – donor M7444; D2 – donor M7267.

DETAILED DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

[0037] The disclosed isolated antibodies, isolated bispecific antibodies, and methods may be understood more readily by reference to the following detailed description taken in connection with the accompanying figures, which form a part of this disclosure. It is to be understood that the disclosed isolated antibodies, isolated bispecific antibodies, and methods are not limited to those described and/or shown herein, and that the terminology used herein is for the purpose of describing particular embodiments by way of example only and is not intended to be limiting of the claimed isolated antibodies, isolated bispecific antibodies, and methods.

[0038] Unless specifically stated otherwise, any description as to a possible mechanism or mode of action or reason for improvement is meant to be illustrative only, and the disclosed isolated antibodies, isolated bispecific antibodies, and methods are not to be constrained by the correctness or incorrectness of any such suggested mechanism or mode of action or reason for improvement.

[0039] Throughout this text, the descriptions refer to antibodies and methods of using said antibodies. Where the disclosure describes or claims a feature or embodiment associated with an antibody, such a feature or embodiment is equally applicable to the methods of using the antibody. Likewise, where the disclosure describes or claims a feature or embodiment associated with a method of using an antibody, such a feature or embodiment is equally applicable to the antibody.

[0040] When a range of values is expressed, another embodiment includes from the one particular value and/or to the other particular value. Further, reference to values stated in ranges include each and every value within that range. All ranges are inclusive and combinable. When values are expressed as approximations, by use of the antecedent “about,” it will be understood that the particular value forms another embodiment. Reference to a particular numerical value includes at least that particular value, unless the context clearly dictates otherwise.

[0041] It is to be appreciated that certain features of the disclosed isolated antibodies, isolated bispecific antibodies, and methods which are, for clarity, described herein in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the disclosed isolated antibodies, isolated bispecific antibodies,

and methods that are, for brevity, described in the context of a single embodiment, may also be provided separately or in any subcombination.

[0042] As used herein, the singular forms “a,” “an,” and “the” include the plural.

[0043] Various terms relating to aspects of the description are used throughout the specification and claims. Such terms are to be given their ordinary meaning in the art unless otherwise indicated. Other specifically defined terms are to be construed in a manner consistent with the definitions provided herein.

[0044] The term “about” when used in reference to numerical ranges, cutoffs, or specific values is used to indicate that the recited values may vary by up to as much as 10% from the listed value. Thus, the term “about” is used to encompass variations of $\pm 10\%$ or less, variations of $\pm 5\%$ or less, variations of $\pm 1\%$ or less, variations of $\pm 0.5\%$ or less, or variations of $\pm 0.1\%$ or less from the specified value.

[0045] “Antibody” refers to all isotypes of immunoglobulins (IgG, IgA, IgE, IgM, IgD, and IgY) including various monomeric, polymeric and chimeric forms, unless otherwise specified. Specifically encompassed by the term “antibody” are polyclonal antibodies, monoclonal antibodies (mAbs), and antibody-like polypeptides, such as chimeric antibodies and humanized antibodies.

[0046] “Antigen-binding fragments” or “bispecific antigen-binding fragments” are any proteinaceous structure that may exhibit binding affinity for a particular antigen. Antigen-binding fragments include those provided by any known technique, such as enzymatic cleavage, peptide synthesis, and recombinant techniques. Some antigen-binding fragments are composed of portions of intact antibodies that retain antigen-binding specificity of the parent antibody molecule. For example, antigen-binding fragments may comprise at least one variable region (either a heavy chain or light chain variable region) or one or more CDRs of an antibody known to bind a particular antigen. Examples of suitable antigen-binding fragments include, without limitation, diabodies and single-chain molecules as well as Fab, F(ab')₂, Fc, Fabc, and Fv molecules, single chain (Sc) antibodies, individual antibody light chains, individual antibody heavy chains, chimeric fusions between antibody chains or CDRs and other proteins, protein scaffolds, heavy chain monomers or dimers, light chain monomers or dimers, dimers consisting of one heavy and one light chain, a monovalent fragment consisting of the VL, VH, CL and CH1 domains, or a monovalent antibody as described in WO2007059782, bivalent fragments comprising two Fab fragments linked by a disulfide bridge at the hinge region, a Fd fragment consisting essentially of the V.sub.H and C.sub.H1 domains; a Fv fragment consisting essentially

of the VL and VH domains of a single arm of an antibody, a dAb fragment (Ward et al., Nature 341, 544-546 (1989)), which consists essentially of a VH domain and also called domain antibodies (Holt et al; Trends Biotechnol. 2003 Nov.; 21(11):484-90); camelid or nanobodies (Revets et al; Expert Opin Biol Ther. 2005 Jan.; 5(1):111-24); an isolated complementarity determining region (CDR), and the like. All antibody isotypes may be used to produce antigen-binding fragments. Additionally, antigen-binding fragments may include non-antibody proteinaceous frameworks that may successfully incorporate polypeptide segments in an orientation that confers affinity for a given antigen of interest, such as protein scaffolds. Antigen-binding fragments may be recombinantly produced or produced by enzymatic or chemical cleavage of intact antibodies. The phrase “an antibody or antigen-binding fragment thereof” may be used to denote that a given antigen-binding fragment incorporates one or more amino acid segments of the antibody referred to in the phrase.

[0047] When used herein in the context of two or more antibodies or antigen-binding fragments, the term “competes with” or “cross-competes with” indicates that the two or more antibodies or antigen-binding fragments compete for binding to ROR1, e.g. compete for ROR1 binding in the assay described in the disclosed Examples.

[0048] The term “CD3” refers to the human CD3 protein multi-subunit complex. The CD3 protein multi-subunit complex is composed to 6 distinctive polypeptide chains. These include a CD3 γ chain (SwissProt P09693), a CD3 δ chain (SwissProt P04234), two CD3 ϵ chains (SwissProt P07766), and one CD3 ζ chain homodimer (SwissProt 20963), and which is associated with the T cell receptor α and β chain. The term “CD3” includes any CD3 variant, isoform and species homolog which is naturally expressed by cells (including T cells) or can be expressed on cells transfected with genes or cDNA encoding those polypeptides, unless noted.

[0049] “Effective amount” or “therapeutically effective amount” refers to an amount effective, at dosages and for periods of time necessary, to achieve a desired therapeutic result. A therapeutically effective amount of a ROR1 x CD3 bispecific antibody or bispecific antigen-binding fragment thereof may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of the antibody to elicit a desired response in the individual. A therapeutically effective amount is also one in which any toxic or detrimental effects of the antibody or antibody portion are outweighed by the therapeutically beneficial effects.

[0050] The term “epitope” means a protein determinant capable of specific binding to an antibody. Epitopes usually consist of surface groupings of molecules such as amino acids or

sugar side chains and usually have specific three dimensional structural characteristics, as well as specific charge characteristics. Conformational and nonconformational epitopes are distinguished in that the binding to the former but not the latter is lost in the presence of denaturing solvents. The epitope may comprise amino acid residues directly involved in the binding and other amino acid residues, which are not directly involved in the binding, such as amino acid residues which are effectively blocked or covered by the specifically antigen binding peptide (in other words, the amino acid residue is within the footprint of the specifically antigen binding peptide).

[0051] “Immunospecifically” when used in the context of antibodies, or antibody fragments, represents binding via domains encoded by immunoglobulin genes or fragments of immunoglobulin genes to one or more epitopes of a protein of interest, without preferentially binding other molecules in a sample containing a mixed population of molecules. Typically, an antibody binds to a cognate antigen with a K_d of less than about 1×10^{-8} M, as measured by a surface plasmon resonance assay or a cell binding assay. Phrases such as “anti-[antigen] antibody” (e.g., anti-ROR1 antibody) are meant to convey that the recited antibody specifically binds the recited antigen.

[0052] “Isolated” means a biological component (such as an antibody) has been substantially separated, produced apart from, or purified away from other biological components of the organism in which the component naturally occurs, i.e., other chromosomal and extrachromosomal DNA and RNA, and proteins. Antibodies that have been “isolated” thus include antibodies purified by standard purification methods. “Isolated antibodies” can be part of a composition and still be isolated if such composition is not part of the native environment of the antibody. The term also embraces antibodies prepared by recombinant expression in a host cell as well as chemically synthesized antibodies. An “isolated antibody or antigen-binding fragment thereof,” as used herein, is intended to refer to an antibody or antigen-binding fragment thereof which is substantially free of other antibodies or antigen-binding fragments having different antigenic specificities (for instance, an isolated antibody that specifically binds to ROR1 is substantially free of antibodies that specifically bind antigens other than ROR1). An isolated antibody that specifically binds to an epitope, isoform or variant of ROR1 may, however, have cross-reactivity to other related antigens, for instance from other species (such as ROR1 species homologs).

[0053] The term “ k_d ” (sec^{-1}), as used herein, refers to the dissociation rate constant of a particular antibody-antigen interaction. Said value is also referred to as the k_{off} value.

[0054] The term “ k_a ” ($M^{-1} \text{ sec}^{-1}$), as used herein, refers to the association rate constant of a particular antibody-antigen interaction.

[0055] The term “ K_D ” (M), as used herein, refers to the dissociation equilibrium constant of a particular antibody-antigen interaction.

[0056] The term “ K_A ” (M^{-1}), as used herein, refers to the association equilibrium constant of a particular antibody-antigen interaction and is obtained by dividing the k_a by the k_d .

[0057] “Subject” refers to human and non-human animals, including all vertebrates, e.g., mammals and non-mammals, such as non-human primates, mice, rabbits, sheep, dogs, cats, horses, cows, chickens, amphibians, and reptiles. In many embodiments of the described methods, the subject is a human.

[0058] “ROR1” (Receptor Tyrosine Kinase-Like Orphan Receptor 1) refers to the 106-kDa member of the receptor tyrosine kinase family having a UniProt Accession Number Q01973 (human) and Q9Z139 (mouse).

[0059] “Treating” or “treatment” refer to any success or indicia of success in the attenuation or amelioration of an injury, pathology, or condition, including any objective or subjective parameter such as abatement, remission, diminishing of symptoms or making the condition more tolerable to the patient, slowing in the rate of degeneration or decline, making the final point of degeneration less debilitating, improving a subject’s physical or mental well-being, or prolonging the length of survival. The treatment may be assessed by objective or subjective parameters, including the results of a physical examination, neurological examination, or psychiatric evaluations.

[0060] The following abbreviations are used herein: Receptor Tyrosine Kinase-Like Orphan Receptor 1 (ROR1); small cell lung cancer (SCLC), non-small cell lung cancer (NSCLC); circulating tumor cell (CTC); extracellular domain (ECD).

ROR1 Specific Antibodies and Antigen-Binding Fragments

[0061] Disclosed herein are isolated antibodies, or antigen-binding fragments thereof, that immunospecifically bind to ROR1. The disclosed isolated antibodies, or antigen-binding fragments thereof, include those provided in **Table 20**.

[0062] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:1 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5. In some

embodiments, the heavy chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:1 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:5.

[0063] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:2,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:3,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:4,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:6,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:7, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:8,

wherein the CDRs are defined according to Kabat.

[0064] The isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and a light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:1 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:1 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:5.

[0065] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1, is RR1B65 or an antigen-binding fragment thereof.

[0066] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:9 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:9 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:5.

[0067] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:10,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:11,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:12,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:6,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:7, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:8,

wherein the CDRs are defined according to Kabat.

[0068] The isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and a light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:9 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:9 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:5.

[0069] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1, can be RR1B66 or an antigen-binding fragment thereof.

[0070] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:13 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:13 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:5.

[0071] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:14,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:15,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:16,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:6,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:7, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:8,

wherein the CDRs are defined according to Kabat.

[0072] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:13 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:13 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:5.

[0073] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1, can be RR1B67 or an antigen-binding fragment thereof.

[0074] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:17 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:17 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:5.

[0075] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:18,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:19,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:20,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:6,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:7, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:8,

wherein the CDRs are defined according to Kabat.

[0076] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:17 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
- b. a heavy chain that comprises, consists of, or consist essentially of the amino acid sequence of SEQ ID NO:17 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:5.

[0077] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B69 or an antigen-binding fragment thereof.

[0078] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:21 and the light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:21 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:5.

[0079] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:22,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:23,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:24,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:6,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:7, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:8,

wherein the CDRs are defined according to Kabat.

[0080] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:21 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:21 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:5.

[0081] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B70 or an antigen-binding fragment thereof.

[0082] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:25 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:29. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:25 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:29.

[0083] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:26,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:27,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:28,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:30,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:31, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:32,

wherein the CDRs are defined according to Kabat.

[0084] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:25 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:29; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:25 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:29.

[0085] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B71 or an antigen-binding fragment thereof.

[0086] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:33 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:36. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:33 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:36.

[0087] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:2,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:34,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:35,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:37,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:7, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:38,

wherein the CDRs are defined according to Kabat.

[0088] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:33 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:36; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:33 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:36.

[0089] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B72 or an antigen-binding fragment thereof.

[0090] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:39 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:41. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:39 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:41.

[0091] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:22,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:23,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:40,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:42,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:43, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:44,

wherein the CDRs are defined according to Kabat.

[0092] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:39 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:41; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:39 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:41.

[0093] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B74 or an antigen-binding fragment thereof.

[0094] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:45 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:49. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:45 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:49.

[0095] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:46,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:47,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:48,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:50,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:51, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:52,

wherein the CDRs are defined according to Kabat.

[0096] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:45 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:49; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:45 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:49.

[0097] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B76 or an antigen-binding fragment thereof.

[0098] The isolated antibody and antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:53 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:57. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:53 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:57.

[0099] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:54,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:55,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:56,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:58,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:59, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:60,

wherein the CDRs are defined according to Kabat.

[0100] In some embodiments, the isolated antibody or antigen-binding fragment can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:53 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:57; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:53 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:57.

[0101] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B77 or an antigen-binding fragment thereof.

[0102] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:61 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:57. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:61 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:57.

[00103] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:54,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:55,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:62,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:58,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:59, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:60,

wherein the CDRs are defined according to Kabat.

[00104] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further have a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:61 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:57; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:61 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:57.

[0105] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B78 or an antigen-binding fragment thereof.

[0106] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:63 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:63 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:5.

[0107] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:64,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:19,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:65,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:6,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:7, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:8,

wherein the CDRs are defined according to Kabat.

[0108] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:63 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:63 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:5.

[0109] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B82 or an antigen-binding fragment thereof.

[0110] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:66 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:66 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:5.

[0111] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:67,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:68,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:69,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:6,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:7, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:8,

wherein the CDRs are defined according to Kabat.

[0112] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:66 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:66 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:5.

[0113] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B83 or an antigen-binding fragment thereof.

[0114] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:70 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:70 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:5.

[0115] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:10,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:71,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:72,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:6,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:7, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:8,

wherein the CDRs are defined according to Kabat.

[0116] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:70 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:70 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:5.

[0117] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B84 or an antigen-binding fragment thereof.

[0118] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:73 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:76. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:73 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:76.

[0119] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:54,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:74,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:75,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:77,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:51, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:78,

wherein the CDRs are defined according to Kabat.

[0120] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:73 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:76;
or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:73 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:76.

[0121] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B85 or an antigen-binding fragment thereof.

[0122] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:79 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:81. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:79 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:81.

[0123] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:22,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:23,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:80,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:82,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:7, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:83,

wherein the CDRs are defined according to Kabat.

[0124] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:79 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:81; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:79 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:81.

[0125] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B86 or an antigen-binding fragment thereof.

[0126] The isolated antibody or antigen-binding fragment thereof can comprise a heavy chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:84 and a light chain comprising an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:87. In some aspects, the heavy chain can comprise, consist of, or consist essentially of the amino acid

sequence of SEQ ID NO:84 and the light chain can comprise, consist of, or consist essentially of the amino acid sequence of SEQ ID NO:87.

[0127] The isolated antibody or antigen-binding fragment thereof can comprise:

- a. a heavy chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:22,
- b. a heavy chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:85,
- c. a heavy chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:86,
- d. a light chain CDR1 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:88,
- e. a light chain CDR2 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:43, and
- f. a light chain CDR3 comprising, consisting of, or consisting essentially of the amino acid sequence of SEQ ID NO:89,

wherein the CDRs are defined according to Kabat.

[0128] In some embodiments, the isolated antibody or antigen-binding fragment thereof can further comprise a heavy chain and light chain that, apart from the CDRs, comprise:

- a. a heavy chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:84 and a light chain amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:87; or
- b. a heavy chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:84 and a light chain that comprises, consists of, or consists essentially of the amino acid sequence of SEQ ID NO:87.

[0129] In some embodiments, the isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1 is RR1B88 or an antigen-binding fragment thereof.

[0130] The isolated antibody, or antigen-binding fragment thereof bind to an epitope within the extracellular domain (ECD) of ROR1. In some embodiments, the isolated antibody or antigen-binding fragment thereof can bind to the Ig-like Domain. In some embodiments, the isolated antibody or antigen-binding fragment thereof can bind to the Frizzled Domain. In some embodiments, the isolated antibody or antigen-binding fragment thereof can bind to the Kringle Domain.

[0131] The isolated antibody, or antigen-binding fragment thereof, can bind to a region of the ROR1 extracellular domain (ECD) spanning residues 324-387 (TVSVTKSGRQCQPWNSQYPHTHTFTALRFPELNGGHSYCRNPGNQKEAPWCFTLDEN FKSDLCD – SEQ ID NO:98). In some aspects, the epitope of the isolated antibody or antigen-binding fragment thereof comprises SEQ ID NO:98. In some aspects, the epitope of the isolated antibody or antigen-binding fragment thereof consists essentially of SEQ ID NO:98. In some aspects, the epitope of the isolated antibody or antigen-binding fragment thereof consists of SEQ ID NO:98. In some aspects, the epitope of the isolated antibody or antigen-binding fragment thereof is 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:98.

[0132] In some embodiments, the isolated antibody or antigen-binding fragment thereof can bind to an epitope on ROR1 comprising T324, V325, S326, V327, T328, S330, G331, R332, Q333, P336, N338, S339, Y341, H359, S360, Y361, L377, D378, and D387. In some embodiments, the isolated antibody or antigen-binding fragment thereof can bind to an epitope on ROR1 consisting essentially of T324, V325, S326, V327, T328, S330, G331, R332, Q333, P336, N338, S339, Y341, H359, S360, Y361, L377, D378, and D387. In some embodiments, the isolated antibody or antigen-binding fragment thereof can bind to an epitope on ROR1 consisting of T324, V325, S326, V327, T328, S330, G331, R332, Q333, P336, N338, S339, Y341, H359, S360, Y361, L377, D378, and D387.

[0133] Also provided are isolated antibodies or antigen-binding fragments thereof that compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof. Suitable reference antibodies include any of the isolated anti-ROR1 antibodies or antigen-binding fragments thereof disclosed above. In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:1 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:1 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5.

[0134] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:9 and a light chain comprising, consisting essentially of, or

consisting of the amino acid sequence of SEQ ID NO:5. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:9 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5.

[0135] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:13 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:13 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5.

[0136] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:17 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:17 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5.

[0137] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:21 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:21 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5.

[0138] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:25 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:29. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:25 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:29.

[0139] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:33 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:36. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:33 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:36.

[0140] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:39 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:41. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:39 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:41.

[0141] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:45 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:49. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising

a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:45 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:49.

[0142] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:53 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:57. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:53 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:57.

[0143] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:61 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:57. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:61 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:57.

[0144] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:63 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:63 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5.

[0145] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:66 and a light chain comprising, consisting essentially of, or

consisting of the amino acid sequence of SEQ ID NO:5. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:66 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5.

[0146] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:70 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:70 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5.

[0147] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:73 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:76. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:73 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:76.

[0148] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:79 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:81. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:79 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:81.

[0149] In some embodiments, the reference antibody or antigen-binding fragment thereof can comprise a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:84 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:87. Thus, the isolated antibody or antigen-binding fragment thereof can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:84 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:87.

[0150] Also provided herein are isolated antibodies, or antigen-binding fragments thereof, that compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, wherein the reference antibody or antigen-binding fragment thereof binds an epitope within residues 324-387

(TVSVTKSGRQCQPWNSQYPHTHTFTALRFPELNGGHSYCRNPGNQKEAPWCFTLDEN FKSDLCD – SEQ ID NO:98) of the ROR1 extracellular domain (ECD). In some aspects, the isolated antibodies, or antigen-binding fragments thereof, compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, wherein the reference antibody or antigen-binding fragment thereof binds an epitope comprising SEQ ID NO:98. In some aspects, the isolated antibodies, or antigen-binding fragments thereof, compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, wherein the reference antibody or antigen-binding fragment thereof binds an epitope consisting essentially of SEQ ID NO:98. In some aspects, the isolated antibodies, or antigen-binding fragments thereof, compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, wherein the reference antibody or antigen-binding fragment thereof binds an epitope consisting of SEQ ID NO:98. In some aspects, the isolated antibodies, or antigen-binding fragments thereof, compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, wherein the reference antibody or antigen-binding fragment thereof binds an epitope that is 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:98.

[0151] The isolated antibody, or antigen-binding fragment thereof, can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, wherein the reference antibody or antigen-binding fragment binds to an epitope on ROR1 comprising T324, V325, S326, V327, T328, S330, G331, R332, Q333, P336, N338, S339, Y341, H359, S360, Y361, L377, D378, and D387. In some embodiments, the isolated antibody, or antigen-binding

fragment thereof, can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, wherein the reference antibody or antigen-binding fragment binds to an epitope on ROR1 consisting essentially of T324, V325, S326, V327, T328, S330, G331, R332, Q333, P336, N338, S339, Y341, H359, S360, Y361, L377, D378, and D387. In some embodiments, the isolated antibody, or antigen-binding fragment thereof, can compete for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, wherein the reference antibody or antigen-binding fragment binds to an epitope on ROR1 consisting of T324, V325, S326, V327, T328, S330, G331, R332, Q333, P336, N338, S339, Y341, H359, S360, Y361, L377, D378, and D387. In some aspects, the reference antibody or antigen-binding fragment thereof comprises a heavy chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:13 and a light chain comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:5.

[0152] The disclosed anti-ROR1 antibodies or antigen-binding fragments thereof include all isotypes, IgA, IgD, IgE, IgG and IgM, and synthetic multimers of the four-chain immunoglobulin (Ig) structure. The disclosed antibodies or antigen-binding fragments also include the IgY isotype generally found in hen or turkey serum and hen or turkey egg yolk.

[0153] The disclosed antibodies or antigen-binding fragments can also be derived from any of the Ig subclasses. For example, the disclosed antibodies, or antigen-binding fragments thereof, can be derived from IgG1, IgG2, IgG3, and IgG4 isotypes. These subtypes share more than 95% homology in the amino acid sequences of the Fc regions but show major differences in the amino acid composition and structure of the hinge region. The Fc region mediates effector functions, such as antibody-dependent cellular cytotoxicity (ADCC) and complement-dependent cytotoxicity (CDC). In ADCC, the Fc region of an antibody binds to Fc receptors (FcγRs) on the surface of immune effector cells such as natural killers and macrophages, leading to the phagocytosis or lysis of the targeted cells. In CDC, the antibodies kill the targeted cells by triggering the complement cascade at the cell surface. The disclosed antibodies include antibodies with the described features of the variable domains in combination with any of the IgG isotypes, including modified versions in which the Fc sequence has been modified to effect different effector functions.

[0154] For many applications of therapeutic antibodies, Fc-mediated effector functions are not part of the mechanism of action. These Fc-mediated effector functions can be detrimental and potentially pose a safety risk by causing off-mechanism toxicity. Modifying effector functions can be achieved by engineering the Fc regions to reduce their binding to FcγRs or the

complement factors. The binding of IgG to the activating (FcγRI, FcγRIIa, FcγRIIIa and FcγRIIIb) and inhibitory (FcγRIIb) FcγRs or the first component of complement (C1q) depends on residues located in the hinge region and the CH2 domain. Mutations can be introduced in IgG1, IgG2 and IgG4 to reduce or silence Fc functionalities. Silencing mutations can include, but are not limited to IgG1 AA (F234A, L235A), IgG4 PAA (S228P, F234A, L235A), IgG2 AA (V234A, G237A), IgG1 FEA (L234F, L235E, D265A), or IgG1 FES (L234F/L235E/P331S). In some embodiments, the disclosed antibody or antigen-binding fragment thereof can contain the IgG1 AA (F234A, L235A) mutation. In some embodiments, the disclosed antibody or antigen-binding fragment thereof can contain the IgG4 PAA (S228P, F234A, L235A) mutation. In some embodiments, the disclosed antibody or antigen-binding fragment thereof can contain the IgG2 AA (V234A, G237A) mutation. In some embodiments, the disclosed antibody or antigen-binding fragment thereof can contain the IgG1 FEA (L234F, L235E, D265A) mutation. In some embodiments, the disclosed antibody or antigen-binding fragment thereof can contain the IgG1 FES (L234F/L235E/P331S) mutation. In some embodiments, the disclosed antibody or antigen-binding fragment thereof can contain the IgG1 L234A, L235A, and/or F405L mutations. In some embodiments, the disclosed antibody or antigen-binding fragment thereof can contain the S228P, L234A, L235A, F405L, and/or R409K mutations. In some embodiments, the disclosed antibody or antigen-binding fragment thereof can contain the IgG-AA Fc-L234A, L235A, and F405L.

[0155] The disclosed antibodies or antigen-binding fragments thereof can comprise an Fc region with one or more of the following properties: (a) reduced effector function when compared to the parent Fc; (b) reduced affinity to Fcγ RI, Fcγ RIIa, Fcγ RIIf, Fcγ RIIfb and/or Fcγ RIIfa; (c) reduced affinity to FcγRI; (d) reduced affinity to FcγRIIa; (e) reduced affinity to FcγRIIf; (f) reduced affinity to Fcγ RIIfb; or (g) reduced affinity to FcγRIIfa.

[0156] The anti-ROR1 antibodies and antigen-binding fragments thereof may be derived from any species by recombinant means. For example, the antibodies or antigen-binding fragments may be mouse, rat, goat, horse, swine, bovine, chicken, rabbit, camelid, donkey, human, or chimeric versions thereof. For use in administration to humans, non-human derived antibodies or antigen-binding fragments may be genetically or structurally altered to be less antigenic upon administration to the human patient.

[0157] In some embodiments, the antibodies or antigen-binding fragments can be chimeric. As used herein, the term “chimeric” refers to an antibody, or antigen-binding fragment thereof, having at least some portion of at least one variable domain derived from the antibody

amino acid sequence of a non-human mammal, a rodent, or a reptile, while the remaining portions of the antibody, or antigen-binding fragment thereof, are derived from a human.

[0158] In some embodiments, the antibodies can be humanized antibodies. Humanized antibodies may be chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) that contain minimal sequence derived from non-human immunoglobulin. For the most part, humanized antibodies are human immunoglobulins (recipient antibody) in which residues from a complementary-determining region (CDR) of the recipient antibody are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity, and capacity. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework regions are those of a human immunoglobulin sequence. The humanized antibody may include at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin.

[0159] The anti-ROR1 antibodies or antigen-binding fragments thereof described herein can have binding affinities for ROR1 that include a dissociation constant (K_D) of less than about 5×10^{-7} M, preferably less than about 5×10^{-8} M. In some embodiments, the anti-ROR1 antibodies or antigen-binding fragments thereof described herein can have binding affinities for ROR1 that include a dissociation constant (K_D) of less than about 5×10^{-7} M, preferably less than about 5×10^{-8} M. The affinity of the described anti-ROR1 antibodies or antigen-binding fragments thereof may be determined by a variety of methods known in the art, such as surface plasmon resonance or ELISA-based methods. Assays for measuring affinity by SPR include assays performed using a BIAcore T200 machine, where the assay is performed at room temperature (*e.g.* at or near 25°C), wherein the antibody capable of binding to ROR1 is captured on the Biacore sensor chip by an anti-Fc antibody (*e.g.* goat anti-human IgG Fc specific antibody Jackson ImmunoResearch laboratories Prod # 109-005-098) to a level around 300 RUs, followed by the collection of association and dissociation data at a flow rate of 50 μ l/min.

[0160] In addition to the described anti-ROR1 antibodies and antigen-binding fragments thereof, also provided are polynucleotide sequences encoding the disclosed antibodies and antigen-binding fragments thereof.

[0161] Vectors comprising the polynucleotides are also provided. The vectors can be expression vectors. Recombinant expression vectors containing a sequence encoding the

disclosed antibodies or antigen-binding fragments thereof are thus contemplated as within the scope of this disclosure. The expression vector may contain one or more additional sequences such as, but not limited to, regulatory sequences (e.g., promoter, enhancer), selection markers, and polyadenylation signals. Vectors for transforming a wide variety of host cells are well known and include, but are not limited to, plasmids, phagemids, cosmids, baculoviruses, bacmids, bacterial artificial chromosomes (BACs), yeast artificial chromosomes (YACs), as well as other bacterial, yeast and viral vectors.

[0162] Also described are cells expressing, and capable of expressing, the disclosed vectors. These cells may be mammalian cells (such as 293F cells, CHO cells), insect cells (such as Sf7 cells), yeast cells, plant cells, or bacteria cells (such as *E. coli*). The disclosed antibodies may also be produced by hybridoma cells.

ROR1 x CD3 Bispecific Antibodies and Bispecific Antigen Binding Fragments

[0163] Disclosed herein are isolated bispecific antibodies, or bispecific antigen-binding fragments thereof, that bind to ROR1 and CD3 (ROR1 x CD3 bispecific antibodies). The ROR1 x CD3 bispecific antibodies have at least a first antigen-binding site that immunospecifically binds ROR1 (ROR1 arm) and a second antigen-binding site that immunospecifically binds CD3 (CD3 arm).

[0164] The isolated ROR1 x CD3 bispecific antibodies, or bispecific antigen-binding fragments thereof, can comprise:

- a) a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site comprising a heavy chain CDR1, CDR2, and CDR3 and a light chain CDR1, CDR2, and CDR3; and
- b) a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site comprising a heavy chain CDR1, CDR2, and CDR3 and a light chain CDR1, CDR2, and CDR3.

[0165] Suitable first antigen-binding sites that immunospecifically bind ROR1 include any of the above disclosed anti-ROR1 antibodies. In some embodiments, the first antigen-binding site that immunospecifically binds ROR1 has:

- a. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:3, a heavy chain CDR3 comprising, consisting essentially of, or consisting of

- the amino acid sequence of SEQ ID NO:4, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- b. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:11, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:12, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- c. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:15, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:16, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- d. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:18, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:20, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of

- the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- e. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:24, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- f. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:26, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:27, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:28, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:30, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:31, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:32, wherein the CDRs are defined according to Kabat;
- g. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:34, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:35, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:37, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:38, wherein the CDRs are defined according to Kabat;

- h. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:40, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:42, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:44, wherein the CDRs are defined according to Kabat;
- i. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:46, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:47, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:48, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:50, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:52, wherein the CDRs are defined according to Kabat;
- j. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:56, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:60, wherein the CDRs are defined according to Kabat;
- k. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID

NO:55, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:62, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:60, wherein the CDRs are defined according to Kabat;

- l. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:64, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:65, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- m. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:67, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:68, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:69, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- n. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:71, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:72, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID

- NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- o. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:74, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:75, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:77, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:78, wherein the CDRs are defined according to Kabat;
 - p. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:80, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:82, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:83, wherein the CDRs are defined according to Kabat; or
 - q. a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:85, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:86, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:88, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising,

consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:89, wherein the CDRs are defined according to Kabat.

[0166] The second antigen-binding site that immunospecifically binds CD3 can have a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat. The second antigen-binding site that immunospecifically binds CD3 can be derived from CD3B219. The second antigen-binding site that immunospecifically binds CD3 can be derived from the CD3 antibodies disclosed in U.S. Patent No. 8,236,308. The second antigen-binding site that immunospecifically binds CD3 can be derived from the CD3 antibodies disclosed in U.S. Patent App. Pub. No. 2010/0260668. The second antigen-binding site that immunospecifically binds CD3 can be derived from the CD3 antibodies disclosed in U.S. Patent App. Pub. No. 2013/0018174. The second antigen-binding site that immunospecifically binds CD3 can be derived from the CD3 antibodies disclosed in EP2647707. The second antigen-binding site that immunospecifically binds CD3 can be derived from the CD3 antibodies disclosed in U.S. Patent App. Pub. No. 2012/0321626. The second antigen-binding site that immunospecifically binds CD3 can be derived from the CD3 antibodies disclosed in Int'l Pub. No. WO2012/162067. The second antigen-binding site that immunospecifically binds CD3 can be derived from the CD3 antibodies disclosed in U.S. Patent App. Pub. No. 2013/0060011. The second antigen-binding site that immunospecifically binds CD3 can be derived from the CD3 antibodies disclosed in U.S. Patent App. Pub. No. 2013/0058936. The second antigen-binding site that immunospecifically binds CD3 can be derived from the CD3 antibodies disclosed in U.S. Patent App. Pub. No. 2013/0078249. The second antigen-binding site that immunospecifically binds CD3 can be derived from the CD3 antibodies disclosed in U.S. Patent App. Pub. No. 2013/0058937. The second antigen-binding site that immunospecifically binds CD3 can be derived from the CD3 antibodies disclosed in Int'l Pub. No. WO2013/065708.

[0167] In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can comprise mutations in the Fc region including, but not limited to, IgG1 AA (F234A, L235A), IgG4 PAA (S228P, F234A, L235A), IgG2 AA (V234A, G237A), IgG1 FEA (L234F, L235E, D265A), or IgG1 FES (L234F/L235E/P331S). In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG1 AA (F234A, L235A) mutation. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG4 PAA (S228P, F234A, L235A) mutation. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG2 AA (V234A, G237A) mutation. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG1 FEA (L234F, L235E, D265A) mutation. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG1 FES (L234F/L235E/P331S) mutation. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG1 L234A, L235A, and/or F405L mutations. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the S228P, L234A, L235A, F405L, and/or R409K mutations. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG-AA Fc-L234A, L235A, and F405L.

[0168] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:3, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:4, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a

heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0169] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:11, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:12, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97,

wherein the CDRs are defined according to Kabat.

[0170] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:15, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:16, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97,

wherein the CDRs are defined according to Kabat.

[0171] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:18, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising, consisting essentially of, or

consisting of the amino acid sequence of SEQ ID NO:20, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8; and

- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0172] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:24, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting

essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0173] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:26, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:27, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:28, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:30, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:31, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:32; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID

NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0174] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:34, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:35, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:37, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:38; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0175] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2

comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:40, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:42, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:44; and

- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0176] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:46, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:47, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:48, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:50, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:52; and

- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0177] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:56, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:60; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising,

consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0178] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:62, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:60; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0179] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or

- consisting of the amino acid sequence of SEQ ID NO:64, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:65, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8;
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0180] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:67, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:68, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:69, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3

comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8; and

- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0181] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:71, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:72, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID

NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0182] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:74, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:75, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:77, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:78; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0183] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:80, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:82, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:83; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0184] In some embodiments, the isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:85, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:86, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:88, a light chain CDR2 comprising, consisting essentially of, or

- consisting of the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:89; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0185] Also provided are isolated ROR1 x CD3 bispecific antibodies, or bispecific antigen-binding fragments thereof, comprising:

- a. a first heavy chain (HC1);
- b. a second heavy chain (HC2);
- c. a first light chain (LC1); and
- d. a second light chain (LC2),

wherein the HC1 and the LC1 form a first antigen-binding site that immunospecifically binds ROR1, and the HC2 and the LC2 form a second antigen-binding site that immunospecifically binds CD3.

[0186] In some embodiments, the first antigen-binding site that immunospecifically binds ROR1 is formed from a HC1 and a LC1, wherein:

- a. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:3, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:4, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially

- of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- b. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:11, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:12, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- c. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:15, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:16, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- d. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:18, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:19, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:20, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;

- e. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:23, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:24, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- f. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:26, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:27, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:28, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:30, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:31, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:32, wherein the CDRs are defined according to Kabat;
- g. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:34, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:35, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:37, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:38, wherein the CDRs are defined according to Kabat;

- h. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:23, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:40, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:42, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:44, wherein the CDRs are defined according to Kabat;
- i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:46, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:47, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:48, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:50, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:52, wherein the CDRs are defined according to Kabat;
- j. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:55, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:56, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:60, wherein the CDRs are defined according to Kabat;

- k. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:55, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:62, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:60, wherein the CDRs are defined according to Kabat;
- l. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:64, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:19, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:65, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- m. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:67, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:68, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:69, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- n. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2

- comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:71, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:72, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat;
- o. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:74, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:75, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:77, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:78, wherein the CDRs are defined according to Kabat;
- p. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:23, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:80, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:82, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:83, wherein the CDRs are defined according to Kabat; or
- q. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of

SEQ ID NO:85, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:86, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:88, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:89, wherein the CDRs are defined according to Kabat.

[0187] In some embodiments, the first antigen-binding site that immunospecifically binds ROR1 is formed from:

- a. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:1 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:1 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5;
- b. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:9 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:9 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5
- c. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:13 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:13 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5
- d. a HC1 and a LC1, wherein

- i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:17 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:17 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5
- e. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:21 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:21 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5
- f. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:25 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:29; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:25 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:29
- g. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:33 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:36; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:33 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:36
- h. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:39 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:41; or

- ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:39 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:41
- i. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:45 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:49; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:45 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:49
- j. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:53 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:57; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:53 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:57
- k. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:61 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:57; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:61 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:57
- l. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:63 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:63 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5
- m. a HC1 and a LC1, wherein

- i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:66 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:66 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5
- n. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:70 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:70 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5
- o. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:73 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:76; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:73 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:76
- p. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:79 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:81; or
 - ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:79 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:81
- q. a HC1 and a LC1, wherein
 - i. the HC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:84 and the LC1 is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:87; or

- ii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:84 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:87.

[0188] In some embodiments, the first antigen-binding site that immunospecifically binds to ROR1 can comprise:

- a. the heavy chain CDRs and light chain CDRs of any one of a-q above and
- b. a heavy chain and light chain that, apart from the CDRs, comprises:
 - i. the HC1 and LC1 of any one of a.i.-q.i. above or
 - ii. the HC1 and LC1 of any one of a.ii.-q.ii. above.

[0189] For example, and without intent to be limiting, the first antigen-binding site that immunospecifically binds to ROR1 can comprise:

a HC1 having a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:15, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:16, and a LC1 having a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat; and

a HC1 that, apart from the CDRs, is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:13 and a LC1 that, apart from the CDRs, is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5.

[0190] The second antigen-binding site that immunospecifically binds CD3 can be formed from a HC2 and a LC2, wherein the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of

SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

[0191] In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can be formed from a HC2 and a LC2, wherein the HC2 is at least 90%, 95%, or 99% identical to SEQ ID NO:90 and the LC2 is at least 90%, 95%, or 99% identical to SEQ ID NO:91. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 is formed from a HC2 and a LC2, wherein the HC2 comprises, consists essentially of, or consists the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists the amino acid sequence of SEQ ID NO:91.

[0192] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:3, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:4, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8;
 - ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:1 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:1 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein

- i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;
- ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
- iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0193] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:11, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:12, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3

- comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8;
- ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:9 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:9 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein
- i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;
 - ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
 - iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0194] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:15, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:16, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8;
 - ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:13 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:13 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein
 - i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;

- ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
- iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0195] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:18, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:19, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:20, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8;
 - ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:17 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:17 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein

- i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;
- ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
- iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0196] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:23, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:24, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3

- comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8;
- ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:21 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:21 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein
- i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;
 - ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
 - iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0197] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:26, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:27, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:28, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:30, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:31, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:32;
 - ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:25 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:29; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:25 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:29; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein
 - i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;

- ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
- iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0198] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:34, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:35, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:37, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:38;
 - ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:33 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:36; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:33 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:36; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein

- i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;
- ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
- iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0199] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:23, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:40, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:42, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:43, and a light chain CDR3

- comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:44;
- ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:39 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:41; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:39 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:41; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein
- i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;
 - ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
 - iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0200] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:46, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:47, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:48, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:50, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:52;
 - ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:45 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:49; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:45 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:49; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein
 - i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;

- ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
- iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0201] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:55, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:56, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:60;
 - ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:53 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:57; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:53 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:57; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein

- i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;
- ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
- iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0202] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:55, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:62, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:59, and a light chain CDR3

- comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:60;
- ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:61 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:57; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:61 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:57; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein
- i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;
 - ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
 - iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0203] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:64, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:19, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:65, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8;
 - ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:63 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:63 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein
 - i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;

- ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
- iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0204] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:67, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:68, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:69, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8;
 - ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:66 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:66 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein

- i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;
- ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
- iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0205] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:71, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:72, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3

- comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:8;
- ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:70 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:5; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:70 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:5; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein
- i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;
 - ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
 - iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0206] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:74, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:75, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:77, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:78;
 - ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:73 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:76; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:73 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:76; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein
 - i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;

- ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
- iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0207] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:23, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:80, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:82, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:83;
 - ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:79 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:81; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:79 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:81; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein

- i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;
- ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
- iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0208] The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, can comprise:

- a. a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site formed from a HC1 and a LC1, wherein
 - i. the HC1 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:85, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:86, and the LC1 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:88, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:43, and a light chain CDR3

- comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:89;
- ii. the HC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:84 and the LC1 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:87; or
 - iii. the HC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:84 and the LC1 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:87; and
- b. a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site formed from a HC2 and a LC2, wherein
- i. the HC2 has a heavy chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:93, and a heavy chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising, consisting essentially of, or consisting of the amino acid sequence of SEQ ID NO:97;
 - ii. the HC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90%, 95%, or 99% identical to the amino acid sequence of SEQ ID NO:91; or
 - iii. the HC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:90 and the LC2 comprises, consists essentially of, or consists of the amino acid sequence of SEQ ID NO:91,

wherein the CDRs are defined according to Kabat.

[0209] The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind to ROR1 with a K_D of less than about 100 nM, less than about 75 nM, less than about 50 nM, less than about 30 nM, less than about 25 nM, less than about 20 nM,

less than about 15 nM, less than about 10 nM, or less than about 7.5 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 5 nM to about 100 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 5 nM to about 75 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 5 nM to about 50 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 5 nM to about 30 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 5 nM to about 25 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 5 nM to about 20 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 5 nM to about 15 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 5 nM to about 10 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 10 nM to about 100 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 15 nM to about 100 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 20 nM to about 100 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 25 nM to about 100 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 30 nM to about 100 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 50 nM to about 100 nM as measured by Biacore. The disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof can bind ROR1 with a K_D of about 75 nM to about 100 nM as measured by Biacore.

[0210] In some embodiments, the first antigen-binding site that immunospecifically binds ROR1 can be derived from an IgG having one or more of the following mutations: IgG1

AA (F234A, L235A); IgG4 PAA (S228P, F234A, L235A); IgG2 AA (V234A, G237A); IgG1 FEA (L234F, L235E, D265A); or IgG1 FES (L234F/L235E/P331S). In some embodiments, the first antigen-binding site that immunospecifically binds ROR1 can contain the IgG1 AA (F234A, L235A) mutation. In some embodiments, the first antigen-binding site that immunospecifically binds ROR1 can contain the IgG4 PAA (S228P, F234A, L235A) mutation. In some embodiments, the first antigen-binding site that immunospecifically binds ROR1 can contain the IgG2 AA (V234A, G237A) mutation. In some embodiments, the first antigen-binding site that immunospecifically binds ROR1 can contain the IgG1 FEA (L234F, L235E, D265A) mutation. In some embodiments, the first antigen-binding site that immunospecifically binds ROR1 can contain the IgG1 FES (L234F/L235E/P331S) mutation. In some embodiments, the first antigen-binding site that immunospecifically binds ROR1 can contain the IgG1 L234A, L235A, and/or F405L mutations. In some embodiments the first antigen-binding site that immunospecifically binds ROR1 can contain the S228P, L234A, L235A, F405L, and/or R409K mutations. In some embodiments, the first antigen-binding site that immunospecifically binds ROR1 can contain the IgG-AA Fc-L234A, L235A, and F405L.

[0211] In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can be derived from an IgG having one or more of the following mutations: IgG1 AA (F234A, L235A); IgG4 PAA (S228P, F234A, L235A); IgG2 AA (V234A, G237A); IgG1 FEA (L234F, L235E, D265A); or IgG1 FES (L234F/L235E/P331S). In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG1 AA (F234A, L235A) mutation. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG4 PAA (S228P, F234A, L235A) mutation. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG2 AA (V234A, G237A) mutation. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG1 FEA (L234F, L235E, D265A) mutation. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG1 FES (L234F/L235E/P331S) mutation. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG1 L234A, L235A, and/or F405L mutations. In some embodiments the second antigen-binding site that immunospecifically binds CD3 can contain the S228P, L234A, L235A, F405L, and/or R409K mutations. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 can contain the IgG-AA Fc-L234A, L235A, and F405L.

[0212] In some embodiments, the the second antigen-binding site that immunospecifically binds CD3 can bind CD3ε on primary human T cells and/or primary cynomolgus T cells. In some embodiments, the second antigen-binding site that immunospecifically binds CD3 activates primary human CD4⁺ T cells and/or primary cynomolgus CD4⁺ T cells.

[0213] In some embodiments, the disclosed ROR1 x CD3 bispecific antibodies are capable of binding to CD3 on human or cynomolgous monkey T-cells with a dissociation constant of less than 500, or less than 100 or less that 20 nM as determined by competition binding with a labeled anti-CD3 antibody with known affinity.

[0214] The ROR1 x CD3 bispecific antibodies, or bispecific antigen-binding fragments thereof, can be single chain bispecific antibodies or bispecific antigen-binding fragments thereof. The ROR1 x CD3 bispecific antibodies, or bispecific antigen-binding fragments thereof, can be BITEs (Micromet). The ROR1 x CD3 bispecific antibodies, or bispecific antigen-binding fragments thereof, can be DARTs (MacroGenics). The ROR1 x CD3 bispecific antibodies, or bispecific antigen-binding fragments thereof, can be Fcab and Mab2 (F-star). The ROR1 x CD3 bispecific antibodies, or bispecific antigen-binding fragments thereof, can be Fc-engineered IgG1s (Xencor). The ROR1 x CD3 bispecific antibodies, or bispecific antigen-binding fragments thereof, can be DuoBodies (Genmab). The ROR1 x CD3 bispecific antibodies, or bispecific antigen-binding fragments thereof, can be TetBiAbs (Merck).

[0215] Methods of preparing bispecific antibodies invention include those described in WO2008/119353, WO2011/131746, van der Neut-Kolfschoten et al. (Science. 2007 Sep. 14; 317(5844):1554-7), PCT/US2015/051314, WO2005/061547, US2014/0170148, and US2016/0009824.

[0216] In addition to the disclosed ROR1 x CD3 bispecific antibodies and bispecific antigen-binding fragments thereof, provided are polynucleotide sequences encoding the described ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof. In some embodiments, the polynucleotide encoding the HC1, the HC2, the LC1 or the LC2 of the ROR1 x CD3 bispecific antibody or bispecific antigen-binding fragment is provided. Vectors comprising the described polynucleotides are also provided, as are cells expressing the ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof. These cells may be mammalian cells (such as 293F cells, CHO cells), insect cells (such as Sf7 cells), yeast cells, plant cells, or bacteria cells (such as E. coli). The disclosed ROR1 x CD3 bispecific antibodies and bispecific antigen-binding fragments thereof may also be produced by hybridoma cells. In

some embodiments, methods for generating the ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments by culturing cells is provided.

[0217] Further provided herein are pharmaceutical compositions comprising the ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments and a pharmaceutically acceptable carrier.

Method of Treating Cancer

[0218] Disclosed herein are methods of treating a subject having cancer, the method comprising administering to the subject a therapeutically effective amount of any of the above disclosed ROR1 x CD3 bispecific antibodies, or bispecific antigen-binding fragments thereof.

[0219] The use of an effective amount of any of the disclosed ROR1 x CD3 bispecific antibody or bispecific antigen-binding fragment thereof in the treatment of cancer is also provided.

[0220] The disclosed ROR1 x CD3 bispecific antibodies and bispecific antigen-binding fragments thereof can be used to inhibit the growth and/or proliferation of cancer cells or other diseased cells that express ROR1. Provided are methods for inhibiting growth or proliferation of cancer cells comprising administering a therapeutically effective amount of any of the disclosed the ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments to inhibit the growth or proliferation of cancer cells.

[0221] The disclosed ROR1 x CD3 bispecific antibodies and bispecific antigen-binding fragments thereof can further be used to enhance the killing of ROR1-expressing diseased cells, such as cancer cells, by targeting CD3 expressing T cells to the ROR1-expressing cell. Provided herein are methods of redirecting a T cell to a ROR1-expressing cancer cell comprising administering a therapeutically effective amount of any of the disclosed the ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments to redirect a T cell to a cancer.

[0222] In some embodiments, the cancer is a ROR1-expressing cancer, such as lung cancer, hematological cancer, breast cancer, prostate cancer, pancreatic cancer, colon cancer, ovarian cancer, renal cancer, uterine cancer, or melanoma. The ROR1-expressing cancer can be a lung cancer, such as non-small cell lung cancer (NSCLC) or small cell lung cancer (SCLC). The ROR1-expressing cancer can be a hematological cancer, such as acute myeloid leukemia (AML), myelodysplastic syndrome (MDS, low or high risk), acute lymphocytic leukemia (ALL, including all subtypes), diffuse large B-cell lymphoma (DLBCL), chronic myeloid leukemia (CML), or blastic plasmacytoid dendritic cell neoplasm (BPDCN). The ROR1-expressing

cancer can be breast cancer. The ROR1-expressing cancer can be prostate cancer. The ROR1-expressing cancer can be pancreatic cancer. The ROR1-expressing cancer can be colon cancer. The ROR1-expressing cancer can be ovarian cancer. The ROR1-expressing cancer can be renal cancer. The ROR1-expressing cancer can be uterine cancer. The ROR1-expressing cancer can be melanoma.

[0223] In some embodiments, the ROR1 x CD3 bispecific antibody or bispecific antigen-binding fragment thereof can be administered to the subject as a pharmaceutical composition. Thus, also disclosed is the use of any of the disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof in the manufacture of a composition for the treatment of cancer.

[0224] The pharmaceutical compositions provided herein can comprise: a) an effective amount of a ROR1 x CD3 bispecific antibody or bispecific antigen-binding fragment thereof, and b) a pharmaceutically acceptable carrier, which may be inert or physiologically active. As used herein, the term “pharmaceutically acceptable carriers” includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, and the like that are physiologically compatible. Examples of suitable carriers, diluents and/or excipients include one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol, and the like, as well as any combination thereof. In many cases, it will be preferable to include isotonic agents, such as sugars, polyalcohols, or sodium chloride in the composition. In particular, relevant examples of suitable carriers include: (1) Dulbecco's phosphate buffered saline, pH about 7.4, containing or not containing about 1 mg/mL to 25 mg/mL human serum albumin, (2) 0.9% saline (0.9% w/v sodium chloride (NaCl)), and (3) 5% (w/v) dextrose; and may also contain an antioxidant such as tryptamine and a stabilizing agent such as Tween 20 ®.

[0225] The ROR1 x CD3 bispecific antibody, bispecific antigen-binding fragment, or composition comprising the same may also contain a further therapeutic agent, as necessary for the particular disorder being treated. The ROR1 x CD3 bispecific antibody or bispecific antigen-binding fragment thereof and the further therapeutic agent preferably have complementary activities that do not adversely affect each other. In a preferred embodiment, the further therapeutic agent can be cytarabine, an anthracycline, histamine dihydrochloride, or interleukin 2. In a preferred embodiment, the further therapeutic agent is a chemotherapeutic agent.

[0226] The ROR1 x CD3 bispecific antibody, bispecific antigen-binding fragment, or composition comprising the same may be in a variety of forms including, for example, liquid, semi-solid, and solid dosage forms. The preferred form depends on the intended mode of

administration and therapeutic application. The ROR1 x CD3 bispecific antibody, bispecific antigen-binding fragment, or composition comprising the same can be in the form of injectable or infusible solutions. The ROR1 x CD3 bispecific antibody, bispecific antigen-binding fragment, or composition comprising the same can be administered parenterally (e.g. intravenous, intramuscular, intraperitoneal, subcutaneous). The ROR1 x CD3 bispecific antibody, bispecific antigen-binding fragment, or composition comprising the same can be administered intravenously as a bolus or by continuous infusion over a period of time. The ROR1 x CD3 bispecific antibody, bispecific antigen-binding fragment, or composition comprising the same can be injected by intramuscular, subcutaneous, intra-articular, intrasynovial, intratumoral, peritumoral, intralesional, or perilesional routes, to exert local as well as systemic therapeutic effects. The ROR1 x CD3 bispecific antibody, bispecific antigen-binding fragment, or composition comprising the same can be administered orally.

[0227] Sterile preparations for parenteral administration can be prepared by incorporating the antibody, or antigen-binding fragment thereof, in the required amount in the appropriate solvent, followed by sterilization by microfiltration. As solvent or vehicle, there may be used water, saline, phosphate buffered saline, dextrose, glycerol, ethanol, and the like, as well as combination thereof. In many cases, isotonic agents, such as sugars, polyalcohols, or sodium chloride can be included in the composition. These compositions may also contain adjuvants, in particular wetting, isotonizing, emulsifying, dispersing and stabilizing agents. Sterile compositions for parenteral administration may also be prepared in the form of sterile solid compositions which may be dissolved at the time of use in sterile water or any other injectable sterile medium.

[0228] Solids for oral administration, including tablets, pills, powders (gelatine capsules, sachets) or granules may be used. In these compositions, the bispecific antibody or antigen-binding fragment thereof can be mixed with one or more inert diluents, such as starch, cellulose, sucrose, lactose or silica, under an argon stream. These compositions may also comprise substances other than diluents, for example one or more lubricants such as magnesium stearate or talc, a coloring, a coating (sugar-coated tablet) or a glaze.

[0229] For liquid compositions for oral administration, there may be used pharmaceutically acceptable solutions, suspensions, emulsions, syrups and elixirs containing inert diluents such as water, ethanol, glycerol, vegetable oils or paraffin oil. These compositions may comprise substances other than diluents, for example wetting, sweetening, thickening, flavoring or stabilizing products.

[0230] The dose of the ROR1 x CD3 bispecific antibody, bispecific antigen-binding fragment, or composition comprising the same depends on the desired effect, the duration of the treatment, and the route of administration used. In general, the doctor will determine the appropriate dosage depending on the age, weight and any other factors specific to the subject to be treated.

[0231] Dosage regimens in the above methods of treatment and uses are adjusted to provide the optimum desired response (e.g., a therapeutic 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. Parenteral compositions may be formulated in dosage unit form for ease of administration and uniformity of dosage.

[0232] The ROR1 x CD3 bispecific antibody or bispecific antigen-binding fragment thereof may also be administered in combination therapy, *i.e.*, combined with other therapeutic agents relevant for the disease or condition to be treated. In some embodiments is provided a method for treating or preventing cancer, the method comprises administering to a subject a therapeutically effective amount of any of the disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof, and a chemotherapeutic agent. In some embodiments, the other therapeutic agent is cytarabine, an anthracycline, histamine dihydrochloride, or interleukin 2. In some embodiments is provided a method for treating or preventing cancer, the method comprising administering to a subject a therapeutically effective amount of any of the disclosed ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof and radiotherapy. Radiotherapy may comprise radiation or associated administration of radiopharmaceuticals. The source of radiation may be either external or internal to the patient being treated (radiation treatment may, for example, be in the form of external beam radiation therapy (EBRT) or brachytherapy (BT)). Radioactive elements include, e.g., radium, cesium-137, iridium-192, americium-241, gold-198, cobalt-57, copper-67, technetium-99, iodide-123, iodide-131, and indium-111. Combined administration of the disclosed bispecific ROR1 x CD3 bispecific antibodies or bispecific antigen-binding fragments thereof and the other therapeutic agent may be simultaneous, separate or sequential, in any order. For simultaneous administration, the agents may be administered as one composition or as separate compositions, as appropriate.

EXAMPLES

[0233] The following examples are provided to further describe some of the embodiments disclosed herein. The examples are intended to illustrate, not to limit, the disclosed embodiments.

General Methods

Transient Transfection and Expression of ROR in HEK expi

[0234] ROR1 extracellular domain c-Mer proto-oncogene tyrosine kinase transmembrane domain (ROR1 ECD MERTK tm) was transiently expressed in cells for anti-ROR1 antibody reactivity confirmation (HEK293F), for characterization of commercial anti-ROR1 antibodies (HEK293F and CHO-S), to test phage and hybridoma panels against ROR2 cross-screen (CHO-S), to check cross-reactivity of ROR1 mAb hits against ROR2-ECD MERTK (CHO-S), to test for binding of anti-CD3 and anti-ROR1 antibodies to ROR1 transiently transfected cells (HEK293F), and to check cross-reactivity of ROR1 mAb hits against ROR2-ECD MERTK (CHO-S). ROR1 ECD MERTK tm (referred to herein as RR1W1; SEQ ID NO:99) has the following amino acid sequence:

QETELSVSAELVPTSSWNISSELNKDSYLTLDPEMNNITSLGQTAELHCKVSGNP
PPTIRWFKNDAPVVQEPRRLSFRSTIYGSRLRIRNLDTTDTGYFQCVATNGKEVV
SSTGVLFVKFGPPPTASPGYSDEYEEDGFCQPYRGIACARFIGNRTVYMESLHM
QGEIENQITAAFTMIGTSSHLSDKCSQFAIPSLCHYAFPYCDETSSVPKPRDL
CRDEC EILENVLCQTEYIFARSNPMILMRLKLPNCEDLPQPESPEAANCIRIGIP
MADPINK NHKCYNSTGVDYRGTVSVTKSGRQCQPWNSQYPHTHTFTALRFPEL
NGGHSYC RNPGNQKEAPWCFTLDENFKSDLCDIPACDSKDSKEKNKMEILFGC
FCGFILIGLI LYISLAIRGGGGSGGGS

[0235] ROR2-ECD MERTK (referred to herein as RR1W2; SEQ ID NO:100) has the following amino acid sequence:

EVEVLDPNDPLGPLDGQDGIPTLKGYFLNFLEPVNNITIVQGQTAILHCKVAGNP
PPNVRWLKNDAPVVQEPRRIIRKTEYGSRLRIQDLDTTDTGYYQCVATNGMKTI
TATGVLFVRLGPTHSPNHNFQDDYHEDGFCQPYRGIACARFIGNRTIYVDSLQM
QGEIENRITAAFTMIGTSTHLSDQCSQFAIPSFCHFVFPLCDARSRTPKPRELCRDE
CEVLES DLCRQEYTIARSNPLILMRLQLPKCEALPMPESPDAANCMRIGIPAERLG

RYHQCYNHSGMDYRGTA STTKSGHQCPWALQHPSHLSSTDFPELGGGHAY
 CRNPGGQMEGPWCFTQNK NVRMELCDVPSCSPRDSSKMGFGCFCGFILIGLILYI
 SLAIRGGGGSGGGS

[0236] HEK 293F cells were placed in Freestyle™ 293 media (Gibco #12338) at a density of 6×10^5 cells/ml to a volume of 30 mls in a 125 ml vented cap shake flask with shaking at 130 RPM, 24 hours prior to transfection. On the day of transfection, the cells were counted by Cedex and determined to have a density between 8×10^5 cells/ml and 1.2×10^6 cells/ml and a viability over 98%. Transfection was carried out using Freestyle max reagent (Invitrogen #16447). For a single 30 ml transfection, in one tube 37.5 µl of freestyle max reagent was diluted in 1 ml of OptiMEM media (Gibco #31985). In a separate tube, 37.5 µg of DNA (18.75 µg target and 18.75 µg pAdVantage) was mixed into 1 ml OptiMEM. The two tubes were then mixed together, incubated in the biosafety cabinet for 3 minutes and then the mixture added directly to the flask of HEK293F cells.

[0237] For CHO-S transfections, CHO-S cells were placed in Freestyle CHO media (Gibco #12651) at a density of 6×10^5 cells/ml to a volume of 30 mls in a 125 ml vented cap shake flask with shaking at 130 RPM, 24 hours prior to transfection. On the day of transfection, the cells were counted by Cedex and determined to have a density between 8×10^5 cells/ml and 1.2×10^6 cells/ml and a viability over 98%. Transfection was carried out using Freestyle max reagent (Invitrogen #16447). For a single 30 ml transfection, in one tube 37.5 µl of freestyle max reagent was diluted in 1 ml of OptiMEM media (Gibco #31985). In a separate tube, 37.5 µg of DNA (18.75 µg target and 18.75 µg pAdVantage) was mixed into 1 ml OptiMEM. The two tubes were then mixed together, incubated in the biosafety cabinet for 3 minutes and then the mixture added directly to the flask of CHO-S cells.

Expression of antibodies in HEK expi cells

[0238] Transient Expression was performed with the Expi293F transfection process (Expi293 Expression System Kit (Life Technologies Corporation Cat # A14635)). Expi293F cells (Life Technologies Corporation Cat #A14527) were grown at 37°C; 7% CO₂; 130 RPM in Expi293 Expression Medium (Life Technologies Corporation Cat # A14351-01). Two days prior to transfection, cells were split at 7×10^5 cells/ml. At the time of transfection, cells were counted and verified to be at a concentration of *at least* 30×10^5 cells/ml and above 95% viable. For each 30-mL transfection, 30 µg of plasmid DNA was mixed with in Opti-MEM I Reduced Serum Medium (Life Technologies Corporation Cat # 31985-070) to a total volume of 1.5 mL. (15 µg of

pAdvantage DNA and 15 µg of expression vector DNA (for antibodies this is 1:3 ratio of HC:LC expression constructs). 81 µL of ExpiFectamine 293 Reagent (Life Technologies Corporation Cat # A14525) was then diluted in Opti-MEM I medium to a total volume of 1.5 mL. The diluted DNA and ExpiFectamine solutions were then mixed gently and incubated for 5 minutes at room temperature. The diluted DNA was added to the diluted ExpiFectamine 293 Reagent, mixed gently, and incubated for 20 minutes at room temperature. After the incubation, the mixture was then added to 25.5 ml of cells in a 125 ml shake flask. Immediately following transfection, 150 µL of ExpiFectamine 293 Transfection Enhancer 1 and 1.5 mL of ExpiFectamine 293 Transfection Enhancer 2 were added to each flask (Life Technologies Corporation Cat # A14525). Five days post transfection, cells supernatant was harvested by centrifugation and clarified through a 0.2 micron filter.

Purification of antibodies

[0239] The antibody in the clarified culture supernatant was captured by MabSelect SuRe™ Protein A resin and eluted with 100 mM sodium acetate (pH 3.5). The fractions containing the antibody were pooled and promptly neutralized with 2.5 M Tris HCl (pH 7.2), then buffer exchanged into 1xD-PBS or other desired buffers if specified. The protein concentration was determined by measurement of OD280 on a NanoDrop spectrophotometer and calculated using its absorbance coefficient. The purity and homogeneity of the antibody was assessed by SDS-PAGE and SE-HPLC. Usually an SEC polishing step using Superdex 200 was performed if the monomer fell below 95% per SE-HPLC.

MSD Cell Binding

[0240] Meso scale discovery (MSD) Streptavidin- Standard (SA-STD) plate was blocked with 50 µL per well of assay buffer for 5 minutes. The plate was inverted to remove assay buffer and tapped on paper towels. 1 µg/mL of 50 µL of biotinylated ROR1 in assay buffer were added to each well of the plate and incubated overnight at 4°C. 150 µL of assay buffer was added to each well of the coated plates without removing the coating reagent and incubated for ~ one hour. The plate was washed three times with wash buffer. The plate was tapped lightly on paper towels to remove residual wash buffer. 50 µL of human anti-ROR1 DuoBody® Ab in assay buffer were added to each well of the plate and incubated ~ one hour at ambient temperature. The plate was washed three times with wash buffer. 50 µL of 1.4 µg/mL of

ruthenium-labeled anti-human IgG (H+L) antibody in assay buffer were added to each well of the plates. The plate was incubated for ~ one hour with gentle vortexing at ambient temp. The plate was washed three times with wash buffer. 150 μ L of read buffer were added to each well of the plate. The plate was immediately read on the MSD sector imager 6000a Reader for luminescence levels.

Flow Cytometry Analysis of Cytotoxicity

[0241] Evaluation of cytotoxicity was performed using a flow cytometry assay. To do this, GFP labeled NCI-H358 target cells were plated in 96-well flat-bottomed plates at 2×10^4 cells/well. The next day, 1×10^5 primary pan T cells were added to each well in combination with the appropriate bispecific molecule in culture media. Cocultures were incubated at 37°C for 72 hours prior to analysis. Cells were harvested using cell dissociation buffer (Life Technologies, USA) and labeled with fixable live/dead dye (Life Technologies, USA) and anti-CD25. These markers were used to evaluate death of target cells by gating on GFP⁺ cells and assessment of T cell activation by gating on GFP⁺ T cells, respectively. Samples were collected on an IntelliCyt iQue High Throughput Flow Cytometry HTFC system and analyzed using ForeCyt software. EC₅₀ values were calculated in GraphPad Prism V6. Acceptance criteria for non-linear regression curve fitting was a confidence interval (CI) range of less than 1.4.

SPR Binding affinity studies

[0242] SPR experiments were performed with a four-channel Biacore T200 optical biosensor system at 25°C. For experiments with soluble ROR1, the four flowcells of a CM5 sensor chip were immobilized with high levels (> 6000 response units (RU)) of goat anti-human Fc antibody (Jackson ImmunoResearch, cat # 109-005-098). Following this step, the control and test antibodies were captured on flow-cells 2, 3 and 4 until desired capture levels to generate sufficient antigen binding response were obtained (~350 RU). Flow cell 1 did not have any captured antibody and was used as a reference surface. Recombinant human ROR1 was prepared in filtered and degassed PBSTE buffer (Bio-Rad # 176-2730) starting from 400 nM to 5 nM at 3-fold dilutions (FIG. 7A, left; FIG. 7B, left). These solutions were injected over all 4 flow-cells at a flow rate of 50 μ L/min and the association was monitored for 4 minutes followed by dissociation for 10 minutes. After each interaction, the sensor-chip surface was regenerated using glycine pH 1.5 to yield a stable baseline for following cycles.

[0243] Binding kinetics analyses of the anti-ROR1 antibody interactions with ROR1 were performed by global kinetics fitting of the sensorgrams using 1:1 Langmuir Model.

Analysis of ROR1 Expression On Various Cells Lines

ROR1 Receptor Expression in Lung, Colon, Prostate and Heme Cancer Cell Lines

[0244] To evaluate the link between ROR1 expression and lung cancer, 70 lung cancer cell lines, including NSCLC derived from adenocarcinoma and squamous cell subtypes, and SCLC-derived lines, were evaluated for ROR1 expression. Binding of a commercially available phycoerythrin (PE) conjugated monoclonal anti-ROR1- antibody (2A2; Biolegend catalog # 357803/357804) that does not crossreact with ROR2 was evaluated using a Fluorescence-Activated Cell Sorting (FACS)-based approach. Positivity was scored as showing a mean fluorescent intensity (MFI) signal that was 2-fold greater than a PE-conjugated mIgG1 isotype control. A significant percentage of the cell lines tested (54%) demonstrated expression of ROR1, including both NSCLC and SCLC-derived lines (data not shown). Within the positive lines, there was a range of expression from cell lines that expressed high levels of ROR1 (such as NCI-1155, LU1901R2 and NCI-H446), intermediate levels (such as NCI-H1975 and NCI-H358), and low to no expression (such as SKMES-1, NCI-H520 and NCI-H1417), using this detection method. Several lines with predominantly intermediate to low expression were selected for use in *in vitro* and *in vivo* assays disclosed herein. **FIG. 1** illustrates the ROR1 expression from select lung cancer cell lines.

[0245] Colon, prostate, and cell lines were also evaluated for ROR1 expression. While the colon and prostate panels were limited, several lines with high ROR1 expression were identified that could be used in binding and functional assays, including HT-29.

Table 1. Summary of ROR1 expression data on *in vitro* tumor cell lines

Tumor Cell Origin	Results	Expression >2-fold over Isotype
Lung	40/74	54%
Colon	9/19	47%
Prostate	4/6	67%

Expression of ROR1 on lung, colon, and prostate-derived tumor cell lines by flow cytometry. A monoclonal anti-ROR1 antibody was used for detection of ROR1 on unfixed samples. For this analysis, MFI values were normalized using binding of an mIgG1 isotype control antibody (Biolegend cat# 400120) at the same concentration to calculate the fold-change over background.

ROR1 Expression in Heme Cancer Cell Lines

[0246] Confluent Mantle Cell Lymphoma (MCL), B Cell Lymphoma, and Multiple Myeloma (MM) cells were stained for ROR1 expression using an in-house developed anti-ROR1 monoclonal antibody (RR1B121) that was conjugated to Alexa Fluor 647 according to manufacture's instructions (A647, ThermoFisher). Cells were washed twice in phosphate-buffered saline (PBS) and stained with Live/Dead (Aqua; ThermoFisher) for 10 minutes at room temperature. Live/Dead stain was washed out with PBS. Cells were either unstained or stained with 300 ng antibody in 50 uL final volume anti-ROR1-A647 in FACS Stain Buffer (BD Biosciences) for 30 minutes at 4 °C. All staining steps were performed in the dark. Unstained sample was used as negative control; fluorescence minus one (FMO). Cells were washed twice with PBS and reconstituted in Stain Buffer for acquisition on the BD FACS Canto cytometer.

[0247] ROR1 expression was assessed in 25 cell lines from selected hematological malignancies (FIG. 14). Specific ROR1 expression was detected in all MCL lines tested and about half of MM lines. However, only two B lymphoma lines showed ROR1 expression.

ROR1 Receptor Density in Heme Cancer Cell Lines

[0248] Confluent Mantle Cell Lymphoma (MCL) cell lines were stained for ROR1 expression using anti-ROR1 MAb conjugated to Phycoerythrin (PE) (clone 2A2, Biolegend). Cells were washed twice in phosphate-buffered saline (PBS) and stained for Live/Dead (Aqua; ThermoFisher) for 10 minutes at room temperature. Live/Dead stain was washed out with PBS. Cells were either unstained or stained with 1 uL/sample in 50 uL final volume anti-ROR1-PE in FACS Stain Buffer (BD Biosciences) for 30 minutes at 4°C. All staining steps were performed in the dark. Unstained sample was used as negative control; fluorescence minus one (FMO). Receptor density was measured using PE Quantibrite Beads according to manufacture's instructions (BD). Cells were washed twice with PBS and reconstituted in Stain Buffer for acquisition on the BD FACS Canto cytometer.

[0249] ROR1 expression was assessed in 5 MCL cell lines and receptor density (number of ROR1 molecules per cell) was quantified using the ABC method (FIG. 15). Data are presented as averages of two independent experiments (mean±SD) per cell line.

ROR1 Expression in Normal Human Tissues

[0250] A tumor microarray (TMA) comprising an extensive array of normal tissues was also assessed for ROR1 positivity using the 4102s polyclonal antibody (Cell Signaling

Technology). The results suggested that ROR1 expression was present on some normal tissues, including breast, colon, kidney, prostate and uterus (**Table 2**). Notably, out of 12 lung specimens analyzed, two showed some degree of positivity, with one demonstrating some level of membrane staining. In addition, fallopian tube sections appeared to be the only tissue with consistent evidence of membranous expression, in which 5 of 7 samples exhibited this staining profile. Overall, a substantial number of normal tissues exhibited some frequency of positivity, which has not been described in the literature. Due to this and the appreciable level of non-specific staining that was noted on control tumor cell lines, it was postulated that much of the positivity seen with this antibody was caused by non-specific staining.

Table 2. ROR1 Positive IHC Staining in a Normal Human TMA

Tissue	Results	Tissue	Results
Adrenal gland	2/15 – likely glomerulosa cells (40% intensity)	Skeletal Muscle: Quadriceps	0/3
Breast	4/6 – no staining in stroma	Ovary	3/12 (70-80% intensity)
Brain	0/29	Pancreas	3/12 (20-40% intensity)
Blood-vessel: Aorta	0/10	Pituitary	0/9
Blood-vessel: Renal artery	0/3	Prostate	8/13 (40-80% intensity)
Esophagus	0/3	Skin	0/7
Fallopian tube	5/7[†] (70-90% intensity)	Small Intestine	3/6 (60-80% intensity)
Heart	0/12	Nerve	0/3
Kidney	12/15 (90% intensity)	Spleen	0/11
Large colon	5/5 - (80% intensity)	Stomach	6/14- oxyntic cells (20-70% intensity)
Liver	3/8 – kupfer cells, hepatocytes negative.	Testis	3/15
Lung	2/12[§] – bronchial epithelium	Ureter	2/9 (70% intensity)
Lymph node	3/13	Uterus: Corpus	6/8 (80% intensity)
Skeletal Muscle	0/4	Uterus: Cervix	0/3
Skeletal Muscle: Diaphragm	0/2		

[†]Membranous staining on all positive samples

[§]Membranous staining on 1 of 2 positive samples

Expression of ROR1 on primary normal tissue sections by IHC. A rabbit anti-ROR1 polyclonal antibody was used for detection of ROR1 on formalin-fixed primary tumor samples. Staining

was scored positive or negative and determined to be cytoplasmic or membranous by a pathologist.

ROR1 Expression on Circulating Tumor Cells (CTCs) from small cell lung cancer (SCLC) patients

[0251] Since a significant number of small cell lung cancer (SCLC) cell lines had demonstrated ROR1 expression, analyses were performed on primary tumor cells from patients with this disease. SCLC is characterized by a high propensity for metastases, and therefore patients have a much higher incidence of circulating tumor cells (CTC) in the peripheral blood, which enabled the analysis of the incidence of ROR1 in this type of lung malignancy. For this analysis, fresh blood was fixed using a slow release formulation of formaldehyde in CellSave tubes. Two detection antibodies, 2A2 and the anti-ROR1 antibody RR1B78 (see *infra*), which binds the frizzled domain of ROR1, were tested. Spiking of control ROR1⁺ cell lines into whole blood demonstrated that RR1B78 was markedly more sensitive than 2A2. Therefore, analysis of CTCs in primary SCLC samples was performed using RR1B78. Analysis of peripheral blood samples from 7 samples showed that 5 patients had detectable ROR1 CTCs. Of these specimens, 3 samples had 10 or more CTCs that could be analyzed for ROR1 expression. Tumor cells from all three patients demonstrated detectable ROR1 on between 7-45% of cells, suggesting that ROR1 expression is a feature of some SCLC tumors (**Table 3**).

Table 3. ROR1 Expression on CTCs from SCLC patients

Patient ID#	# of total CTCs detected [§]	# ROR1 ⁺ CTCs (%)
B11-SCLC	296	21 (7%)
MT0820-SCLC	1	0
CNV265-SCLC	1	1 (100%)
B12-SCLC	0	0
CNV505-SCLC	0	0
CNV678-SCLC	10	1 (10%)
B13-SCLC	234	106 (45%)

[§]CTCs were identified as having a cytokeratin⁺CD45⁻ phenotype.

Detection of ROR1 on circulating tumor cells from SCLC patients. Patient blood samples were fixed in CellSave collection tubes from primary breast, colon, lung and prostate tumors by IHC. RR1B78 was used for detection of ROR1 on formalin-fixed primary tumor samples. Staining was scored positive or negative by a pathologist. All expression was scored as being cytoplasmic.

ROR1 Expression on Tumor Cells from Chronic lymphocytic leukemia and Mantle cell lymphoma patients

[0252] Frozen peripheral blood mononuclear cells (PBMC) or bone marrow mononuclear cells (BMMC) from patients with Chronic lymphocytic leukemia (CLL, all BMMC) or Mantle cell lymphoma (MCL, 2 donors matched PBMC and BMMC) were purchased from Conversant Bio. Samples were thawed quickly at 37°C and transferred to warm 12mL of RPMI medium (containing 10% fetal bovine serum) (Invitrogen). After wash in ice cold PBS (Invitrogen) and filtration, cells were counted and seeded at 1×10^6 live cells/well in 96-well round bottom plate. First, cells were stained with 50uL of NearIR L/D IR (ThermoFisher) according to manufacture's protocol at room temperature in the dark for 10-15min. After wash with ice cold PBS and FACs Stain Buffer (BD) cells were stained with antibody cocktail, anti-CD45-PerCP-Cy5.5 (eBioscience), anti-CD5-FITC and anti-CD19-PE-Cy7 (BD Bioscience), anti-CD38-PE, anti-CD40-BV605 and anti-CD137-BV421 (BioLegend) in 50uL final volume Brilliant Stain buffer (BD Bioscience) for 30 min at 4°C in the dark. Following a wash with FACs buffer, cells were reconstituted with 200uL FACS buffer and analyzed by Fortessa II cytometer. Data analysis was performed using FlowJo and Prism software. Tumor cells were identified as CD19+CD5+ of live lymphocytes.

[0253] ROR1 was highly expressed in all of the CLL samples on the majority of tumor cells ($\text{MFI}_{\text{avg}} = 853$) and independent of % tumor cells in the sample (FIG. 16). ROR1 was expressed at ~1.5 fold lower level in MCL, as compared to CLL, ($\text{MFI}_{\text{avg}} = 575$) on >50% tumor cells (FIG. 16).

Generation Of Anti-ROR1 mAbs From Phage Panels

Phage Panning and Panel Selection

[0254] ROR1-binding Fabs were selected from *de novo* pIX phage display libraries as described in Shi, L., *et al.* (2010) De novo selection of high-affinity antibodies from synthetic fab libraries displayed on phage as pIX fusion proteins. *J Mol Biol* 397, 385-396. Briefly, the libraries were generated by diversifying human scaffolds where germline V_H genes IGHV1-69*01, IGHV3-23*01, and IGHV5-51*01 were recombined with the human IGHJ-4 minigene *via* the H-CDR3 loop, and human germline V_L kappa genes O12 (IGKV1-39*01), L6 (IGKV3-11*01), A27 (IGKV3-20*01), and B3 (IGKV4-1*01) were recombined with the IGKJ-1 minigene to assemble complete V_H and V_L domains. Library design is detailed in Shi *et al.*, *J Mol Biol* 397:385-96, 2010. The three heavy chain libraries were combined with the four germline light chains, known as Version 2, or combined with the diversified light chain libraries, known as Version 3, to generate 12 unique $V_H:V_L$ combinations. These libraries were later

combined further based on heavy chain gene to generate six libraries for panning experiments against ROR1.

[0255] Additional *de novo* pIX libraries based on the same heavy chains (1-69, 3-23, 5-51) and germline light chains (A27, B3, L6, 012), were generated by Sloning Biotech mutagenesis technologies. These were made as phage libraries, and were combined based on heavy chain gene to generate three additional libraries for panning experiments against ROR1.

[0256] The libraries were panned against biotinylated human ROR1-Fc (Sino Biological Inc Cat #13968-H02H1). Biotinylated antigen was captured on streptavidin magnetic beads (Dyna) and exposed to the *de novo* pIX Fab libraries at a final concentration of 100 nM or 10 nM. Non-specific phage were washed away in PBS-Tween and bound phage were recovered by infection of MC1061F⁺ *E. coli* cells. Phage were amplified from these cells overnight and panning was repeated for a total of four rounds. Following four rounds of biopanning, monoclonal Fabs were screened for binding to human ROR1 Fc in two formats: 1) in an ELISA where Fabs were captured on an ELISA plate by sheep anti-human FD, biotinylated ROR1-Fc was added to the captured Fabs, followed by detection of btROR-Fc with Streptavidin HRP; and 2) in an ELISA where btROR1-Fc was captured on an ELISA plate by Streptavidin, Fab supernatant was added to the captured antigen, followed by detection of the Fabs with goat AntiFab²:HRP. Clones that demonstrated 10-fold over background binding to btROR1-Fc in either format were sequenced in the heavy and light chain variable regions.

[0257] A total of 69 clones were selected from the *de novo* selections based on human ROR1-Fc binding. 64 of the 69 Fabs (labeled RR1B1-RR1B64) were cloned into IgG2sigma/k backbone to generate full length antibodies, expressed, and further characterized in the sections below.

ROR1 antibody affinity maturation:

[0258] To affinity mature the ROR1 antibodies, light chain libraries, generated using Sloning Biotech mutagenesis technologies, were constructed. The heavy chain variable regions from ROR1 Kringle domain binders - RR1B66, RR1B67, RR1B69, RR1B82, RR1B83, and RR1B84 (Table 9) – were cloned into a pIX phagemid vector containing this diversified VLk3-11 library. Once expressed and displayed these phage libraries were then panned stringently against ROR1 to obtain higher affinity binders.

[0259] Specifically, the libraries were panned against biotinylated human ROR1-Fc (Sino Biological Inc Cat #13968-H02H1). Biotinylated ROR1 was captured on streptavidin

magnetic beads (Dyna) and exposed to the maturation pIX Fab libraries at a final concentration of 10 nM or 1 nM. Non-specific phage were washed away in PBS-Tween and bound phage were recovered by infection of MC1061F⁺ E. coli cells. Phage were amplified from these cells overnight and panning was repeated for a total of three rounds. Following three rounds of biopanning, monoclonal Fabs were screened for binding to human ROR1 Fc in three formats: 1) in an ELISA where Fabs were captured on an ELISA plate by sheep anti-human FD, biotinylated ROR1-Fc was added to the captured Fabs, followed by detection of btROR-Fc with Streptavidin HRP; 2) in an ELISA where btROR1-Fc was captured on an ELISA plate by Streptavidin, Fab supernatant was added to the captured antigen, followed by detection of the Fabs with goat AntiFab²:HRP; and 3) in a proximity based luminescence immunoassay where the Fabs were allowed to bind in solution with bt-ROR-1, antiFab²:HRP, and SA-acridin (BMG LabTech Lumistar Omega). Clones that demonstrated a signal to background ratio greater than 10-fold were sequenced in the heavy and light chain variable regions. Those clones that were unique and not matching the parental VL sequence were then selected for further characterization. These Fabs were tested in a ranking ELISA where Fabs were captured on an ELISA plate by sheep anti-human FD, biotinylated ROR1-Fc was added in a dilution series to the captured Fabs, followed by detection of bt-ROR-1-Fc with Streptavidin HRP. Fabs that demonstrated improved binding curves relative to the parental Fabs were then selected for conversion to mAb, also considering absence of possible PTM risks, and diversity of the LC sequence. A total of 36 clones were cloned into IgG4-PAA backbone to generate full length antibodies, expressed, and further characterized (see Table 22).

[0260] SPR experiments were performed using a ProteOn XPR36 system (Bio-Rad) at 25°C to measure the binding of affinity matured anti-human ROR1 antibodies and the parental RR1B67 to human ROR1. Goat anti-human Fc IgG (Jackson ImmunoResearch, cat # 109-005-098) was directly immobilized via amine coupling at 30 µg/mL in acetate buffer, pH 5.0 on all 6 ligand channels in horizontal orientation on GLC Sensor Chip (Bio-Rad, catalog no. 176-5011) with a flow rate of 30 µL/min for 300 seconds in PBS containing 0.005% Tween-20. The immobilization densities averaged about 6000 Response Units (RU) with less than 5% variation among different channels. Five different mAbs were captured on the anti-human Fc IgG surface at 0.5 µg/ml (~400 RU) in vertical ligand orientation, with the 6th ligand channel as no ligand surface control. Recombinant Human ROR1-ECD with a C terminal human serum albumin (HSA) fusion and a histag, RR1W27. in house) at 300 nM concentration in 3-fold dilution series of 5 concentrations flew in as analyte to bind to captured mAbs in the horizontal orientation. A

buffer sample was also injected to monitor the dissociation of captured mAb and baseline stability. The dissociation phase for all concentrations of Ag was monitored at a flow rate of 100 μ L/min for 30 minutes. The binding surface was regenerated for the next interaction cycle using a 18 second pulse of 0.8% phosphoric acid. The raw data were processed by subtracting two sets of reference data from the response data: 1) the inter-spot signals to correct for the non-specific interactions between the Ag and the empty chip surface; 2) the buffer channel signals to correct for baseline drifting due to the dissociation of captured mAb over time. The processed data at all concentrations for each mAb were globally fit to a 1:1 simple Langmuir binding model to extract the kinetic (k_{on} , k_{off}) and affinity (K_D) constants. An arbitrary criteria using the %Chi2/Rmax <30% was set to measure the quality of fit, quantitative kinetic results for only those with valid fit in the summary Table 3A should be considered quantitatively reliable.

[0261] In some experiments a mammalian expression construct encoding the extracellular domain of human ROR1 (Uniprot Accession #Q01973| residues 30-406) fused at the N-terminus of human serum albumin (C34S)-6xHis (RR1W27) was used to transiently transfect Expi293F cells. Six days post-transfection the culture supernatant was harvested by centrifugation. The RR1W27 was purified from the Expi293F supernatant by immobilized metal affinity chromatography (IMAC) followed by buffer exchange into 1X PBS by exhaustive dialysis.

[0262] Table 3A: Summary of binding results of affinity matured anti-ROR1 antibodies measured by ProteOn SPR.

Protein AA	ka(M-1s-1)	kd (s-1)	KD (nM)	Fold of affinity increase over parental mAb	Comments
RR1B177	2.89E+05	1.90E-04	0.7	2.4	
RR1B178	1.43E+05	5.87E-04	4.1	0.4	
RR1B179	8.15E+04	4.00E-04	4.9	0.3	
RR1B181	1.71E+05	2.30E-04	1.4	1.2	
RR1B183	1.85E+05	3.49E-04	1.9	0.8	
RR1B184	1.74E+05	1.95E-04	1.1	1.4	
RR1B185	1.91E+05	2.91E-04	1.5	1.1	
RR1B186	1.63E+05	1.94E-04	1.2	1.3	
RR1B187	2.02E+05	1.04E-03	5.1	0.3	
RR1B188	1.89E+05	6.32E-04	3.4	0.5	
RR1B189	1.12E+05	6.13E-04	5.5	0.3	
RR1B190	1.23E+05	2.54E-04	2.1	0.8	
RR1B191	2.79E+05	3.40E-04	1.2	1.3	
RR1B193	2.24E+05	6.23E-04	2.8	0.6	

RR1B194	2.06E+05	4.90E-04	2.4	0.7	
RR1B196	1.87E+05	4.45E-04	2.4	0.7	
RR1B197	1.74E+05	7.85E-04	4.5	0.4	
RR1B199	3.75E+05	7.44E-04	2.0	0.8	
RR1B200	1.58E+05	2.91E-04	1.8	0.9	
RR1B201	2.25E+05	9.97E-05	0.4	3.6	
RR1B202	1.47E+05	1.07E-03	7.2	0.2	
RR1B203	1.25E+05	2.75E-04	2.2	0.7	
RR1B206	1.06E+05	7.28E-05	0.7	2.3	
RR1B207	9.66E+04	1.47E-04	1.5	1.1	
RR1B208	8.66E+04	1.37E-03	15.9	0.1	
RR1B210	3.41E+05	7.85E-04	2.3	0.7	
RR1B211	8.19E+04	7.08E-04	8.7	0.2	
RR1B213	2.48E+05	1.30E-04	0.5	3.1	
RR1B67	1.51E+05	2.48E-04	1.6	1.0	parental molecule
RR1B180					Binding observed; fit not valid
RR1B212					Binding observed; fit not valid
RR1B209					Binding observed; fit not valid
RR1B205					Binding observed; fit not valid
RR1B204					Binding observed; fit not valid
RR1B198					Binding observed; fit not valid
RR1B192					Binding observed; fit not valid
RR1B182					Binding observed; fit not valid

Anti-ROR1 Antibody Cell Binding Characterization

[0263] The 64 anti-ROR1 antibodies were characterized by binding to CHO-S cell lines that expressed ROR1 or ROR2. Transfected CHO-S cells ROR1 (RR1W1) and ROR2 (RR1W2) and mock control CHO-S were provided for one set of binding experiments. In addition to flow based analysis, Western blot was used to confirm the expression of ROR1 on the CHO-S cells before characterization of the phage-derived hits.

[0264] The anti-ROR1 antibodies were screened using transiently transfected CHO-S cells 24 hours following transfection. Four commercial monoclonal anti-ROR1 antibodies (Creative Diagnostics catalog # DMAB8606MH; Biolegend (2A2 Ab) catalog #357803, 357804; AVIVA Systems Biology catalog # OAAD00316; ACRIS Antibodies, Inc. catalog

#AM06399SU-N) and the goat polyclonal antibody from R&D systems (catalog # AF2000) were used as positive controls. Parental and mock-transfected CHO cells, as well as RSV isotype controls (B23B31) were used as negative controls. Binding of the test antibodies was determined using a polyclonal anti-human antibody labeled with alexafluor 674. Of the 64 antibodies tested, 63 showed robust binding to the ROR1 transfected CHO-S cells. Binding affinity was measured using standard deviation (SD) from the mean of the test articles with those less than the mean minus 1 SD being called low binders, those within 1 SD of the mean being called intermediate binders, and those with stronger binding than the mean plus 1 SD being called strong binders. Using this approach, 12 low, 44 intermediate and 7 strong ROR1 binders were identified. This set of antibodies was further characterized using endogenously expressing tumor cell lines by flow and western blot.

[0265] Transiently transfected ROR2 CHO cells were also analyzed in this experiment. No ROR2 expression was detected by any of the positive control antibodies tested (data not shown). With the anti-ROR1 antibodies, 11/64 were considered to be high ROR2 binders; RR1B3, B11, B14, B15, B17, B32, B43, B46, B51, B55 and B61 were eliminated based on the data.

[0266] The binding of anti-ROR1 antibodies to CHO-S cells transiently transfected with the ROR1 extracellular domain (ROR1-ECD) was repeated. An anti-human secondary (Goat Anti-human IgG AlexaFluor 647; Life Technologies catalog #A21445) was used for visualization of binding. A monoclonal anti-ROR1 antibody from Biolegend (A2A; Biolegend) was run in triplicate as a positive control. Parental and mock-transfected CHO cells, as well as isotype controls (B23B31) were run as negative controls. Binding of the antibodies were read out using a polyclonal anti-human antibody labeled with alexafluor 674 (Goat Anti-human IgG AlexaFluor 647; Life Technologies cat#A21445). Of the 64 antibodies tested, 62 showed robust binding to a fraction of the ROR1-ECD transfected cells that correlated with that shown by the positive control antibody (data not shown). This is in comparison with 63 of 64 which were identified in the previous experiment. RR1B31, which appeared to bind well in the previous experiment, did not bind in this experiment. Data was compared to that from the initial experiment using MFI values to rank the antibodies (**Table 4**). There were differences in the ranking between the two experiments probably due to the fact that the binders mostly bound within a very small range of MFI values. However, given the intrastudy variation, the data suggests that the majority of these antibodies bind ROR1 expressed by CHO cells following transient transfection.

Table 4. Activity of anti-ROR1 antibodies against ROR transfected CHO cells

Antibody	MFI Values		
	Parental CHO	ROR2-Transfected CHO	ROR1-Transfected CHO
Isotype Control	1630	8903	1735
RR1B1	2930	85223	1807
RR1B2	4317	28981	5072
RR1B3	5386	72524	11694
RR1B4	5006	85459	4586
RR1B5	4749	42152	5400
RR1B6	5036	65166	4007
RR1B7	4813	47028	4517
RR1B8	5591	49271	5809
RR1B9	7438	44950	6107
RR1B10	6386	68761	8408
RR1B11	3756	88144	15011
RR1B12	7904	42268	6375
RR1B13	1769	36671	1479
RR1B14	3534	93611	11635
RR1B15	3240	66981	12490
RR1B16	2618	42469	4481
RR1B17	4407	68602	12085
RR1B18	2386	44097	3022
RR1B19	1716	24990	1529
RR1B20	2554	5420	1790
RR1B21	5158	60139	4065
RR1B22	3757	45408	3920
RR1B23	4824	58357	4464
RR1B24	5478	65416	5081
RR1B25	4301	56058	4144
RR1B26	3558	64312	5197
RR1B27	6307	34511	7196
RR1B28	3020	29951	2540
RR1B29	3199	31030	4296
RR1B30	3010	33126	2733
RR1B31	4237	61410	3163
RR1B32	3914	47957	13480
RR1B33	4489	61314	4710
RR1B34	4434	41971	4402
RR1B35	5435	57284	4635
RR1B36	4559	59947	4793
RR1B37	3154	27367	3789

RR1B38	21015	60174	12327
RR1B39	3087	33765	3327
RR1B40	3487	30990	2930
RR1B41	1701	25963	1697
RR1B42	3852	64131	10862
RR1B43	5697	87621	5603
RR1B44	6929	133040	3313
RR1B45	6561	112695	5408
RR1B46	6775	133631	12699
RR1B47	4289	55285	3474
RR1B48	14354	52064	9804
RR1B49	3158	74413	5091
RR1B50	8189	74438	7165
RR1B51	4946	89028	11147
RR1B52	5954	56117	2125
RR1B53	14248	28490	9006
RR1B54	9508	72969	8183
RR1B55	5283	77480	7709
RR1B56	4329	79419	3473
RR1B57	2624	76578	2216
RR1B58	13984	57324	8851
RR1B59	3497	85595	2828
RR1B60	4588	62703	3137
RR1B61	3893	50742	10919
RR1B62	3850	24006	3632
RR1B63	4647	23244	3244
RR1B64	1532	17221	1181

[0267] In addition to these CHO-S transfected cells, various cell lines were evaluated for use in characterization of the panel of the anti-ROR1 antibodies. MCF-7 cells were determined to be negative for ROR1 and ROR2 (data not shown). The cell line U266 was determined to be negative for ROR1 and positive for ROR2 (data not shown). MDA-MB231 cells were strongly positive for ROR1 (**Table 5** and **Table 6**). HEK293 appeared to be positive for ROR2 (data not shown). CHO-S showed a relatively small shift compared to HEK293 and 3T3 cells, which correlated with the absence of a specific band by western blotting (data not shown). Interestingly, a smaller band was present in the blots indicating that the antibody (R&D Systems catalog #AF2000; Goat polyclonal) could bind to a protein expressed by these cells. Whether this is a truncated form of ROR1 or a different protein is not clear and needs further investigation. However, the shift seen in all cell lines could be caused by binding to this smaller

species. It was also shown that HEK293 cells could be transiently transfected with ROR1 and cell surface expression detected (data not shown).

[0268] The anti-ROR1 antibodies were assessed for binding to two breast tumor lines: MDA-MB231 breast tumor cells expressing endogenous ROR1 (**Table 5** and **Table 6**) and MCF-7 which are ROR1 negative (data not shown). An anti-human secondary was used for visualization of binding. Four monoclonal anti-ROR1 commercial antibodies (Creative Diagnostics catalog # DMAB8606MH; Biolegend (2A2 Ab) catalog #357803, 357804; AVIVA Systems Biology catalog # OAAD00316; ACRIS Antibodies, Inc. catalog #AM06399SU-N) and the goat polyclonal antibody from R&D systems (catalog # AF2000) were used as positive controls. A panel of six RSV controls (B23B31) were run to gauge background binding. Binding of the test antibodies was read out using a polyclonal anti-human antibody labeled with alexafluor 674. Mouse and goat positive control antibodies were detected using the appropriate polyclonal secondary antibodies conjugated to the same fluorochrome. Of the 64 antibodies tested, 61 showed binding above the mean of the isotype controls. Thirty-nine (39) antibodies demonstrated binding better than the best positive control antibody. Relative affinity was measured using standard deviation (SD) from the mean of the test articles, with those greater than the mean being called intermediate and those greater than the mean plus 1 SD being called high binders. Using this approach, 24 intermediate and 7 strong ROR1 binders were identified.

[0269] Next, the anti-ROR1 antibodies were assessed for binding to the ROR1 positive cell line, SKMES-1 and CHO-S ROR1 by Western Blot (data not shown). No bands were detected in the SKMES-1 lysates using the Phage hit supernatants. The ROR1 polyclonal antibody served as the control. Multiple bands were observed in the ROR1-CHO-S transfected lysate possibly due to glycosylation. A band of approximately 70 kDa was observed in the Western with phage RR1B31, RR1B20, RR1B51, RR1B61 and RR1B28, respectively. This observed band is believed to be a glycosylated form of ROR1. A faint band was observed using a control antibody in the SKMES-1 lysate at ~130 kDa. This band is believed to be full length ROR1.

[0270] The anti-ROR1 antibodies were assessed for binding to two lung tumor cell lines: H358 and SKMES-1, as well as a mantle cell carcinoma line, JEKO-1 using flow cytometry. All of these lines have been shown to express endogenous ROR1 protein. The JEKO-1 (a mantle cell line) showed significant background (data not shown). SK-SH5Y cells, a neuroblastoma line shown in the literature to express ROR2, was also run, although the ROR1 status of these cells is not known (data not shown). Four monoclonal anti-ROR1 commercial

antibodies (Creative Diagnostics catalog # DMAB8606MH; Biolegend (2A2 Ab) catalog #357803, 357804; AVIVA Systems Biology catalog # OAAD00316; ACRIS Antibodies, Inc. catalog #AM06399SU-N) and the goat polyclonal antibody from R&D systems (catalog # AF2000) were used as positive controls. A panel of six RSV isotype controls (B23B31) was used to gauge background binding. Binding of the test antibodies was read out using a polyclonal anti-human antibody labeled with alexafluor 674. Mouse and goat anti-ROR1 positive control antibodies were detected using the appropriate polyclonal secondary antibodies conjugated to the same fluorochrome.

[0271] Of the 64 anti-ROR1 antibodies tested, over half showed binding above the mean of the isotype controls. A handful of antibodies showed binding above that seen in the positive controls. RR1B48 showed consistently good binding across the cell lines tested, as did RR1B46, RR1B11, RR1B55 and RR1B58, which were all ranked in the top 10 for SKMES-1, H358 and MDA-MB231 (**Table 6**). RR1B48 and RR1B11 did not appear to be affected by formaldehyde-based fixation as much as RR1B46, RR1B55 and RR1B58. This may suggest that these two groups bind to non-fixation and fixation-sensitive epitopes, respectively. RR1B48 and RR1B11 may be useful for IHC which requires fixation prior to labeling. Overall, this data suggests that over half of the panel binds to endogenous ROR1 and allows the selection of the best binders for affinity testing and epitope binning. The fixation data also allows the selection of several antibodies for further testing as tool reagents for IHC.

Table 5. ROR1 expression in SKMES-1 and MDA-MB231 cell lines

Antibody	MFI Values	
	SKMES-1	MDA-MB231
Isotype Control	1372	1608
RR1B1	6174	8105
RR1B2	7735	6669
RR1B3	6727	7158
RR1B4	12921	10954
RR1B5	9977	13225
RR1B6	10234	17264
RR1B7	5185	10501
RR1B8	10711	15299
RR1B9	7628	12996
RR1B10	9225	16057
RR1B11	26803	29792
RR1B12	10346	17252

RR1B13	9615	14810
RR1B14	9176	14233
RR1B15	10626	15113
RR1B16	5453	8586
RR1B17	4216	7933
RR1B18	2528	4704
RR1B19	1658	3097
RR1B20	646	736
RR1B21	5372	8057
RR1B22	3375	5596
RR1B23	7643	10673
RR1B24	10483	13518
RR1B25	8762	11918
RR1B26	12992	15803
RR1B27	4281	5641
RR1B28	1558	1461
RR1B29	2155	5743
RR1B30	2253	3968
RR1B31	2710	3855
RR1B32	7218	12210
RR1B33	6183	9347
RR1B34	11124	12108
RR1B35	5368	11495
RR1B36	4912	9761
RR1B37	2752	5543
RR1B38	9102	10194
RR1B39	2178	3382
RR1B40	1695	2842
RR1B41	1910	3014
RR1B42	11407	7704
RR1B43	8884	18478
RR1B44	13163	18825
RR1B45	18460	20915
RR1B46	29141	31312
RR1B47	12139	15842
RR1B48	30169	40620
RR1B49	21938	23400
RR1B50	6932	7006
RR1B51	4790	7504
RR1B52	6039	8420
RR1B53	18675	8125
RR1B54	9302	14947
RR1B55	15690	18968
RR1B56	7453	8512

RR1B57	16212	17335
RR1B58	20628	22610
RR1B59	18977	15606
RR1B60	13838	12539
RR1B61	3179	3434
RR1B62	8360	7631
RR1B63	6096	6574
RR1B64	2910	1863

Table 6. ROR1 expression in SKMES-1, H358, and MDA-MB231 cell lines

		Weighted 2X for Lung (SKMES and H358)						
		SKMES		H358		MDA-MB231		Score
		Expt 1	Expt2	Expt 1	Expt2	Expt 1	Expt2	
	Binding Domain							
RR1B01	Not Determined	50	22	32	62	14	25	205
RR1B02	Ig Domain	66	24	20	102	11	17	240
RR1B03	Frz Domain	54	20	26	86	12	19	217
RR1B04	Frz Domain	102	72	72	108	49	35	438
RR1B05	Frz Domain	84	44	36	84	22	42	312
RR1B06	Frz Domain	86	64	84	74	59	54	421
RR1B07	Frz Domain	38	26	30	48	28	33	203
RR1B08	Frz Domain	94	48	58	50	50	48	348
RR1B09	Frz Domain	62	40	38	30	51	41	262
RR1B10	Frz Domain	78	108	98	116	40	52	492
RR1B11	Frz Domain	124	116	120	122	60	62	604
RR1B12	Ig Domain	88	62	62	94	18	53	377
RR1B13	Ig Domain	82	82	70	68	15	45	362
RR1B14	Frz Domain	76	80	102	64	24	44	390
RR1B15	Frz Domain	92	94	108	52	42	47	435
RR1B16	Frz Domain	44	78	86	38	34	29	309
RR1B17	Frz Domain	30	68	68	24	32	23	245
RR1B18	Frz Domain	18	34	40	10	16	11	129
RR1B19	Frz Domain	6	18	22	6	9	6	67
RR1B20	Not Determined	2	2	2	2	2	1	11
RR1B21	Krg Domain	42	58	48	54	45	24	271
RR1B22	Krg Domain	28	74	94	82	37	13	328
RR1B23	Krg Domain	64	92	92	112	47	34	441
RR1B24	Krg Domain	90	100	90	110	41	43	474
RR1B25	Krg Domain	70	66	66	78	55	37	372
RR1B26	Ig Domain	104	86	76	96	29	50	441
RR1B27	Krg Domain	32	42	28	42	25	14	183
RR1B28	Frz Domain	4	28	24	14	13	2	85
RR1B29	Krg Domain	12	10	14	20	17	15	88
RR1B30	Krg Domain	16	14	6	18	10	10	74

RR1B31	Ig Domain	20	4	4	16	1	9	54
RR1B32	Ig Domain	58	88	82	92	31	39	390
RR1B33	Krg Domain	52	52	50	76	19	30	279
RR1B34	Krg Domain	96	98	46	88	46	38	412
RR1B35	Krg Domain	40	56	44	98	23	36	297
RR1B36	Krg Domain	36	90	74	80	57	31	368
RR1B37	Krg Domain	22	30	34	44	4	12	146
RR1B38	Frz Domain	74	118	96	66	56	32	442
RR1B39	Krg Domain	14	16	16	34	8	7	95
RR1B40	Krg Domain	8	12	12	12	5	4	53
RR1B41	Krg Domain	10	8	10	8	6	5	47
RR1B42	Frz Domain	98	32	18	28	26	22	224
RR1B43	Frz Domain	72	112	110	120	38	56	508
RR1B44	Ig Domain	106	114	118	128	39	57	562
RR1B45	Frz Domain	114	124	104	118	52	59	571
RR1B46	Ig Domain	126	126	126	124	63	51	616
RR1B47	Ig Domain	100	38	60	90	20	63	371
RR1B48	Frz Domain	128	128	128	106	64	64	618
RR1B49	Ig Domain	122	102	88	58	43	61	474
RR1B50	Ig Domain	56	110	112	46	62	18	404
RR1B51	Frz Domain	34	54	78	40	53	20	279
RR1B52	Ig Domain	46	50	52	36	27	27	238
RR1B53	Ig Domain	116	36	80	22	44	26	324
RR1B54	Ig Domain	80	104	54	104	33	46	421
RR1B55	Ig Domain	110	122	116	126	61	58	593
RR1B56	Frz Domain	60	60	42	70	7	28	267
RR1B57	Ig Domain	112	96	56	114	36	55	469
RR1B58	Ig Domain	120	120	114	100	58	60	572
RR1B59	Ig Domain	118	106	122	72	35	49	502
RR1B60	Ig Domain	108	70	64	56	21	40	359
RR1B61	Frz Domain	26	76	106	26	48	8	290
RR1B62	Ig Domain	68	46	124	60	30	21	349
RR1B63	Ig Domain	48	84	100	32	54	16	334
RR1B64	Ig Domain	24	6	8	4	3	3	48

[0272] Most of the phage hit antibodies bound to both ROR1+ cell lines, SKMES-1, and MDA-MB-231. The phage hits were sorted by mean fluorescence index (MFI), first on SKMES, and followed by sorting on MDA-MB-231. Overall, the intensity correlated well in each case. The phage hits could be loosely grouped as high binders, medium binders, and low or non-binders, regardless of whether they were sorted on SKMES-1 or MDA-MB-231. The commercial antibody controls for this assay did not work as well as expected. A similar

experiment was carried out with H358 and SH-SY-5Y cells. Generally, the phage hits which were good binders to H358 were also good binders to SH-SY-5Y, and those that were poor binders were poor for both cell lines as well (data not shown). The phage hits were generally in the same “category” whether they were sorted by rank on H358 or on SH-SY-5Y. That is, the high binders were generally the same for both cell lines, the medium binders were generally the same for both, and the low or non-binders were also the same for both cell lines. In addition, the binding rankings generally followed the trend seen in the other ROR1+ cell lines tested, SKMES-1 and MDA-MB-231.

Binning of the Panel by ROR1 ECD domain

[0273] In order to characterize the initial panel of phage-derived anti-ROR1 antibodies, a set of Fc fusion proteins were created (RR1W4 IgC2 domain, RR1W5 frizzled domain, and RR1W6 kringle domain) as key reagents. In this experiment the binding of each mAb to these Fc-fusion proteins was carried out by MSD. Briefly, 5 µl of 10 µg/ml of ROR1 ECD domain constructs (RR1W4 IgC2 domain, RR1W5 frizzled domain, and RR1W6 kringle domain) were absorbed on Meso Scale Discovery (MSD) HighBind plates (Gaithersburg, MD) for 2 hours then washed 3X with 150 µl 0.1M HEPES. The plate was blocked with 5% BSA buffer overnight at 4°C. The next day, the plate was washed 3X in preparation for addition of anti-ROR mAb supernatants. 25 µl of 10 µg/ml mAb supernatant was added for each variant, and samples were incubated for 2 hrs at room temperature with gentle shaking. The plate was washed 3X, then 25 µl of 20nM Ru-labeled anti-human Kappa chain (Clone# SB81a, Southernbiotech, Birmingham, AL) was added to each well to detect binding of the mAbs to the various ROR1 domain constructs. Incubation was for 1 hour at room temperature with gentle shaking. Domain variants were mixed with 20 nM Ru-labeled anti-human Kappa chain and commercial anti-ROR1 (MAB2000; Clone # 291608, R&D Systems) at 200nM as controls. The plate was then washed 3 times with HEPES wash buffer. MSD read buffer (150 µl) was added to each well, and the plate was then analyzed using an MSD Sector Imager 6000 (MSD, Gaithersburg, MD).

[0274] The results of the binning assessment provided a consistent binning of the mAbs, which was used in subsequent analyses. Frizzled and Kringle Domain selective binding appeared to be strong; IgC2 binding was overall very weak when it was noted. RR1B46 and RR1B55 seemed clearly better than average IgC2 binders. The molecules RR1B01 and RR1B20 clearly did not bind to any of the ROR1 or ROR2 proteins. In **Table 7**, Tier 1, 2, and 3 refer to

sets of mAbs that were grouped together for evaluation. **Table 7** shows that the panel of anti-ROR1 antibodies were fairly evenly divided across the 3 domains of the ECD of ROR1.

Table 7. Results of binning assessment

Domain	IgC2-Fc	Fr-Fc	Kr-Fc	ND*
1	RR1B26	RR1B04		RR1B01
2	RR1B44	RR1B06		
3	RR1B46	RR1B10		
4	RR1B47	RR1B11		
5	RR1B49	RR1B14		
6	RR1B50	RR1B15		
7	RR1B55	RR1B19		
8	RR1B57	RR1B43		
9	RR1B58	RR1B45		
10	RR1B59	RR1B48		
11	RR1B60			
1	RR1B02	RR1B08	RR1B22	
2	RR1B12	RR1B09	RR1B23	
3	RR1B13	RR1B17	RR1B24	
4	RR1B32	RR1B18	RR1B34	
5	RR1B52	RR1B38	RR1B36	
6	RR1B53	RR1B42		
7	RR1B54	RR1B51		
8	RR1B62	RR1B61		
9	RR1B63			
1	RR1B31	RR1B03	RR1B21	RR1B20
2	RR1B64	RR1B05	RR1B25	
3		RR1B07	RR1B27	
4		RR1B16	RR1B29	
5		RR1B28	RR1B30	
6		RR1B56	RR1B33	
7			RR1B35	
8			RR1B37	
9			RR1B39	
10			RR1B40	
11			RR1B41	
Total No.	22	24	16	2

ND* : Not determined

Tabulation of the binning data for the set of 64 anti-ROR1 antibodies shows that antibodies to each of the three extracellular domains were identified. Molecules that bind to the Ig-Like domain (IgC2-Fc), Frizzled domain (Fz-FC), and Kringle (Kz-Fc) were identified. Two molecules did not appear to bind to ROR1 in this analysis.

[0275] Experiments were also carried out to evaluate the binding of the phage-derived panel to ROR1-Fc (Sino Biologicals) and ROR2-His (Origene) protein by Meso scale discovery (MSD). The molecules RR1B43, RR1B45 and RR1B55 displayed low levels of ROR2 binding and RR1B11, RR1B44, RR1B46 had measurable ROR2 binding (data not shown). Molecule RR1B36 was identified as a potential ROR2 binder and RR1B25 had very low level of ROR2 binding. Comparison with binding data to CHO-ROR2 cells suggests some overlap (bold): RR1B3, **B11**, B14, B15, B17, B32, **B43**, B46, B51, **B55** and B61 (data not shown).

[0276] A series of antibody supernatants were tested for their ability to bind ROR1 and ROR2 wt, single domain Fc fusion proteins, and ROR1/ROR2 domain-swapped variants in order to identify the binding domain. In the experiment, ROR1-ECD-Fc and ROR2-ECD-Fc binding data were compared to a version of the ROR2 ECD in which the IgC2 domain was replaced with the ROR1 IgC2 domain (IgC2(1)-Fz-(2)-Kg(2)-Fc) and a similar domain reconstructed chimeric ECD in which the ROR2 IgC2 domain would be presented (IgC2(2)-Fz(1)-Kr(2)-Fc). In these experiments, one would expect that ROR1-ECD-Fc binding would correlate with the IgC2(1) chimera. Likewise, the ROR2-ECD-Fc binding would be expected to correlate with IgC2(2) chimera. An expected pairing was observed in some experiments: RR1B26, RR1B49, RR1B50, RR1B58, RR1B59 and RR1B60. However, the binding to the chimera was generally very low and in no case was the chimera above 50% of the binding value for the WT ECD (data not shown).

[0277] The binning data for the anti-ROR1 antibodies was used to determine the epitope for the commercial antibody 2A2. A competition experiment was performed using parental anti-ROR1 antibodies. Three cell lines were tested: H520 cells as a negative control, and H358 and SK-MES-1 as ROR1+ test cells. As expected, H520 cells showed an absence of binding as shown in the similarity in the MFI values between the no mAb control (without pretreatment with blocking mAb) and the no 2A2 control (well D12) (data not shown). In contrast the, data from the H358 and SKMES definitively demonstrated that the 2A2 antibody binds to the Ig-like domain. Pre-incubation with antibodies RR1B76 (RR1B58), RR1B85 (RR1B44) and RR1B86 (RR1B47) inhibited 2A2 binding. Interestingly, RR1B65 (RR1B12) only inhibited 2A2 binding only slightly, while RR1B88 did not inhibit 2A2 binding at all, indicating that there are at least two epitopes in the Ig-like region.

[0278] A weight of evidence approach was adopted to enable the selection of a group of anti-ROR1 antibodies that were to be advanced to expression and purification as IgG4 PAA molecules. The data in **Table 6** was combined with ROR2 selectivity data. After elimination of

non-binders and cross reactive ROR2 binders, a few very weak binders were deprioritized. Then the molecules were binned by epitope and a high binder, medium binder and a weak binder were selected for each of the three epitopes in the ROR1 ECD. Backup molecules were then selected for each of these molecules. This selection exercise resulted in a table of 24 molecules that was divided into two panels of 12 each (**Table 8 and FIG. 2**). This set of molecules was advanced to expression and purification.

Table 8. Anti-ROR1 antibodies from phage display advanced to expression and purification

Panel (A)	Panel (B)
RR1B06	RR1B23
RR1B24	RR1B36
RR1B48	RR1B33
RR1B35	RR1B21
RR1B22	RR1B39
RR1B45	RR1B04
RR1B38	RR1B08
RR1B56	RR1B09
RR1B57	RR1B44
RR1B58	RR1B54
RR1B12	RR1B47
RR1B52	RR1B50

Generation of anti-ROR1 mAbs on IgG4 PAA platform

[0279] The 24 anti-ROR1 antibodies were prepared on the IgG4 PAA platform, which naturally includes R409 (**Table 9**).

Table 9. Anti-ROR1 Antibodies on IgG4 PAA platform

Panel (A) Parental	IgG4 PAA K409R		Panel (B) Parental	IgG4 PAA K409R
RR1B06	RR1B78		RR1B23	RR1B67
RR1B24	RR1B68		RR1B36	RR1B83
RR1B48	RR1B72		RR1B33	RR1B82
RR1B35	RR1B69		RR1B21	RR1B81

RR1B22	RR1B66		RR1B39	RR1B84
RR1B45	RR1B71		RR1B04	RR1B77
RR1B38	RR1B70		RR1B08	RR1B79
RR1B56	RR1B74		RR1B09	RR1B80
RR1B57	RR1B75		RR1B44	RR1B85
RR1B58	RR1B76		RR1B54	RR1B88
RR1B12	RR1B65		RR1B47	RR1B86
RR1B52	RR1B73		RR1B50	RR1B87

These 24 molecules were re-cloned as IgG4 PAA with DuoBody® K409R mutation.

[0280] Some of the selected mAbs did not express well – the mAbs RR1B68, RR1B73, RR1B75, RR1B79, RR1B80, RR1B81 and RR1B87 were not advanced (shaded gray in the above table). This resulted in 17 anti-ROR1 mAbs for evaluation.

Surface plasmon resonance to test binding of CD3 arm to ROR1

[0281] Binding of the anti-CD3 antibody CD3B219. Experiments were carried out on H358 cells, primary T-cells, SK-MES-1 cells, and the ROR1 expressed in HEK293F cells.. The binding results showed concentration dependent binding of commercial mouse anti-ROR1 antibodies to the ROR1 expressing H358 cells and no specific binding of the anti-CD3 antibodies to these cells. The binding results showed concentration dependent binding of anti-CD3 antibodies to the T cells and no specific binding of anti-ROR1 antibody to the T cells. These results confirm that the anti-CD3 antibodies bind specifically to T cells as expected. The binding results showed concentration dependent binding of anti-ROR1 antibodies to the ROR1 expressing SK-MES-1 cells and no specific binding to the anti-CD3 antibodies to the ROR1 expressing SK-MES-1 cells. The binding results showed concentration dependent binding of anti-ROR1 antibodies to the ROR1 transiently transfected HEK293F cells and parental HEK293F cells and no specific binding to the anti-CD3 antibodies to the ROR1 transiently transfected HEK293F cells and parental HEK293F cells. These data are summarized in **Table 10** below.

Table 10. Summary of experiments testing anti-CD3 antibody binding to ROR1 expressing cells

Cell Line	ROR1 expression?	Anti-ROR1 binding?	CD3 expression?	Anti-CD3 binding?
H358	Yes, endogenous	Yes	No	No

Primary T cells	No	No	Yes, endogenous	Yes
SK-MES-1	Yes, endogenous	Yes	No	No
ROR1 transfected 293F	Yes, overexpressed	Yes	No	No
Parental 293F	Yes, endogenous	Yes	No	No

Cross Competition of anti-ROR1 mAb Panel

[0282] The panel of IgG4 PAA K409R anti-ROR1 antibodies were evaluated in a cross-competition experiment. Five μ L of recombinant human ROR1-Fc Chimera (10 μ g/mL; Sino Biologicals, Cat# 13968-H02H1) was directly coated on MSD HighBind plates for 2 hours at room temperature then blocked with 5% MSD Blocker A buffer for an additional 2 hours at room temperature. The plates were washed 3x with 0.1 M HEPES buffer, pH 7.4, followed by the addition of a mixture of Ruthenium (Ru)-labeled anti-ROR1 mAb, which was pre-incubated at room temperature for 30 minutes with different concentrations, from 1 μ M to 1 nM, of other anti-ROR1 mAbs. After incubation with gentle shaking at room temperature 2 hours, the plates were washed 3x with 0.1M HEPES buffer (pH 7.4). MSD Read Buffer T was diluted with distilled water (4-fold) and dispensed into each well. The plates were analyzed with a SECTOR Imager 6000 (Meso Scale Discovery, Gaithersburg, MD) and the data were processed with GraphPad.

[0283] The IgG4 PAA K409R anti-ROR1 antibodies that had been assigned to the Kringle Domain binding family, including RR1B67, gave very clear cross competition readout. RR1B66, RR1B67, RR1B69, RR1B82, RR1B83 and RR1B84 competed for binding of the Ru-labeled RR1B69 molecule (**FIG. 3** and **Table 11**). From this data it was concluded that all of the Kringle binding molecules bound to the same epitope. In addition, the commercial antibody 2A2 was shown to bind to the Ig-like domain (**Table 11**).

Table 11. Summary of cross competition data

Competitor	Ru-labeled anti-ROR1 mAb						
	RR1B69	RR1B71	RR1B72	RR1B78	RR1B85	RR1B86	RR1B88
RR1B66	+	—	—	—	—	—	—
RR1B67	+	—	—	—	—	—	—
RR1B69	+	—	—	—	—	—	—
RR1B82	+	—	—	—	—	—	—
RR1B83	+	—	—	—	—	—	—
RR1B84	+	—	—	—	—	—	—

RR1B71	—	+	—	—	—	—	—
RR1B70	—	—	+	+	—	—	—
RR1B72	—	—	+	+	—	—	—
RR1B74	—	±	+	+	—	—	—
RR1B77	—	±	+	+	—	—	—
RR1B78	—	±	+	+	—	—	—
RR1B65	—	—	—	—	—	—	+
RR1B76	—	—	—	—	—	±	+
RR1B85	—	—	—	—	+	+	—
RR1B86	—	—	—	—	+	+	—
RR1B88	—	—	—	—	—	—	+
	Kringle	Frizzle			Ig-Like		

[0284] The cross competition experiment identified 6 binding groups on the ECD of ROR1 (Table 12). One competition group was found for the Kringle binding molecules (Group 1). All of the Frizzled domain binding molecules with the exception of RR1B71 bound to the same epitope (Group 2). RR1B71 formed Group 3. Three epitope groups were identified for the Ig-like domain. The commercial molecule 2A2 formed Group 5.

Table 12. Binding Groups on the ECD of ROR1

Kringle	Frizzled		Ig-Like		
Group I	Group II	Group III	Group IV	Group V	Group VI
RR1B66	RR1B70	RR1B71	RR1B85	2A2	RR1B65
RR1B67	RR1B72		RR1B86		RR1B76
RR1B69	RR1B74				RR1B88
RR1B82	RR1B77				
RR1B83	RR1B78				
RR1B84					

Generation of ROR1 x CD3 Bispecific Antibodies

[0285] ROR1 x CD3 bispecific antibodies were prepared using the DuoBody® platform. See, for example, U.S. Patent App. Pub. No. US2014/0170148. Briefly, a controlled Fab arm exchange (cFAE) between 2 intentionally designed monoclonal antibodies, one harboring F405L mutation and another having K409R. The cFAE was initiated by mixing equal molar ratio of the 2 parental antibodies – IgG4 PAA K409R anti-ROR1 antibodies (ROR1 arm) and CD3B219 (CD3 arm) –or in some cases 6% extra of one parental to deplete another, with 75

mM (final concentration) of cysteamine HCl (2-MEA). After incubation for 5 hrs at 31°C, the antibody mixture was dialyzed against 1xD-PBS, during which period 2-MEA was removed to allow the reduced disulfide bonds to reconnect. The formation of DuoBody® heterodimer was analyzed by either cation exchange (CEX) HPLC or hydrophobic interaction chromatography (HIC) HPLC. The bispecific antibodies were polished by preparative CEX or HIC to remove the residual parental(s). The 17 ROR1 x CD3 bispecific antibodies created using this approach are listed in **Table 13**.

Table 13. ROR1 x CD3 bispecific antibodies

ROR1 x CD3 Bispecific Antibody	Parental IgG4 PAA anti-ROR1 antibody	Domain
RCDB3	RR1B65	Ig-Like
RCDB11	RR1B76	Ig-Like
RCDB17	RR1B85	Ig-Like
RCDB18	RR1B86	Ig-Like
RCDB19	RR1B88	Ig-Like
RCDB7	RR1B70	Frizzled
RCDB8	RR1B71	Frizzled
RCDB9	RR1B72	Frizzled
RCDB10	RR1B74	Frizzled
RCDB12	RR1B77	Frizzled
RCDB13	RR1B78	Frizzled
RCDB4	RR1B66	Kringle
RCDB5	RR1B67	Kringle
RCDB6	RR1B69	Kringle
RCDB14	RR1B82	Kringle
RCDB15	RR1B83	Kringle
RCDB16	RR1B84	Kringle

The IDs that correspond between phage-hits (column 1) and the IgG4 PAA ROR1 antibodies (column 2), and the ROR1 x CD3 bispecific antibody (DuoBody®).

[0286] ROR1 x CD3 DuoBody® molecules used in the remainder of the studies were those having a CD3B219 arm. Thus, as used in the remainder of the Examples section, ROR1 x CD3 bispecific antibody refers to those having a CD3B219 arm, unless otherwise stated.

Relative Cell Binding for the ROR1 x CD3 Bispecific Antibodies

[0287] The set of 17 ROR1 x CD3 bispecific antibodies were tested for binding to ROR1 expressing HCC827 cells. Briefly, cells were harvested using cell dissociation buffer

(Gibco, USA) and washed in PBS. Labeling with bispecific antibody was performed for 45 minutes at 4°C in FACS staining buffer (BD Biosciences, USA). Cells were washed in staining buffer prior to incubation with an alexa-fluor 647-labeled anti-human secondary antibody (Life Technologies, USA). Samples were collected on an IntelliCyt High Throughput Flow Cytometry HTFC system and analyzed using ForeCyt software. EC₅₀ values were calculated in GraphPad Prism V6. Acceptance criteria for non-linear regression curve fitting was a confidence interval (CI) range of less than 1.4.

[0288] Control antibodies used were a CD3 x B21M isotype and a commercial anti-ROR1 antibody from BioLegend (2A2) and the corresponding isotype. The antibodies were titrated starting from 15 µg/mL or about 100 nM. Each antibody dilution was run in duplicate and the CD3 x B21M isotype was included on all plates. All ROR1 CD3 bispecific antibodies bound to the cells in a concentration dependent manner, while the CD3 x B21M and BioLegend isotype did not bind to the cells in a concentration dependent manner. The isotype subtracted geo mean fluorescence index (geoMFI) data for all samples was used for analysis. The isotype subtracted values were calculated by subtracting the respective plate CD3 x B21M isotype GeoMFI from the antibody GeoMFI at each concentration. The EC₅₀ values were calculated using the isotype subtracted geoMFI values. The data was graphed in Prism, the nM concentration values were LOG transformed and the EC₅₀ values were calculated using non linear regression with the log(agonist) vs. response - Variable slope (four parameters) analysis with bottom constrained to 0 since the data was isotype background subtracted. Some curves did not appear to fully plateau at the highest concentration of antibody tested and some curves also have different maximal binding signals.

[0289] These data were replotted by grouping according to Domain Binding for graphical representation (**FIG. 4**). The isotype subtracted data was graphed in Prism, the nM concentration values were LOG transformed and the curve was fitted using non linear regression with the log(agonist) vs. response - Variable slope (four parameters) with the bottom constrained to 0 since the data was isotype background subtracted. The EC₅₀ binding values were calculated and are shown in **Table 14**.

Table 14. EC₅₀ of ROR1 x CD3 Bispecific Antibodies

ROR1 x CD3 Bispecific Ab	Domain	Binding EC ₅₀ (nM)
RCDB3	Ig-Like	3.77
RCDB11	Ig-Like	2.36

RCDB17	Ig-Like	4.72
RCDB18	Ig-Like	5.07
RCDB19	Ig-Like	16.2
RCDB7	Frizzled	1
RCDB8	Frizzled	10.63
RCDB9	Frizzled	16.94
RCDB10	Frizzled	14.8
RCDB12	Frizzled	1.25
RCDB13	Frizzled	1.64
RCDB4	Kringle	9.14
RCDB5	Kringle	3.74
RCDB6	Kringle	6.25
RCDB14	Kringle	6.21
RCDB15	Kringle	6.34
RCDB16	Kringle	10.43

[0290] The binding data indicated that the relative affinity of the Frizzled and Ig-Like domain molecules were more potent, while the Kringle domain binders were on average less potent. These data were in the context of the CD3 arm and were only determined on one ROR1 expressing cell line. The EC₅₀ values for the Fizzled domain binders were slightly tighter than either the best Ig-like or the best Kringle domain binding ROR1 x CD3 bispecific antibodies.

Functional Evaluation of the ROR1 x CD3 Bispecific Antibodies

[0291] A variety of approaches were utilized to evaluate the functional activity of the set of 17 ROR1 x CD3 bispecific antibodies. In one experiment, a subset of these molecules were tested in T cell re-direction killing assay. The IncuCyte based assay was used because it is more amenable to studies measuring killing of adherent cell lines and, in contrast to the flow-based assays, allows the calculation of absolute target cell numbers per well and the kinetics of their expansion. This is possible due to the use of RFP-labeled target cells which were generated using a lentiviral construct from Essen BioSciences. In this experiment, two independent readouts were used to measure cytotoxicity: target cell growth inhibition (**FIG. 5**) and Caspase 3,7 activity (data not shown). This allowed the loss of target cells and apoptotic target cell death, which is a feature of T cell mediated killing, to be correlated. An analysis protocol was developed which enabled the calculation of growth inhibition based on the expansion index generated from the number of target cells/well at each timepoint of the experiment. These kinetics curves were used to generate area under the curve values that were plotted to generate titration curves for each ROR1 x CD3 bispecific antibody. Interpolation was then used to

generate single values that could be used to directly compare the potency of the test molecules. Interpolation was used rather than EC50's because the maximum values were very different when comparing the different sets of molecules binned based on binding domain. Rankings from the growth inhibition and Caspase readouts were compared and, although not identical, showed a strong correlation (data not shown).

[0292] The growth inhibition data clearly showed that there was a difference between the groups of molecules binding to distinct domains in their ability to kill (**FIG. 5** and **Table 15**). The curves generated by the Kringle domain binders had higher maximum value compared to the Frizzled domain binders. The Ig-like domain binders demonstrated the lowest maximum values for target cell growth inhibition, suggesting that there was a relationship between the position of the epitope and killing potential, with those binding the more membrane proximal region being more efficacious than those binding more distal parts of the ECD molecule. Within each of the groups of molecules, those with the highest relative affinities demonstrated the best killing, suggesting that affinity is important, but is secondary to the position of the epitope.

Table 15. Killing EC50 for ROR1 x CD3 bispecific antibodies

ROR1 x CD3 Bispecific Ab	Domain	Killing EC50 (nM)
RCDB3	Ig-Like	2.485
RCDB11	Ig-Like	0.2473
RCDB17	Ig-Like	5.166
RCDB7	Frizzled	16.92
RCDB9	Frizzled	3.213
RCDB13	Frizzled	0.5392
RCDB4	Kringle	0.6769
RCDB5	Kringle	0.4543
RCDB6	Kringle	0.4371
RCDB15	Kringle	1.278
RCDB16	Kringle	2.913

[0293] The caspase readout also showed that the Kringle binders generally had greater killing potential compared to those binding the Frizzled and Ig-like domains. There were, however, some differences in the data. Curve fits were not generated for RCDB11 and RCDB5 although the individual data points demonstrated good killing similar to that seen with the target cell growth inhibition readout. RCDB13 and RCDB9 were the best killers in the Frizzled group,

while RCDB5 and RCDB15 appeared to be slightly better than RCDB4 and RCDB16 within the Kringle group. These observations are similar to that seen for the other readout.

[0294] Overall, this data suggests strongly that membrane proximity is a key determinant of killing potential, with affinity having a secondary impact. Of the panel of ROR1 x CD3 bispecific antibodies tested, the Kringle domain binders showed the best killing efficacy. The higher affinity molecules in the Frizzled and Ig-like domain binding groups also showed good activity, suggesting that several distinct molecules are available for lead selection.

[0295] The ROR1 x CD3 bispecific antibodies were also assessed in a novel T cell mediated cytotoxicity assay. In this assay, the target cells were engineered with a cytosolic fusion to half-BetaGal by DiscoverX, which generated target cell lines that were transfected with a fusion protein composed of a non-secreted housekeeping gene fused with part of the b-gal molecule. This would be released into the media following lysis of the cell and could be used to readout (chemiluminescence). The lysis released b-gal would be fully reconstituted following addition of the complementary part of b-gal and a substrate. Three cell lines were transfected: H520 (negative control), H358 and SKMES-1.

[0296] Two different housekeeping proteins were used in the cell lines. Based on preliminary data, the background signal in the non-lysed ADO-fusion transfected cells was higher than desired. Hence, the FKBP1A cells were selected for a pilot T cell killing experiment. The H520 cell line was examined by Flow Cytometry analysis and shown to be negative for ROR1 (as expected). The H358 and SK-MES-1 cell lines were positive as expected.

[0297] The DiscoverX killing assay provided comparable data to other T-cell mediated cytotoxicity assays. In this example (**FIG. 6**), the Kringle domain binding ROR1 x CD3 bispecific antibodies were among the best killing molecules and constituted a single group of molecules. More diverse responses were seen with Frizzled and Ig-like domain binders. However, two Frizzled binders and one of the Ig-like binders were comparable to the set of Kringle binding ROR1 x CD3 bispecific antibodies.

[0298] The ROR1 x CD3 bispecific antibodies RR1B69, B67, B78, B76, B72, B77, and B89 were further analyzed.

Cytotoxicity in comparison with published ROR1xCD3 bispecific antibodies.

[0299] The redirected T cell killing of lung tumor cells activated by ROR1 x CD3 bispecific antibodies was compared between RCDB5 and a prior art antibody, published in WO2014167022A1, Example 3C, Bispecific (Fab)₂x(Fab) antibody bivalent for ROR1 and

monovalent for CD3, with Fc, for brevity termed “Engmab” antibody. Flow cytometry-based assays were used to measure cytotoxicity. Triplicate samples were set up per condition. Briefly, 10,000 GFP-transfected NCI-H1975 lung tumor cells were plated per well in 96 well flat-bottomed plates and left to adhere for 4-6 hours. Cryopreserved, purified T cells were then thawed and added to each well at 50,000 cells/well (5:1 E:T) concomitant with bi-specific antibodies, which were plated at a final titration range of 0.0064 – 6667pM. Plates were incubated at 37°C for 72 hours.

[0300] At harvest, cells were released with trypsin, labelled with fixable viability dye (Thermo Fisher Scientific, Bridgewater) and anti-human CD25 (clone M-A251; BioLegend, San Diego), and collected using the IntelliCyt iQue high throughput flow cytometer. Data analysis was performed in ForeCyt software (IntelliCyt, Albuquerque) and exported to Microsoft Excel. Log-transformed values were then used for non-linear regression using the “sigmoidal dose-response (variable slope)” function in Prism v6.02 (GraphPad, La Jolla). A LogEC50 95% confidence interval range of less than 1.4. was set as acceptance criteria for curve fitting. Charts show mean values $\pm$ SEM. Statistical analysis was performed using an unpaired two tail t-test.

[0301] The data demonstrates that the RCDB5-activated cytotoxicity was greater than Engmab-activated cytotoxicity at various antibody concentrations (FIG. 13A). The number of live lung tumor cells per well was 4.6-fold lower in RCDB5-treated wells than in Engmab-treated wells at the highest concentration tested (6.67 nM, FIG. 13B). Because the induction of CD25 expression on T cells is associated with their activation, our data suggested that loss of target cells was mediated in a T cell-dependent manner (FIG. 13C).

ROR1xCD3 mediates potent killing of MCL lines in whole blood cytotoxicity assay in vitro

[0302] Confluent MCL cells, MAVER-1, JeKo-1, Z-138 and NAMALWA, Burkitt's lymphoma line (data not shown) were washed in PBS and labeled with 500 nM carboxyfluorescein succinimidyl ester (CFSE) dye (Invitrogen) for 5 min at room temperature. Reaction was quenched with heat-inactivated fetal bovine serum for 1 min. CFSE-labeled tumor cells were washed with culture media and reconstituted at 1×10^6 cells/mL. 20,000 tumor cells were co-cultured with 40uL whole blood from 4 healthy donors in the presence of either ROR1xCD3 RCDB13 or null arm control MAbs (nullxCD3 or ROR1xnull) reconstituted in RPMI medium (containing 10% FBS). Cells were cultured in 96-well plates at a final volume of 200uL/well at 37°C 5% CO₂ for 60 hours. Red blood cells were lysed using Multispecies Red Cell Lysis Buffer (eBioscience) diluted 1:10 with water on ice for 3 minutes. Cells were washed

with PBS and stained with Live/Dead (Near-IR; ThermoFisher) according to manufacture's protocol. Cell pellets were stained with anti-CD4-PerCP/Cy5.5, anti-CD8-PE-Cy7, anti-CD25-PE (BioLegend) in 50 μ L volumes of FACs Stain Buffer (BD) for 30 min at 4°C in the dark. Cells were washed twice with Stain Buffer and reconstituted with Stain Buffer. % Cytotoxicity (100%- % Live CFSE+) and T cell activation (% CD25 expression on CD4+ and CD8+ lymphoid fractions) were measured by flow cytometry. Data were acquired on the BD FACs Canto cytometer and analyzed by CytoBank software and GraphPad Prism 6. Data are representative of two independent experiments.

[0303] ROR1xCD3 mediated potent killing of MCL lines in whole blood cytotoxicity assay *in vitro* (FIG. 17A-F). Specific engagement of T cells with tumor cells mediated by ROR1xCD3 was required to induce dose-dependent T cell activation (activation marker, CD25 upregulation, FIG. 17D-F) and cytotoxicity (FIG. 17A-C). Specificity of T cell – tumor engagement was also confirmed by the lack of cytotoxicity below 1 nM when null controls were used. Although $\Delta E_{\max}$ (% of maximum cytotoxicity - % spontaneous cytotoxicity in the absence of antibody) varied between donors, EC50 were comparable between all cell lines tested and ranged between 0.2-1 nM.

ROR1xCD3 mediates potent killing of MCL lines in cytotoxicity assay in vitro using PBMC as effector cells

[0304] Confluent MCL cells, MAVER-1, Z-138, JeKo-1, REC-1, Mino (data not shown for JeKo-1, REC-1, Mino) were washed in PBS and labeled with 500nM carboxyfluorescein succinimidyl ester (CFSE) dye (Invitrogen) for 5 min at room temperature. Reaction was quenched with heat-inactivated fetal bovine serum for 1 min. CFSE-labeled tumor cells were washed with RPMI culture media (containing 10% fetal bovine serum) and reconstituted at 1×10^6 cells/mL. PBMCs were washed in RPMI culture medium and adjusted to 2.5×10^6 cells/mL. 20,000 tumor cells were co-cultured with 100,000 PBMC from 2 healthy donors (E:T=1:5) in the presence of either ROR1xCD3 RCDB13 or null arm control MAbs (nullxCD3 or ROR1xnull) reconstituted in culture medium. Cells were cultured in 96-well plates, final volume 200 μ L/well at 37°C 5% CO₂ for 60 hours. Staining and data analysis were performed as in Fig. 4. Data are representative of 2 independent experiments.

[0305] ROR1xCD3 mediated potent killing of MCL lines when PBMCs were used as effector cells in cytotoxicity assay *in vitro* (FIG. 18A, C show data for MAVER-1 cells, and FIG. 18B, D show data for Z-138 cells). Specific engagement of T cells with tumor cells mediated by

ROR1xCD3 DuoBody was required to induce dose-dependent T cell activation (activation marker, CD25 upregulation, FIG. 18C-D) and cytotoxicity (FIG. 18A-B). Specificity of T cell – tumor engagement was also confirmed by the lack of cytotoxicity below 1 nM when null controls were used. EC50 were comparable between all cell lines tested and ranged between 0.2-1 nM similar to EC50 derived from whole blood assays using the same MCL lines as target cells. These data also suggested lack of association between ROR1 receptor density (FIG. 15) and EC50.

Deamidation of the CD3 arm

[0306] In the analysis of ROR1xCD3 bispecific antibodies, CD3 deamidation was observed on the CD3 Heavy Chain CDR3 in all release samples, which increases upon stress at high pH. Analytical evaluation of the CD3 deamidation was carried out twice. RCDB5 and RCDB11 release samples exhibited similar amount of deamidation levels ($17 \pm 2\%$ and $19 \pm 3\%$) compared to previous study ($17 \pm 2\%$ and $20 \pm 4\%$). A slightly higher level was observed in RCDB13 ($24 \pm 2\%$ vs. $19 \pm 5\%$), although within the error range (**Table 16**).

Table 16. Anti-CD3 antibody CD3B219 deamidation levels

mAb	parental	PTM	CDR	Motif	Residue	%PTM Release	%PTM HighPH
RCDB5	CD3B219	Deamid.	H3	NS	N106+N103	17 ± 2	72 ± 6
RCDB11	CD3B219	Deamid.	H3	NS	N106+N103	19 ± 3	75 ± 5
RCDB13	CD3B219	Deamid.	H3	NS	N106+N103	24 ± 2	78 ± 5

Biophysical and Cell Binding of ROR1 x CD3 Bispecific Antibodies

[0307] Based upon early results for cell binding (**FIG. 5**) it was expected that Ig-like and Frizzled Domain binders might bind to ROR1 expression cells tighter than Kringle Domain binders. Since Kringle Domain binders were apparently better mediators of T cell directed cytotoxicity, a solid understanding of the cell binding was desired.

[0308] The affinity of select ROR1 x CD3 bispecific antibodies to ROR1 was evaluated with the cell affinity technique using MesoScale Discovery technology (MSD-CAT). The MSD-CAT experiments were performed either using H358 cells endogenously expressing ROR1 or HEK293 transfected human ROR1. The receptor density of HEK293 transfected human ROR1

was measured by flow cytometry, which was then translated to molar concentration of receptor in the reaction mixture and was used in these studies. DuoBody® CD3B288 with single null arm of anti-RSV was used as negative control. Parental (mock) HEK293 cells were used to evaluate nonspecific binding to the cell surface. In order to measure the affinity of an interaction using the MSD-CAT method, a series of mixtures with a fixed concentration of the soluble reactant (A) and varying concentrations of cells (B) were prepared and allowed to reach equilibrium. After equilibration, the concentration of free A was determined and the data was analyzed for affinity. For these studies, the reaction mixture was prepared by adding antibody at four different but fixed concentrations and the cells were serially diluted starting at 6×10^7 cells/mL. After incubation and equilibration of the reaction mixture, free anti-ROR1 was captured via biotin-ROR1-DDK captured on SA plate and followed by detection using ruthenium-labeled anti-human IgG. The binding profiles of the ROR1 x CD3 bispecific antibody interactions with ROR1 were performed by nonlinear least-square fitting of the binding curves using 1:1 binding model.

[0309] In order to perform the MSD-CAT experiments, an assay for detection of free mAb in the reaction mixture was developed. Two detection methods were tested. The first method in which ROR1 flag-tagged (aka ROR1-DDK) was captured using an anti-flag tag antibody, followed by binding of free anti-ROR1 to the captured ROR1-DDK and detection with ruthenium-labeled anti-human IgG failed due to poor assay performance : low assay signal and narrow assay window. Therefore, a second detection assay was developed and finally used for the MSD-CAT experiment. In this detection assay, free anti-ROR1 was captured via biotin-ROR1-DDK on SA plate and the captured mAb detected using ruthenium-labeled anti-human IgG.

[0310] MSD-CAT for ROR1 DuoBody binding to HEK cells expressing hu ROR1 (Lentiviral plasmid pDR25226) were generated and used to transfect HEK293F cells. The ROR1 x CD3 bispecific antibodies (RCDB5, RCDB6, RCDB9, RCDB11, RCDB12, RCDB13) were analyzed using this cell line (**Table 17**). These data were fit using the receptor density of 1.8 million human ROR1 per HEK293 as measured by flow cytometry (data not shown). Example data are shown in Figure 7A and 7B. From these measurements the DuoBody RCDB5 had a K_D of 331 ± 152 pM and the RR1B67 parental (bivalent) antibody had an apparent K_D of 55 ± 13 pM. RR1B67 Mab displayed a ~ 6-fold tighter binding than RCDB5 (the DuoBody for RR1B67xCD3B219). This higher affinity of the parental to the HEK293 ROR1 expressing cells was attributed to avidity effects. The binding profiles of RCDB13, RCDB11, RCDB12, RCDB5, RCDB6 were similar with affinity in the sub-nM range; however, weaker affinity was observed

for RCDB9 in the nM range. For RCDB9, there was a cell concentration dependent titration on the control (mock) cells that showed non-specific binding for RCDB9. The negative DuoBody®, CD3B288, showed no binding to ROR1 expressing cells nor to HEK293 mock cell.

Table 17. Compiled cell affinity of ROR1 x CD3 DuoBody® Abs to HEK293 cells expressing human ROR1

Antibody	Human ROR1 Cell (Ave ± SD) K_D [pM]	n
RCDB5	331 ± 152	20
RCDB6	648 ± 325	12
RCDB9	2268 ± 1748	8
RCDB11	382 ± 142	12
RCDB12	236 ± 170	12
RCDB13	254 ± 122	12
*RR1B67	*55 ± 13	6

Summary of cell affinity (MSD-CAT) data for the binding of six ROR1 x CD3 bispecific antibodies and the anti-ROR1 antibody RR1B67 to HEK293 cells engineered to overexpress ROR1 (# human ROR1 receptor/cell = 1.8×10^6). The data corresponds to the average and standard deviation of all acceptable (total indicated by n) affinity values obtained in 3 independent experiments. All of the molecules had sub-nanomolar affinity, with the exception of RCDB9. The binding of the parental molecule RR1B67 suggest avidity effect in binding due to the bivalent nature of the antibody which could potentially cross-link two neighboring ROR1 in the cell surface.

* Referred to as the “apparent K_D ” because it could be affected by avidity due to bivalent binding

[0311] Biacore (surface plasmon resonance; SPR) was also used to determine the affinity of the ROR1 x CD3 bispecific antibodies (RCDB5, RCDB6, RCDB9, RCDB11, RCDB12, RCDB13) to a recombinant human ROR1 (Table 18). Example SPR sensograms are shown in Figure 7A and 7B.

Table 18. Biacore analysis of ROR1 x CD3 bispecific antibodies

Ab ID	k_{on} Ave ($M^{-1}s^{-1}$)	k_{on} STDEV ($M^{-1}s^{-1}$)	k_{off} ave (s^{-1})	k_{off} STDEV (s^{-1})	K_D ave (nM)	K_D Stdev (nM)	n
RCDB5	1.54E+04	1.21E+03	1.17E-04	9.33E-06	8	0.9	3
RCDB13	1.84E+04	2.29E+03	1.95E-04	3.49E-05	11	2.3	3

RCDB6	1.84E+04	2.05E+03	2.22E-04	5.80E-06	12	1.4	3
RCDB11	1.94E+04	2.52E+03	3.01E-04	5.36E-05	15	3.4	3
RCDB12	2.33E+04	5.82E+02	6.45E-04	1.61E-05	28	1.0	3
RCDB9	2.79E+04	1.65E+03	2.20E-03	2.70E-04	79	10.7	3
RRIB67	2.09E+04	(1.8-2.3)E+04	1.33E-04	(1.2-1.4)E-04	6	7.8 - 5.3	2
RRIB69	1.91E+04	(1.9-1.9)E+04	2.13E-04	(1.0-2.2)E-04	11	11.8- 10.4	2

Summary of Biacore data for the binding of six ROR1 x CD3 bispecific antibodies and the anti-ROR1 antibodies RRIB67 and RRIB69 to recombinant human ROR1. The data corresponds to the average and standard deviation of all acceptable (total indicated by n) affinity values obtained in 3 independent experiments. All of the molecules had sub-nanomolar affinity, with the exception of RCDB9. The binding of the parental molecule RRIB67 suggest avidity effect in binding due to the bivalent nature of the antibody which could potentially cross-link two neighboring ROR1 in the cell surface.

[0312] Both Biacore (SPR) and MSD-CAT demonstrated that the weakest binder to ROR1 is RCDB9 regardless of the form of antigen used (recombinant or cell-surface expressed). In addition, both methods show that the other 5 ROR1 x CD3 bispecific antibodies (RCDB5, RCDB13, RCDB6, RCDB11, RCDB12) bind with affinities that are within 3.6-fold or less of each other. MSD-CAT affinities of ROR1 x CD3 bispecific antibodies for cell-surface ROR1 are >20-fold tighter than SPR data for recombinant ROR1. The difference in SPR versus MSD-CAT affinities for cell-surface ROR1 is most likely due to the presentation of the antigen on the cell surface in comparison to the recombinant antigen. The binding observed by SPR is representative of monovalent affinity which is not influenced by avidity effects regardless of the type of molecule analyzed (monospecific or bispecific antibody), but in the context of the cellular assay, the binding of the monospecific antibody, in contrast to the ROR1 x CD3 bispecific antibodies, is affected by avidity due to the bivalent nature of the antibody. An example of this avidity effect is shown by the binding of RCDB5 and its parental anti-ROR1 mAb (RRIB67) (**FIG. 7**). The parental mAb showed twice the response of RCDB5 in Biacore (left panels) indicating occupation of the two arms in the parental mAb, but the binding profiles

are similar. However, in the case of MSD-CAT (right panels) the curves are shifted to the left and the slope is steeper for the parental mAb indicating tighter binding.

[0313] In summary, the SPR data for RCDB5 and RR1B67 suggested a low nanomolar K_D . This was consistent with the expectation of monovalency in this experiment. ROR1-ECD was bound to the sensor-surface captured antibodies in a monomeric format. Binding of RCDB5 to cells was about 25 fold more potent (~300 pM). It could be possible that the membrane anchored format of ROR1 as expressed on the cell surface presents the antigen in a more favorable conformation for binding. The large shift in potency for the RR1B67 molecule to cells was most likely due to an avidity effect. The high density of exogenous ROR1 surface expression on HEK293 cells would suggest that receptor crosslinking could occur and increase the apparent binding constant.

In vivo activity of ROR1 x CD3 bispecific antibodies

[0314] An admixture mouse model was used to evaluate the *in vivo* efficacy of RCDB13 and RCDB5. In the model, 5 million H1975 cells were mixed with 1 million human T cells (E:T ratio of 5:1) in 50% Cultrex. The mixture was implanted into the right flank of female athymic nude mice (0.1 ml/mouse). Treatment with ROR1 x CD3 bispecific antibodies began on day zero and continued for 5 doses (IV). A PBS control group, and 0.1, 1, and 10 ug/mouse were administered for each ROR1 x CD3 bispecific antibody (**FIG. 8**). The ROR1 x CD3 bispecific antibody RCDB5 at 1 and 10 ug/mouse suppressed the growth of the H1975 tumor when compared to the PBS control. An overall weaker effect was observed with RCDB13.

Fc receptor binding of RCDB5

[0315] The purpose of this study was to characterize by competition AlphaScreen the interaction of the ROR1 x CD3 bispecific antibody RCDB5 with human FcγR1, FcγRIIa, FcγRIIb, FcγRIIIa, and FcRn relative to wild type hIgG1 and a collection of related IgG4 PAA control parental (bivalent) and null-arm (monovalent) molecules. The antibodies used in the AlphaScreen are provided in **Table 19**. The AlphaScreen is a bead-based assay system used to study biomolecular interactions in microplate format. AlphaScreen assays used two types of bead: Donor beads and Acceptor beads. Both bead types were coated with a hydrogel which minimized non-specific binding and self-aggregation while providing reactive groups for conjugating molecules to the bead surface. Donor beads contained a photosensitizer, which converted ambient oxygen to singlet oxygen upon illumination at 680 nm. Singlet oxygen is not

a free-radical and, like other excited molecules, has a limited lifetime before it reverts to ground state. Within its 4 μ sec half-life, singlet oxygen can diffuse approximately 200 nm in solution. If an Acceptor bead is within that distance, chemical energy can be transferred from singlet oxygen to thioxene derivatives within the Acceptor bead which results in light production at 520–620 nm. Proximity-dependent chemical energy transfer is the basis for the homogeneous nature of AlphaScreen. In the disclosed experiments, competition was scored as a reduction in AlphaScreen signal. Briefly, control biotinylated IgG bound Streptavidin Donor beads bring His-tagged Fc γ R/FcRn bound Ni²⁺ Acceptor beads into proximity producing, upon illumination, a chemiluminescent signal. Unlabeled competitor test Abs were serially diluted and applied. Signal was reduced when a test Ab competed with control biotinylated IgG for binding to Fc γ R/FcRn.

Table 19. Roster of Competitor Abs Used in AlphaScreen

FcγR	Supplier	Cat. No.	Comments
Fc γ RI (CD64)	R&D Systems	1257-FC	Formulated w/o BSA
Fc γ RIIa (CD32a)	R&D Systems	1330-CD/CF	Formulated w/o BSA
Fc γ RIIb/c (CD32b/c)	R&D Systems	1875-CD	Formulated w/o BSA
Fc γ RIIIa (CD16a)	R&D Systems	4325-FC	Formulated w/o BSA
FcRn	Supplier	Cat. No.	Comments
FCGRT/B2M Heterodimer	Sino Biological	CT009-H08H	Formulated w/o BSA

Sample
B21M IgG1, CNT03930, ICAB7.005, 11.7 mg/mL
B21M IgG4PAA, I3CB15.I3CB15.001, 7.26 mg/mL
CD3B219 x B23B39 huIgG4 PAA null arm DuoBody, 11.4 mg/mL
Control DuoBody for ROR1,RR1B78xRSV B21M huIgG4_PAA_F405L, CBIS ID: RR1B120.001, DPR lot: 8661-B120, 3.99 mg/mL
RR1B67 ELM, anti-ROR1, huIgG4_PAA, DPR lot: 9057, CBIS ID: RR1B67.006, 6.13 mg/mL

RR1B67 X CD3B219, huIgG4_PAA Duobody, DPR lot: 9051, CBIS
ID: RCDB5.005, 6.9 mg/mL

[0316] Ranking in competition binding assays is often carried out on the basis of the EC50 values derived from dose-response curves. In AlphaScreen assays, however, competitor Abs do not always generate sigmoidal dose-response curves. Hence EC50 values cannot always be derived. Instead, degree of silence was established by comparing the % maximum signal at any given concentration across the entire cohort of Abs tested. Test Abs were assayed over two replicate experimental rounds carried out on different days. Only one (representative) set of results is shown.

[0317] On FcγRI, RCDB5 bound to the same extent as the hIgG4 PAA isotype controls (not shown). RCDB5 bound to FcγRIIIa (**FIG. 9**) and FcγRIIb (not shown) in a manner that is nearly identical to that of IgG4 PAA isotype control. On FcγRIIIa, RCDB5 was no more competitive than the hIgG4 PAA isotype Abs (**FIG. 10**). RCDB5 binds FcRn as efficiently as hIgG1 WT (see **FIG. 10A**; B21M IgG1 represents RSV IgG1 WT control). In summary, the ROR1 x CD3 bispecific antibody RCDB5 bound all Fc receptors tested to essentially the same extent as matched IgG4 PAA isotype.

Crystallization of the Kringle Domain of Human ROR1 and RR1B67

[0318] The human ROR1 Kringle Domain / RR1B67 Fab complex was prepared by a four-step procedure. First, the Fab and Kringle Domain were mixed together (1.2 molar excess of Fab) and incubated over the weekend at 4 °C while dialyzing into 20 mM Tris pH 8.0. Second, the complex was bound to a monoS 5/50 column (GE Healthcare) in 20 mM Tris pH 8.0 and eluted with a NaCl gradient using an ÄKTA purifier system (GE Healthcare). Due to poor separation, the peak fractions were pooled together, diluted 8 times in 20mM Hepes pH 7.5, and the complex was purified using the mono S 5/50 column in 20mM Hepes pH 7.5 and a NaCl gradient. Finally, the complex was concentrated to 7.8 mg/mL by ultrafiltration (Amicon Ultra-4 3kDa).

[0319] Crystallization trials for the free Fab and Kringle/Fab complex were carried out using the sitting drop vapor-diffusion method at 20 °C, Corning 3550 96-well plates (Hampton, cat no. HR8-146), and the crystallization screens IH1M, IH2M, JCSG+, CS, and. The screen solutions were dispensed into the plate wells with a Liquidator 96, model 200uL (Mettler Toledo) and the nanodrops were prepared with a Mosquito LCP robot (TTP Labtech) at room

temperature. The crystallization drops were monitored for at least 21 days using a Formulatrix imager that automatically recorded the drop image. Diffraction quality crystals of the ROR1 Kringle/RR1B67 Fab complex were grown from 18% PEG 3k, 0.2M (NH₄)₂SO₄, 0.1M acetate pH 4.5 with the complex initially at 7.8 mg/mL. Crystals of RR1B67 Fab were obtained from 2M (NH₄)₂SO₄, 5% MPD, 0.1M MES pH 6.5 with the Fab initially at 13 mg/mL. For data collection, the crystals were soaked for few seconds in a cryo-protectant solution containing the corresponding mother liquor supplemented with 20% glycerol and then, flash frozen in liquid nitrogen.

[0320] X-ray diffraction datasets were collected with a Pilatus 6M detector at beamline 22-ID of the Advanced Photon Source (APS) at Argonne National Laboratory. The X-ray diffraction datasets were processed with the program HKL2000. The structures were solved by molecular replacement with the program Phaser, human germline antibody 1-69/B3 (PDB code 3QOT) as search model for the free RR1B67 Fab, and human plasminogen kringle 3 domain (PDB code: 2LOS, NMR model 1) and free RR1B67 Fab as search models for the ROR1 kringle / RR1B67 Fab complex. The structures were refined with the program PHENIX. Model adjustments and structural overlays were carried out using the program COOT. Crystallographic calculations, contact distances for definition of epitope and paratope residues, and epitope area calculations were performed with the CCP4 suite of programs. All molecular graphics were generated with PyMol (*PyMOL Molecular Graphics System, Version 1.4.1, Schrödinger, LLC*) and the CDRs were determined using the Kabat definition.

[0321] Crystal structures for the Fab of RR1B67 bound to the isolated human ROR1 Kringle domain (with Fc removed by TEV digestion) was determined to 3.2 Å resolution. The structure of the antibody/antigen complex allowed the characterization of the interactions in atomic detail, increased the understanding of the antibody mechanism of action, and enhanced the knowledge about the ROR1 extracellular region. There is no available structure of any part of the ROR1 extracellular domain in public literature. The ROR1 structure includes residues 310-391, corresponding to the whole Kringle domain, and one N-linked glycan in Asn-315. The structure reveals all important interactions with the Fab. Some protein residues were present in the crystalline environment but are not ordered: six N-terminal and 15 C-terminal ROR1 residues, as well as 14 amino acid residues leftover from the Fc fusion. These disordered residues were not resolved in the structure and were excluded from the final model. The RR1B67 Fab structures included light chain residues 1-213 and heavy chain residues 1-220 (except for heavy chain residues 134-140, which are disordered and were not included). There

was one RR1B67/Kringle complex in the asymmetric unit with the Fab/antigen combining site well defined by the electron density map, which allowed reliable positioning of the binding residues. The Fab was numbered sequentially in all Figures and ROR1 numbering starts at the signal peptide.

[0322] The structure of the complex between RR1B67 Fab and the ROR1 Kringle domain demonstrated that the epitope is discontinuous and involves residues distributed throughout loop regions of the membrane-proximal Kringle domain (residues T324-T328, S330-Q333, P336, N338, S339, Y341, H359-Y361, L377, D378, and D387) (**FIG. 11** and **FIG. 12**). The Kringle surface area buried by the Fab was around 882 Å² and there were extensive contacts between the Kringle and Fab (**FIG. 11C-FIG. 11D**), which was consistent with the antibody/antigen subnanomolar affinity determined by SPR. The RR1B67 paratope was composed of residues in CDR-L1, -L3, -H2, and -H3 (**FIG. 12**). Gly331, Gln333, and His359 contact both the heavy and light chains of RR1B67, while all the other epitope residues contact either heavy or light chain. (**FIG. 11C-FIG. 11D**). The only residue that differ between human/cyno and mouse ROR1 Kringle is T396S. This residue is not in the antibody/antigen interface.

[0323] Those skilled in the art will appreciate that numerous changes and modifications can be made to the preferred embodiments of the disclosed isolated anti-ROR1 antibodies, ROR1 x CD3 bispecific antibodies, and methods of using the same, and that such changes and modifications can be made without departing from the spirit of the invention. It is, therefore, intended that the appended claims cover all such equivalent variations as fall within the true spirit and scope of the invention.

[0324] The disclosures of each patent, patent application, and publication cited or described in this document are hereby incorporated herein by reference, in its entirety.

Table 20. Anti-ROR1 Ab Sequences (CDRs defined by Kabat)

Anti-ROR1 mAb	Chain Peptide Id Isotype	Sequence
RR1B65	Heavy Chain	EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYWMSVVRQAPGKGLEWVSAISGSGGSTY
	RR1H31	YADSVKGRFTISRDN SKNTLYLQMNSLR AEDTAVYYCAKDLIGSWGMYFDYWGGQGLV
	hulG4_nG4m(a)_PAA	TVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
		QSSGLYSLSSVTVTPSSSLGTKTYTCNVVDHKPSNTKVDKRVESKYGPPCPAPAEEAAGGP
		SVFLFPPKPKD TLMISRTPEVTCVVVDV/SQEDPEVQFNWYVDGVEVHNAKTKPREEQFN
		TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTKSKAKGQPREPQVYITLPPSQEEM
		TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSRLLTVDKSRWQ
		EGNVFSCSVMEALHNHYTQKSLSLGLGK
		SEQ ID NO:1
	HC CDR1	NYWMS
		SEQ ID NO:2
	HC CDR2	AISGSGSTYYADSVKG
		SEQ ID NO:3
	HC CDR3	DLIGSWGMYFDY
		SEQ ID NO:4
	Light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARF
	PH9L3	SGSGSGTDFTLTISSELEPEDFAVYYCQQRSNWPLTFGGGTKVEIKRTV/AAPSVFIFPPSDEQ
		LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKA
		DYEKHKVYACEVTHQGLSPVTKSFNRGEC
		SEQ ID NO:5
	huKappa_Km3	RASQSVSSYLA
	LC CDR1	SEQ ID NO:6
	LC CDR2	DASNRAT
		SEQ ID NO:7
	LC CDR3	QQRSNWPLT
		SEQ ID NO:8
RR1B66	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGDTFTSDAIHWVRQAPGQGLEWMGRIPISGTANY

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	RR1H51 huIgG4_nG4m(a)_PAA	AQKFQGRV/TITADESTSTAYMELSSLRSEDTAVYYCARGRYSYYYFDYWGGQTLVTVS SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPCPAEAAGGPSVF LFPPKPKDITLMISRTPETCVVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSRLTVDKSRWQEGN VFSCSVMHREALHNHYTQKSLSLGLGK SEQ ID NO:9
	HC CDR1	TDAlH SEQ ID NO:10
	HC CDR2	RIIPISGTANYAQKFQG SEQ ID NO:11
	HC CDR3	GRYSYYFYFDY SEQ ID NO:12
	Light Chain PH9L3	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAITGIPARF SGSGSGTDFTLTSSLEPEDFAVYYCQQRSNWPLTFGGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTLKA DYEKHKVYACEVTHQGLSPVTKSFNRGEC SEQ ID NO:5
	huKappa_Km3 LC CDR1	RASQSVSSYLA SEQ ID NO:6
	LC CDR2	DASNRAT SEQ ID NO:7
	LC CDR3	QQRSNWPLT SEQ ID NO:8
	Heavy Chain RR1H52	QVQLVQSGAEVKKPGSSVKVSCKASGGTFTSTYAIHWVRQAPGQGLEWMGRIPIEGRAY YAQKFQGRV/TITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRYWFDYWGGQTLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
	RR1B67	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	hulG4_nG4m(a)_PAA	SSGLYSLSVVTVPSSSLGKTYTCNVVDHDKPSNTKVVDKRVESKYGPPPCPAPEAAGGPS VFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTKSKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLGLGK SEQ ID NO:13
	HC CDR1	TYAIH
		SEQ ID NO:14
	HC CDR2	RIPIEGRAYYAQKFQG
		SEQ ID NO:15
	HC CDR3	GRYSRYWFDY
		SEQ ID NO:16
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAITGIPARF SGSGSGTDFTLTISSELPEDFAVYYCQQRSNWPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVCLLNINFPYREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKA DYEKHKVYACEVTHQGLSPVTKSFNRGEC SEQ ID NO:5
	huKappa_Km3	RASQSVSSYLA
	LC CDR1	SEQ ID NO:6
	LC CDR2	DASNRAT
		SEQ ID NO:7
	LC CDR3	QQRSNWPLT
		SEQ ID NO:8
RR1B69	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGDTFSDAAIHVVIRQAPGQGLEWMGYIIPISGTAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRARIYRWAFDYWGQGTLLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVPSSSLGKTYTCNVVDHDKPSNTKVVDKRVESKYGPPPCPAPEAAGGPS VFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST
	RR1H65	
	hulG4_nG4m(a)_PAA	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
		YRVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLGLK SEQ ID NO:17
	HC CDR1	DAAIH SEQ ID NO:18
	HC CDR2	YIIPISGTANYAQKFQG SEQ ID NO:19
	HC CDR3	GRARYRWAFDY SEQ ID NO:20
	Light Chain PH9L3	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAITGIPARF SGSGGTDFLTLSLEPEDEFAVYYCQQRSNWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKA DYEKHKVYACEVTHQGLSPVTKSFNRGEC SEQ ID NO:5
	huKappa Km3 LC CDR1	RASQSVSSYLA SEQ ID NO:6
	LC CDR2	DASNRAT SEQ ID NO:7
	LC CDR3	QQRSNWPLT SEQ ID NO:8
	Heavy Chain RR1H68 hulG4_nG4m(a)_PAA	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGGIPIFGTANY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARDGYYSRYRGYFLYYGMDVWG QGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHT FPAVLQSSGLYSLSSVTVTPSSSLGTKITYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPE AAGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPR EEQFNSTYRVSVSLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLTP PSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTV
	RR1B70	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
		DKSRWQEGNVFSCSVMHEALHNHYTQKSLSLGK SEQ ID NO:21
	HC CDR1	SYAIS SEQ ID NO:22
	HC CDR2	GIPIFGTANYAQKFQG SEQ ID NO:23
	HC CDR3	DGYYSRYRGYFLYYGMDV SEQ ID NO:24
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSELEPEDEFAVYYCQQRSNWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPRQAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:5
	huKappa_Km3	RASQSVSSYLA SEQ ID NO:6
	LC CDR1	DASNRAT SEQ ID NO:7
	LC CDR2	QQRSNWPLT SEQ ID NO:8
	LC CDR3	EVQLLESGGGLVQPGGSLRLSCAASGFTTFSSYAMSWVRQAPGKGLEWVSAIRYDGGSTY YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKMFGGQLDYWGQGTLVTVSS ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVTVTPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPCCPPCPAPEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR VVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLGK SEQ ID NO:25
	Heavy Chain	
RR1B71	RR1H11 hulG4_nG4m(a)_PAA	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	HC CDR1	SYAMS SEQ ID NO:26
	HC CDR2	AIRYDGGSTYYADSVKG SEQ ID NO:27
	HC CDR3	MFGGQLDY SEQ ID NO:28
	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQSIDRHLN WYQQKPGKAPKLLIYKASSLQSGVPSR FSGSGGTDFLTITSSLPEDFATY CQQPHTFPLTFGQGTKVEIKRTVAAPS VFI FPPSDEQ LKSGTASV VCLLN FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:29
	huKappa Km3	RASQSIDRHLN SEQ ID NO:30
	LC CDR1	KASSLQS SEQ ID NO:31
	LC CDR2	QQPHTFPLT SEQ ID NO:32
	LC CDR3	EVQLLESGGGLVQPGGSLRLSCAASGFTFSN YWMSWVRQAPGKGLWVSGISYNGGSTY YADSVKGRFTISRDN SKNTLYLQMNSLR AEDTAVYYCAKPYFGFDYWGQGT LVTVSSAS TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLY SLSSVTVTPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPAPEAAGGPSVFLFP PKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGV E VHN A KTKPREEQFNSTYRVV SVLT V L H Q D W L N G K E Y K C K V S N K G L P S S I E K T I S K A K G Q P R E P Q V Y T L P P S Q E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S R L T V D K S R W Q E G N V F S C S V M H E A L H N H Y T Q K S L S L S L G K SEQ ID NO:33
	Heavy Chain	NYWMS SEQ ID NO:2
	RR1H14 huIgG4_nG4m(a)_PAA	
RR1B72	HC CDR1	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B74	HC CDR2	GISYNGGSTYYADSVKG SEQ ID NO:34
	HC CDR3	PYFGFDY SEQ ID NO:35
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVADFLAWYQQKPGQAPRLIYDASNRATGIPAR FSGSGSTDFLTLSISLEPEDFAVYYCQQGNRWPIFGGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:36
	huKappa_Km3	SEQ ID NO:36
	LC CDR1	RASQSVADFLA SEQ ID NO:37
	LC CDR2	DASNRAT SEQ ID NO:7
	LC CDR3	QQGNRWPIIT SEQ ID NO:38
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTSSYAISWVRQAPGQGLEWMGGIPIFGTANY AQKFQGRV/TITADESTSTAYMELSSLRSEDTAVYYCARTGNKLDYWGGGTLVTVSSAST KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYS LSSVVTVPSSSLGTQTYTCNVVDHMKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLFPP KPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYK'TTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLGLGK SEQ ID NO:39
	HC CDR1	SYAIS SEQ ID NO:22
	HC CDR2	GIPIFGTANYAQKFQG SEQ ID NO:23

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B76	HC CDR3	TGNKLDY SEQ ID NO:40
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVAKFLAWYQQKPGQAPRLLIYFASNRA TDIPARF SGSGSGTDFTLTISSELPEDFAVYYCQQRDHWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVCLLNINFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:41
	huKappa Km3 LC CDR1	RASQSVAKFLA SEQ ID NO:42
	LC CDR2	FASNRAT SEQ ID NO:43
	LC CDR3	QQRDHWPLT SEQ ID NO:44
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGFTSSYGISWVRQAPGQGLEWMGWISAIFGTAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGVASWYLDYWGGTLVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG LYSLSSVTVPSSSLGTKITYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSRLTVDKSRWQEGN VFSCSVMHREALHNHYTQKSLSLGLK SEQ ID NO:45
	HC CDR1	SYGIS SEQ ID NO:46
	HC CDR2	WISAIFGTANYAQKFQG SEQ ID NO:47
	HC CDR3	GVASWYLDY SEQ ID NO:48

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	Light Chain	DIQMTQSPSSLSASVGDRTTITCRASQSNKWLNWYQQKPGKAPKLLIYAASSLQSGVPSR FSGSGGTDFLTISSLQPEDFATYYCQQDYNFPYTFGGGTKVEIKRTVAAPSVFIFPPSDE QLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:49
	huKappa_Km3	
	LC CDR1	RASQSINKWLN SEQ ID NO:50
	LC CDR2	AASSLQS SEQ ID NO:51
	LC CDR3	QQDYNFPYT SEQ ID NO:52
	Heavy Chain	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIHYPGDS DTR YSPFQGGQVTTISADKSISTAYLQWSSLKASDTAMYCARVFAASRGYGIFFDYWGQGTLV TVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSVTVTPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPAPAEEAAGGP SVFLFPPKPKDITLMISRTPEVTCVVVDV/SQEDPEVQFNWYVDGVEVHNAKTKPREEQFN TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTKSKAKGQPREPQVYTLPPSQEEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSRLTVDKSRWQ EGNVFSCSVMEALHNHYTQKSLSLGLK SEQ ID NO:53
	HC CDR1	SYWIG SEQ ID NO:54
	HC CDR2	IIVPGDSDTRYSPSFQG SEQ ID NO:55
	HC CDR3	VFASRSGYGIPFDY SEQ ID NO:56
	Light Chain	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPKLLIYWASTR ESGVPDRFSGSGGTDFLTISLQAEDEVAVYYCQQYYSTPLTFGGGTKVEIKRTVAAPSV
RR1B77		

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B78	PH9L2	FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:57
	hu\LC\kappa\constant	
	LC CDR1	KSSQSVLYSSNNKNYLA SEQ ID NO:58
	LC CDR2	WASTRES SEQ ID NO:59
	LC CDR3	QQYYSTPLT SEQ ID NO:60
	Heavy Chain	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGIHYPGDS DTR YSPFQGGQVTISADKSISTAYLQWSSLKASDTAMYCARDVGRWAPGGFLDYWGQGTLV TVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL QSSGLYSLSSVTVTPSSSLGKTKTYTCNVVDHKPSNTKVDKRVESKYGPPCPPCAPEAAGGP SVFLFPPKPKDITLMISRTPETVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNS TYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAKGQPREPQVYITLPPSQEEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSRLTVDKSRWQ EGNVFSCSVMMHEALHNHYTQKSLSLGLK SEQ ID NO:61
	HC CDR1	SYWIG SEQ ID NO:54
	HC CDR2	IYPGDSDTRYSPSFQG SEQ ID NO:55
	HC CDR3	DVGRWAPGGFLDY SEQ ID NO:62
	Light Chain	DIVMTQSPDLSAVSLGERATINCKSSQSVLYSSNNKNYLA WYQQKPGQPPKLLIYWASTR ESGVPDFRFGSGSGTDFTLTISSLQAEDVAVYCCQQYYSTPLTFGQGTKVEIKRTVAAPSV FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTSL SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	PH9L2	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	hu\LC\kappa\constant	SEQ ID NO:57
	LC CDR1	KSSQSVLYSSNNKNYLA
		SEQ ID NO:58
	LC CDR2	WASTRES
		SEQ ID NO:59
	LC CDR3	QQYYSTPLT
		SEQ ID NO:60
RR1B82	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGFTFDSDAIHWVRQAPGQGLEWMGYIPIISGTAN
	RR1H62	YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRWTFDYWGQGLVTV
	hulgG4_nG4m(a)_PAA	SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
		SGLYSLSSVTVTPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPAPEAAGGPSV
		FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTY
		RVVSVLTVLIHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYVYTLPPSQEEMTK
		NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQEG
		NVFCSCVMHEALHNHYTQKSLSLGLK
		SEQ ID NO:63
	HC CDR1	SDAIH
		SEQ ID NO:64
	HC CDR2	YIIPISGTANYAQKFQG
		SEQ ID NO:19
	HC CDR3	GRYSYRWTFDY
		SEQ ID NO:65
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAATGIPARF
	PH9L3	SGSGSGTDFTLTISSELPEDFAVYYCQQRSNWPLTFGGQGTKVEIKRTVAAPSVFIFPPSDEQ
	huKappa_Km3	LKSGTASVCLLNFNFPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTLKA
		DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
		SEQ ID NO:5
	LC CDR1	RASQSVSSYLA

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B83		SEQ ID NO:6
	LC CDR2	DASNRAT
		SEQ ID NO:7
	LC CDR3	QQRSNWPLT
		SEQ ID NO:8
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFKSAIHWVVRQAPGQGLEWMGYISPPYGS
	RR1H66	YYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRIAYYYVFDYWGQGLVT
	hulG4_nG4m(a)_PAA	VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
		SSGLYSLSSVTVTPSSSLGTTKTYTCNVVDHDKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPS
		VFLFPPKPKDTLMISRTPEVTCVVVDV/SQEDPEVQFNWYVDGVEVHNATKTPREEQFNST
		YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT
		KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSRLTVDKSRWQE
		GNVFCSCVMHEALHNHYTQKSLSLGLK
		SEQ ID NO:66
	HC CDR1	SAYIH
		SEQ ID NO:67
	HC CDR2	YISPPYGSAYYAQKFQG
		SEQ ID NO:68
	HC CDR3	GRIAYYYVFDY
		SEQ ID NO:69
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRATGIPARF
	PH9L3	SGSGGTDFLTLSLEPEDEFAVYYCQQRSNWPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQ
		LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKA
	huKappa Km3	DYEKHKVYACEVTHQGLSPVTKSFNRGEC
		SEQ ID NO:5
	LC CDR1	RASQSVSSYLA
		SEQ ID NO:6
	LC CDR2	DASNRAT

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B84	LC CDR3	SEQ ID NO:7 QQRSNWPLT SEQ ID NO:8
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSKKASGFTSTDAIHWVRQAPGQGLEWMGYIPIISGNAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYAYNWGFDYWGGQGLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVPSSSLGKTYTCNVDPKPSNTKVDKRVESKYGPPCPAPEAAGGPS VFLFPPKPKDITLMISRTPETVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTITLVHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMEALHNHYTQKSLSLGLK SEQ ID NO:70
	HC CDR1	TDAIH SEQ ID NO:10
	HC CDR2	YIIPISGNANYAQKFQG SEQ ID NO:71
	HC CDR3	GRYAYNWGFDY SEQ ID NO:72
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRAATGIPARF SGSGSGTDFTLTSSLEPEDEFAVYYCQQRSNWPLTFGGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSTLTLSKA DYEKHKVYACEVTHQGLSPVTKSFNRGEC SEQ ID NO:5
	huKappa_Km3	
	LC CDR1	RASQSVSSYLA SEQ ID NO:6
	LC CDR2	DASNRAT SEQ ID NO:7
	LC CDR3	QQRSNWPLT

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B85		SEQ ID NO:8
	Heavy Chain	EVQLVQSGAEVKKPGESLKISKKSGYSFTSYWIGWVRQMPGKGLEWMGIIDPGDSDTR
	RR1H30	YSPFQGGVTTISADKSISTAYLQWSSLKASDTAMYCYCARGNDPWPDFDYWGQGTLLVTVS
	hulG4_nG4m(a)_PAA	SASTKGPSVFPLAPCSRSTSESTAALGLCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
		GLYSLSSVTVTPSSSLGKTYTCNVVDHDKPSNTKVDKRVESKYGPCCPPCPAPEAAGGPSVF
		LFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR
		VVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTYLPPSQEEMTKN
		QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSRLLTVDKSRWQEGN
		VFSCSVMEALHNHYTQKSLSLGLGK
		SEQ ID NO:73
	HC CDR1	SYWIG
		SEQ ID NO:54
	HC CDR2	IIDPGDSDTRYSPSFQG
		SEQ ID NO:74
	HC CDR3	GNDPWPDFDY
		SEQ ID NO:75
	Light Chain	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRF
	PH9L4	SGSGGTDFLTITSSLPQEDFATYCYQQSYSTPLTFGGQGTKVEIKRTVAAPSVFIFPPSDEQL
	huKappa Km3	KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKA
		DYEEKHKVYACEVTHQGLSSPVTKSFNRGEC
		SEQ ID NO:76
	LC CDR1	RASQSISSYLN
		SEQ ID NO:77
	LC CDR2	AASSLQS
		SEQ ID NO:51
	LC CDR3	QQSYSTPLT
RR1B86	Heavy Chain	SEQ ID NO:78 QVQLVQSGAEVKKPGSSVKVSCKASGDTFSSYAISWVRQAPGQGLEWMGGIIPFGTANY

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	RR1H13 huIgG4_nG4m(a)_PAA	AQKFQGRV/TITADESTSTAYMELSSLRSEDTAVYYCARGQDESGLDYWGQGTLLVTVSSA STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL YSLSSVTVTPSSSLGKTKYTCNVVDHKPSNTKVDKRVESKYGPPCPCPAPEAAGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNV FSCVMHEALHNHYTQKSLSLGLGK SEQ ID NO:79
	HC CDR1	SYAIS SEQ ID NO:22
	HC CDR2	GIPIFGTANYAQKFQG SEQ ID NO:23
	HC CDR3	GQDESGLDY SEQ ID NO:80
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSDWLAWYQQKPGQAPRLLIYDASNRAATGIPAR FSGSGSTDFLTISSELEPEDFAVYYCQQSGDWPYTFGQGTKVEIKRTVAAPSVFIFPPSDE QLKSGTASVCLLNNFYPREAKVQWVKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLISK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:81
	huKappa_Km3 LC CDR1	RASQSVSDWLA SEQ ID NO:82
	LC CDR2	DASNRAAT SEQ ID NO:7
	LC CDR3	QQSGDWPYT SEQ ID NO:83
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTSSYAIWVVRQAPGQGLEWMGGISAFIGNAN YAQKFQGRV/TITADESTSTAYMELSSLRSEDTAVYYCARLRLGNLDYWGQGTLLVTVSSA STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGL
	RR1H20	
RR1B88		

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	hulG4_nG4m(a)_PAA	YSLSSVVTVPSSSLGTKTYTCNVVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVGVHNAAKTKPREEQFNSTYRV VSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQ VSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSRLTVDKSRWQEGNV FSCSVMHREALHNHYTQKSLSLGLGK SEQ ID NO:84
	HC CDR1	SYAIS SEQ ID NO:22
	HC CDR2	GISAIFGNANYAQKFQG SEQ ID NO:85
	HC CDR3	LR LGNLDY SEQ ID NO:86
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVANFLAWYQQKPKGQAPRLLIYFASNRAATGIPARF SGSGSGTDFTLTISSELEPEDFAVYYCQQYYGAPITFGQGTKVEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSPVTKSFNRGEC SEQ ID NO:87
	huKappa_Km3	RASQSVANFLA SEQ ID NO:88
	LC CDR1	FASNRAT SEQ ID NO:43
	LC CDR2	QQYYGAPIT SEQ ID NO:89
	LC CDR3	

Table 21. Sequence of CD3B219

CD3 Chain	Sequence
Heavy Chain	EVQLVESGGGLVQPGGSLRLSCAASGFTFTNTYAMNWVRQAPGKGLEWVARIRSKYNNYATYYAASVKGRF TISRDDSKNSLYLQMNSLKTEDTAVYYCARHGNFGNSYVSWFAYWGQGTLVTVSSASTKGPSVFPLAPCSR STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGTKITYTCNVVDHKP SNTKVDKRVESKYGPPCPAPAAAGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVVDG VEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPP SQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFLLYSKLTVDKSRWQEGNVFS CSVMHEALHNHYTQKSLSLGLGK SEQ ID NO:90
HC CDR1	GFTFTNTYAMN SEQ ID NO:92
HC CDR2	RIRSKYNNYATY SEQ ID NO:93
HC CDR3	HGNFGNSYVSWFAY SEQ ID NO:94
Light Chain	QTVVTQEPSLTVSPGGTVTLTCRSSTGAVTTSNYANWVQKPGQAPRGLIGGTNKRAPGTPARFSGSLGKG AALTLSGVQPEDEAEYYCALWYSNLWVFGGGTKLTVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYP GAVTVAWKADSSPVKAGVETTTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS SEQ ID NO:91
LC CDR1	RSSTGAVTTSNYAN SEQ ID NO:95
LC CDR2	GTNKRAP SEQ ID NO:96
LC CDR3	ALWYSNLWV SEQ ID NO:97

Table 22. Sequences for affinity matured anti-ROR1 antibodies (CDRs defined by Kabat)

Anti-ROR1 mAb	Chain Peptide Id Isotype	Sequence
RR1B177	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFTSDAIHWVRQAPGQGLEWMGRIPIISGTANY AOKFQGRV/TITADESTSTAYMELSSLRSEDTAVYYCARGYSYYYYFDYWGGTGLVTVS SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYTCNVVDHKSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVF LFPPKPKDTLMISRTPETVTCVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR VVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYITLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSRLLTVDKSRWQEGN VFSCSVMHREALHNHYTQKSLSLGLGK SEQ ID NO:101
	HC CDR1	TDAIH SEQ ID NO:103
	HC CDR2	RIPISGTANYAQKFQG SEQ ID NO:104
	HC CDR3	GRYSYYYYFDY SEQ ID NO:105
	Light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLEWYQQKPGQAPRLLIYDASNRAIGIPARF SGSGGTDFLTITSSLEPEDFAVYYCQQRSNWPLTFGGGTKVEIKRTV/AAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:102
	huKappa Km3	RASQSVSSYLE SEQ ID NO:106
	LC CDR1	DASNRAT SEQ ID NO:107
	LC CDR2	QQRSNWPLT SEQ ID NO:108
	LC CDR3	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B178	Heavy Chain	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSDA AIHWVVRQAPGQG LEWMGYIIPISGTAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRARYRWAFDYWGQGTLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVTPSSSLGTKTYTCNVVDHKSNTKVDKRVESKYGPPCPAPEAAGGPS VFLFPPKPKD TLMISRTPETVCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLYSRLTVDKSRWQE GNVFSCSVMEALHNHYTQKSLSLGLK SEQ ID NO:109
	HC CDR1	DAAIH
		SEQ ID NO:111
	HC CDR2	YIIPISGTANYAQKFG
		SEQ ID NO:112
	HC CDR3	GRARYRWAFDY
		SEQ ID NO:113
	Light chain	EIVLTQSPATLSLSPGERATLSCRASQSVRNLYAWYQQKPGQAPRLLIYDASN RATGIPAR FSGSGGTDFLTITSSLEPEDFAVYYCQQRSNWPLTFGGGTKVEIKRTVAAPSVFIFPPSDE QLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	hulKappa_Km3	SEQ ID NO:110
	LC CDR1	RASQSVRNLYA
		SEQ ID NO:114
RR1B179	LC CDR2	DASN RAT
		SEQ ID NO:115
	LC CDR3	QQRSNWPLT
		SEQ ID NO:116
	Heavy Chain	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSDA AIHWVVRQAPGQG LEWMGYIIPISGTAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRARYRWAFDYWGQGTLVT

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	RR1H65 hulG4_nG4m(a)_PAA	VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVPSSSLGTKTYTCNVVDHKPSNTKVDKRVESKYGPPCPPAPEAAGGPS VFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTKSKAKGQPREPQVYTTLPSSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE GNVFCSVMHEALHNHYTQKSLSLGLGK SEQ ID NO:117
	HC CDR1	DAAIH SEQ ID NO:119
	HC CDR2	YIIPISGTANYAQKFQG SEQ ID NO:120
	HC CDR3	GRARYRWAFDY SEQ ID NO:121
	Light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSTYLAWYQQKPGQAPRLLIYDASNRATGIPARF SGSGSGTDFTLTISSELEPEFAVYYCQQRSNWPLTFGGQTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTLKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:118
	huKappa_Km3 LC CDR1	RASQSVSTYLA SEQ ID NO:122
	LC CDR2	DASNRAT SEQ ID NO:123
	LC CDR3	QQRSNWPLT SEQ ID NO:124
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSDAAIHWVVRQAPGQGLEWMGYIIPISGTAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRARYRWAFDYWGQGTLLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVPSSSLGTKTYTCNVVDHKPSNTKVDKRVESKYGPPCPPAPEAAGGPS
	RR1H65	
RR1B180		

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	hulG4_nG4m(a)_PAA	VFLFPPKPKDTLMISRTPEVTCVVVDV/SQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLGLK SEQ ID NO:125
	HC CDR1	DAAIH SEQ ID NO:127
	HC CDR2	YIIPISGTANYAQKFQG SEQ ID NO:128
	HC CDR3	GRARYRWAFDY SEQ ID NO:129
	Light chain	EIVLTQSPATLSLSPGERATLSCRASQSVRNLYAWYQQKPGQAPRLIEDASNRAITGIPAR FSGSGGTDFLTITISSELEDFAVYYCQQRSNWPLTFGGTKVEIKRTV/AAPSVFIFPPSDE QLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:126
	huKappa Km3	RASQSVRNLYA SEQ ID NO:130
	LC CDR1	DASNRAT SEQ ID NO:131
	LC CDR2	QQRSNWPLT SEQ ID NO:132
	LC CDR3	
	Heavy Chain	QVQLVQSGAEVKKPGSSVKV/SCKASGDTFTDAIHWVRQAPGQGLEWMGYIPIISGNAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYAYNWGFDYWGGTGLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVSVTVPSSSLGKTYTCNVVDHKPSNTKVDKRVESKYGPPCPAPEAAGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV/SQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT
	RR1H69	
	hulG4_nG4m(a)_PAA	
RR1B181		

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
		KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLGLK SEQ ID NO:133
	HC CDR1	TDAlH SEQ ID NO:135
	HC CDR2	YIIPISGNANYAQKFG SEQ ID NO:136
	HC CDR3	GRYAYNWGFDY SEQ ID NO:137
	Light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIKDASNRATGIPARF SGSGSGTDFTLTISSELEPEDEFAVYYCQQRSNWPLTFGGGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVCLLNNFYPRFAKVVQWVKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSPVTKSFNRGEC SEQ ID NO:134
	huKappa_Km3	RASQSVSSYLA SEQ ID NO:138
	LC CDR1	DASNRA SEQ ID NO:139
	LC CDR2	QQRSNWPLT SEQ ID NO:140
	LC CDR3	QQRSNWPLT SEQ ID NO:140
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFTSDAIHWVRQAPGQGLEWMGYIPIISGNAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYAYNWGFDYWGQGLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVSVTVPSSSLGKTYTCNVVDHKSNTKVDKRVESKYGPPCPPCPAPEAAGGPS VFLFPPKPKDITLMISRTPETVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLGLK
	RR1B69	
	hulG4_nG4m(a)_PAA	
RR1B182		

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	HC CDR1	SEQ ID NO:141 TDAIH
	HC CDR2	SEQ ID NO:143 YIIPISGNANYAQKFQG
	HC CDR3	SEQ ID NO:144 GRYAYNWGFDY
	Light chain	SEQ ID NO:145 EIVLTQSPATLSLSPGERATLSCRASQSVRNLYAWYQQKPGQAPRLIIKDAASNRATGIPAR FSGSGGTDFLTITISLSEPEDEFAVYYCQQRSNWPLTFGGGTKVEIKRTVAAPSVFIFPPSDE QLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	huKappa_Km3	SEQ ID NO:142 RASQSVRNLYLA
	LC CDR1	SEQ ID NO:146 DASNRAT
	LC CDR2	SEQ ID NO:147 QQRSNWPLT
	LC CDR3	SEQ ID NO:148 QVQLVQSGAEVKKPGSSVKVSCKASGGTFTSDAIHWVRQAPGQGLEWMGYIIPISGNAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYAYNWGFDYWGQGLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVSVTVPSSSLGKTKYTCNVVDHDKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPS VFLFPPKPKDITLMISRTPETVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLGLK
	Heavy Chain	SEQ ID NO:149 TDAIH
	RR1H69 huIgG4_nG4m(a)_PAA	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
		SEQ ID NO:151
	HC CDR2	YIIPISGNANYAQKFQG
		SEQ ID NO:152
	HC CDR3	GRYAYNWGFDY
		SEQ ID NO:153
	Light chain	EIVLTQSPATLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLIKDASDRATGIPARF
	RR1L65	SGSGGTDFLTLSLEPEDFAVYYCQQRSNWPLTFGGQGTKVEIKRTVAAPSVFIFPPSDEQ
		LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSKA
		DYEKHKVYACEVTHQGLSPVTKSFNRGEC
	huKappa Km3	SEQ ID NO:150
	LC CDR1	RASQSVRSYLA
		SEQ ID NO:154
	LC CDR2	DASDRAT
		SEQ ID NO:155
	LC CDR3	QQRSNWPLT
		SEQ ID NO:156
RR1B184	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFTSDAIHWVRQAPGQGLEWMGYIIPISGNAN
	RR1H69	YAAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYAYNWFQGYWGGTGLVT
		VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
	hulG4_nG4m(a)_PAA	SSGLYSLSVVTVPSSSLGKTYTCNVVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPS
		VFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST
		YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTKSKAKGQPREPQVYTLPPSQEEMT
		KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSRLTVDKSRWQE
		GNVFSCSVMHEALHNHYTQKSLSLGLK
		SEQ ID NO:157
	HC CDR1	TDAlH
		SEQ ID NO:159
	HC CDR2	YIIPISGNANYAQKFQG

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	HC CDR3	SEQ ID NO:160 GRYAYNWGFDY SEQ ID NO:161
	Light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIKDASTRATGIPARF SGSGSGTDFTLTISSELEPEDFAVYYCQQRSNWPLTFGGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:158
	huKappa_Km3	RASQSVSSYLA SEQ ID NO:162
	LC CDR1	DASTRAT SEQ ID NO:163
	LC CDR2	QQRSNWPLT SEQ ID NO:164
	LC CDR3	QVQLVQSGAEVKKPGSSVKVSCKASGGTFTSDAIHWVRQAPGQGLEWMGYIPIISGNAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYAYNWGFDYWGQGLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVPSSSLGKTKYTCNVVDHKPSNTKVDKRVESKYGPPCPAPAEAGGPS VFLFPPKPKDITLMISRTPETVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMEALHNHYTQKSLSLGLK SEQ ID NO:165
	Heavy Chain	TDAIH
	RR1H69	SEQ ID NO:167
	hulG4_nG4m(a)_PAA	YIIPISGNANYAQKFOG SEQ ID NO:168
	HC CDR1	GRYAYNWGFDY
RR1B185	HC CDR2	
	HC CDR3	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B186	Light chain	SEQ ID NO:169 EIVLTQSPATLSLSPGERATLSCRASQSVNTYLAWYQQKPGQAPRLLIKDASTRATGIPARF SGSGGTDFLTLSLEPEDFAVYYCQQRSNWPLTFGGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	huKappa Km3	SEQ ID NO:166
	LC CDR1	RASQSVNTYLA SEQ ID NO:170
	LC CDR2	DASTRAT SEQ ID NO:171
	LC CDR3	QQRSNWPLT SEQ ID NO:172
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGFTFTDAIHWVRQAPGQGLEWMGYIIPISGNAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYAYNWGFDYWGGTGLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPAPEAAGGPS VFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTKSKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMEALHNHYTQKSLSLGLK SEQ ID NO:173
	HC CDR1	TDAIH SEQ ID NO:175
	HC CDR2	YIIPISGNANYAQKFG SEQ ID NO:176
	HC CDR3	GRYAYNWGFDY SEQ ID NO:177
	Light chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIKDASTRATGIPARF

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B187	RR1L73	SGSGSGTDFTLTISSELEPEFAVYYCQQRSNWPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:174
	LC CDR1	RASQSVSSYLA SEQ ID NO:178
	LC CDR2	DASYRAT SEQ ID NO:179
	LC CDR3	QQRSNWPLT SEQ ID NO:180
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFKSAIYHWVRQAPGQGLEWMGYISPYGSA YYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRIAYYYVFDYWQGTLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVVTVPSSSLGTQTYTCNVVDHFKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV/SQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTTISKAKGQPREPQVYITLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLYSRLTVDKSRWQE GNVFSCSVMEALHNHYTQKSLSLGLK SEQ ID NO:181
	HC CDR1	SAYIH SEQ ID NO:183
	HC CDR2	YISPYGSAYYAQKFQG SEQ ID NO:184
	HC CDR3	GRIAYYYVFDY SEQ ID NO:185
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASYRATGIPARF SGSGSGTDFTLTISSELEPEFAVYYCQQRSNWPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKA
	RR1L102	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	huKappa_Km3	DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	LC CDR1	SEQ ID NO:182 RASQVSSYLA
	LC CDR2	SEQ ID NO:186 DASYRAT
	LC CDR3	SEQ ID NO:187 QQRSNWPLT
		SEQ ID NO:188
RR1B188	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAIHWVRQAPGQGLEWMGRIPIEGRAY
	RR1H52	YAKQFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRYWFDYWGQGTLLVT
	huIgG4_nG4m(a)_PAA	VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ
		SSGLYSLSVVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPAPAEAGGPS
		VFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST
		YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT
		KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE
		GNVFSCSVMHEALHNHYTQKSLSLGLK
		SEQ ID NO:189
	HC CDR1	TYAIH
		SEQ ID NO:191
	HC CDR2	RIPIEGRAYYAQKFQG
		SEQ ID NO:192
	HC CDR3	GRYSYRYWFDY
		SEQ ID NO:193
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASSRATGIPARF
	RR1L196	SGSGSGTDFTLTISSELPEDFAVYYCQQRSNWPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQ
	huKappa_Km3	LKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTLKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:190

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	LC CDR1	RASQSVSSYLA SEQ ID NO:194
	LC CDR2	DASSRAT SEQ ID NO:195
	LC CDR3	QQRSNWPLT SEQ ID NO:196
	Heavy Chain RR1H65 hulG4_nG4m(a)_PAA	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSDAIIHWVRQAPGQGLEWMGYIIPISGTAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRARYRWAFDYWGQGTLLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVTPSSSLGKTYTCNVVDHKSNTKVDKRVESKYGPPCPPCPAPEAAGGPS VFLFPPKPKDTLMISRTPEVTCVVVDV/SQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLGLGK SEQ ID NO:197
RR1B189	HC CDR1	DAAIH SEQ ID NO:199
	HC CDR2	YIIPISGTANYAQKFQG SEQ ID NO:200
	HC CDR3	GRARYRWAFDY SEQ ID NO:201
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVNNYLAWYQQKPGQAPRLLIYDASYRATGIPAR FSGSGGTDFLTLSISLEPEDFAVYYCQQRSNWPLTFGGGTKVEIKRTV/AAPSVFIFFPPSDE QLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLTK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:198
	huKappa Km3 LC CDR1	RASQSVNNYLA SEQ ID NO:202

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B190	LC CDR2	DASYRAT SEQ ID NO:203
	LC CDR3	QQRSNWPLT SEQ ID NO:204
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAIHWVRQAPGQGLEWMGRIPIEGRAY YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRYWFDYWGQGTLLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVTPSSSLGTKITYTCNVLDHDKPSNTKVDKRVESKYGPPCPPAPEAAGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTTISKAKGQPREPQVYITLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCVMHEALHNHYTQKSLSLGLK SEQ ID NO:205
	HC CDR1	TYAIH SEQ ID NO:207
	HC CDR2	RIPIEGRAYYAQKFQG SEQ ID NO:208
	HC CDR3	GRYSRYWFDY SEQ ID NO:209
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSTYLAWYQQKPGQAPRLLIHDASYRATGIPARF SGSGSGTDFTLTISSELEPEDEFAVYYCQQRRAHWPIITFGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVCLLNNFYPRFAKVVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKA DYEKHKVYACEVTHQGLSPVTKSFNRGEC SEQ ID NO:206
	huKappa_Km3 LC CDR1	RASQSVSTYLA SEQ ID NO:210
	LC CDR2	DASYRAT SEQ ID NO:211

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	LC CDR3	QQRHWPIT SEQ ID NO:212
RR1B191	Heavy Chain	QQLVQSGAEVKKPGSSVKV SCKASGGTFTDAIHWVRQAPGQGLEWMGRIPISGTANY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGYSYYFYFDYWGQGLVTVS SASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTTKTYTCNVVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR VVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLGLK SEQ ID NO:213
	HC CDR1	TDAIH
	HC CDR2	SEQ ID NO:215 RIIPISGTANYAQKFQG
	HC CDR3	SEQ ID NO:216 GRYSYYFYFDY SEQ ID NO:217
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSTYLAWYQQKPGQAPRLLIYDASNRAATGIPARF SGSGSGTDFTLTISSELEPEDEFAVYYCQQRRAHWPNPTFGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVCLLNINFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTL SKA DYEKHKVYACEVTHQGLSPVTKSFNRGEC SEQ ID NO:214
	huKappa_Km3 LC CDR1	RASQSVSTYLA SEQ ID NO:218
	LC CDR2	DASNRAT SEQ ID NO:219
	LC CDR3	QQRHWPNT SEQ ID NO:220

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B192	Heavy Chain	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSTY AIHWVRQAPGQGLEWMGRIPIEGRAY YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRYWFDYWGGQTLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVPSSSLGKTKYTCNVVDHKSNTKVDKRVESKYGPPCPAPEAAGGPS VFLFPPKPKDITLMISRTPETVCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLGLK SEQ ID NO:221
	HC CDR1	TYAIH
		SEQ ID NO:223
	HC CDR2	RIPIEGRAYYAQKFGQ
		SEQ ID NO:224
	HC CDR3	GRYSYRYWFDY
		SEQ ID NO:225
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSTYLAWYQQKPGQAPRLLIYDASNRTATGIPARF SGSGSGTDFTLTISSELEPEDEFAVYYCQQRASPLTFGGQGTKVEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWVKVDNALQSGNSQESVTEQDSKDSITYSLSTLTLSKA DYEKHKVYACEVTHQGLSPVTKSFNRGEC
	hukappa_Km3	SEQ ID NO:222
	LC CDR1	RASQSVSTYLA
		SEQ ID NO:226
	LC CDR2	DASNRTAT
		SEQ ID NO:227
	LC CDR3	QQRASPLT
		SEQ ID NO:228
RR1B193	Heavy Chain	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSTY AIHWVRQAPGQGLEWMGRIPIEGRAY YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRYWFDYWGGQTLVT

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	RR1H52 hulG4_nG4m(a)_PAA	VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVPSSSLGTKTYTCNVVDHKPSNTKVDKRVESKYGPPCPPAPEAAGGPS VFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTITLVLHQDWLNNGKEYKCKVSNKGLPSSIEKTKSKAKGQPREPQVYTTLPSSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE GNVFCSVMHEALHNHYTQKSLSLGLGK SEQ ID NO:229
	HC CDR1	TYAIH SEQ ID NO:231
	HC CDR2	RIPIEGRAYYAQKFQG SEQ ID NO:232
	HC CDR3	GRYSRYWFDY SEQ ID NO:233
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSNYLAWYQQKPGQAPRLIHDAASNRATGIPAR FSGSGSTDFLTITSSLEPEDFAVYYCQQRAHSPNTFGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCCLNNFYFPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTLKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:230
	huKappa_Km3 LC CDR1	RASQSVSNYLA SEQ ID NO:234
	LC CDR2	DASNRAT SEQ ID NO:235
	LC CDR3	QQRHSPNT SEQ ID NO:236
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAIHWVRQAPGQGLEWMGRIPIEGRAY YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRYWFDYWGGQTLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVPSSSLGTKTYTCNVVDHKPSNTKVDKRVESKYGPPCPPAPEAAGGPS
	RR1H52	
RR1B194		

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	hulG4_nG4m(a)_PAA	VFLFPPKPKDITLMISRTPEVTCVVVDV/SQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVQLHQLDNLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGGSFFLYSRLTVDKSRWQE GNVFSCSVMHREALHNHYTQKSLSLGLK SEQ ID NO:237
	HC CDR1	TYAIH SEQ ID NO:239
	HC CDR2	RIPIEGRAYYAQKFG SEQ ID NO:240
	HC CDR3	GRYSRYWFDY SEQ ID NO:241
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLIEDASDRATGIPARF SGSGGTDFLTITSSLEPEDFAVYYCQQRSHWPLTFGGTKVEIKRTV/AAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:238
	huKappa Km3	RASQSVSSYLA SEQ ID NO:242
	LC CDR1	DASDRAT SEQ ID NO:243
	LC CDR2	QQRSHWPLT SEQ ID NO:244
	LC CDR3	
	Heavy Chain	QVQLVQSGAEVKKPGSSVKV/SCKASGFTSTDAIHWVRQAPGQGLEWMGRIIPISGTANY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGYSYYFYFDYWGGTLVTVS SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVTPSSSLGTTKTYTCNVDPHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVF LFPPKPKDITLMISRTPEVTCVVVDV/SQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR VVSVLTQLHQLDNLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKN
	RR1H51	
	hulG4_nG4m(a)_PAA	
RR1B196		

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
		QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLGLGK SEQ ID NO:245
	HC CDR1	TDAIH SEQ ID NO:247
	HC CDR2	RIIPISGTANYAQKFQG SEQ ID NO:248
	HC CDR3	GRYSYYFYFDY SEQ ID NO:249
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSNYLAWYQQKPGQAPRLLIYDASNRAATGIPAR FSGSGSGTDFTLTISSELEPEDFAVYYCQQRSHWPNTFGQGTKVEIKRTVAAPSVFIFPPSDE QLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:246
	huKappa_Km3	RASQSVSNYLA SEQ ID NO:250
	LC CDR1	DASNRAAT SEQ ID NO:251
	LC CDR2	QQRSHWPNT SEQ ID NO:252
	LC CDR3	QVQLVQSGAEVKKPGSSVKVSKCASGGTFTSDAIHWVRQAPGQGLEWMGRIPIISGTANY AQKFQGRV/TITADESTSTAYMELSSLRSEDTAVYYCARGYSYYFYFDYWGQGLVTVS SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVVTVPSSSLGTQTYTCNVDPHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVF LFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVVEVHNAKTKPREEQFNSTYR VVSVLTVLHQDWLNGKEYCKVKSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLGLGK
	Heavy Chain	
	RR1H51	
	hulG4_nG4m(a)_PAA	
RR1B197		

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	HC CDR1	SEQ ID NO:253 TDAIH
	HC CDR2	SEQ ID NO:255 RIIPISGTANYAQKFQG
	HC CDR3	SEQ ID NO:256 GRYSYYFYFDY
	Light Chain	SEQ ID NO:257 EIVLTQSPATLSLSPGERATLSCRASQSVNNYLAWYQQKPGQAPRLLIYDASNRAATGIPAR FSGSGGTDFLTITISLEPEDFAVYYCQQRSHWPNTFGQGTKVEIKRTVAAPSVFIFPPSDE QLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	huKappa_Km3	SEQ ID NO:254 RASQSVNNYLA
	LC CDR1	SEQ ID NO:258 DASNRAT
	LC CDR2	SEQ ID NO:259 QQRSHWPNT
	LC CDR3	SEQ ID NO:260 QVQLVQSGAEVKKPGSSVKVSCKASGGTFSTYAIHWVRQAPGQGLEWMGRIPIEGRAY YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRYWFDYWGGGTLV VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVPSSSLGKTKYTCNVVDHDKPSNTKVDKRVESKYGPPCPAPAEAGGPS VFLFPPKPKDITLMISRTPETVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMEALHNHYTQKSLSLGLK
	Heavy Chain	SEQ ID NO:261 TYAIH
	RR1H52 huIgG4_nG4m(a)_PAA	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
		SEQ ID NO:263
	HC CDR2	RIPIEGRAYYAQKFQG
		SEQ ID NO:264
	HC CDR3	GRYSRYWFDY
		SEQ ID NO:265
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASYRATGIPARF
	RR1L216	SGSGGTDFLTITSSLEPEDFAVYQCQRSHSPLTFGQGTKVEIKRTVAAPSVFIFPPSDEQL
	huKappa Km3	KSGTASVVCLLNIFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSSTLTLSKA
	LC CDR1	DYEKHKVYACEVTHQGLSPVTKSFNRGEC
		SEQ ID NO:262
	LC CDR2	RASQSVSSYLA
		SEQ ID NO:266
RR1B199	LC CDR3	DASYRAT
		SEQ ID NO:267
	Heavy Chain	QQRSHSPLT
		SEQ ID NO:268
	RR1H62	QVQLVQSGAEVKKPGSSVKVSCKASGGTFTDSDAIHWVRQAPGQGLEWMGYIIPISGTAN
	hulG4_nG4m(a)_PAA	YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRWTFDYWGQGTLLVTV
		SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS
		SGLYSLSVVTVPSSSLGTTKTYTCNVVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSV
		FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY
		RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTK
		NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFFLYSRLTVDKSRWQEG
		NVDFSCVMHEALHNHYTQKSLSLGLGK
		SEQ ID NO:269
	HC CDR1	SDAIH
		SEQ ID NO:271
	HC CDR2	YIIPISGTANYAQKFQG

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B200	HC CDR3	SEQ ID NO:272 GRYSYRWTFDY SEQ ID NO:273
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVRNLYAWYQQKPGQAPRLIEDASNRATGIPAR FSGSGGTDFLTITSSLEPEDFAVYYCQQRSHSPITFGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:270
	huKappa_Km3	RASQSVRNLYA SEQ ID NO:274
	LC CDR1	DASNRAT SEQ ID NO:275
	LC CDR2	QQRSHSPIT SEQ ID NO:276
	LC CDR3	QVQLVQSGAEVKKPGSSVKVSCKASGGTFKSAYIHVVVRQAPGQGLEWMGYISPYYGSA YYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRIAYYYVFDYWGGTTLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSSVTVTPSSSLGTTKTYTCNVVDHKPSNTKVDKRVESKYGPPCPAPAEAGGPS VFLFPPKPKDITLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLGLK SEQ ID NO:277
	Heavy Chain	SAYIH
	RR1H66	SEQ ID NO:279
	hulG4_nG4m(a)_PAA	YISPYYGSAYYAQKFQG SEQ ID NO:280
	HC CDR1	GRIAYYYVFDY
	HC CDR2	
	HC CDR3	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B201	Light Chain	SEQ ID NO:281 EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRRATGIPARF SGSGGTDFLTLSLEPEDEFAVYYCQQRSNWPITFGQGTKVEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTSKA DYEKHKVYACEVTHQGLSPVTKSFNRGEC
	huKappa Km3	SEQ ID NO:278
	LC CDR1	RASQSVSSYLA SEQ ID NO:282
	LC CDR2	DASNRRAT SEQ ID NO:283
	LC CDR3	QQRSNWPIT SEQ ID NO:284
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGCTFDSDAIHWVRQAPGQGLLEWMGYIPIISGTAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRWTFDYWGQGTLLVTV SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS SGLYSLSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPAPEAAGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSDPEDEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLIHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLGLK SEQ ID NO:285
	HC CDR1	SDAIH SEQ ID NO:287
	HC CDR2	YIIPISGTANYAQKFQG SEQ ID NO:288
	HC CDR3	GRYSYRWTFDY SEQ ID NO:289
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASNRRATGIPAR

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B202	RR1L143	FSGSGSGTDFTLTISSELEPEDEFAVYYCQQRSNWPITFGQGTKVEIKRTVAAPSVFIFPPSDEQ
	huKappa_Km3	LKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTL SKA
	LC CDR1	DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:286
	LC CDR1	RASQSVSNYLA SEQ ID NO:290
	LC CDR2	DASNRAI SEQ ID NO:291
	LC CDR3	QQRSNWPIT SEQ ID NO:292
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSKKASGGTFTSDAIHWVRQAPGQGLEWMGRIPIISGTANY
	RR1H51	AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGYSYYFYFDYWGQGLVTVS
	huIgG4_nG4m(a)_PAA	SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
		GLYSLSSVTVTPSSSLGKTYTCNVVDHKSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVF
		LFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVGVHNAKTKPREEQFNSTYR
		VVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVYITLPPSQEEMTKN
		QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFFLYSRLTVDKSRWQEGN
		VFSCSVMHAEALHNHYTQKSLSLGLGK SEQ ID NO:293
	HC CDR1	TDAIH SEQ ID NO:295
	HC CDR2	RIIPISGTANYAQKFQG SEQ ID NO:296
	HC CDR3	GRYSYYFYFDY SEQ ID NO:297
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVRSYLAWYQQKPGQAPRLIYDASNRAITGIPARF
	RR1L225	SGSGSGTDFTLTISSELEPEDEFAVYYCQQRSNWPITFGQGTKVEIKRTVAAPSVFIFPPSDEQL
		KSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTL SKA

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	huKappa_Km3	DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	LC CDR1	SEQ ID NO:294 RASQSVRSYLA
	LC CDR2	SEQ ID NO:298 DASNRAT
	LC CDR3	SEQ ID NO:299 QQRSNWPIT
		SEQ ID NO:300
RR1B203	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFKSAIYHWVRQAPGQGLEWMGYISPYYSYGA YYAQQFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRIAYYYVFDYWGGQTLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVSVTVPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPAPAEAAGGPS VFLFPPKPKDITLMISRTPETVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMHEALHNHYTQKSLSLGLK
		SEQ ID NO:301
	HC CDR1	SAYIH
		SEQ ID NO:303
	HC CDR2	YISPYYSAYYAQKFQG
		SEQ ID NO:304
	HC CDR3	GRIAYYYVFDY
		SEQ ID NO:305
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVRNLYAWYQQKPGQAPRLLIYDASNRATGIPAR FSGSGSTDFLTITSSLEPEDFAVYYCQQRSNWPITFGQGTKVEIKRTVAAPSVFIFPPSDEQ LKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	RR1L117	
	huKappa_Km3	SEQ ID NO:302

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	LC CDR1	RASQSVRNLYA SEQ ID NO:306
	LC CDR2	DASNRAI SEQ ID NO:307
	LC CDR3	QQRSNWPIT SEQ ID NO:308
	Heavy Chain RR1H69 hulG4_nG4m(a)_PAA	QVQLVQSGAEVKKPGSSVKVSCKASGGTFTSDAIHWVRQAPGQGLEWMGYIIPISGNAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYAYNWGFDYWGQGLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVTVTPSSSLGKTYTCNVVDHKSNTKVDKRVESKYGPPCPPCPAPEAAGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVFQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLYSRLTVDKSRWQE GNVFCSCVMHEALHNHYTQKSLSLGLGK SEQ ID NO:309
RR1B204	HC CDR1	TDIAIH SEQ ID NO:311
	HC CDR2	YIIPISGNANYAQKFQG SEQ ID NO:312
	HC CDR3	GRYAYNWGFDY SEQ ID NO:313
	Light Chain RR1L95	EIVLTQSPATLSLSPGERATLSCRASQSVSTYLAWYQQKPGQAPRLLIKDASNRATGIPARF SGSGGTDFTLTISSELPEDFAVYYCQQRSNWPIITFGQGTKVEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:310
	huKappa Km3 LC CDR1	RASQSVSTYLA SEQ ID NO:314

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B205	LC CDR2	DASNRAT SEQ ID NO:315
	LC CDR3	QQRSNWPIT SEQ ID NO:316
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSKASGGTFKSAIHWVVRQAPGQGLEWMGYISPYYGSA YYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRIAYYYVFDYWGGGTLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVPSSSLGTTKTYTCNVVDHGPSNTKVDKRVESKYGPPCPAPAEAGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCVMHEALHNHYTQKSLSLGLK SEQ ID NO:317
	HC CDR1	SAYIH SEQ ID NO:319
	HC CDR2	YISPYYGSAYYAQKFQG SEQ ID NO:320
	HC CDR3	GRIAYYYVFDY SEQ ID NO:321
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIKDASDRATGIPARF SGSGSGTDFTLTISSELEPEDEFAVYYCQQRSNWPITFGQGTKVEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTLKA DYEKHKVYACEVTHQGLSPVTKSFNRGEC SEQ ID NO:318
	huKappa_Km3 LC CDR1	RASQSVSSYLA SEQ ID NO:322
	LC CDR2	DASDRAT SEQ ID NO:323

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	LC CDR3	QQRSNWPIT SEQ ID NO:324
RR1B206	Heavy Chain	QQLVQSGAEVKKPGSSVKV SCKASGFTSTY AIHWV RQAPGQGLEWMGRIP IEGRAY Y A Q K F Q G R V T I T A D E S T S T A Y M E L S S L R S E D T A V Y Y C A R G R Y S Y R Y W F D Y W G Q G T L V T V S S A S T K G P S V F L A P C S R S T S E S T A A L G C L V K D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V T V P S S S L G T K T Y T C N V D H K P S N T K V D K R V E S K Y G P P C P A P E A A G G P S V F L F P P K P K D T L M I S R T P E V T C V V D V S Q E D P E V Q F N W Y V D G V E V H N A K T K P R E E Q F N S T Y R V V S V L T V L H Q D W L N G K E Y K C K V S N K G L P S S I E K T I S K A K G Q P R E P Q V Y T L P P S Q E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S R L T V D K S R W Q E G N V F S C S V M H E A L H N H Y T Q K S L S L G K SEQ ID NO:325
	HC CDR1	TYAIH SEQ ID NO:327
	HC CDR2	RIPIEGRAYYAQKFQG SEQ ID NO:328
	HC CDR3	GRYSRYWFDY SEQ ID NO:329
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSNYLA WYQQKPGQAPRLIYDASNRA TGIPAR FSGSGGTDFLTITISSELEPEDFAVY YCQQRSNWPNTFTGQGTKVEIKRTVAAPS VFIFPPSDE QLKSGTASVCLLN NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS TYSLSSTLTLSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:326
	huKappa_Km3 LC CDR1	RASQSVSNYLA SEQ ID NO:330
	LC CDR2	DASNRAT SEQ ID NO:331
	LC CDR3	QQRSNWPNT SEQ ID NO:332

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
RR1B207	Heavy Chain	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSTY AIHWVRQAPGQGLEWMGRIPIEGRAY YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRYWFDYWGQGTLLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVSVTVPSSSLGKTKYTCNVVDHKSNTKVDKRVESKYGPPCPAPEAAGGPS VFLFPPKPKDMLISRTPETCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGGSFFLYSRLTVDKSRWQE GNVFSCSVMEALHNHYTQKSLSLGLK SEQ ID NO:333
	HC CDR1	TYAIH
		SEQ ID NO:335
	HC CDR2	RIPIEGRAYYAQKFGQ
		SEQ ID NO:336
	HC CDR3	GRYSYRYWFDY
		SEQ ID NO:337
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSNYLA WYQQKPGQAPRLIHDA SNRATGIPAR FSGSGSGTDFTLTISSELPEDFAVYYCQQRSNWPNTFGQGTKVEIKRTVAAPSVFIFPPSDE QLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTSK ADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	hukappa_Km3	SEQ ID NO:334
	LC CDR1	RASQSVSNYLA
		SEQ ID NO:338
	LC CDR2	DASNRAT
		SEQ ID NO:339
	LC CDR3	QQRSNWPNT
		SEQ ID NO:340
RR1B208	Heavy Chain	QVQLVQSGAEVKKPGSSVKV SCKASGGTFSTDAIHWVRQAPGQGLEWMGRIPISGTANY AQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRYWFDYWGQGTLLVTVS

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	RR1H51 hulG4_nG4m(a)_PAA	SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS GLYSLSSVTVTPSSSLGTTKTYTCNVVDHGPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSVF LFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR VVSFLTIVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFFLYSRLTVDKSRWQEGN VFSCSVMHEALHNHYTQKSLSLGLGK SEQ ID NO:341
	HC CDR1	TDAIH SEQ ID NO:343
	HC CDR2	RIIPISGTANYAQKFQG SEQ ID NO:344
	HC CDR3	GRYSYYFYFDY SEQ ID NO:345
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSTYLAWYQQKPGQAPRLIYDASNRTATGIPARF SGSGSGTDFTLTISSELEPEDEFAVYYCQQRSNWPIITFGQGTKEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:342
	huKappa_Km3 LC CDR1	RASQSVSTYLA SEQ ID NO:346
	LC CDR2	DASNRTAT SEQ ID NO:347
	LC CDR3	QQRSNWPIIT SEQ ID NO:348
	Heavy Chain	QVQLVQSGAEVKKPKGSSVKVSCKASGGTFTSDAIHWVVRQAPGQGLEWMGYIIPISGTAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRWTFDYWGQGTLLVTV SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS SGLYSLSSVTVTPSSSLGTTKTYTCNVVDHGPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSV
	RR1H62	
RR1B209		

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	hulG4_nG4m(a)_PAA	FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSRLTVDDKSRWQEG NVFSCSVMEALHNHYTQKSLSLGLGK SEQ ID NO:349
	HC CDR1	SDAIH SEQ ID NO:351
	HC CDR2	YIIPISGTANYAQKFQG SEQ ID NO:352
	HC CDR3	GRYSYRWTFDY SEQ ID NO:353
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSTYLAWYQQKPGQAPRLLIYDASNATGIPARF SGSGGTDFLTITSSLEPEDFAVYYCQQRNSPITFGQGTKVEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSITLTSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC SEQ ID NO:350
	huKappa Km3	RASQSVSTYLA SEQ ID NO:354
	LC CDR1	DASNRAT SEQ ID NO:355
	LC CDR2	QQRNSPIT SEQ ID NO:356
	LC CDR3	
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGCTFDSDAIHWVVRQAPGQGLEWMGYIPIISGTAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRWTFDYWGQGTLLVTV SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSVSVTVPSSSLGTTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTK
	RR1H62	
	hulG4_nG4m(a)_PAA	
RR1B210		

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
		NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLGLK SEQ ID NO:357
	HC CDR1	SDAIH SEQ ID NO:359
	HC CDR2	YIIPISGTANYAQKFQG SEQ ID NO:360
	HC CDR3	GRYSYRWTFDY SEQ ID NO:361
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVSTYLAWYQQKPGQAPRLIEDASYRATGIPARF SGSGGTDFLTISSELEPEFAVYYCQQRNSPITFGQGTKVEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKA DYEKHKVYACEVTHQGLSPVTKSFNRGEC SEQ ID NO:358
	huKappa_Km3	RASQSVSTYLA SEQ ID NO:362
	LC CDR1	DASYRAT SEQ ID NO:363
	LC CDR2	QQRNSNPIT SEQ ID NO:364
	LC CDR3	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSDAIIHWVVRQAPGQGLEWMGYIIPISGTAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRARYRWAFDYWGQGLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ SSGLYSLSVVTVPPSSSLGKTYTCNVVDHKSNTKVDKRVESKYGPPCPPCPAPEAAGGPS VFLFPPKPKDITLMISRTPEVTCVVVDV/SQEDPEVQFNWYVDGVEVHNAKTKPREEQFNST YRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQE GNVFSCSVMEALHNHYTQKSLSLGLK
	Heavy Chain	
	RR1H65	
	hulG4_nG4m(a)_PAA	
RR1B211		

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
	HC CDR1	SEQ ID NO:365 DAAIH
	HC CDR2	SEQ ID NO:367 YIIPISGTANYAQKFQG
	HC CDR3	SEQ ID NO:368 GRARYRWAFDY
	Light Chain	SEQ ID NO:369 EIVLTQSPATLSLSPGERATLSCRASQSVSNYLAWYQQKPGQAPRLIEDASNRATGIPARF SGSGSGTDFTLTISLSEPEDEFAVYYCQQRSNYPPLTFGQGTKEIKRTVAAPSVFIFPPSDEQL KSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYLSSTLTLSKA DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
	huKappa_Km3	SEQ ID NO:366 RASQSVSNYLA
	LC CDR1	SEQ ID NO:370 DASNRAT
	LC CDR2	SEQ ID NO:371 QQRSNYPPLT
	LC CDR3	SEQ ID NO:372 QVQLVQSGAEVKKPGSSVKVSCKASGGTFTSDAIHWVVRQAPGQGLEWMGYIPIISGTAN YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGYSYRWTFDYWGQGTLLVTV SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS SGLYSLSSVTVTPSSSLGTTKTYTCNVVDHDKPSNTKVDKRVESKYGPPCPPCPAPEAAGGPSV FLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY RVVSVLTVLIHQDWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYITLPPSQEEMTK NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEG NVFSCSVMEALHNHYTQKSLSLGK
	Heavy Chain	SEQ ID NO:373 SDAIH
	RR1H62 huIgG4_nG4m(a)_PAA	

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
		SEQ ID NO:375
	HC CDR2	YIIPISGTANYAQKFQG
		SEQ ID NO:376
	HC CDR3	GRYSYRWTFDY
		SEQ ID NO:377
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVRNLYAWYQQKPGQAPRLLIYDASSRATGIPARF
	RR1L174	SGSGSGTDFLTISSELEPEDEFAVYYCQQRSNYPITFGGQGTKVEIKRTVAAPSVFIFPPSDEQL
	huKappa Km3	KSGTASVVCLLNIFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYSLSSSTLTLSKA
	LC CDR1	DYEKHKVYACEVTHQGLSPVTKSFNRGEC
		SEQ ID NO:374
		RASQSVRNLYA
		SEQ ID NO:378
RR1B213	LC CDR2	DASSRAT
		SEQ ID NO:379
	LC CDR3	QQRSNYPIT
		SEQ ID NO:380
	Heavy Chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFTDSDAIHWVVRQAPGQGLEWMGYIIPISGTAN
	RR1H62	YAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCARGRYSYRWTFDYWGQGTLLVTV
	hulG4_nG4m(a)_PAA	SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS
		SGLYSLSVVTVPSSSLGTKTYTCNVVDHKPSNTKVDKRVESKYGPPCPPCPAPEAAGGSPV
		FLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTY
		RVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYVTLPPSQEEMTK
		NQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFFLYSRLTVDKSRWQEG
		NVDFSCVMHEALHNHYTQKSLSLGLGK
		SEQ ID NO:381
	HC CDR1	SDAIH
		SEQ ID NO:383
	HC CDR2	YIIPISGTANYAQKFQG

Anti-RORI mAb	Chain Peptide Id Isotype	Sequence
		SEQ ID NO:384
	HC CDR3	GRYSYRWTFDY
		SEQ ID NO:385
	Light Chain	EIVLTQSPATLSLSPGERATLSCRASQSVRN ^Y LAWYQQKPGQAPRLLIYDASN ^R ATGIPAR
	RR1L117	FSGSGGTDFLTITSSLEPEDFAVYYCQQRSNWPITFGGQGTKVEIKRTVAAPSVFIFPPSDEQ
	huKappa_Km3	LKSGTASVVCLLNNFYPR ^E AKVQWKVDNALQSGNSQESVTEQDSKDS ^T YSLSS ^T LTLSKA
		DYEKHKVYACEVTHQGLSSPVTKSFNRGEC
		SEQ ID NO:382
	LC CDR1	RASQSVRN ^Y LA
		SEQ ID NO:386
	LC CDR2	DASN ^R AT
		SEQ ID NO:387
	LC CDR3	QQRSNWPIT
		SEQ ID NO:388

What is claimed:

1. An isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1, the antibody or antigen-binding fragment thereof comprising:
 - a. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:3, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:4, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - b. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:11, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:12, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - c. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:15, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:16, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - d. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:18, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:20, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - e. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:24, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;

- f. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:26, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:27, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:28, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:30, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:31, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:32;
- g. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:34, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:35, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:37, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:38;
- h. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:40, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:42, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:44;
- i. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:46, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:47, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:48, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:50, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:52;
- j. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:56, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60;
- k. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:62, a light

- chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60;
- l. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:64, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:65, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - m. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:67, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:68, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:69, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - n. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:71, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:72, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - o. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:74, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:75, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:77, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:78;
 - p. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:80, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:82, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:83; or

- q. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:85, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:86, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:88, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:89; wherein the CDRs are defined according to Kabat.

2. The isolated antibody, or antigen-binding fragment thereof, of claim 1 wherein the antibody, or antigen-binding fragment thereof, comprises a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:15, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:16, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8, wherein the CDRs are defined according to Kabat.

3. The isolated antibody, or antigen-binding fragment thereof, of claim 1 wherein the antibody, or antigen-binding fragment thereof, comprises a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:62, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60, wherein the CDRs are defined according to Kabat.

- 4. The isolated antibody, or antigen-binding fragment thereof, of claim 1 wherein:
 - a. the antibody, or antigen-binding fragment thereof, of (a) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:1 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - b. the antibody, or antigen-binding fragment thereof, of (b) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid

- sequence of SEQ ID NO:9 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- c. the antibody, or antigen-binding fragment thereof, of (c) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:13 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - d. the antibody, or antigen-binding fragment thereof, of (d) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:17 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - e. the antibody, or antigen-binding fragment thereof, of (e) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:21 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - f. the antibody, or antigen-binding fragment thereof, of (f) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:25 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:29;
 - g. the antibody, or antigen-binding fragment thereof, of (g) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:33 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:36;
 - h. the antibody, or antigen-binding fragment thereof, of (h) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:39 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:41;
 - i. the antibody, or antigen-binding fragment thereof, of (i) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:45 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:49;
 - j. the antibody, or antigen-binding fragment thereof, of (j) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid

- sequence of SEQ ID NO:53 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:57;
- k. the antibody, or antigen-binding fragment thereof, of (k) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:61 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:57;
 - l. the antibody, or antigen-binding fragment thereof, of (l) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:63 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - m. the antibody, or antigen-binding fragment thereof, of (m) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:66 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - n. the antibody, or antigen-binding fragment thereof, of (n) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:70 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - o. the antibody, or antigen-binding fragment thereof, of (o) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:73 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:76;
 - p. the antibody, or antigen-binding fragment thereof, of (p) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:79 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:81; or
 - q. the antibody, or antigen-binding fragment thereof, of (q) has a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:84 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:87.

5. The isolated antibody or antigen-binding portion thereof of claim 4, wherein the heavy chain has the amino acid sequence of SEQ ID NO:13 and a light chain has the amino acid sequence of SEQ ID NO:5.

6. The isolated antibody or antigen-binding portion thereof of claim 4, wherein the heavy chain has the amino acid sequence of SEQ ID NO:61 and a light chain has the amino acid sequence of SEQ ID NO:57.

7. An isolated antibody, or antigen-binding fragment thereof, that immunospecifically binds to ROR1, the antibody or antigen-binding fragment thereof comprising:

- a. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:1 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- b. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:9 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- c. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:13 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- d. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:17 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- e. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:21 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- f. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:25 and a light chain comprising an amino

- acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:29;
- g. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:33 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:36;
 - h. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:39 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:41;
 - i. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:45 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:49;
 - j. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:53 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:57;
 - k. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:61 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:57;
 - l. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:63 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - m. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:66 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - n. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:70 and a light chain comprising an amino

acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;

- o. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:73 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:76;
- p. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:79 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:81; or
- q. a heavy chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:84 and a light chain comprising an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:87.

8. An isolated antibody, or antigen-binding fragment thereof, that binds to an epitope on ROR1 comprising T324, V325, S326, V327, T328, S330, G331, R332, Q333, P336, N338, S339, Y341, H359, S360, Y361, L377, D378, and D387.

9. The isolated antibody, or antigen-binding fragment thereof, of any one of claims 1-8 wherein the antibody or antigen-binding fragment is a human antibody or antigen-binding fragment.

10. The isolated antibody, or antigen-binding fragment thereof, of any one of claims 1-9 wherein the antibody or antigen-binding fragment is recombinant.

11. The isolated antibody, or antigen-binding fragment thereof, of any one of claims 1-10 wherein the antigen-binding fragment is a Fab fragment, a Fab2 fragment, or a single chain antibody.

12. A nucleic acid molecule encoding the isolated antibody, or antigen-binding fragment thereof, of any one of claims 1-11.

13. A vector comprising the nucleic acid molecule of claim 12.

14. A cell expressing the isolated antibody, or antigen-binding fragment thereof, of any one of claims 1-11.

15. An isolated antibody, or antigen-binding fragment thereof, that competes for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, the reference antibody or antigen-binding fragment thereof comprising:

- a. a heavy chain comprising the amino acid sequence of SEQ ID NO:1 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- b. a heavy chain comprising the amino acid sequence of SEQ ID NO:9 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- c. a heavy chain comprising the amino acid sequence of SEQ ID NO:13 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- d. a heavy chain comprising the amino acid sequence of SEQ ID NO:17 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- e. a heavy chain comprising the amino acid sequence of SEQ ID NO:21 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- f. a heavy chain comprising the amino acid sequence of SEQ ID NO:25 and a light chain comprising the amino acid sequence of SEQ ID NO:29;
- g. a heavy chain comprising the amino acid sequence of SEQ ID NO:33 and a light chain comprising the amino acid sequence of SEQ ID NO:36;
- h. a heavy chain comprising the amino acid sequence of SEQ ID NO:39 and a light chain comprising the amino acid sequence of SEQ ID NO:41;
- i. a heavy chain comprising the amino acid sequence of SEQ ID NO:45 and a light chain comprising the amino acid sequence of SEQ ID NO:49;
- j. a heavy chain comprising the amino acid sequence of SEQ ID NO:53 and a light chain comprising the amino acid sequence of SEQ ID NO:57;
- k. a heavy chain comprising the amino acid sequence of SEQ ID NO:61 and a light chain comprising the amino acid sequence of SEQ ID NO:57;
- l. a heavy chain comprising the amino acid sequence of SEQ ID NO:63 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- m. a heavy chain comprising the amino acid sequence of SEQ ID NO:66 and a light chain comprising the amino acid sequence of SEQ ID NO:5;

- n. a heavy chain comprising the amino acid sequence of SEQ ID NO:70 and a light chain comprising the amino acid sequence of SEQ ID NO:5;
- o. a heavy chain comprising the amino acid sequence of SEQ ID NO:73 and a light chain comprising the amino acid sequence of SEQ ID NO:76;
- p. a heavy chain comprising the amino acid sequence of SEQ ID NO:79 and a light chain comprising the amino acid sequence of SEQ ID NO:81; or
- q. a heavy chain comprising the amino acid sequence of SEQ ID NO:84 and a light chain comprising the amino acid sequence of SEQ ID NO:87.

16. An isolated antibody, or antigen-binding fragment thereof, that competes for binding to ROR1 with a reference antibody or antigen-binding fragment thereof, wherein the reference antibody or antigen-binding fragment binds to an epitope on ROR1 comprising T324, V325, S326, V327, T328, S330, G331, R332, Q333, P336, N338, S339, Y341, H359, S360, Y361, L377, D378, and D387.

17. The isolated antibody or antigen-binding fragment thereof of claim 16, wherein the reference antibody comprises a heavy chain comprising the amino acid sequence of SEQ ID NO:13 and a light chain comprising the amino acid sequence of SEQ ID NO:5.

18. An isolated ROR1 x CD3 bispecific antibody, or a bispecific antigen-binding fragment thereof, comprising:

- a) a first antigen-binding site that immunospecifically binds ROR1, the first antigen-binding site comprising a heavy chain CDR1, CDR2, and CDR3 and a light chain CDR1, CDR2, and CDR3; and
- b) a second antigen-binding site that immunospecifically binds CD3, the second antigen-binding site comprising a heavy chain CDR1, CDR2, and CDR3 and a light chain CDR1, CDR2, and CDR3.

19. The isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of claim 18, wherein the first antigen-binding site that immunospecifically binds ROR1 has:

- a. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:3, a heavy

- chain CDR3 comprising the amino acid sequence of SEQ ID NO:4, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- b. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:11, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:12, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - c. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:15, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:16, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - d. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:18, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:20, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - e. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:24, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
 - f. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:26, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:27, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:28, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:30, a light chain

- CDR2 comprising the amino acid sequence of SEQ ID NO:31, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:32;
- g. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:34, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:35, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:37, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:38;
- h. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:40, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:42, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:44;
- i. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:46, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:47, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:48, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:50, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:52;
- j. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:56, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60;
- k. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:62, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60;

- l. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:64, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:65, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- m. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:67, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:68, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:69, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- n. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:71, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:72, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- o. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:74, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:75, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:77, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:78;
- p. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:80, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:82, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:83; or
- q. a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:85, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:86, a light

chain CDR1 comprising the amino acid sequence of SEQ ID NO:88, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:89; wherein the CDRs are defined according to Kabat.

20. The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of any one of claims 18-19, wherein the second antigen-binding site that immunospecifically binds CD3 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

21. The isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of claim 20, wherein:

- a. the first antigen-binding site that immunospecifically binds ROR1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:15, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:16, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8; and
- b. the second antigen-binding site that immunospecifically binds CD3 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

22. The isolated ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of claim 20, wherein:

- a. the first antigen-binding site that immunospecifically binds ROR1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:62, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60; and
- b. the second antigen-binding site that immunospecifically binds CD3 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:94, a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

23. An isolated ROR1 x CD3 bispecific antibody, or a bispecific antigen-binding fragment thereof, comprising:

- a) a first heavy chain (HC1);
- b) a second heavy chain (HC2);
- c) a first light chain (LC1); and
- d) a second light chain (LC2),

wherein the HC1 and the LC1 form a first antigen-binding site that immunospecifically binds ROR1, and the HC2 and the LC2 form a second antigen-binding site that immunospecifically binds CD3.

24. The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of claim 23, wherein

- a. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:3, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:4, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- b. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:11, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:12, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- c. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:15, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:16, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- d. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:18, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:20, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- e. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:24, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of

- SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- f. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:26, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:27, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:28, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:30, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:31, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:32;
 - g. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:2, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:34, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:35, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:37, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:38;
 - h. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:40, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:42, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:44;
 - i. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:46, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:47, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:48, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:50, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:52;
 - j. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID

- NO:56, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60;
- k. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:62, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60;
- l. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:64, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:19, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:65, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- m. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:67, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:68, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:69, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;
- n. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:10, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:71, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:72, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8;

- o. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:74, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:75, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:77, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:51, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:78;
 - p. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:23, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:80, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:82, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:83; or
 - q. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:22, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:85, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:86, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:88, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:43, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:89;
- wherein the CDRs are defined according to Kabat.

25. The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of claim 24, wherein

- a. the HC1 of (a) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:1 and the LC1 of (a) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- b. the HC1 of (b) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:9 and the LC1 of (b) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;

- c. the HC1 of (c) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:13 and the LC1 of (c) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- d. the HC1 of (d) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:17 and the LC1 of (d) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- e. the HC1 of (e) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:21 and the LC1 of (e) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- f. the HC1 of (f) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:25 and the LC1 of (f) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:29;
- g. the HC1 of (g) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:33 and the LC1 of (g) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:36;
- h. the HC1 of (h) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:39 and the LC1 of (h) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:41;
- i. the HC1 of (i) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:45 and the LC1 of (i) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:49;
- j. the HC1 of (j) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:53 and the LC1 of (j) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:57;

- k. the HC1 of (k) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:61 and the LC1 of (k) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:57;
- l. the HC1 of (l) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:63 and the LC1 of (l) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- m. the HC1 of (m) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:66 and the LC1 of (m) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- n. the HC1 of (n) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:70 and the LC1 of (n) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- o. the HC1 of (o) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:73 and the LC1 of (o) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:76;
- p. the HC1 of (p) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:79 and the LC1 of (p) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:81; or
- q. the HC1 of (q) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:84 and the LC1 of (q) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:87.

26. The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of claim 23, wherein

- a. the HC1 of (a) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:1 and the LC1 of (a) comprises an amino

- acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
- b. the HC1 of (b) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:9 and the LC1 of (b) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - c. the HC1 of (c) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:13 and the LC1 of (c) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - d. the HC1 of (d) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:17 and the LC1 of (d) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - e. the HC1 of (e) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:21 and the LC1 of (e) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - f. the HC1 of (f) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:25 and the LC1 of (f) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:29;
 - g. the HC1 of (g) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:33 and the LC1 of (g) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:36;
 - h. the HC1 of (h) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:39 and the LC1 of (h) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:41;
 - i. the HC1 of (i) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:45 and the LC1 of (i) comprises an

- amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:49;
- j. the HC1 of (j) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:53 and the LC1 of (j) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:57;
 - k. the HC1 of (k) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:61 and the LC1 of (k) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:57;
 - l. the HC1 of (l) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:63 and the LC1 of (l) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - m. the HC1 of (m) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:66 and the LC1 of (m) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - n. the HC1 of (n) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:70 and the LC1 of (n) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:5;
 - o. the HC1 of (o) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:73 and the LC1 of (o) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:76;
 - p. the HC1 of (p) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:79 and the LC1 of (p) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:81; or
 - q. the HC1 of (q) comprises an amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:84 and the LC1 of (q) comprises an

amino acid sequence that is at least 90% identical to the amino acid sequence of SEQ ID NO:87.

27. The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of any one of claims 23-26, wherein the HC2 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:97, wherein the CDRs are defined according to Kabat.

28. The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of any one of claims 23-27, wherein the HC2 comprises an amino acid sequence that is at least 90% identical to SEQ ID NO:90 and the LC2 comprises an amino acid sequence that is at least 90% identical to SEQ ID NO:91.

29. The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of any one of claims 23-27, wherein:

- a. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:14, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:15, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:16, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:6, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:7, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:8; and
- b. the HC2 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:97,

wherein the CDRs are defined according to Kabat.

30. The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of any one of claims 23-27, wherein:

- a. the HC1 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:54, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:55, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:62, and the LC1 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:58, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:59, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:60; and
- b. the HC2 has a heavy chain CDR1 comprising the amino acid sequence of SEQ ID NO:92, a heavy chain CDR2 comprising the amino acid sequence of SEQ ID NO:93, a heavy chain CDR3 comprising the amino acid sequence of SEQ ID NO:94, and the LC2 has a light chain CDR1 comprising the amino acid sequence of SEQ ID NO:95, a light chain CDR2 comprising the amino acid sequence of SEQ ID NO:96, and a light chain CDR3 comprising the amino acid sequence of SEQ ID NO:97,

wherein the CDRs are defined according to Kabat.

31. The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of any one of claims 23-28, wherein:

- a. the HC1 has the amino acid sequence of SEQ ID NO:13 and the LC1 has the amino acid sequence of SEQ ID NO:5; and
- b. the HC2 has the amino acid sequence of SEQ ID NO:90 and the LC2 has the amino acid sequence of SEQ ID NO:91.

32. The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of any one of claims 23-28, wherein:

- a. the HC1 has the amino acid sequence of SEQ ID NO:61 and the LC1 has the amino acid sequence of SEQ ID NO:57; and
- b. the HC2 has the amino acid sequence of SEQ ID NO:90 and the LC2 has the amino acid sequence of SEQ ID NO:91.

33. The ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of any one of claims 18-32, wherein the bispecific antigen-binding fragment is a single chain.

34. An isolated cell expressing the ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of any one of claims 18-33.

35. A method of treating a subject having cancer, the method comprising:
administering to the subject a therapeutically effective amount of the ROR1 x CD3 bispecific antibody, or bispecific antigen-binding fragment thereof, of any one of claims 18-33.

36. The method of claim 35, wherein the cancer is lung cancer or a hematological cancer.

37. Use of an effective amount of a ROR1 x CD3 bispecific antibody or bispecific antigen-binding fragment thereof of any one of claims 18-33 in the treatment of cancer.

38. Use of a ROR1 x CD3 bispecific antibody or bispecific antigen-binding fragment thereof of any one of claims 18-33 in the manufacture of a composition for the treatment of cancer.

39. The use of claims 37 or 38, wherein the cancer is lung cancer, hematological cancer, breast cancer, prostate cancer, pancreatic cancer, colon cancer, ovarian cancer, renal cancer, uterine cancer, or melanoma.

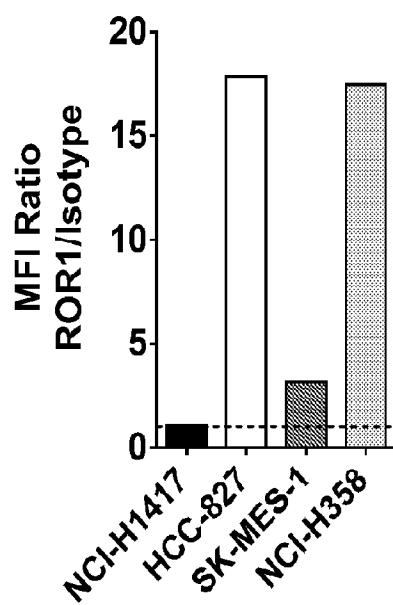


FIG. 1

FIG. 2A

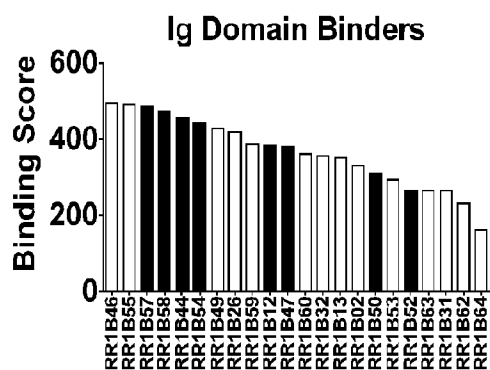


FIG. 2B

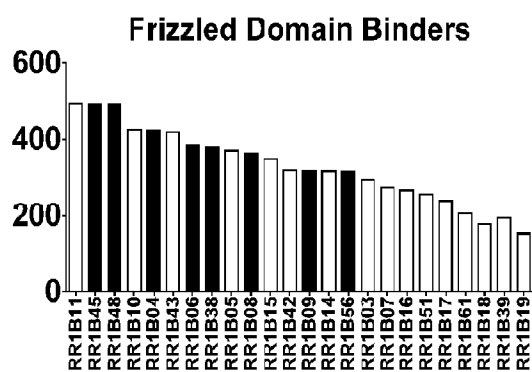
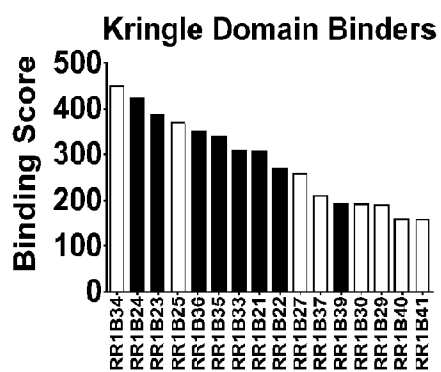


FIG. 2C



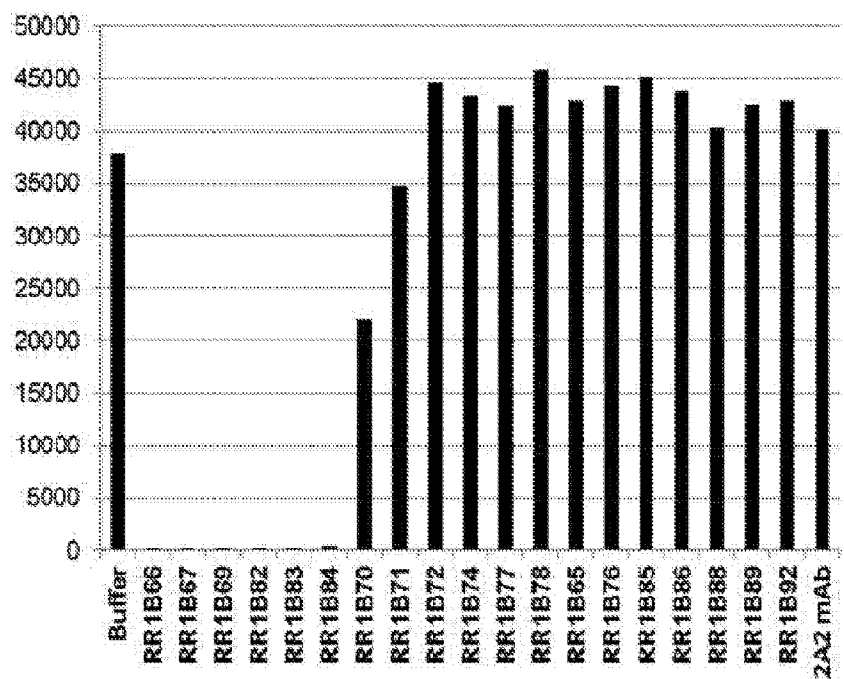


FIG. 3

FIG. 4A

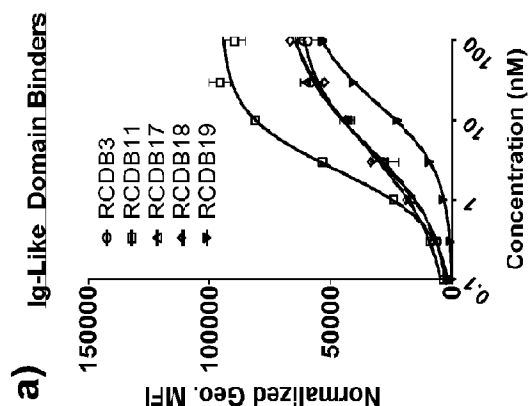


FIG. 4B

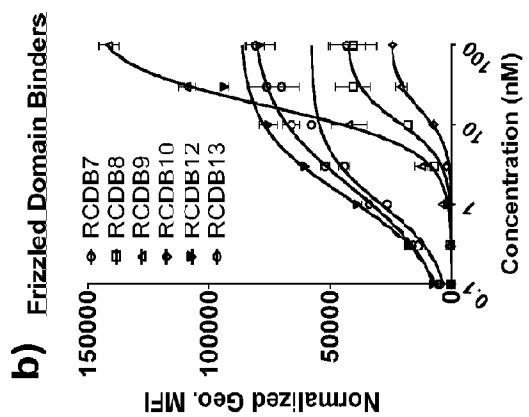


FIG. 4C

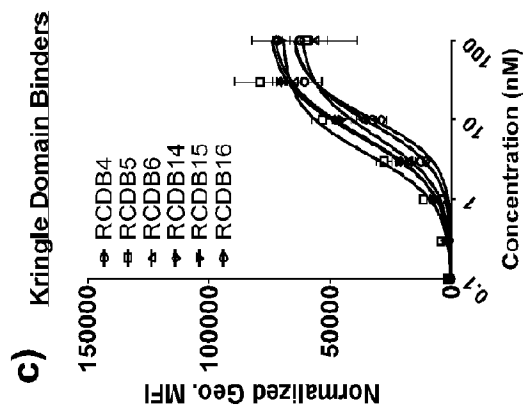


FIG. 5A

FIG. 5B

FIG. 5C

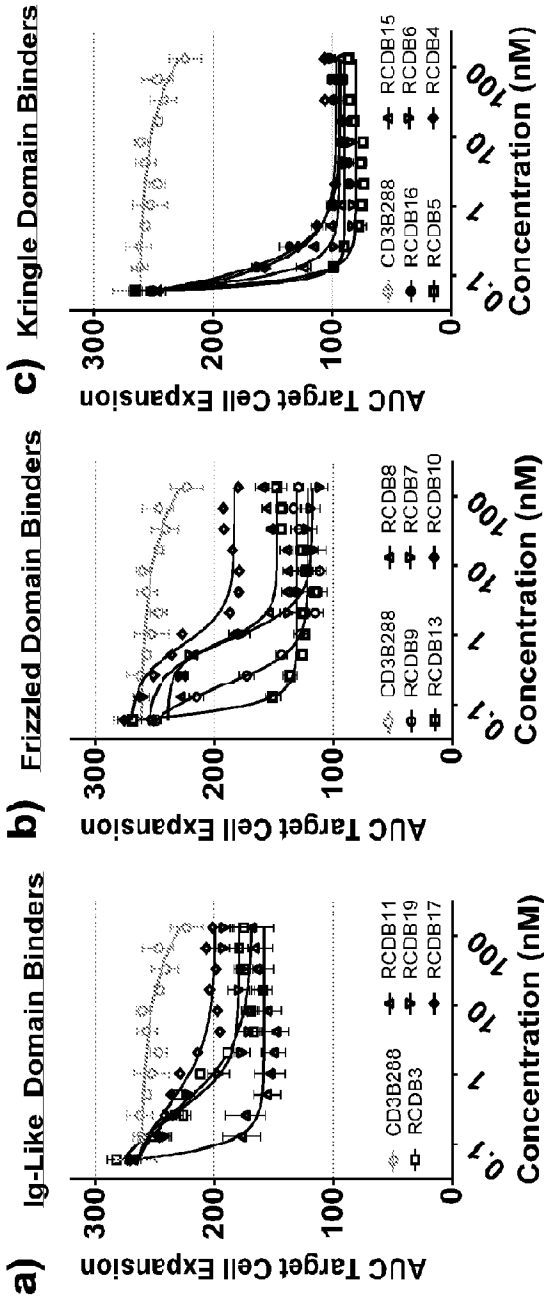
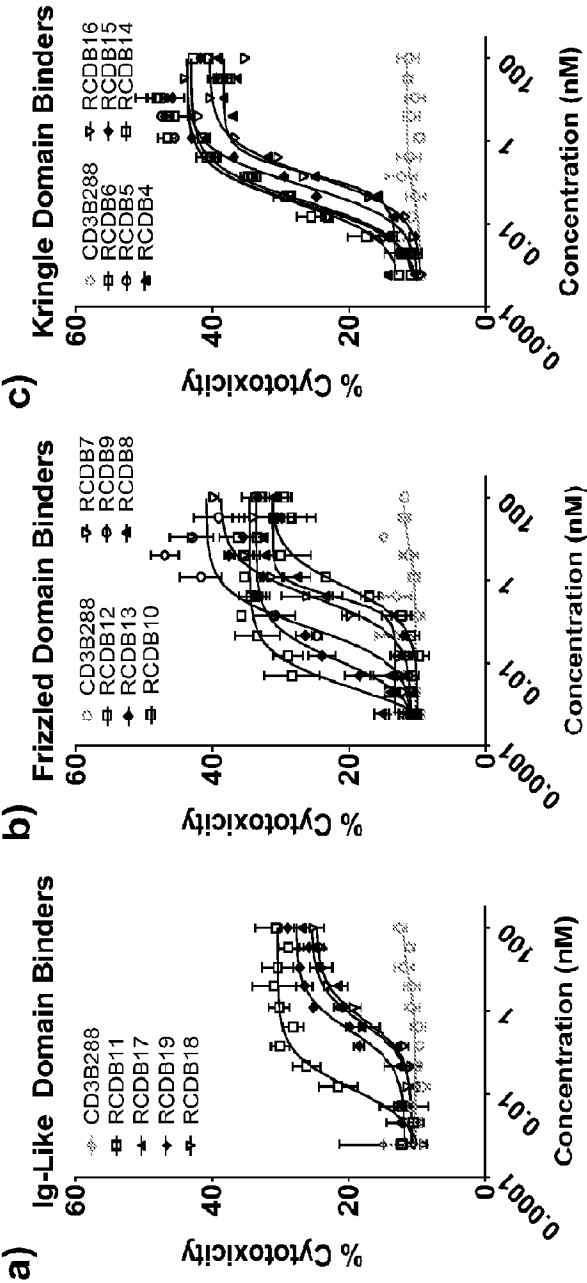


FIG. 6A

FIG. 6B

FIG. 6C



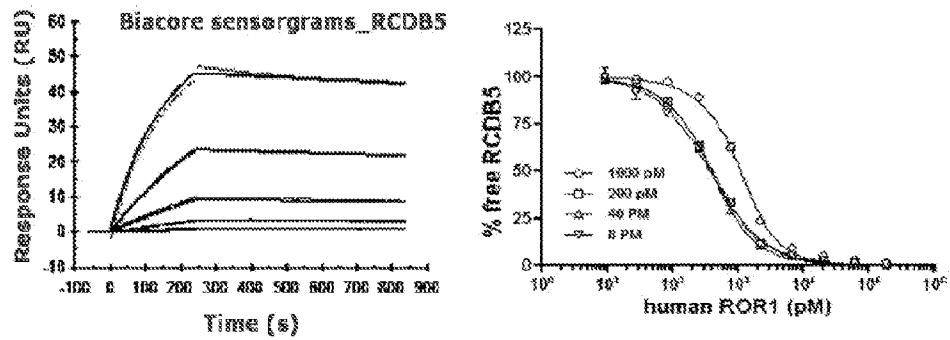


FIG. 7A

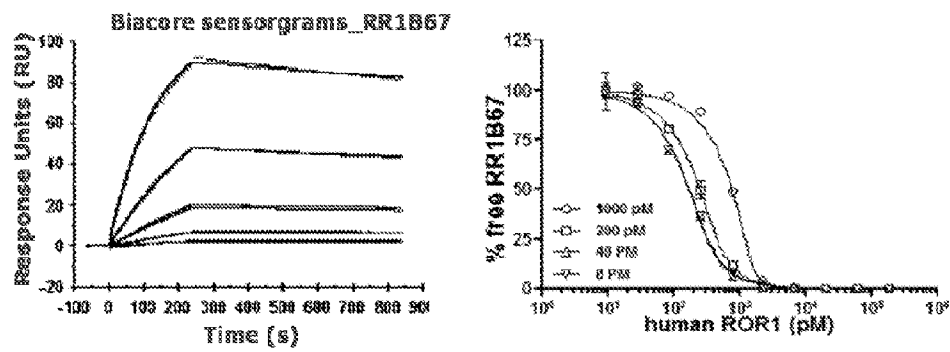


FIG. 7B

SUBSTITUTE SHEET (RULE 26)

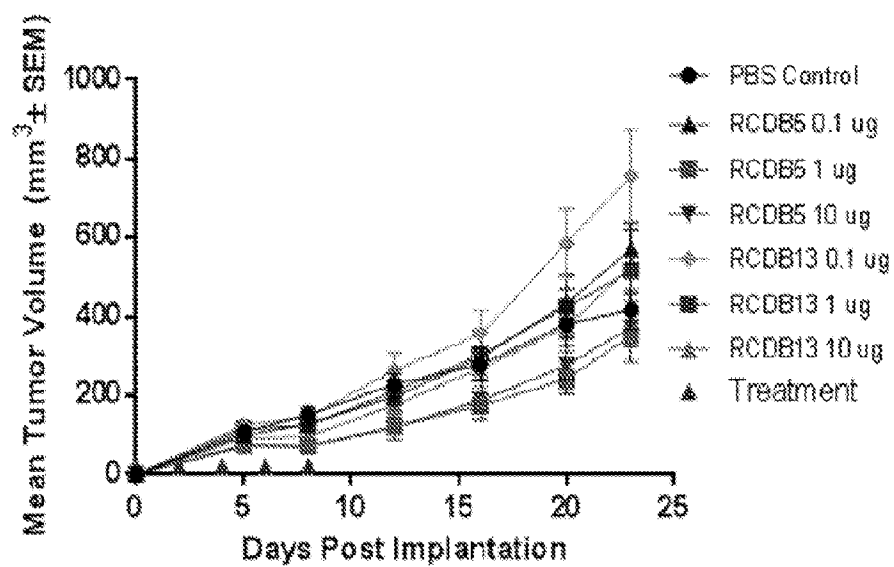


FIG. 8

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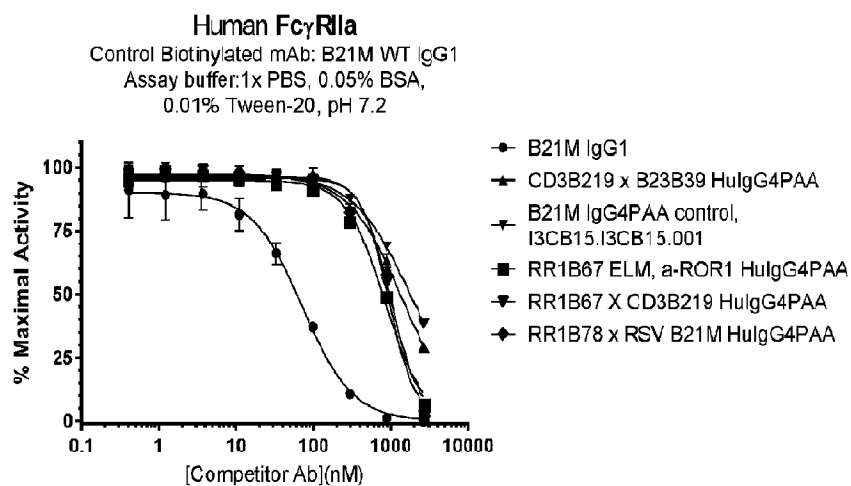


FIG. 9A

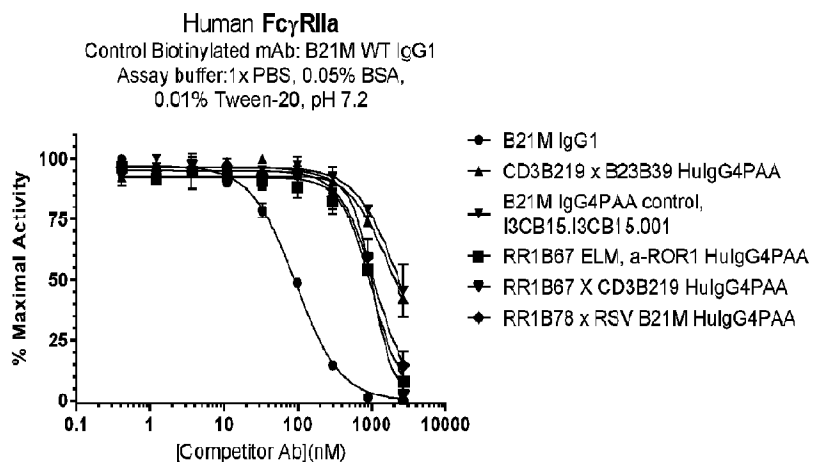


FIG. 9B

SUBSTITUTE SHEET (RULE 26)

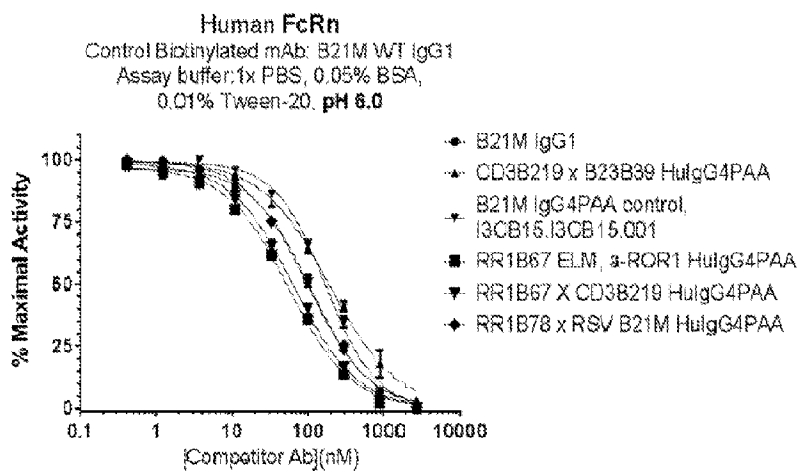


FIG. 10A

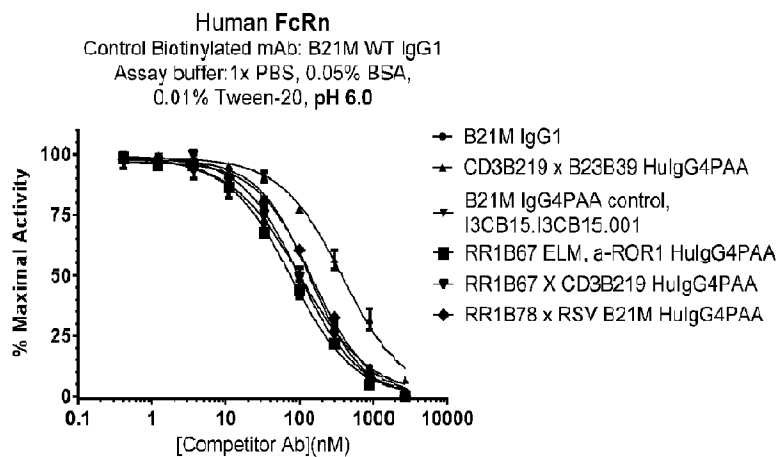


FIG. 10B

SUBSTITUTE SHEET (RULE 26)

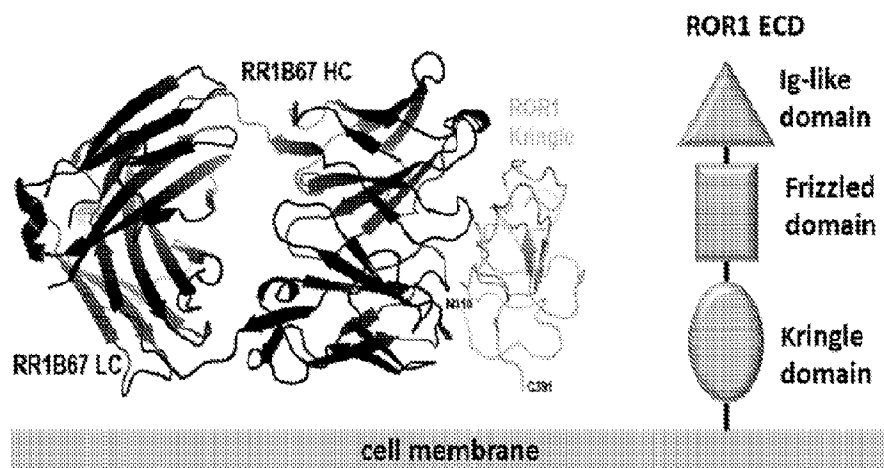


FIG. 11A

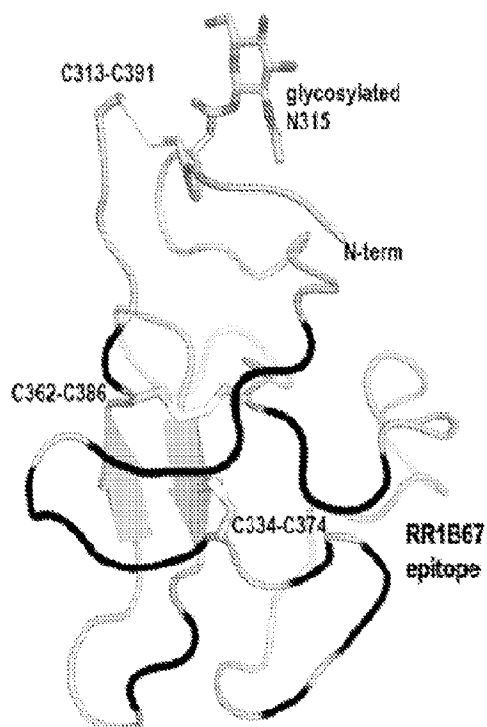


FIG. 11B

SUBSTITUTE SHEET (RULE 26)

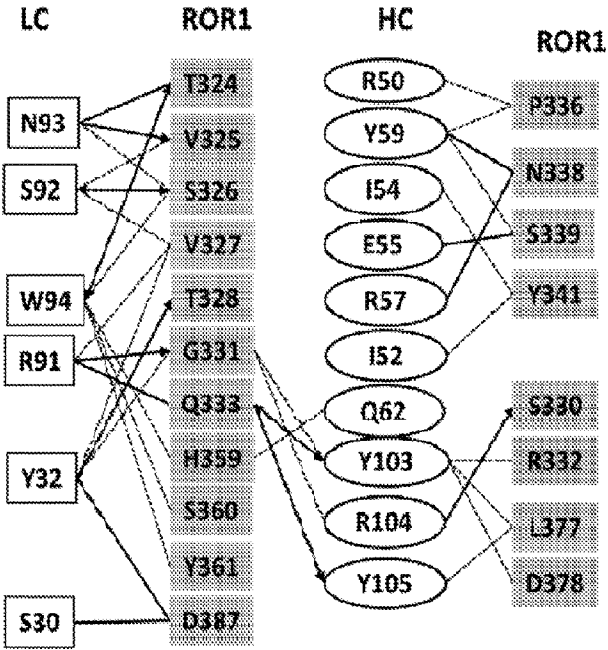


FIG. 11C

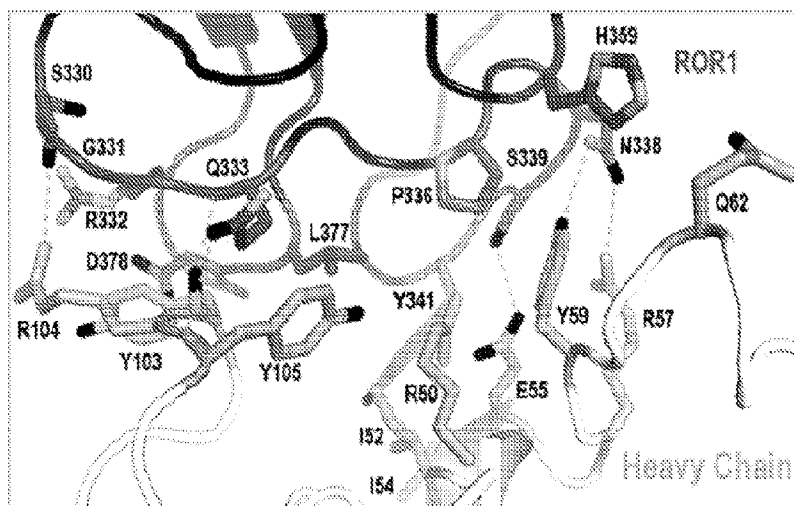
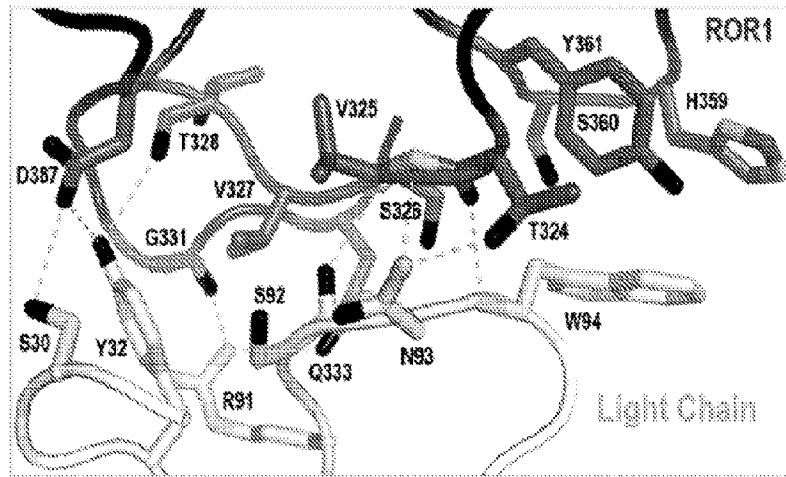


FIG. 11D

Epitope	Ig-like Domain	Frizzled Domain	Xringle Domain
R0R1_30	QETELSVSAELVPTSSNNISSELNKLUSYLELDEPMNITTSLSQTAELHCKVSGNPPETISWFKMDAPVCEPRRL	109	
R0R1_106	SEKSTIYGSRIIRIRNLDTDTGNFQCVATNGKIVVSSFGULEVNFKEPPPTASPGYSDEVEELGECQPYRGLACARE	181	
R0R1_182	ICNETVNESLHMQGEIENQITAFATWIGTSSHLSDKCSQFAIPSLCHYAFPYCDETSSEVFPFOLCECECIEN	257	
R0R1_258	VLCQTEVFARSNEMILMRKLKFNCEDLQPKPSPEANCIKIGFEMADFINNNKNCINSTEVDYRSTWTKSGRQ	333	
R0R1_334	COFNSQEFTHHTTIALRFPPELNGCHSICRNPNGCKEAFPCFTIDENFESDLCDIPACDCKDSKERKRMELLY	406	
Paratope			
RR1B67_HC	1 QVQLVQSGAEVYKPGSSVYVSKKASGGTFTYAIHWYRQAFQGGLEWNGHIIPTFCRAFIAGFQGRVITIADES	75	CDR-H1 CDR-H2
RR1B67_HC	76 TSTAYMELSLRSEDTAVIYCARGRYSTKWFDDYWGQGLVIVSSASTKGPSVEFLAFSSKSTSGTAALGCIYK	150	CDR-H3
RR1B67_HC	151 DYFFEPVIVSWNGALISGVHTFPNAVIGSSGLYSLSVVTVPSSSLGTQYICNVNKKPSNTRKVKKVERKSC	223	
RR1B67_LC	1 EIVLTQSPATLSLSPGERATLSCRASQSVSSHLAWYQKPGQAPRLIYYDA SNRAIGIFARFSGSSSGTDFTITL	75	CDR-L1 CDR-L2
RR1B67_LC	76 SSLEPEDEAVIYCQQESNMLTFQGGIKVEIKRTVAAPSVFIFPPSDEQLKSTGSAVYVCLINNYFREAKVQKVK	150	CDR-L3
RR1B67_LC	151 ENALQSGNSQESVTEQDSKSTYSLSLTLSKADYENKKVYACEVTHQGLSSPVTKSENRCGC	214	

FIG. 12

SUBSTITUTE SHEET (RULE 26)

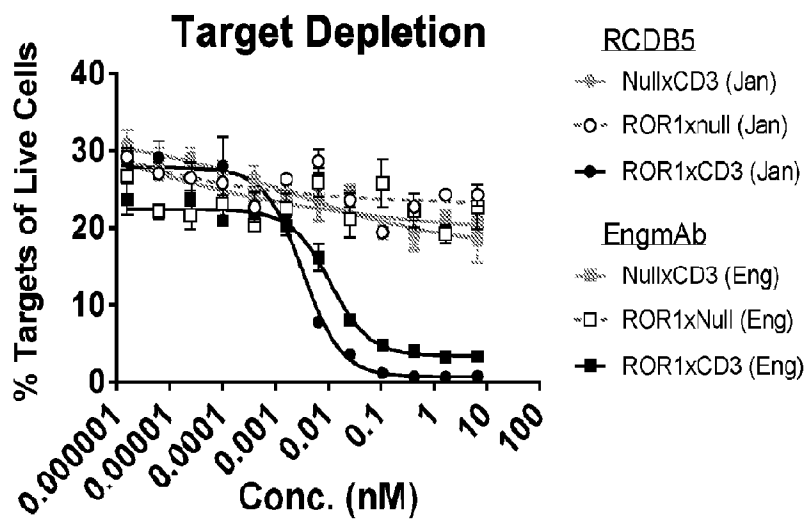


FIG. 13A

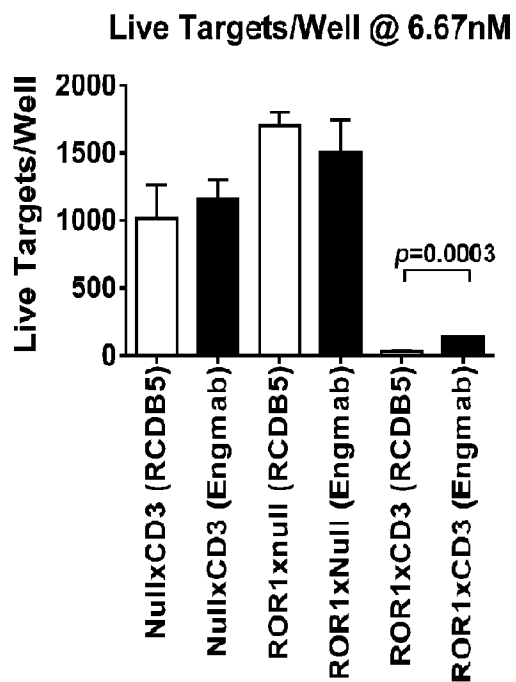


FIG. 13B

SUBSTITUTE SHEET (RULE 26)

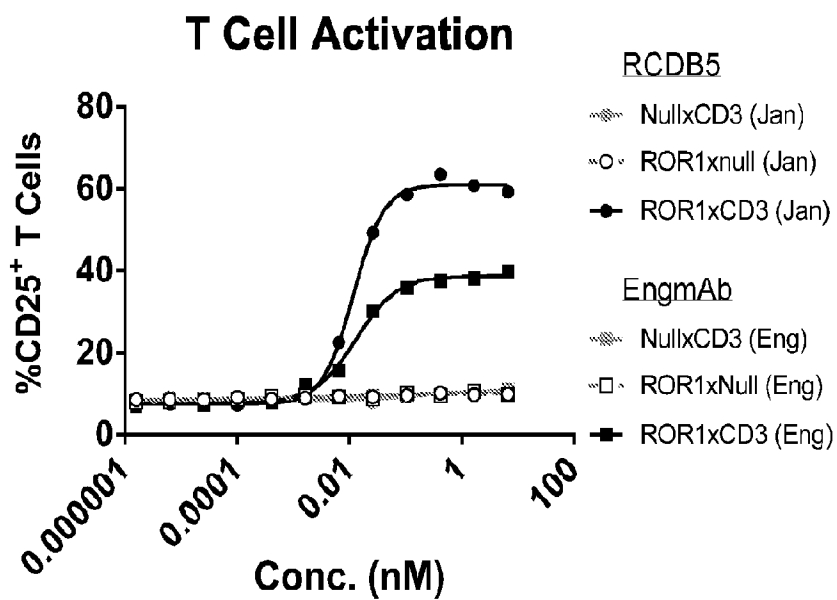


FIG. 13C

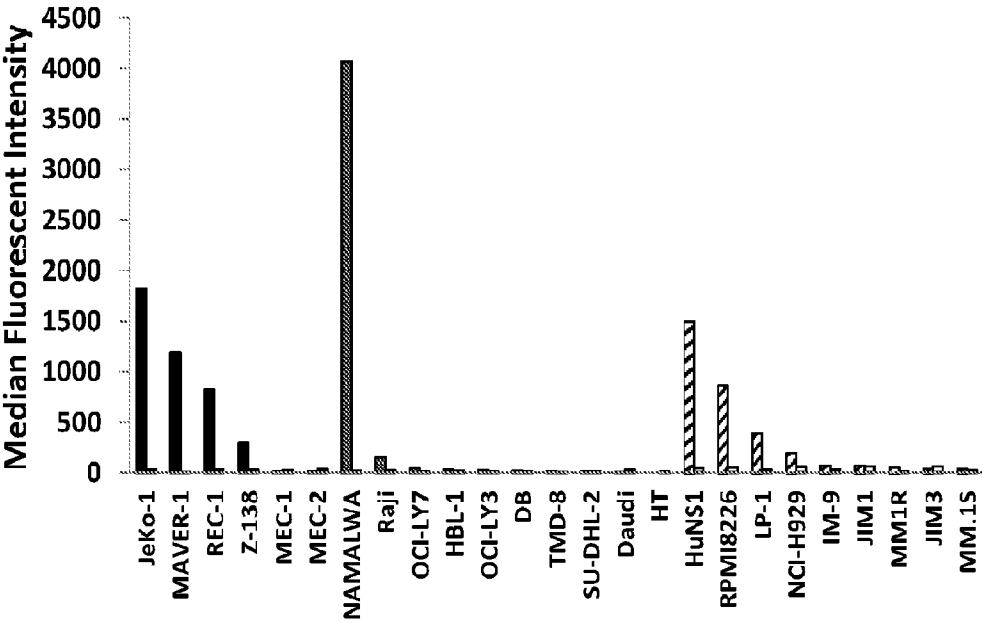


FIG. 14A

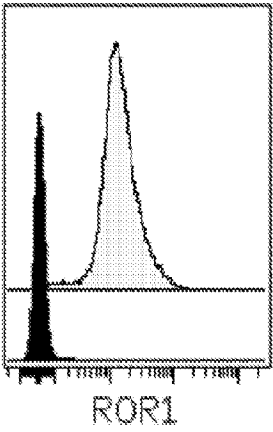


FIG. 14B

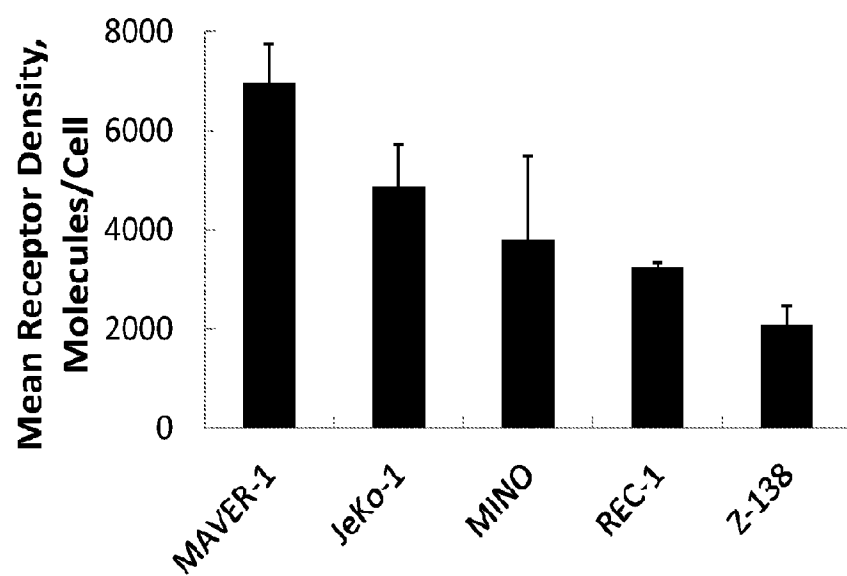


FIG. 15

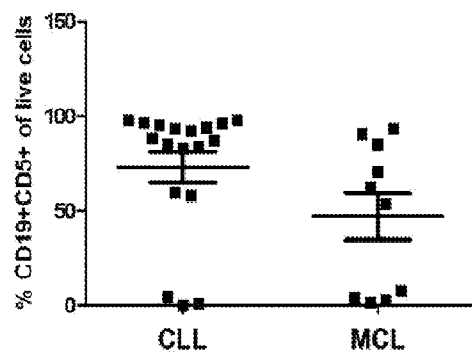


FIG. 16A

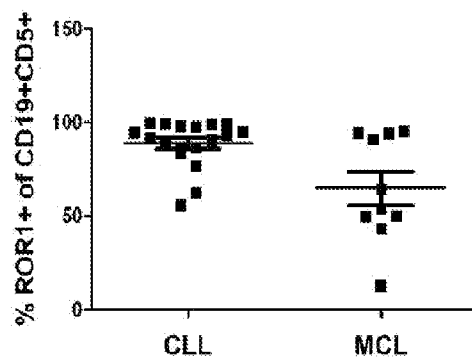


FIG. 16B

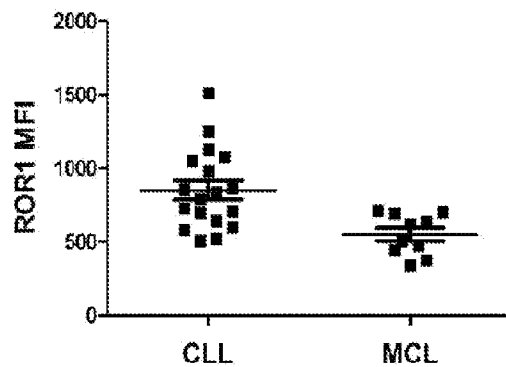


FIG. 16C

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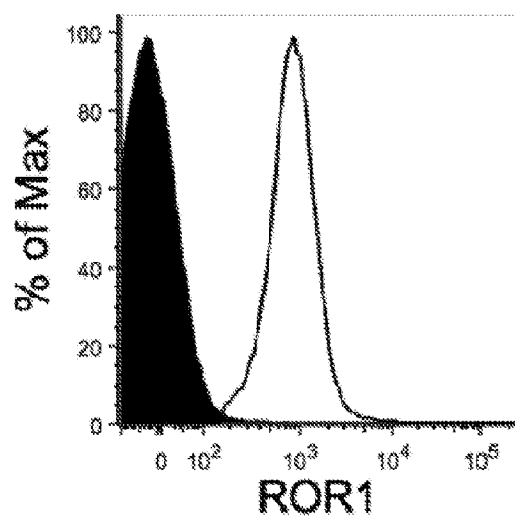


FIG. 16D

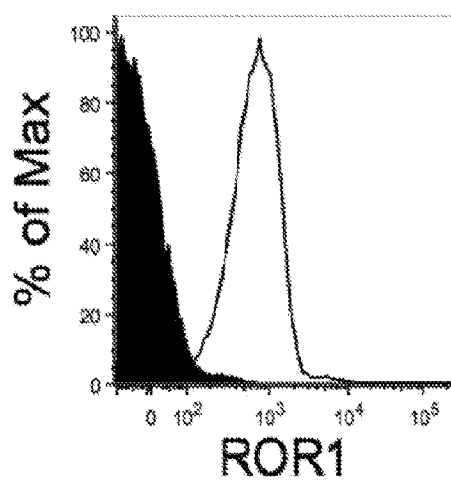


FIG. 16E

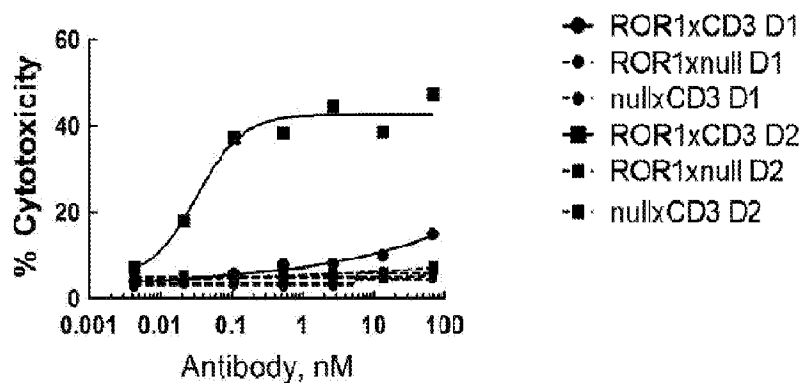


FIG. 17A

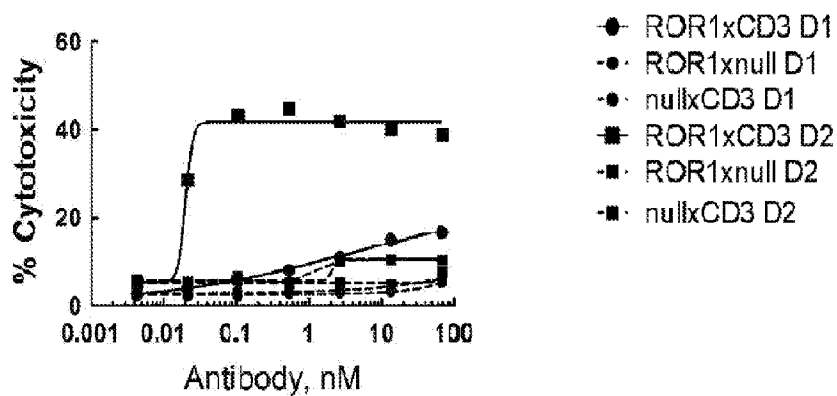


FIG. 17B

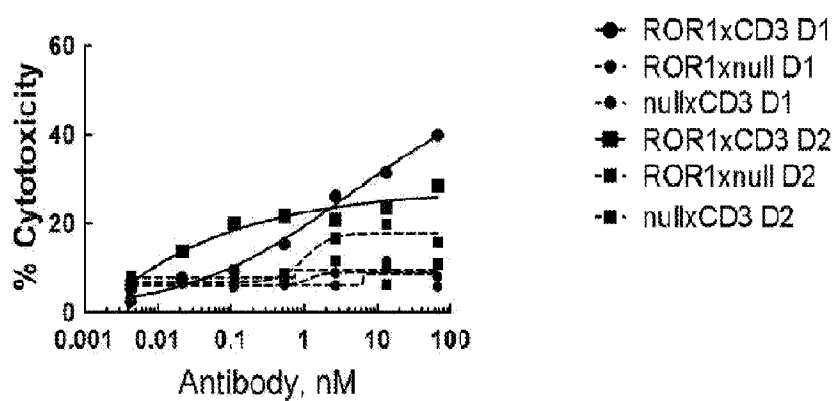


FIG. 17C

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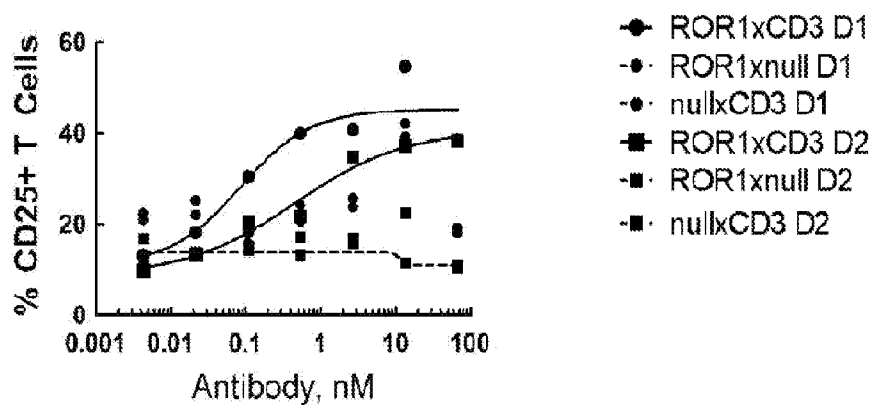


FIG. 17D

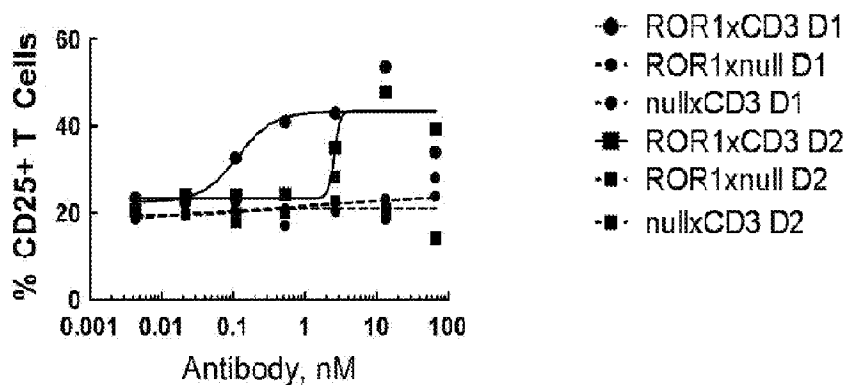


FIG. 17E

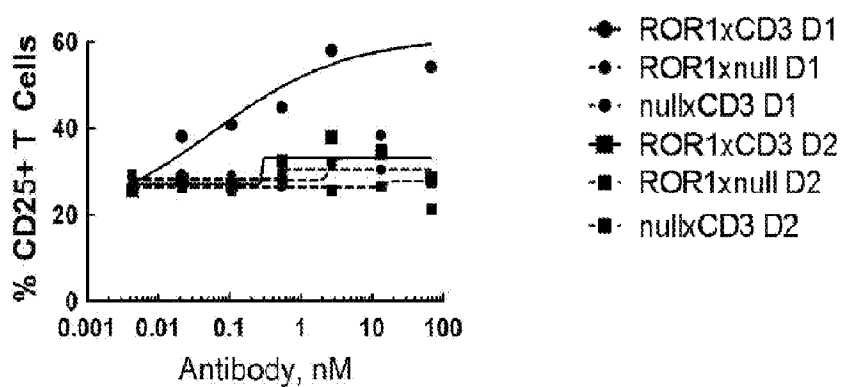


FIG. 17F

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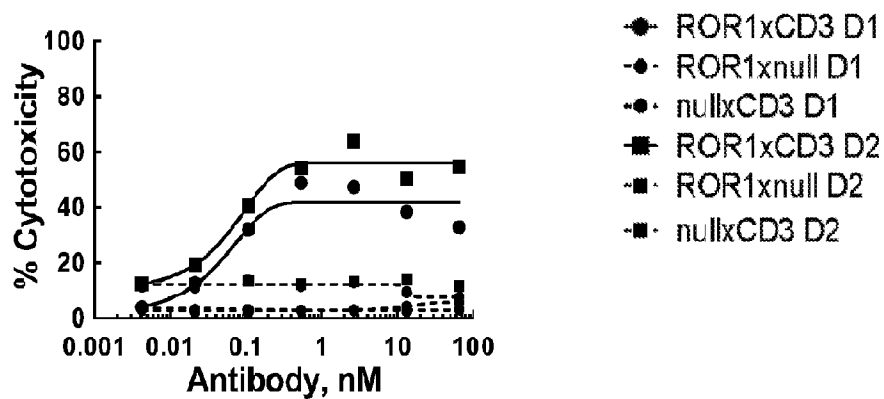


FIG. 18A

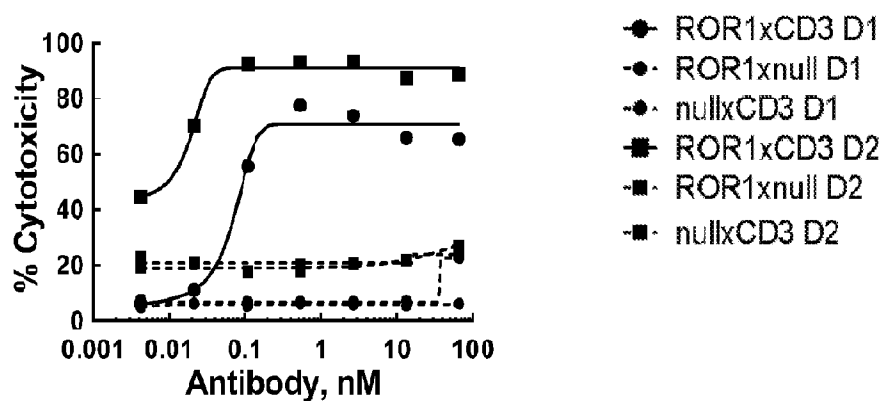


FIG. 18B

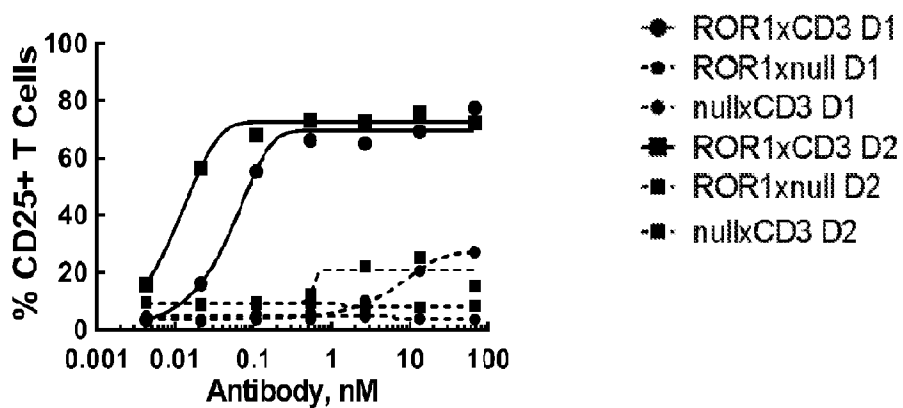


FIG. 18C

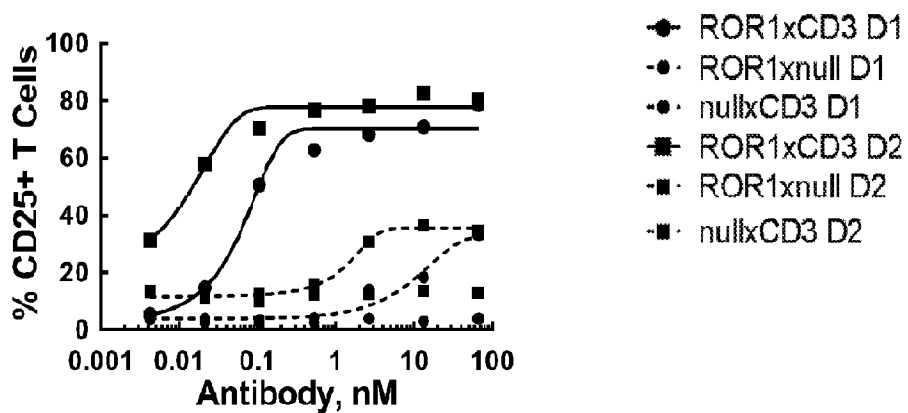


FIG. 18D

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BALDWIN, ERIC T.
HARMAN, BENJAMIN
CARDOSO, ROSA M.F.
NEMETH-SEAY, JENNIFER F.
ATTAR, RICARDO
GAUDET, FRANCOIS
LI, YINGZHE
LUO, JINQUAN
MCDAID, RONAN
POMERANTZ, STEVEN C.
TAM, SUSAN H.
TEPLYAKOV, ALEXEY
WU, SHENG-JIUN

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METHODS OF USING THE SAME

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<151> 2016-01-22

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20 25 30
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35 40 45
Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95
Ala Lys Asp Leu Ile Gly Ser Trp Gly Met Tyr Phe Asp Tyr Trp Gly
100 105 110

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Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115 120 125

Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala
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Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
145 150 155 160

Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala
165 170 175

Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val
180 185 190

Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His
195 200 205

Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly
210 215 220

Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser
225 230 235 240

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
245 250 255

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro
260 265 270

Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
275 280 285

Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val
290 295 300

Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
305 310 315 320

Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr
325 330 335

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
340 345 350

Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys
355 360 365

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
370 375 380

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
385 390 395 400

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser
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Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
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20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
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<213> Artificial Sequence

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

<400> 7

Asp Ala Ser Asn Arg Ala Thr
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<210> 8

<211> 9

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

<400> 8

Gln Gln Arg Ser Asn Trp Pro Leu Thr
1 5

<210> 9

<211> 447

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 9

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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Ala Arg Gly Arg Tyr Ser Tyr Tyr Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 10
Thr Asp Ala Ile His
1 5

<210> 11
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 11
Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 12
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 12
Gly Arg Tyr Ser Tyr Tyr Tyr Tyr Phe Asp Tyr
1 5 10

<210> 13

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 13

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Tyr
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 14

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 14

Thr Tyr Ala Ile His
1 5

<210> 15
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 15
 Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 16
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 16
 Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr
 1 5 10

<210> 17
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 17
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asp Ala
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Arg Ala Arg Tyr Arg Trp Ala Phe Asp Tyr Trp Gly Gln
 100 105 110

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Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 18
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 18
Asp Ala Ala Ile His
1 5

<210> 19
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 19
Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 20
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 20
Gly Arg Ala Arg Tyr Arg Trp Ala Phe Asp Tyr
1 5 10

<210> 21
<211> 454
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 21

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Gly Tyr Tyr Ser Arg Tyr Arg Gly Tyr Phe Leu Tyr Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala
115 120 125

Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser
130 135 140

Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe
145 150 155 160

Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170 175

Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu
180 185 190

Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr
195 200 205

Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg
210 215 220

Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
225 230 235 240

Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
245 250 255

JB15075USNPSL.txt

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
260 265 270

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
275 280 285

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
290 295 300

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
305 310 315 320

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
325 330 335

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
340 345 350

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
355 360 365

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
370 375 380

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
385 390 395 400

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
405 410 415

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
420 425 430

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
435 440 445

Ser Leu Ser Leu Gly Lys
450

<210> 22

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 22

Ser Tyr Ala Ile Ser
1 5

<210> 23
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 23
 Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 24
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 24
 Asp Gly Tyr Tyr Ser Arg Tyr Arg Gly Tyr Phe Leu Tyr Tyr Gly Met
 1 5 10 15

Asp Val

<210> 25
 <211> 444
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 25
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ser Ala Ile Arg Tyr Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

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Ala Lys Met Phe Gly Gly Gln Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205

Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
210 215 220

Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
340 345 350

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 26
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 26
Ser Tyr Ala Met Ser
1 5

<210> 27
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 27
Ala Ile Arg Tyr Asp Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 28
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 28
Met Phe Gly Gly Gln Leu Asp Tyr
1 5

<210> 29

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 29

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Arg His
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Lys Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Pro His Thr Phe Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 30

<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 30
Arg Ala Ser Gln Ser Ile Asp Arg His Leu Asn
1 5 10

<210> 31
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 31
Lys Ala Ser Ser Leu Gln Ser
1 5

<210> 32
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 32
Gln Gln Pro His Thr Phe Pro Leu Thr
1 5

<210> 33
<211> 443
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 33
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Gly Ile Ser Tyr Asn Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Lys Pro Tyr Phe Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110
 Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 115 120 125
 Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
 130 135 140
 Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 145 150 155 160
 Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 165 170 175
 Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu
 180 185 190
 Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn Thr
 195 200 205
 Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro
 210 215 220
 Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe Pro
 225 230 235 240
 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 245 250 255
 Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn
 260 265 270
 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 275 280 285
 Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
 290 295 300
 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 305 310 315 320
 Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys
 325 330 335
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu
 340 345 350

Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
355 360 365

Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
370 375 380

Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
385 390 395 400

Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly
405 410 415

Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
420 425 430

Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440

<210> 34
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 34
Gly Ile Ser Tyr Asn Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val Lys
1 5 10 15

Gly

<210> 35
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 35
Pro Tyr Phe Gly Phe Asp Tyr
1 5

<210> 36
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 36

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Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ala Asp Phe
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Gly Asn Arg Trp Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 37

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 37

Arg Ala Ser Gln Ser Val Ala Asp Phe Leu Ala
1 5 10

<210> 38
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 38
 Gln Gln Gly Asn Arg Trp Pro Ile Thr
 1 5

<210> 39
 <211> 443
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 39
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
 20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Thr Gly Asn Lys Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val
 100 105 110

Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
 115 120 125

Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys Leu
 130 135 140

Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly
 145 150 155 160

Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser
 165 170 175

JB15075USNPSL.txt

Gly Leu Tyr Ser₁₈₀ Leu Ser Ser Val₁₈₅ Val Thr Val Pro Ser Ser₁₉₀ Ser Leu

Gly Thr Lys₁₉₅ Thr Tyr Thr Cys Asn₂₀₀ Val Asp His Lys Pro₂₀₅ Ser Asn Thr

Lys Val₂₁₀ Asp Lys Arg Val Glu₂₁₅ Ser Lys Tyr Gly Pro₂₂₀ Pro Cys Pro Pro

Cys₂₂₅ Pro Ala Pro Glu Ala₂₃₀ Ala Gly Gly Pro Ser₂₃₅ Val Phe Leu Phe Pro₂₄₀

Pro Lys Pro Lys Asp₂₄₅ Thr Leu Met Ile Ser₂₅₀ Arg Thr Pro Glu Val₂₅₅ Thr

Cys Val Val₂₆₀ Val Asp Val Ser Gln Glu₂₆₅ Asp Pro Glu Val Gln₂₇₀ Phe Asn

Trp Tyr Val₂₇₅ Asp Gly Val Glu Val₂₈₀ His Asn Ala Lys Thr₂₈₅ Lys Pro Arg

Glu Glu₂₉₀ Gln Phe Asn Ser Thr₂₉₅ Tyr Arg Val Val Ser₃₀₀ Val Leu Thr Val

Leu₃₀₅ His Gln Asp Trp Leu₃₁₀ Asn Gly Lys Glu Tyr₃₁₅ Lys Cys Lys Val Ser₃₂₀

Asn Lys Gly Leu Pro₃₂₅ Ser Ser Ile Glu Lys₃₃₀ Thr Ile Ser Lys Ala₃₃₅ Lys

Gly Gln Pro Arg₃₄₀ Glu Pro Gln Val Tyr₃₄₅ Thr Leu Pro Pro Ser₃₅₀ Gln Glu

Glu Met Thr₃₅₅ Lys Asn Gln Val Ser₃₆₀ Leu Thr Cys Leu Val₃₆₅ Lys Gly Phe

Tyr Pro₃₇₀ Ser Asp Ile Ala Val₃₇₅ Glu Trp Glu Ser Asn₃₈₀ Gly Gln Pro Glu

Asn₃₈₅ Asn Tyr Lys Thr Thr₃₉₀ Pro Pro Val Leu Asp₃₉₅ Ser Asp Gly Ser Phe₄₀₀

Phe Leu Tyr Ser Arg₄₀₅ Leu Thr Val Asp Lys₄₁₀ Ser Arg Trp Gln Glu₄₁₅ Gly

Asn Val Phe Ser₄₂₀ Cys Ser Val Met His₄₂₅ Glu Ala Leu His Asn₄₃₀ His Tyr

Thr Gln Lys₄₃₅ Ser Leu Ser Leu Ser₄₄₀ Leu Gly Lys

<210> 40
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 40
 Thr Gly Asn Lys Leu Asp Tyr
 1 5

<210> 41
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 41
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ala Lys Phe
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Phe Ala Ser Asn Arg Ala Thr Asp Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Asp His Trp Pro Leu
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 42
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 42
Arg Ala Ser Gln Ser Val Ala Lys Phe Leu Ala
1 5 10

<210> 43
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 43
Phe Ala Ser Asn Arg Ala Thr
1 5

<210> 44
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 44
Gln Gln Arg Asp His Trp Pro Leu Thr
1 5

<210> 45
<211> 445
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 45
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Val Ala Ser Trp Tyr Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

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Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 46
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 46
Ser Tyr Gly Ile Ser
1 5

<210> 47
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 47
Trp Ile Ser Ala Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 48
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 48
 Gly Val Ala Ser Trp Tyr Leu Asp Tyr
 1 5

<210> 49
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 49
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Lys Trp
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asp Tyr Asn Phe Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 50
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 50
Arg Ala Ser Gln Ser Ile Asn Lys Trp Leu Asn
1 5 10

<210> 51
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 51
Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 52
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 52
Gln Gln Asp Tyr Asn Phe Pro Tyr Thr
1 5

<210> 53
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

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<400> 53

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Val Phe Ala Ser Arg Ser Gly Tyr Gly Ile Pro Phe Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly
115 120 125

Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser
130 135 140

Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val
145 150 155 160

Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe
165 170 175

Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
180 185 190

Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val
195 200 205

Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys
210 215 220

Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly
225 230 235 240

Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
245 250 255

Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu
260 265 270

Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
275 280 285

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg
290 295 300

Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
305 310 315 320

Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu
325 330 335

Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
340 345 350

Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu
355 360 365

Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
370 375 380

Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
385 390 400

Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp
405 410 415

Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His
420 425 430

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu
435 440 445

Gly Lys
450

<210> 54
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 54
Ser Tyr Trp Ile Gly
1 5

<210> 55
<211> 17
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 55

Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 56

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 56

Val Phe Ala Ser Arg Ser Gly Tyr Gly Ile Pro Phe Asp Tyr
1 5 10

<210> 57

<211> 220

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 57

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Ser Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
100 105 110

Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
210 215 220

<210> 58
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 58
Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn Tyr Leu
1 5 10 15

Ala

<210> 59
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 59
Trp Ala Ser Thr Arg Glu Ser
1 5

<210> 60
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 60

Gln Gln Tyr Tyr Ser Thr Pro Leu Thr
1 5

<210> 61

<211> 449

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 61

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Tyr Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Asp Val Gly Arg Trp Ala Pro Gly Gly Phe Leu Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
115 120 125

Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr
130 135 140

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
145 150 155 160

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
165 170 175

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
180 185 190

Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp
195 200 205

His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr
210 215 220

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Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro
 225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp
 260 265 270

Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr
 340 345 350

Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr
 355 360 365

Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu
 370 375 380

Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu
 385 390 395 400

Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys
 405 410 415

Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 420 425 430

Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly
 435 440 445

Lys

<210> 62
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 62

Asp Val Gly Arg Trp Ala Pro Gly Gly Phe Leu Asp Tyr
1 5 10

<210> 63

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 63

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Asp Ser Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

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Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 64
<211> 5
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 64
Ser Asp Ala Ile His
1 5

<210> 65
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 65
Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr
1 5 10

<210> 66
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 66
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Lys Ser Ala
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ser Pro Tyr Tyr Gly Ser Ala Tyr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Ile Ala Tyr Tyr Tyr Val Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

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Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
 405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 67
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 67
Ser Ala Tyr Ile His
1 5

<210> 68
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 68
Tyr Ile Ser Pro Tyr Tyr Gly Ser Ala Tyr Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 69
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 69
Gly Arg Ile Ala Tyr Tyr Tyr Val Phe Asp Tyr
1 5 10

<210> 70
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 70
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

JB15075USNPSL.txt

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 71

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 71

Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 72

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 72

Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr
1 5 10

<210> 73

<211> 446

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 73

Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Glu
1 5 10 15

Ser Leu Lys Ile Ser Cys Lys Gly Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asp Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe
50 55 60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65 70 75 80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Ala Arg Gly Asn Asp Pro Trp Pro Asp Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu
130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
180 185 190

Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro
195 200 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro
210 215 220

Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe
225 230 235 240

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
245 250 255

Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val
260 265 270

Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
275 280 285

Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val
290 295 300

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
305 310 315 320

Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser
325 330 335

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
340 345 350

Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
355 360 365

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
370 375 380

Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp
385 390 395 400

Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp
405 410 415

Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His
420 425 430

Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 74

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 74

Ile Ile Asp Pro Gly Asp Ser Asp Thr Arg Tyr Ser Pro Ser Phe Gln
1 5 10 15

Gly

<210> 75
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 75
Gly Asn Asp Pro Trp Pro Asp Phe Asp Tyr
1 5 10

<210> 76
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 76
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

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Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 77

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 77

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 78

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 78

Gln Gln Ser Tyr Ser Thr Pro Leu Thr
1 5

<210> 79

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 79

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Gln Asp Glu Ser Gly Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
115 120 125

Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly
130 135 140

Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
165 170 175

Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
180 185 190

Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser
195 200 205

Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys
210 215 220

Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu
225 230 235 240

Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
245 250 255

Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln
260 265 270

Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys
275 280 285

Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu
290 295 300

Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys
305 310 315 320

Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys
325 330 335

Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser
340 345 350

Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
355 360 365

Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln
370 375 380

Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly
385 390 395 400

Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln
405 410 415

Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn
420 425 430

His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 80
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 80
Gly Gln Asp Glu Ser Gly Leu Asp Tyr
1 5

<210> 81
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 81
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asp Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

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Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Asp Trp Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 82
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 82
Arg Ala Ser Gln Ser Val Ser Asp Trp Leu Ala
1 5 10

<210> 83
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 83

Gln Gln Ser Gly Asp Trp Pro Tyr Thr
1 5

<210> 84

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 84

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ser Ala Ile Phe Gly Asn Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Leu Arg Leu Gly Asn Leu Asp Tyr Trp Gly Gln Gly Thr Leu
100 105 110

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
115 120 125

Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
130 135 140

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
145 150 155 160

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
165 170 175

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
180 185 190

Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
195 200 205

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Thr  Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
 210                215                220

Pro  Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val Phe Leu Phe
225                230                235

Pro  Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                245                250                255

Thr  Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
                260                265                270

Asn  Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
                275                280                285

Arg  Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290                295                300

Val  Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305                310                315                320

Ser  Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
                325                330                335

Lys  Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
                340                345                350

Glu  Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
                355                360                365

Phe  Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370                375                380

Glu  Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385                390                395                400

Phe  Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
                405                410                415

Gly  Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
                420                425                430

Tyr  Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
                435                440

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<210> 85

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 85

Gly Ile Ser Ala Ile Phe Gly Asn Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 86

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 86

Leu Arg Leu Gly Asn Leu Asp Tyr
1 5

<210> 87

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 87

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ala Asn Phe
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Phe Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Gly Ala Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 88
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 88
Arg Ala Ser Gln Ser Val Ala Asn Phe Leu Ala
1 5 10

<210> 89
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 89
Gln Gln Tyr Tyr Gly Ala Pro Ile Thr
1 5

<210> 90
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 90
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Thr Tyr
20 25 30

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Ala Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr Tyr Ala Ala
50 55 60

Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Ser
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Ala Arg His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe
100 105 110

Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
115 120 125

Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser
130 135 140

Glu Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu
145 150 155 160

Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His
165 170 175

Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser
180 185 190

Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys
195 200 205

Asn Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu
210 215 220

Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala
225 230 235 240

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
245 250 255

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
260 265 270

Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
275 280 285

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
290 295 300

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Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
305 310 315 320

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser
325 330 335

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
340 345 350

Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val
355 360 365

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
370 375 380

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
385 390 395 400

Pro Val Leu Asp Ser Asp Gly Ser Phe Leu Leu Tyr Ser Lys Leu Thr
405 410 415

Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val
420 425 430

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
435 440 445

Ser Leu Gly Lys
450

<210> 91

<211> 215

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 91

Gln Thr Val Val Thr Gln Glu Pro Ser Leu Thr Val Ser Pro Gly Gly
1 5 10 15

Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
20 25 30

Asn Tyr Ala Asn Trp Val Gln Gln Lys Pro Gly Gln Ala Pro Arg Gly
35 40 45

Leu Ile Gly Gly Thr Asn Lys Arg Ala Pro Gly Thr Pro Ala Arg Phe
50 55 60

Ser Gly Ser Leu Leu Gly Gly Lys Ala Ala Leu Thr Leu Ser Gly Val
65 70 75 80

Gln Pro Glu Asp Glu Ala Glu Tyr Tyr Cys Ala Leu Trp Tyr Ser Asn
85 90 95

Leu Trp Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
100 105 110

Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu
115 120 125

Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro
130 135 140

Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala
145 150 155 160

Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala
165 170 175

Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Arg
180 185 190

Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr
195 200 205

Val Ala Pro Thr Glu Cys Ser
210 215

<210> 92
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 92
Gly Phe Thr Phe Asn Thr Tyr Ala Met Asn
1 5 10

<210> 93
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 93
Arg Ile Arg Ser Lys Tyr Asn Asn Tyr Ala Thr Tyr
1 5 10

<210> 94
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 94
His Gly Asn Phe Gly Asn Ser Tyr Val Ser Trp Phe Ala Tyr
1 5 10

<210> 95
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 95
Arg Ser Ser Thr Gly Ala Val Thr Thr Ser Asn Tyr Ala Asn
1 5 10

<210> 96
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 96
Gly Thr Asn Lys Arg Ala Pro
1 5

<210> 97
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 97
Ala Leu Trp Tyr Ser Asn Leu Trp Val
1 5

<210> 98
<211> 64
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Human or mouse polypeptide

<400> 98
Thr Val Ser Val Thr Lys Ser Gly Arg Gln Cys Gln Pro Trp Asn Ser
1 5 10 15

Gln Tyr Pro His Thr His Thr Phe Thr Ala Leu Arg Phe Pro Glu Leu
20 25 30

Asn Gly Gly His Ser Tyr Cys Arg Asn Pro Gly Asn Gln Lys Glu Ala
35 40 45

Pro Trp Cys Phe Thr Leu Asp Glu Asn Phe Lys Ser Asp Leu Cys Asp
50 55 60

<210> 99

<211> 406

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 99

Gln Glu Thr Glu Leu Ser Val Ser Ala Glu Leu Val Pro Thr Ser Ser
1 5 10 15

Trp Asn Ile Ser Ser Glu Leu Asn Lys Asp Ser Tyr Leu Thr Leu Asp
20 25 30

Glu Pro Met Asn Asn Ile Thr Thr Ser Leu Gly Gln Thr Ala Glu Leu
35 40 45

His Cys Lys Val Ser Gly Asn Pro Pro Pro Thr Ile Arg Trp Phe Lys
50 55 60

Asn Asp Ala Pro Val Val Gln Glu Pro Arg Arg Leu Ser Phe Arg Ser
65 70 75 80

Thr Ile Tyr Gly Ser Arg Leu Arg Ile Arg Asn Leu Asp Thr Thr Asp
85 90 95

Thr Gly Tyr Phe Gln Cys Val Ala Thr Asn Gly Lys Glu Val Val Ser
100 105 110

Ser Thr Gly Val Leu Phe Val Lys Phe Gly Pro Pro Pro Thr Ala Ser
115 120 125

Pro Gly Tyr Ser Asp Glu Tyr Glu Glu Asp Gly Phe Cys Gln Pro Tyr
130 135 140

Arg Gly Ile Ala Cys Ala Arg Phe Ile Gly Asn Arg Thr Val Tyr Met
145 150 155 160

Glu Ser Leu His Met Gln Gly Glu Ile Glu Asn Gln Ile Thr Ala Ala
165 170 175

Phe Thr Met Ile Gly Thr Ser Ser His Leu Ser Asp Lys Cys Ser Gln
180 185 190

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Phe Ala Ile Pro Ser Leu Cys His Tyr Ala Phe Pro Tyr Cys Asp Glu
195 200 205

Thr Ser Ser Val Pro Lys Pro Arg Asp Leu Cys Arg Asp Glu Cys Glu
210 215 220

Ile Leu Glu Asn Val Leu Cys Gln Thr Glu Tyr Ile Phe Ala Arg Ser
225 230 235 240

Asn Pro Met Ile Leu Met Arg Leu Lys Leu Pro Asn Cys Glu Asp Leu
245 250 255

Pro Gln Pro Glu Ser Pro Glu Ala Ala Asn Cys Ile Arg Ile Gly Ile
260 265 270

Pro Met Ala Asp Pro Ile Asn Lys Asn His Lys Cys Tyr Asn Ser Thr
275 280 285

Gly Val Asp Tyr Arg Gly Thr Val Ser Val Thr Lys Ser Gly Arg Gln
290 295 300

Cys Gln Pro Trp Asn Ser Gln Tyr Pro His Thr His Thr Phe Thr Ala
305 310 315 320

Leu Arg Phe Pro Glu Leu Asn Gly Gly His Ser Tyr Cys Arg Asn Pro
325 330 335

Gly Asn Gln Lys Glu Ala Pro Trp Cys Phe Thr Leu Asp Glu Asn Phe
340 345 350

Lys Ser Asp Leu Cys Asp Ile Pro Ala Cys Asp Ser Lys Asp Ser Lys
355 360 365

Glu Lys Asn Lys Met Glu Ile Leu Phe Gly Cys Phe Cys Gly Phe Ile
370 375 380

Leu Ile Gly Leu Ile Leu Tyr Ile Ser Leu Ala Ile Arg Gly Gly Gly
385 390 395 400

Gly Ser Gly Gly Gly Ser
405

<210> 100
<211> 400
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 100

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Glu Val Glu Val Leu Asp Pro Asn Asp Pro Leu Gly Pro Leu Asp Gly
 1 5 10 15
 Gln Asp Gly Pro Ile Pro Thr Leu Lys Gly Tyr Phe Leu Asn Phe Leu
 20 25 30
 Glu Pro Val Asn Asn Ile Thr Ile Val Gln Gly Gln Thr Ala Ile Leu
 35 40 45
 His Cys Lys Val Ala Gly Asn Pro Pro Pro Asn Val Arg Trp Leu Lys
 50 55 60
 Asn Asp Ala Pro Val Val Gln Glu Pro Arg Arg Ile Ile Ile Arg Lys
 65 70 75 80
 Thr Glu Tyr Gly Ser Arg Leu Arg Ile Gln Asp Leu Asp Thr Thr Asp
 85 90 95
 Thr Gly Tyr Tyr Gln Cys Val Ala Thr Asn Gly Met Lys Thr Ile Thr
 100 105 110
 Ala Thr Gly Val Leu Phe Val Arg Leu Gly Pro Thr His Ser Pro Asn
 115 120 125
 His Asn Phe Gln Asp Asp Tyr His Glu Asp Gly Phe Cys Gln Pro Tyr
 130 135 140
 Arg Gly Ile Ala Cys Ala Arg Phe Ile Gly Asn Arg Thr Ile Tyr Val
 145 150 155 160
 Asp Ser Leu Gln Met Gln Gly Glu Ile Glu Asn Arg Ile Thr Ala Ala
 165 170 175
 Phe Thr Met Ile Gly Thr Ser Thr His Leu Ser Asp Gln Cys Ser Gln
 180 185 190
 Phe Ala Ile Pro Ser Phe Cys His Phe Val Phe Pro Leu Cys Asp Ala
 195 200 205
 Arg Ser Arg Thr Pro Lys Pro Arg Glu Leu Cys Arg Asp Glu Cys Glu
 210 215 220
 Val Leu Glu Ser Asp Leu Cys Arg Gln Glu Tyr Thr Ile Ala Arg Ser
 225 230 235 240
 Asn Pro Leu Ile Leu Met Arg Leu Gln Leu Pro Lys Cys Glu Ala Leu
 245 250 255
 Pro Met Pro Glu Ser Pro Asp Ala Ala Asn Cys Met Arg Ile Gly Ile
 260 265 270

JB15075USNPSL.txt

Pro Ala Glu Arg Leu Gly Arg Tyr His Gln Cys Tyr Asn Gly Ser Gly
275 280 285

Met Asp Tyr Arg Gly Thr Ala Ser Thr Thr Lys Ser Gly His Gln Cys
290 295 300

Gln Pro Trp Ala Leu Gln His Pro His Ser His His Leu Ser Ser Thr
305 310 315 320

Asp Phe Pro Glu Leu Gly Gly Gly His Ala Tyr Cys Arg Asn Pro Gly
325 330 335

Gly Gln Met Glu Gly Pro Trp Cys Phe Thr Gln Asn Lys Asn Val Arg
340 345 350

Met Glu Leu Cys Asp Val Pro Ser Cys Ser Pro Arg Asp Ser Ser Lys
355 360 365

Met Gly Phe Gly Cys Phe Cys Gly Phe Ile Leu Ile Gly Leu Ile Leu
370 375 380

Tyr Ile Ser Leu Ala Ile Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser
385 390 395 400

<210> 101

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 101

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Tyr Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

JB15075USNPSL.txt

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 102

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 102

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Glu Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 103
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 103
Thr Asp Ala Ile His
1 5

<210> 104
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 104
Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 105
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 105
Gly Arg Tyr Ser Tyr Tyr Tyr Tyr Phe Asp Tyr
1 5 10

<210> 106
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 106

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Glu
1 5 10

<210> 107

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 107

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 108

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 108

Gln Gln Arg Ser Asn Trp Pro Leu Thr
1 5

<210> 109

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 109

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asp Ala
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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Ala Arg Gly Arg Ala Arg Tyr Arg Trp Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 110

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 110

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 111
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 111
Asp Ala Ala Ile His
1 5

<210> 112
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 112
Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 113
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 113
Gly Arg Ala Arg Tyr Arg Trp Ala Phe Asp Tyr
1 5 10

<210> 114
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 114
Arg Ala Ser Gln Ser Val Arg Asn Tyr Leu Ala
1 5 10

<210> 115
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 115
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 116
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 116
Gln Gln Arg Ser Asn Trp Pro Leu Thr
1 5

<210> 117
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 117
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asp Ala
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

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Met Glu Leu Ser Ser₈₅ Leu Arg Ser Glu Asp₉₀ Thr Ala Val Tyr Tyr₉₅ Cys

Ala Arg Gly Arg₁₀₀ Ala Arg Tyr Arg Trp₁₀₅ Ala Phe Asp Tyr Trp₁₁₀ Gly Gln

Gly Thr Leu₁₁₅ Val Thr Val Ser Ser₁₂₀ Ala Ser Thr Lys Gly₁₂₅ Pro Ser Val

Phe Pro₁₃₀ Leu Ala Pro Cys Ser₁₃₅ Arg Ser Thr Ser Glu₁₄₀ Ser Thr Ala Ala

Leu₁₄₅ Gly Cys Leu Val Lys₁₅₀ Asp Tyr Phe Pro Glu₁₅₅ Pro Val Thr Val Ser₁₆₀

Trp Asn Ser Gly Ala₁₆₅ Leu Thr Ser Gly Val₁₇₀ His Thr Phe Pro Ala₁₇₅ Val

Leu Gln Ser Ser₁₈₀ Gly Leu Tyr Ser Leu₁₈₅ Ser Ser Val Val Thr₁₉₀ Val Pro

Ser Ser Ser₁₉₅ Leu Gly Thr Lys Thr₂₀₀ Tyr Thr Cys Asn Val₂₀₅ Asp His Lys

Pro Ser₂₁₀ Asn Thr Lys Val Asp₂₁₅ Lys Arg Val Glu Ser₂₂₀ Lys Tyr Gly Pro

Pro₂₂₅ Cys Pro Pro Cys Pro₂₃₀ Ala Pro Glu Ala Ala₂₃₅ Gly Gly Pro Ser Val₂₄₀

Phe Leu Phe Pro Pro₂₄₅ Lys Pro Lys Asp Thr₂₅₀ Leu Met Ile Ser Arg₂₅₅ Thr

Pro Glu Val Thr₂₆₀ Cys Val Val Val Asp₂₆₅ Val Ser Gln Glu Asp₂₇₀ Pro Glu

Val Gln Phe₂₇₅ Asn Trp Tyr Val Asp₂₈₀ Gly Val Glu Val His₂₈₅ Asn Ala Lys

Thr Lys₂₉₀ Pro Arg Glu Glu Gln₂₉₅ Phe Asn Ser Thr Tyr₃₀₀ Arg Val Val Ser

Val₃₀₅ Leu Thr Val Leu His₃₁₀ Gln Asp Trp Leu Asn₃₁₅ Gly Lys Glu Tyr Lys₃₂₀

Cys Lys Val Ser Asn₃₂₅ Lys Gly Leu Pro Ser₃₃₀ Ser Ile Glu Lys Thr₃₃₅ Ile

Ser Lys Ala Lys₃₄₀ Gly Gln Pro Arg Glu₃₄₅ Pro Gln Val Tyr Thr₃₅₀ Leu Pro

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 118

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 118

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 119
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 119
Asp Ala Ala Ile His
1 5

<210> 120
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 120
Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 121
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 121
Gly Arg Ala Arg Tyr Arg Trp Ala Phe Asp Tyr
1 5 10

<210> 122
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 122
 Arg Ala Ser Gln Ser Val Ser Thr Tyr Leu Ala
 1 5 10

<210> 123
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 123
 Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 124
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 124
 Gln Gln Arg Ser Asn Trp Pro Leu Thr
 1 5

<210> 125
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 125
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asp Ala
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

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Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Ala Arg Tyr Arg Trp Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 126

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 126

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Glu Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 127
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 127
Asp Ala Ala Ile His
1 5

<210> 128
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 128
Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 129
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 129

Gly Arg Ala Arg Tyr Arg Trp Ala Phe Asp Tyr
1 5 10

<210> 130

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 130

Arg Ala Ser Gln Ser Val Arg Asn Tyr Leu Ala
1 5 10

<210> 131

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 131

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 132

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 132

Gln Gln Arg Ser Asn Trp Pro Leu Thr
1 5

<210> 133

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 133

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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Gly Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

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Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 134

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 134

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Lys Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 135
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 135
Thr Asp Ala Ile His
1 5

<210> 136
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 136
Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 137
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 137

Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr
1 5 10

<210> 138

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 138

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 139

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 139

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 140

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 140

Gln Gln Arg Ser Asn Trp Pro Leu Thr
1 5

<210> 141

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 141

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

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Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 142

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 142

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Lys Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

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Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 143
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 143
Thr Asp Ala Ile His
1 5

<210> 144
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 144
Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 145
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 145
 Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr
 1 5 10

<210> 146
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 146
 Arg Ala Ser Gln Ser Val Arg Asn Tyr Leu Ala
 1 5 10

<210> 147
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 147
 Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 148
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 148
 Gln Gln Arg Ser Asn Trp Pro Leu Thr
 1 5

<210> 149
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 149
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 150

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 150

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Lys Asp Ala Ser Asp Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

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Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 151
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 151
Thr Asp Ala Ile His
1 5

<210> 152
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 152
Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 153
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 153
 Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr
 1 5 10

<210> 154
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 154
 Arg Ala Ser Gln Ser Val Arg Ser Tyr Leu Ala
 1 5 10

<210> 155
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 155
 Asp Ala Ser Asp Arg Ala Thr
 1 5

<210> 156
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 156
 Gln Gln Arg Ser Asn Trp Pro Leu Thr
 1 5

<210> 157
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

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<400> 157

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 158

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 158

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

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Lys Asp Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 159
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 159
Thr Asp Ala Ile His
1 5

<210> 160
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 160

Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 161
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 161
 Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr
 1 5 10

<210> 162
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 162
 Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
 1 5 10

<210> 163
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 163
 Asp Ala Ser Thr Arg Ala Thr
 1 5

<210> 164
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 164
 Gln Gln Arg Ser Asn Trp Pro Leu Thr
 1 5

<210> 165
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 165

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 166

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 166

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Thr Tyr
20 25 30

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Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Lys Asp Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 167

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 167

Thr Asp Ala Ile His
1 5

<210> 168

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 168

Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 169

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 169

Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr
1 5 10

<210> 170

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 170

Arg Ala Ser Gln Ser Val Asn Thr Tyr Leu Ala
1 5 10

<210> 171

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 171

Asp Ala Ser Thr Arg Ala Thr
1 5

<210> 172

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 172

Gln Gln Arg Ser Asn Trp Pro Leu Thr
1 5

<210> 173

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 173

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

JB15075USNPSL.txt

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 174

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 174

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Lys Asp Ala Ser Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 175

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 175

Thr Asp Ala Ile His
1 5

<210> 176

<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 176
Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 177
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 177
Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr
1 5 10

<210> 178
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 178
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 179
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 179
Asp Ala Ser Tyr Arg Ala Thr
1 5

<210> 180
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 180

Gln Gln Arg Ser Asn Trp Pro Leu Thr
1 5

<210> 181

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 181

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Lys Ser Ala
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ser Pro Tyr Tyr Gly Ser Ala Tyr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Ile Ala Tyr Tyr Tyr Val Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
 405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440 445

<210> 182
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 182

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Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 183

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 183

Ser Ala Tyr Ile His
1 5

<210> 184
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 184
 Tyr Ile Ser Pro Tyr Tyr Gly Ser Ala Tyr Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 185
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 185
 Gly Arg Ile Ala Tyr Tyr Tyr Val Phe Asp Tyr
 1 5 10

<210> 186
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 186
 Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
 1 5 10

<210> 187
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 187
 Asp Ala Ser Tyr Arg Ala Thr
 1 5

<210> 188
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 188

Gln Gln Arg Ser Asn Trp Pro Leu Thr
1 5

<210> 189

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 189

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Tyr
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

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Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 190
<211> 214
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 190

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 191

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 191
 Thr Tyr Ala Ile His
 1 5

<210> 192
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 192
 Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 193
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 193
 Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr
 1 5 10

<210> 194
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 194
 Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
 1 5 10

<210> 195
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 195
 Asp Ala Ser Ser Arg Ala Thr
 1 5

<210> 196
 <211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 196

Gln Gln Arg Ser Asn Trp Pro Leu Thr
1 5

<210> 197

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 197

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asp Ala
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Ala Arg Tyr Arg Trp Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

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Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 198

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 198

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 199

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 199

Asp Ala Ala Ile His
1 5

<210> 200

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 200

Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 201

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 201

Gly Arg Ala Arg Tyr Arg Trp Ala Phe Asp Tyr
1 5 10

<210> 202

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 202

Arg Ala Ser Gln Ser Val Asn Asn Tyr Leu Ala
1 5 10

<210> 203

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 203

Asp Ala Ser Tyr Arg Ala Thr
1 5

<210> 204
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 204
 Gln Gln Arg Ser Asn Trp Pro Leu Thr
 1 5

<210> 205
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 205
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Tyr
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

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Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
 405 410 415
 Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440 445

<210> 206
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 206
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

His Asp Ala Ser Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ala His Trp Pro Ile
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 207
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 207
 Thr Tyr Ala Ile His
 1 5

<210> 208
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 208
 Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 209
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 209
 Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr
 1 5 10

<210> 210
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 210
 Arg Ala Ser Gln Ser Val Ser Thr Tyr Leu Ala
 1 5 10

<210> 211
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 211
Asp Ala Ser Tyr Arg Ala Thr
1 5

<210> 212
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 212
Gln Gln Arg Ala His Trp Pro Ile Thr
1 5

<210> 213
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 213
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

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Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
 405 410 415
 Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440 445

<210> 214
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 214
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ala His Trp Pro Asn
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 215
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 215
Thr Asp Ala Ile His
1 5

<210> 216
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 216
Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 217
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 217
Gly Arg Tyr Ser Tyr Tyr Tyr Tyr Phe Asp Tyr
1 5 10

<210> 218
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 218
Arg Ala Ser Gln Ser Val Ser Thr Tyr Leu Ala
1 5 10

<210> 219
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 219

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 220

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 220

Gln Gln Arg Ala His Trp Pro Asn Thr
1 5

<210> 221

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 221

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Tyr
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

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Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
 405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 222

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 222

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ala His Ser Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 223
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 223
 Thr Tyr Ala Ile His
 1 5

<210> 224
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 224
 Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 225
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 225
 Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr
 1 5 10

<210> 226
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 226
 Arg Ala Ser Gln Ser Val Ser Thr Tyr Leu Ala
 1 5 10

<210> 227
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 227
 Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 228
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 228
 Gln Gln Arg Ala His Ser Pro Leu Thr
 1 5

<210> 229
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 229
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Tyr
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

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Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 230
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 230
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

His Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ala His Ser Pro Asn
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 231
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 231
Thr Tyr Ala Ile His
1 5

<210> 232
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 232
Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 233
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 233
Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr
1 5 10

<210> 234
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 234

Arg Ala Ser Gln Ser Val Ser Asn Tyr Leu Ala
1 5 10

<210> 235

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 235

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 236

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 236

Gln Gln Arg Ala His Ser Pro Asn Thr
1 5

<210> 237

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 237

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Tyr
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 238

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 238

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Glu Asp Ala Ser Asp Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser His Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 239
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 239
Thr Tyr Ala Ile His
1 5

<210> 240
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 240
Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 241
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 241
Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr
1 5 10

<210> 242
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 242

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 243

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 243

Asp Ala Ser Asp Arg Ala Thr
1 5

<210> 244

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 244

Gln Gln Arg Ser His Trp Pro Leu Thr
1 5

<210> 245

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 245

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Tyr Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 246

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 246

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser His Trp Pro Asn
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 247
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 247
Thr Asp Ala Ile His
1 5

<210> 248
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 248
Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 249
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 249
Gly Arg Tyr Ser Tyr Tyr Tyr Tyr Phe Asp Tyr
1 5 10

<210> 250
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 250
Arg Ala Ser Gln Ser Val Ser Asn Tyr Leu Ala
1 5 10

<210> 251
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 251
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 252
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 252
Gln Gln Arg Ser His Trp Pro Asn Thr
1 5

<210> 253
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 253
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

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Met Glu Leu Ser Ser₈₅ Leu Arg Ser Glu Asp₉₀ Thr Ala Val Tyr Tyr₉₅ Cys

Ala Arg Gly Arg₁₀₀ Tyr Ser Tyr Tyr₁₀₅ Tyr Phe Asp Tyr Trp₁₁₀ Gly Gln

Gly Thr Leu₁₁₅ Val Thr Val Ser Ser₁₂₀ Ala Ser Thr Lys Gly₁₂₅ Pro Ser Val

Phe Pro₁₃₀ Leu Ala Pro Cys Ser₁₃₅ Arg Ser Thr Ser Glu₁₄₀ Ser Thr Ala Ala

Leu Gly Cys Leu Val Lys₁₅₀ Asp Tyr Phe Pro Glu₁₅₅ Pro Val Thr Val Ser₁₆₀

Trp Asn Ser Gly Ala₁₆₅ Leu Thr Ser Gly Val₁₇₀ His Thr Phe Pro Ala Val₁₇₅

Leu Gln Ser Ser₁₈₀ Gly Leu Tyr Ser Leu₁₈₅ Ser Ser Val Val Thr₁₉₀ Val Pro

Ser Ser Ser₁₉₅ Leu Gly Thr Lys Thr₂₀₀ Tyr Thr Cys Asn Val₂₀₅ Asp His Lys

Pro Ser₂₁₀ Asn Thr Lys Val Asp₂₁₅ Lys Arg Val Glu Ser₂₂₀ Lys Tyr Gly Pro

Pro Cys Pro Pro Cys Pro₂₃₀ Ala Pro Glu Ala Ala₂₃₅ Gly Gly Pro Ser Val₂₄₀

Phe Leu Phe Pro Pro₂₄₅ Lys Pro Lys Asp Thr₂₅₀ Leu Met Ile Ser Arg₂₅₅ Thr

Pro Glu Val Thr₂₆₀ Cys Val Val Val Asp₂₆₅ Val Ser Gln Glu Asp₂₇₀ Pro Glu

Val Gln Phe Asn Trp Tyr Val Asp₂₈₀ Gly Val Glu Val His₂₈₅ Asn Ala Lys

Thr Lys Pro Arg Glu Glu Gln₂₉₅ Phe Asn Ser Thr Tyr₃₀₀ Arg Val Val Ser

Val Leu Thr Val Leu His₃₁₀ Gln Asp Trp Leu Asn₃₁₅ Gly Lys Glu Tyr Lys₃₂₀

Cys Lys Val Ser Asn₃₂₅ Lys Gly Leu Pro Ser₃₃₀ Ser Ile Glu Lys Thr₃₃₅ Ile

Ser Lys Ala Lys₃₄₀ Gly Gln Pro Arg Glu₃₄₅ Pro Gln Val Tyr Thr₃₅₀ Leu Pro

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 254

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 254

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Asn Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser His Trp Pro Asn
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

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Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 255
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 255
Thr Asp Ala Ile His
1 5

<210> 256
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 256
Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 257
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 257
Gly Arg Tyr Ser Tyr Tyr Tyr Tyr Phe Asp Tyr
1 5 10

<210> 258
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 258
 Arg Ala Ser Gln Ser Val Asn Asn Tyr Leu Ala
 1 5 10

<210> 259
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 259
 Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 260
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 260
 Gln Gln Arg Ser His Trp Pro Asn Thr
 1 5

<210> 261
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 261
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Tyr
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe
 50 55 60

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Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 262

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 262

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser His Ser Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

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Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 263
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 263
Thr Tyr Ala Ile His
1 5

<210> 264
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 264
Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 265
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 265
Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr
1 5 10

<210> 266
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 266
Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 267
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 267
Asp Ala Ser Tyr Arg Ala Thr
1 5

<210> 268
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 268
Gln Gln Arg Ser His Ser Pro Leu Thr
1 5

<210> 269
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 269
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Asp Ser Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

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Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320

JB15075USNPSL.txt

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 270

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 270

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Glu Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser His Ser Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 271
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 271
Ser Asp Ala Ile His
1 5

<210> 272
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 272
Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 273
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 273

Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr
1 5 10

<210> 274

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 274

Arg Ala Ser Gln Ser Val Arg Asn Tyr Leu Ala
1 5 10

<210> 275

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 275

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 276

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 276

Gln Gln Arg Ser His Ser Pro Ile Thr
1 5

<210> 277

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 277

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Lys Ser Ala
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45
 Gly Tyr Ile Ser Pro Tyr Tyr Gly Ser Ala Tyr Tyr Ala Gln Lys Phe
 50 55 60
 Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80
 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Gly Arg Ile Ala Tyr Tyr Tyr Val Phe Asp Tyr Trp Gly Gln
 100 105 110
 Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125
 Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300

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Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 278

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 278

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

JB15075USNPSL.txt

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 279
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 279
Ser Ala Tyr Ile His
1 5

<210> 280
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 280
Tyr Ile Ser Pro Tyr Tyr Gly Ser Ala Tyr Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 281
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 281
 Gly Arg Ile Ala Tyr Tyr Tyr Val Phe Asp Tyr
 1 5 10

<210> 282
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 282
 Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
 1 5 10

<210> 283
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 283
 Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 284
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 284
 Gln Gln Arg Ser Asn Trp Pro Ile Thr
 1 5

<210> 285
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 285
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

JB15075USNPSL.txt

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Asp Ser Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 286

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 286

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

JB15075USNPSL.txt

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 287

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 287

Ser Asp Ala Ile His
1 5

<210> 288

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 288

Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 289
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 289
 Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr
 1 5 10

<210> 290
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 290
 Arg Ala Ser Gln Ser Val Ser Asn Tyr Leu Ala
 1 5 10

<210> 291
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 291
 Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 292
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 292
 Gln Gln Arg Ser Asn Trp Pro Ile Thr
 1 5

<210> 293
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

JB15075USNPSL.txt

<400> 293

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Tyr Tyr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 294

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 294

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

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Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 295
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 295
Thr Asp Ala Ile His
1 5

<210> 296
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 296

Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 297
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 297
 Gly Arg Tyr Ser Tyr Tyr Tyr Tyr Phe Asp Tyr
 1 5 10

<210> 298
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 298
 Arg Ala Ser Gln Ser Val Arg Ser Tyr Leu Ala
 1 5 10

<210> 299
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 299
 Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 300
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 300
 Gln Gln Arg Ser Asn Trp Pro Ile Thr
 1 5

<210> 301
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 301

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Lys Ser Ala
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ser Pro Tyr Tyr Gly Ser Ala Tyr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Ile Ala Tyr Tyr Tyr Val Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

JB15075USNPSL.txt

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 302

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 302

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Asn Tyr
20 25 30

JB15075USNPSL.txt

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 303

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 303

Ser Ala Tyr Ile His
1 5

<210> 304

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 304

Tyr Ile Ser Pro Tyr Tyr Gly Ser Ala Tyr Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 305

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 305

Gly Arg Ile Ala Tyr Tyr Tyr Val Phe Asp Tyr
1 5 10

<210> 306

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 306

Arg Ala Ser Gln Ser Val Arg Asn Tyr Leu Ala
1 5 10

<210> 307

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 307

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 308

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 308

Gln Gln Arg Ser Asn Trp Pro Ile Thr
1 5

<210> 309

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 309

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

JB15075USNPSL.txt

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 310

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 310

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

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Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Lys Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 311

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 311

Thr Asp Ala Ile His
1 5

<210> 312

<211> 17

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 312
Tyr Ile Ile Pro Ile Ser Gly Asn Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 313
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 313
Gly Arg Tyr Ala Tyr Asn Trp Gly Phe Asp Tyr
1 5 10

<210> 314
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 314
Arg Ala Ser Gln Ser Val Ser Thr Tyr Leu Ala
1 5 10

<210> 315
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 315
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 316
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 316

Gln Gln Arg Ser Asn Trp Pro Ile Thr
1 5

<210> 317

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 317

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Lys Ser Ala
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ser Pro Tyr Tyr Gly Ser Ala Tyr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Ile Ala Tyr Tyr Tyr Val Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 318

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 318

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Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15
 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
 20 25 30
 Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45
 Lys Asp Ala Ser Asp Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80
 Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Ile
 85 90 95
 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190
 Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205
 Phe Asn Arg Gly Glu Cys
 210

<210> 319

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 319

Ser Ala Tyr Ile His
1 5

<210> 320
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 320
 Tyr Ile Ser Pro Tyr Tyr Gly Ser Ala Tyr Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 321
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 321
 Gly Arg Ile Ala Tyr Tyr Tyr Val Phe Asp Tyr
 1 5 10

<210> 322
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 322
 Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
 1 5 10

<210> 323
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 323
 Asp Ala Ser Asp Arg Ala Thr
 1 5

<210> 324
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 324

Gln Gln Arg Ser Asn Trp Pro Ile Thr
1 5

<210> 325

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 325

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Tyr
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

JB15075USNPSL.txt

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 326
<211> 214
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 326

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Asn
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 327

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 327
 Thr Tyr Ala Ile His
 1 5

<210> 328
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 328
 Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 329
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 329
 Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr
 1 5 10

<210> 330
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 330
 Arg Ala Ser Gln Ser Val Ser Asn Tyr Leu Ala
 1 5 10

<210> 331
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 331
 Asp Ala Ser Asn Arg Ala Thr
 1 5

<210> 332
 <211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 332

Gln Gln Arg Ser Asn Trp Pro Asn Thr
1 5

<210> 333

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 333

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Tyr
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

JB15075USNPSL.txt

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 334

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 334

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

His Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Asn
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 335

<211> 5

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 335
Thr Tyr Ala Ile His
1 5

<210> 336
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 336
Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 337
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 337
Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr
1 5 10

<210> 338
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 338
Arg Ala Ser Gln Ser Val Ser Asn Tyr Leu Ala
1 5 10

<210> 339
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 339
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 340
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 340
 Gln Gln Arg Ser Asn Trp Pro Asn Thr
 1 5

<210> 341
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 341
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Asp
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Tyr Tyr Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
 405 410 415
 Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
 420 425 430
 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440 445

<210> 342
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 342
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Ile
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 343
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 343
 Thr Asp Ala Ile His
 1 5

<210> 344
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 344
 Arg Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 345
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 345
 Gly Arg Tyr Ser Tyr Tyr Tyr Tyr Phe Asp Tyr
 1 5 10

<210> 346
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 346
 Arg Ala Ser Gln Ser Val Ser Thr Tyr Leu Ala
 1 5 10

<210> 347
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 347
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 348
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 348
Gln Gln Arg Ser Asn Trp Pro Ile Thr
1 5

<210> 349
<211> 447
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 349
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Asp Ser Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

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Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 435 440 445

<210> 350
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 350
 Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Tyr
 20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
 35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
 65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Ser Pro Ile
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
 100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
 115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
 130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 351
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 351
Ser Asp Ala Ile His
1 5

<210> 352
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 352
Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 353
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 353
Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr
1 5 10

<210> 354
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 354
Arg Ala Ser Gln Ser Val Ser Thr Tyr Leu Ala
1 5 10

<210> 355
<211> 7
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 355

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 356

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 356

Gln Gln Arg Ser Asn Ser Pro Ile Thr
1 5

<210> 357

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 357

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Asp Ser Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

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Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400
 Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
 405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 358

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 358

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Thr Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Glu Asp Ala Ser Tyr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Ser Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 359
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 359
 Ser Asp Ala Ile His
 1 5

<210> 360
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 360
 Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
 1 5 10 15

Gly

<210> 361
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 361
 Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr
 1 5 10

<210> 362
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 362
 Arg Ala Ser Gln Ser Val Ser Thr Tyr Leu Ala
 1 5 10

<210> 363
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 363
 Asp Ala Ser Tyr Arg Ala Thr
 1 5

<210> 364
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 364
 Gln Gln Arg Ser Asn Ser Pro Ile Thr
 1 5

<210> 365
 <211> 447
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 365
 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Asp Ala
 20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
 35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
 50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Gly Arg Ala Arg Tyr Arg Trp Ala Phe Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
 115 120 125

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Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
 130 135 140
 Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
 145 150 155 160
 Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
 165 170 175
 Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
 180 185 190
 Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
 195 200 205
 Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
 210 215 220
 Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
 225 230 235 240
 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
 245 250 255
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
 260 265 270
 Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
 275 280 285
 Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
 290 295 300
 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
 305 310 315 320
 Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
 325 330 335
 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
 340 345 350
 Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
 355 360 365
 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
 370 375 380
 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 366

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 366

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Glu Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 367
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 367
Asp Ala Ala Ile His
1 5

<210> 368
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 368
Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 369
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 369
Gly Arg Ala Arg Tyr Arg Trp Ala Phe Asp Tyr
1 5 10

<210> 370
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 370

Arg Ala Ser Gln Ser Val Ser Asn Tyr Leu Ala
1 5 10

<210> 371

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 371

Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 372

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 372

Gln Gln Arg Ser Asn Tyr Pro Leu Thr
1 5

<210> 373

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 373

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Asp Ser Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr Trp Gly Gln
100 105 110

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Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 374

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 374

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Tyr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 375
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 375
Ser Asp Ala Ile His
1 5

<210> 376
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 376
Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 377
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 377
Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr
1 5 10

<210> 378
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 378

Arg Ala Ser Gln Ser Val Arg Asn Tyr Leu Ala
1 5 10

<210> 379

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 379

Asp Ala Ser Ser Arg Ala Thr
1 5

<210> 380

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 380

Gln Gln Arg Ser Asn Tyr Pro Ile Thr
1 5

<210> 381

<211> 447

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 381

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Asp Ser Asp
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

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Ala Arg Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro
210 215 220

Pro Cys Pro Pro Cys Pro Ala Pro Glu Ala Ala Gly Gly Pro Ser Val
225 230 235 240

Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
245 250 255

Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu
260 265 270

Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
275 280 285

Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser
290 295 300

Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
305 310 315 320

Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile
325 330 335

Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
340 345 350

Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
355 360 365

Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
370 375 380

Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
385 390 395 400

Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg
405 410 415

Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
420 425 430

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
435 440 445

<210> 382

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 382

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Arg Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 383
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 383
Ser Asp Ala Ile His
1 5

<210> 384
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 384
Tyr Ile Ile Pro Ile Ser Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln
1 5 10 15

Gly

<210> 385
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 385
Gly Arg Tyr Ser Tyr Arg Trp Thr Phe Asp Tyr
1 5 10

<210> 386
<211> 11

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 386
Arg Ala Ser Gln Ser Val Arg Asn Tyr Leu Ala
1 5 10

<210> 387
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 387
Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 388
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 388
Gln Gln Arg Ser Asn Trp Pro Ile Thr
1 5

<210> 389
<211> 377
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown: Human or mouse polypeptide

<400> 389
Gln Glu Thr Glu Leu Ser Val Ser Ala Glu Leu Val Pro Thr Ser Ser
1 5 10 15

Trp Asn Ile Ser Ser Glu Leu Asn Lys Asp Ser Tyr Leu Thr Leu Asp
20 25 30

Glu Pro Met Asn Asn Ile Thr Thr Ser Leu Gly Gln Thr Ala Glu Leu
35 40 45

His Cys Lys Val Ser Gly Asn Pro Pro Pro Thr Ile Arg Trp Phe Lys
50 55 60

Asn Asp Ala Pro Val Val Gln Glu Pro Arg Arg Leu Ser Phe Arg Ser
65 70 75 80

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Thr Ile Tyr Gly Ser Arg Leu Arg Ile Arg Asn Leu Asp Thr Thr Asp
85 90 95

Thr Gly Tyr Phe Gln Cys Val Ala Thr Asn Gly Lys Glu Val Val Ser
100 105 110

Ser Thr Gly Val Leu Phe Val Lys Phe Gly Pro Pro Pro Thr Ala Ser
115 120 125

Pro Gly Tyr Ser Asp Glu Tyr Glu Glu Asp Gly Phe Cys Gln Pro Tyr
130 135 140

Arg Gly Ile Ala Cys Ala Arg Phe Ile Gly Asn Arg Thr Val Tyr Met
145 150 155 160

Glu Ser Leu His Met Gln Gly Glu Ile Glu Asn Gln Ile Thr Ala Ala
165 170 175

Phe Thr Met Ile Gly Thr Ser Ser His Leu Ser Asp Lys Cys Ser Gln
180 185 190

Phe Ala Ile Pro Ser Leu Cys His Tyr Ala Phe Pro Tyr Cys Asp Glu
195 200 205

Thr Ser Ser Val Pro Lys Pro Arg Asp Leu Cys Arg Asp Glu Cys Glu
210 215 220

Ile Leu Glu Asn Val Leu Cys Gln Thr Glu Tyr Ile Phe Ala Arg Ser
225 230 235 240

Asn Pro Met Ile Leu Met Arg Leu Lys Leu Pro Asn Cys Glu Asp Leu
245 250 255

Pro Gln Pro Glu Ser Pro Glu Ala Ala Asn Cys Ile Arg Ile Gly Ile
260 265 270

Pro Met Ala Asp Pro Ile Asn Lys Asn His Lys Cys Tyr Asn Ser Thr
275 280 285

Gly Val Asp Tyr Arg Gly Thr Val Ser Val Thr Lys Ser Gly Arg Gln
290 295 300

Cys Gln Pro Trp Asn Ser Gln Tyr Pro His Thr His Thr Phe Thr Ala
305 310 315 320

Leu Arg Phe Pro Glu Leu Asn Gly Gly His Ser Tyr Cys Arg Asn Pro
325 330 335

Gly Asn Gln Lys Glu Ala Pro Trp Cys Phe Thr Leu Asp Glu Asn Phe
340 345 350

Lys Ser Asp Leu Cys Asp Ile Pro Ala Cys Asp Ser Lys Asp Ser Lys
355 360 365

Glu Lys Asn Lys Met Glu Ile Leu Tyr
370 375

<210> 390

<211> 223

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 390

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Thr Tyr
20 25 30

Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Arg Ile Ile Pro Ile Glu Gly Arg Ala Tyr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Arg Tyr Ser Tyr Arg Tyr Trp Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val
115 120 125

Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala
130 135 140

Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser
145 150 155 160

Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val
165 170 175

Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro
180 185 190

Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
195 200 205

Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys
210 215 220

<210> 391

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 391

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
195 200 205

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Phe Asn Arg Gly Glu Cys
210