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(54) Title: ANTIGEN-BINDING PROTEIN CONSTRUCTS AND ANTIBODIES AND USES THEREOF

(57) Abstract: Provided herein are antigen-binding protein constructs and antibodies and uses of the same.

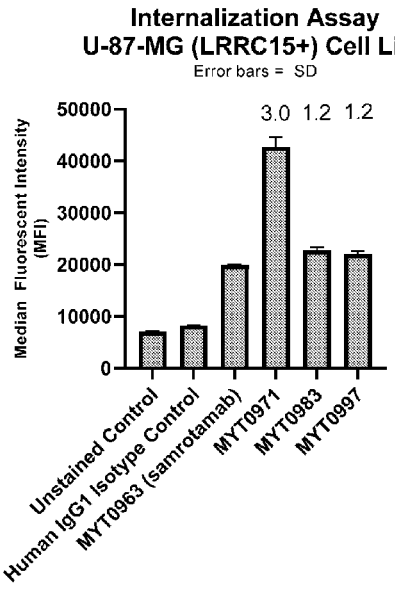


FIG. 41A

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ANTIGEN-BINDING PROTEIN CONSTRUCTS AND ANTIBODIES AND USES THEREOF

CROSS-REFERENCE TO RELATED APPLICATION

This application claims priority to U.S. Provisional Patent Application Serial No. 63/171,705, filed April 7, 2021; the entire contents of which are herein incorporated by reference.

TECHNICAL FIELD

The present disclosure relates to the field of biotechnology, and more specifically, to antigen-binding molecules.

SEQUENCE LISTING

This application contains a Sequence Listing that has been submitted electronically as an ASCII text file named 45395-0045WO_SL.txt. The ASCII text file, created on April 4, 2022, is 515 kilobytes in size. The material in the ASCII text file is hereby incorporated by reference in its entirety.

BACKGROUND

Antibody-drug-conjugates have been designed to combat a variety of diseases. One particular advantage of this approach is the ability for antibody-drug conjugates to have cytostatic or cytotoxic effects. Despite years of development, improved antibody-drug conjugates are desired.

SUMMARY

The present invention is based on the concept that antigen-binding protein constructs and antibodies can be generated that display enhanced efficacy (e.g., one or more of an increase (e.g., a detectable increase) in toxin liberation in a target mammalian cell, an increase (e.g., a detectable increase) in target mammalian cell killing, and an increase (e.g., a detectable increase) in endolysosomal delivery).

Provided herein are antibodies, where the antibody includes (a) a heavy chain variable domain and a light chain variable domain selected from the group of: (i) a heavy chain variable

domain that is at least 90% identical to SEQ ID NO: 1 and where the heavy chain variable domain includes a histidine at one or more positions in SEQ ID NO: 1 selected from the group consisting of: 33, 34, 50, 52, 57, 59, 100, 102, 103, 107, 108, and 109; and/or a light chain variable domain that is at least 90% identical to SEQ ID NO: 2, where the light chain variable domain includes a histidine at one or more positions in SEQ ID NO: 2 selected from the group consisting of: 32, 34, 50, 51, 89, 90, 92, 93, 94, and 96; (ii) a heavy chain variable domain that is at least 90% identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at one or more positions in SEQ ID NO: 84 selected from the group consisting of: 27, 29, 32, 50, 54, 58, 99, 100, 102, 104, and 105 and/or a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, where the light chain variable domain includes a histidine at one or more positions in SEQ ID NO: 85 selected from the group consisting of: 29, 31, 32, 34, 36, 37, 38, 40, 56, 60, 61, 95, 96, 97, and 100; (iii) a heavy chain variable domain that is at least 90% identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at one or more positions in SEQ ID NO: 178 selected from the group consisting of: 33, 52, 56, 57, or 106; and/or a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, where the light chain variable domain includes a histidine at one or more positions in SEQ ID NO: 179 selected from the group consisting of 25, 26, 28, 29, 31, 36, 37, 57, 59, 94, 95, 96, and 100; and (iv) a heavy chain variable domain that is at least 90% identical to SEQ ID NO: 272, where the heavy chain variable domain includes a histidine at one or more positions in SEQ ID NO: 272 selected from the group consisting of: 24, 27, 29, 62, 63, 98, and 108 and/or a light chain variable domain that is at least 90% identical to SEQ ID NO: 273, where the light chain variable domain includes a histidine at one or more positions in SEQ ID NO: 273 selected from the group consisting of 27, 28, 29, 31, 32, 89, 92, and 93; (b) a heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 including one or more of the following: (i) a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139; (ii) a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317; and (iii) an alanine to a cysteine substitution at amino acid position 1; and/or a light chain C_L sequence of SEQ ID NO: 353 including a valine to cysteine substitution at amino acid position 98.

In some embodiments the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317. In some embodiments, the antibody includes heavy chain and light chain sequences selected from the group of: (i) SEQ ID NO: 354 and SEQ ID NO: 2, respectively; (ii) SEQ ID NO: 360 and SEQ ID NO: 85, respectively; (iii) SEQ ID NO: 366 and SEQ ID NO: 179, respectively; and (iv) SEQ ID NO: 372 and SEQ ID NO: 273, respectively.

In some embodiments, the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139. In some embodiments, the antibody includes heavy chain and light chain sequences selected from the group of: (i) SEQ ID NO: 355 and SEQ ID NO: 2, respectively; (ii) SEQ ID NO: 361 and SEQ ID NO: 85, respectively; (iii) SEQ ID NO: 366 and SEQ ID NO: 179, respectively; and (iv) SEQ ID NO: 373 and SEQ ID NO: 273, respectively.

In some embodiments, the antibody includes the light chain C_L sequence of SEQ ID NO: 353 includes a valine to cysteine substitution at amino acid position 98. In some embodiments, the antibody includes heavy chain and light chain sequences selected from the group of: (i) SEQ ID NO: 1 and SEQ ID NO: 359, respectively; (ii) SEQ ID NO: 84 and SEQ ID NO: 365, respectively; (iii) SEQ ID NO: 178 and SEQ ID NO: 371, respectively; and (iv) SEQ ID NO: 272 and SEQ ID NO: 377, respectively.

In some embodiments, the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317; and the light chain C_L sequence of SEQ ID NO: 353 includes a valine to cysteine substitution at amino acid position 98. In some embodiments, the antibody includes heavy chain and light chain sequences selected from the group of: (i) SEQ ID NO: 354 and SEQ ID NO: 359, respectively; (ii) SEQ ID NO: 360 and SEQ ID NO: 365, respectively; (iii) SEQ ID NO: 366 and SEQ ID NO: 371, respectively; and (iv) SEQ ID NO: 372 and SEQ ID NO: 377, respectively;

In some embodiments, the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: a methionine to tyrosine substitution at amino acid position 135, a

serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139; and the light chain C_L sequence of SEQ ID NO: 353 includes a valine to cysteine substitution at amino acid position 98. In some embodiments, the antibody includes heavy chain and light chain sequences selected from the group of: (i) SEQ ID NO: 355 and SEQ ID NO: 359, respectively; (ii) SEQ ID NO: 361 and SEQ ID NO: 365, respectively; (iii) SEQ ID NO: 367 and SEQ ID NO: 371, respectively; and (iv) SEQ ID NO: 373 and SEQ ID NO: 377, respectively.

In some embodiments, the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: an alanine to a cysteine substitution at amino acid position 1. In some embodiments, the antibody includes heavy chain and light chain sequences selected from the group of: (i) SEQ ID NO: 356 and SEQ ID NO: 2, respectively; (ii) SEQ ID NO: 362 and SEQ ID NO: 85, respectively; (iii) SEQ ID NO: 368 and SEQ ID NO: 179, respectively; and (iv) SEQ ID NO: 374 and SEQ ID NO: 273, respectively.

In some embodiments, the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317; and an alanine to a cysteine substitution at amino acid position 1. In some embodiments, the antibody includes a heavy chain and a light chain sequence selected from the group of: (i) SEQ ID NO: 357 and SEQ ID NO: 2, respectively; (ii) SEQ ID NO: 363 and SEQ ID NO: 85, respectively; (iii) SEQ ID NO: 369 and SEQ ID NO: 179, respectively; and (iv) SEQ ID NO: 375 and SEQ ID NO: 273, respectively.

In some embodiments, the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139; and an alanine to a cysteine substitution at amino acid position 1. In some embodiments, the antibody includes a heavy chain and a light chain sequence selected from the group of: (i) SEQ ID NO: 358 and SEQ ID NO: 2, respectively; (ii) SEQ ID NO: 364 and SEQ ID NO: 85, respectively; (iii) SEQ ID NO: 370 and SEQ ID NO: 179, respectively; and (iv) SEQ ID NO: 376 and SEQ ID NO: 273, respectively.

In some embodiments, the antibody includes a cytotoxic drug conjugated to one or more of the following: (a) a heavy chain CH1-CH2-CH3 of SEQ ID NO: 351 or SEQ ID NO: 352 including one or more of the following: (i) the cysteine at amino acid position 103; (ii) the

cysteine at amino acid position 109; (iii) the cysteine at amino acid position 112; and/or (b) the cysteine at amino acid position 107 of SEQ ID NO: 353.

In some embodiments, the antibody includes a cytotoxic or cytostatic agent is conjugated to the cysteine at position 98 of SEQ ID NO: 353. In some embodiments, the antibody includes a cytotoxic or cytostatic agent is conjugated to the cysteine at position 1 of SEQ ID NO: 351 or SEQ ID NO: 352. In some embodiments, the cytotoxic or cytostatic agent is a conjugated toxin, a radioisotope, drug, or a small molecule.

In some embodiments, the (a) the dissociation rate of the antibody at a pH of about 4.0 to about 6.5 is faster than the dissociation rate at a pH of about 7.0 to about 8.0; or (b) the dissociation constant (K_D) of the antibody at a pH of about 4.0 to about 6.5 is greater than the K_D at a pH of about 7.0 to about 8.0.

In some embodiments, a composition including the antibody: provides for one or more of: an increase in toxin liberation in a target mammalian cell as compared to a composition including the same amount of a control antibody; an increase in target mammalian cell killing as compared to a composition including the same amount of a control antibody; and an increase in endolysosomal delivery in the target mammalian cell as compared to a composition including the same amount of a control antibody.

In some embodiments, where a composition including the antibody: results in a less of a reduction in the level of LRRC15presented on the surface of a target mammalian cell as compared to a composition including the same amount of a control antibody; or does not result in a detectable reduction in the level of LRRC15presented on the surface of the target mammalian cell.

In some embodiments, the antibody is degraded in a target mammalian cell following internalization of the antibody by a target mammalian cell. In some embodiments, the target mammalian cell is a cancer cell. In some embodiments, the antibody is cytotoxic or cytostatic to the target mammalian cell. In some embodiments, the antibody has an avidity that results in increased selectivity for cancer cells over non-cancerous cells.

In some embodiments, the antibody is: cross-reactive with a non-human primate LRRC15 and human LRRC15; or cross-reactive with a non-human primate LRRC15, a human LRRC15, and one or both of rat LRRC15 and a mouse LRRC15.

In some embodiments, the half-life of the antibody in vivo is increased as compared to the half-life of a control antibody in vivo.

Also provided herein are pharmaceutical compositions including an effective amount of any one of the antibodies described herein where the first antigen-binding domain includes one of (a) through (d): (a) a light chain variable domain of SEQ ID NO: 2, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, or SEQ ID NO: 78 and/or a heavy chain variable domain of SEQ ID NO: 1, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, or SEQ ID NO: 83, where the first antigen-binding domain does not include (i) a light chain variable domain of SEQ ID NO: 2 and a heavy chain variable domain of SEQ ID NO: 1; (ii) a light chain variable domain of SEQ ID NO: 2 and heavy chain variable domain that is not one of SEQ ID NOs: 20, 21, 23, 25, 30, 32, 43, 45, 46, 50-52, or 80-83; or (iii) a heavy chain variable domain of SEQ ID NO: 1 and a light chain variable domain that is not one of SEQ ID NOs: 61, 63-65, 71, 72, 74-76, or 78; (b) a light chain variable domain of SEQ ID NO: 85, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 149, SEQ ID NO: 153, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 157, SEQ ID NO: 158, SEQ ID NO: 161, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, or SEQ ID NO: 177, and/or a heavy chain variable domain of SEQ ID NO: 84, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 98, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 106, SEQ ID NO: 110, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, or SEQ ID NO: 166, where the first antigen-binding domain does not include (i) a light chain variable domain of SEQ ID NO: 85 and a heavy chain variable domain of SEQ ID NO: 84; (ii) a light chain variable domain of SEQ ID NO: 85 and heavy chain variable domain that is not one of SEQ ID NOs: 93, 95, 98, 101, 102, 106, 110, 120-122, 124, 126, 127, or 166; or (iii) a heavy chain variable domain of SEQ ID NO: 84 and a light chain variable domain that is not one of SEQ ID NOs: 137, 139, 140, 142, 144-146, 148, 149, 153, 154, 156-158, 161, or 169-177; (c) a light chain variable domain of SEQ ID NO: 179, SEQ ID NO: 229, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO:

240, SEQ ID NO: 241, SEQ ID NO: 246, SEQ ID NO: 248 SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 253, SEQ ID NO: 257, SEQ ID NO: 263, SEQ ID NO: 264, SEQ ID NO: 268, SEQ ID NO: 269, SEQ ID NO: 270, or SEQ ID NO: 271, and/or a heavy chain variable domain of SEQ ID NO: 178, SEQ ID NO: 196, SEQ ID NO: 201, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 225, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261, where the first antigen-binding domain does not include (i) a light chain variable domain of SEQ ID NO: 179 and a heavy chain variable domain of SEQ ID NO: 178; (ii) a light chain variable domain of SEQ ID NO: 179 and heavy chain variable domain that is not one of SEQ ID NOs: 196, 201, 205, 206, 225, or 258-261; or (iii) a heavy chain variable domain of SEQ ID NO: 178 and a light chain variable domain that is not one of SEQ ID NOs: 229, 230, 232, 233, 235, 240, 241, 246, 248, 251-253, 257, 263, 264, or 268-271; and (d) a light chain variable domain of SEQ ID NO: 273, SEQ ID NO: 327, SEQ ID NO: 328, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 332, SEQ ID NO: 342, SEQ ID NO: 345, or SEQ ID NO: 346 and/or a heavy chain variable domain of SEQ ID NO: 272, SEQ ID NO: 281, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 311, or SEQ ID NO: 321, where the first antigen-binding domain does not include (i) a light chain variable domain of SEQ ID NO: 273 and a heavy chain variable domain of SEQ ID NO: 272; (ii) a light chain variable domain of SEQ ID NO: 273 and heavy chain variable domain that is not one of SEQ ID NOs: 281, 284, 286, 305, 306, 311, or 321; or (iii) a heavy chain variable domain of SEQ ID NO: 272 and a light chain variable domain that is not one of SEQ ID NOs: 327-329, 331, 332, 342, 345, or 346.

Also provided herein are kits including at least one dose of the antibody of any of the antibodies described herein or any of the pharmaceutical compositions described herein.

Also provided herein are method of treating a cancer characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface, the method including: administering a therapeutically effective amount of the antibody of any one of the antibodies described herein or any one of the pharmaceutical compositions described herein to a subject identified as having a cancer characterized by having the population of cancer cells.

Also provided herein are methods of reducing the volume of a tumor in a subject, where the tumor is characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface, the method including: administering a

therapeutically effective amount of the antibody of any one of the antibodies described herein or any of the pharmaceutical compositions described herein to a subject identified as having a cancer characterized by having the population of cancer cells.

Also provided herein are methods of inducing cell death in a cancer cell in a subject, where the cancer cell has LRRC15 or an epitope of LRRC15 presented on its surface, where the method includes: administering a therapeutically effective amount of the antibody of any one of the antibodies described herein or any one of the pharmaceutical compositions described herein to a subject identified as having a cancer characterized by having a population of the cancer cells.

Also provided herein are methods of decreasing the risk of developing a metastasis or decreasing the risk of developing an additional metastasis in a subject having a cancer, where the cancer is characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface the method including: administering a therapeutically effective amount of the antibody of any one of the antibodies described herein or the any one of the pharmaceutical compositions described herein to a subject identified as having a cancer characterized by having the population of cancer cells.

Also provided herein are antibodies, where the antibody includes: (a) heavy chain variable domain and a light chain variable domain selected from the group consisting of: (i) SEQ ID NO: 1 and SEQ ID NO: 2, respectively; (ii) SEQ ID NO: 84 and SEQ ID NO: 85, respectively; (iii) SEQ ID NO: 178 and SEQ ID NO: 179, respectively; and (iv) SEQ ID NO: 272 and SEQ ID NO: 273, respectively; (b) a heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 including one or more of the following substitution(s): (i) a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139; (ii) a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317; and (iii) an alanine to cysteine substitution at amino acid position 1; and/or a light chain C_L sequence of SEQ ID NO: 353 including a valine to cysteine substitution at position 98.

In some embodiments, the heavy CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317. In some embodiments, the antibody

includes heavy chain and light chain sequences selected from the group of: (i) SEQ ID NO: 354 and SEQ ID NO: 2, respectively; (ii) SEQ ID NO: 360 and SEQ ID NO: 85, respectively; (iii) SEQ ID NO: 366 and SEQ ID NO: 179, respectively; and (iv) SEQ ID NO: 372 and SEQ ID NO: 273, respectively.

In some embodiments, the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139. In some embodiments, the antibody includes a heavy chain and a light chain sequence selected from the group of: (i) SEQ ID NO: 355 and SEQ ID NO: 2, respectively; (ii) SEQ ID NO: 361 and SEQ ID NO: 85, respectively; (iii) SEQ ID NO: 366 and SEQ ID NO: 179, respectively; and (iv) SEQ ID NO: 373 and SEQ ID NO: 273, respectively.

In some embodiments, the light chain C_L sequence of SEQ ID NO: 353 includes a valine to cysteine substitution at amino acid position 98. In some embodiments, the antibody includes heavy chain and light chain sequences selected from the group of: (i) SEQ ID NO: 1 and SEQ ID NO: 359, respectively; (ii) SEQ ID NO: 84 and SEQ ID NO: 365, respectively; (iii) SEQ ID NO: 178 and SEQ ID NO: 371, respectively; and (iv) SEQ ID NO: 272 and SEQ ID NO: 377, respectively.

In some embodiments, the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317; and the light chain C_L sequence of SEQ ID NO: 353 includes a valine to cysteine substitution at amino acid position 98.

In some embodiments, the antibody includes heavy chain and light chain sequences selected from the group of: (i) SEQ ID NO: 354 and SEQ ID NO: 359, respectively; (ii) SEQ ID NO: 360 and SEQ ID NO: 365, respectively; (iii) SEQ ID NO: 366 and SEQ ID NO: 371, respectively; and (iv) SEQ ID NO: 372 and SEQ ID NO: 377, respectively.

In some embodiments, the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139; and the light chain C_L sequence of SEQ ID NO: 353 includes a valine to cysteine substitution at amino acid position 98. In some embodiments, the

antibody includes heavy chain and light chain sequences selected from the group of: (i) SEQ ID NO: 355 and SEQ ID NO: 359, respectively; (ii) SEQ ID NO: 361 and SEQ ID NO: 365, respectively; (iii) SEQ ID NO: 367 and SEQ ID NO: 371, respectively; and (iv) SEQ ID NO: 373 and SEQ ID NO: 377, respectively.

In some embodiments, the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: an alanine to a cysteine substitution at amino acid position 1. In some embodiments, the antibody includes heavy chain and light chain sequences selected from the group of: (i) SEQ ID NO: 356 and SEQ ID NO: 2, respectively; (ii) SEQ ID NO: 362 and SEQ ID NO: 85, respectively; (iii) SEQ ID NO: 368 and SEQ ID NO: 179, respectively; and (iv) SEQ ID NO: 374 and SEQ ID NO: 273, respectively.

In some embodiments, the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317; and an alanine to a cysteine substitution at amino acid position 1. In some embodiments, the antibody includes a heavy chain and a light chain sequence selected from the group of: (i) SEQ ID NO: 357 and SEQ ID NO: 2, respectively; (ii) SEQ ID NO: 363 and SEQ ID NO: 85, respectively; (iii) SEQ ID NO: 369 and SEQ ID NO: 179, respectively; and (iv) SEQ ID NO: 375 and SEQ ID NO: 273, respectively.

In some embodiments, the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 includes: a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139; and an alanine to a cysteine substitution at amino acid position 1. In some embodiments, the antibody includes heavy chain and light chain sequences selected from the group of: (i) SEQ ID NO: 358 and SEQ ID NO: 2, respectively; (ii) SEQ ID NO: 364 and SEQ ID NO: 85, respectively; (iii) SEQ ID NO: 370 and SEQ ID NO: 179, respectively; and (iv) SEQ ID NO: 376 and SEQ ID NO: 273, respectively.

In some embodiments, the antibody includes a cytotoxic drug conjugated to one or more of the following: (a) a heavy chain CH1-CH2-CH3 of SEQ ID NO: 351 or SEQ ID NO: 352 including one or more of the following: (i) the cysteine at amino acid position 103; (ii) the cysteine at amino acid position 109; and (iii) the cysteine at amino acid position 112; and/or (b) the cysteine at amino acid position 107 of SEQ ID NO: 353.

In some embodiments, the antibody includes a cytotoxic or cytostatic agent is conjugated to the cysteine at position 98 of SEQ ID NO: 353.

In some embodiments, the antibody includes a cytotoxic or cytostatic agent is conjugated to the cysteine at position 1 of SEQ ID NO: 351 or SEQ ID NO: 352.

In some embodiments, the cytostatic or cytotoxic agent is a conjugated toxin, a radioisotope, drug, or a small molecule. In some embodiments, the antibody is cytotoxic or cytostatic to a target mammalian cell. In some embodiments, the antibody is degraded in the target mammalian cell following internalization of the antibody by the target mammalian cell. In some embodiments, the target mammalian cell is a cancer cell. In some embodiments, the antibody has an avidity that results in increased selectivity for cancer cells over non-cancerous cells.

In some embodiments, the antibody is cross-reactive with a non-human primate LRRC15 and human LRRC15; or cross-reactive with a non-human primate LRRC15, a human LRRC15, and one or both of rat LRRC15 and a mouse LRRC15.

In some embodiments, the half-life of the antibody in vivo is increased as compared to the half-life of a control antibody in vivo.

In some embodiments, the target mammalian cell is a cancer cell.

Also provided herein are pharmaceutical compositions including an effective amount of any one of the antibodies described herein.

Also provided herein are kits including at least one dose of the antibody of any one of the antibodies described herein or any one of the pharmaceutical compositions described herein.

Also provided herein are methods of treating a cancer characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface, the method including: administering a therapeutically effective amount of the antibody of any one of the antibodies described herein or any one of the pharmaceutical compositions described herein to a subject identified as having a cancer characterized by having the population of cancer cells.

Also provided herein are methods of reducing the volume of a tumor in a subject, where the tumor is characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface, the method including: administering a therapeutically effective amount of the antibody of any one of the antibodies described herein or

any one of the pharmaceutical compositions described herein to a subject identified as having a cancer characterized by having the population of cancer cells.

Also provided herein are methods of inducing cell death in a cancer cell in a subject, where the cancer cell has LRRC15 or an epitope of LRRC15presented on its surface, where the method includes: administering a therapeutically effective amount of the antibody of any one of the antibodies described herein or any one of the pharmaceutical compositions described herein to a subject identified as having a cancer characterized by having a population of the cancer cells.

Also provided herein are methods of decreasing the risk of developing a metastasis or decreasing the risk of developing an additional metastasis in a subject having a cancer, where the cancer is characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface the method including: administering a therapeutically effective amount of the antibody of any one of the antibodies described herein or any one of the pharmaceutical compositions described herein to a subject identified as having a cancer characterized by having the population of cancer cells.

As used herein, the term "antigen-binding protein construct" is (i) a single polypeptide that includes at least one antigen-binding domain or (ii) a complex of two or more polypeptides (e.g., the same or different polypeptides) that together form at least one antigen-binding domain. Non-limiting examples and aspects of antigen-binding protein constructs are described herein. Additional examples and aspects of antigen-binding protein constructs are known in the art.

A "multi-specific antigen-binding protein construct" is an antigen-binding protein construct that includes two or more different antigen-binding domains that collectively specifically bind two or more different epitopes. The two or more different epitopes may be epitopes on the same antigen (e.g., a single polypeptide present on the surface of a cell) or on different antigens (e.g., different proteins present on the surface of the same cell or present on the surface of different cells). In some aspects, the antigen is present on the surface of the cell. In some aspects, a multi-specific antigen-binding protein construct binds two different epitopes (i.e., a "bispecific antigen-binding protein construct"). In some aspects, a multi-specific antigen-binding protein construct binds three different epitopes (i.e., a "trispecific antigen-binding protein construct"). In some aspects, a multi-specific antigen-binding protein construct binds four different epitopes (i.e., a "quadspecific antigen-binding protein construct"). In some

aspects, a multi-specific antigen-binding protein construct binds five different epitopes (i.e., a "quintspecific antigen-binding protein construct"). Each binding specificity may be present in any suitable valency. Non-limiting examples of multi-specific antigen-binding protein constructs are described herein.

An "antigen-binding domain" is one or more protein domain(s) (e.g., formed from amino acids from a single polypeptide or formed from amino acids from two or more polypeptides (e.g., the same or different polypeptides) that is capable of specifically binding to one or more different antigen(s). In some examples, an antigen-binding domain can bind to an antigen or epitope with specificity and affinity similar to that of naturally-occurring antibodies. In some embodiments, the antigen-binding domain can be an antibody or a fragment thereof. In some embodiments, an antigen-binding domain can include an alternative scaffold. Non-limiting examples of antigen-binding domains are described herein. Additional examples of antigen-binding domains are known in the art. In some examples, an antigen-binding domain can bind to a single antigen.

The term "antibody" is used herein in its broadest sense and includes certain types of immunoglobulin molecules that include one or more antigen-binding domains that specifically bind to an antigen or epitope. An antibody specifically includes, e.g., intact antibodies (e.g., intact immunoglobulins, e.g., human IgG (e.g., human IgG1, human IgG2, human IgG3, human IgG4)), antibody fragments, and multi-specific antibodies. One example of an antigen-binding domain is an antigen-binding domain formed by a VH -VL dimer. Additional examples of an antibody are described herein. Additional examples of an antibody are known in the art.

The phrase "endosomal/lysosomal pathway" refers to a network of endosomes (early endosomes, multi-vesicular bodies, late endosomes, and lysosomes) in the cytoplasm of a mammalian cell, wherein molecules internalized through cell-mediated internalization processes, e.g., pinocytosis, micropinocytosis, receptor-mediated endocytosis, and/or phagocytosis, are sorted.

Once the endosomes in the endosomal/lysosomal pathway are purified or isolated, assays for a target protein (e.g., an antigen-binding protein construct described herein) can be performed using methods known in the art (ELISA, Western blot, immunofluorescence, and immunoprecipitation followed by an assay for protein concentration), and can be used to determine the concentration or relative level of the target protein in the endosomes.

Alternatively, endosomes in the endosomal/lysosomal pathway can be imaged using immunofluorescence microscopy using an detectably-labelled antibody (e.g., a fluorophore-labelled, a dye-labelled, or a GFP-labelled antibody, e.g., CellLight™ Early Endosome-GFP) that specifically binds to a characteristic protein present in the endosomes (e.g., EEA1 for early endosomes) and a fluorophore-labelled antibody that specifically binds to the protein of interest (e.g., an antigen-binding protein construct), and the level of the target protein in the endosomes can be determined by quantitation of the overlap in the fluorescence emissions of the two different antibodies.

The phrase "endolysosomal delivery" refers to rate of accumulation over time or the total accumulation at a specific timepoint of an antigen-binding protein construct (e.g., any of the antigen-binding protein constructs described herein) in the endosomal/lysosomal pathway in a mammalian cell (e.g., any of the exemplary target mammalian cells described herein).

An exemplary method to calculate the increase in endolysosomal delivery of a pH engineered ABPC variant as compared to its corresponding starting ABPC from cellular fluorescence data is to measure the ratio of the variant's mean fluorescence intensity minus the mean fluorescence intensity of a non-binding IgG control, then all divided by the variant's corresponding starting ABPC's mean fluorescence intensity minus the mean fluorescence intensity of the IgG control.

An exemplary assay for measuring endolysosomal delivery of any of the ABPCs described herein include those which involve labeling of an ABPC with a fluorescent dye, followed by incubation of the labeled ABPC with cells and measurement of cellular fluorescence as an indicator of endolysosomal delivery of the ABPC (e.g., as described generally in Wustner, *Traffic* 7(6):699-715, 2006). Alternatively, pH-sensitive dyes which preferentially fluoresce at acidic pH but not neutral pH can be used to label any of the ABPCs described herein, which can then be incubated with cells and the cellular fluorescence measured as an indicator of delivery of the ABPC into acidic endolysosomal compartments.

The term "population" when used before a noun means two or more of the specific noun. For example, the phrase "a population of cancer cells" means "two or more cancer cells." Non-limiting examples of cancer cells are described herein.

The phrase "cytostatic to a cell" refers to a direct or indirect decrease in the proliferation (cell division) of the cell (e.g., a cancer cell) *in vivo* or *in vitro*. When an agent is cytostatic to a

cell, the agent can, e.g., directly or indirectly result in cell cycle arrest of the cell (e.g., a cancer cell). In some examples, an agent that is cytostatic to a cell can reduce the number of cells in a population of the cells that are in S phase (as compared to the number of cells in a population of the cells that are in S phase prior to contact with the agent). In some examples, an agent that is cytostatic to a cell can reduce the percentage of the cells in S phase by at least 20%, at least 40%, at least 60%, or at least 80% (e.g., as compared to the percentage of cells in a population of the cells that are in S phase prior to contact with the agent).

The phrase "cytotoxic to a cell" refers to the inducement, directly or indirectly, in the death (e.g., necrosis or apoptosis) of the cell (e.g., a mammalian cell, e.g., a cancer cell).

"Affinity" refers to the strength of the sum total of non-covalent interactions between an antigen-binding site and its binding partner (e.g., an antigen or epitope). Unless indicated otherwise, as used herein, "affinity" refers to intrinsic binding affinity, which reflects a 1:1 interaction between members of an antigen-binding domain and an antigen or epitope. The affinity of a molecule X for its partner Y can be represented by the dissociation equilibrium constant (K_D). Affinity can be measured by common methods known in the art, including those described herein. Affinity can be determined, for example, using surface plasmon resonance (SPR) technology (e.g., BIACORE®) or biolayer interferometry (e.g., FORTEBIO®). Additional methods for determining the affinity for an antigen-binding domain and its corresponding antigen or epitope are known in the art.

The term "epitope" means a portion of an antigen that is specifically bound by an antigen-binding domain through a set of physical interactions between: (i) all monomers (e.g. individual amino acid residues, sugar side chains, and post-translationally modified amino acid residues) on the portion of the antigen-binding domain that specifically binds the antigen and (ii) all monomers (e.g. individual amino acid residues, sugar side chains, post-translationally modified amino acid residues) on the portion of the antigen that is specifically bound by the antigen-binding domain. Epitopes can, e.g., consist of surface-accessible amino acid residues, sugar side chains, phosphorylated amino acid residues, methylated amino acid residues, and/or acetylated amino acid residues and may have specific three-dimensional structural characteristics, as well as specific charge characteristics. Conformational and non-conformational epitopes are distinguished in that binding to the former, but not the latter, may be lost in the presence of denaturing solvents. In some embodiments, an epitope is defined by a

linear amino acid sequence of at least about 3 to 6 amino acids, or about 10 to 15 amino acids. In some embodiments, an epitope refers to a portion of a full-length protein or a portion thereof that is defined by a three-dimensional structure (e.g., protein folding). In some embodiments, an epitope is defined by a discontinuous amino acid sequence that is brought together via protein folding. In some embodiments, an epitope is defined by a discontinuous amino acid sequence that is brought together by quaternary structure (e.g., a cleft formed by the interaction of two different polypeptide chains). The amino acid sequences between the residues that define the epitope may not be critical to three-dimensional structure of the epitope. A conformational epitope may be determined and screened using assays that compare binding of antigen-binding protein construct to a denatured version of the antigen, such that a linear epitope is generated. An epitope may include amino acid residues that are directly involved in the binding, and other amino acid residues, which are not directly involved in the binding.

Methods for identifying an epitope to which an antigen-binding domain specifically binds are known in the art, e.g., structure-based analysis (e.g. X-ray crystallography, NMR, and/or electron microscopy) (e.g. on the antigen and/or the antigen-antigen binding domain complex) and/or mutagenesis-based analysis (e.g. alanine scanning mutagenesis, glycine scanning mutagenesis, and homology scanning mutagenesis) wherein mutants are measured in a binding assay with a binding partner, many of which are known in the art.

The term "paratope" means a portion of an antigen-binding domain that specifically binds to an antigen through a set of physical interactions between: (i) all monomers (e.g. individual amino acid residues, sugar side chains, posttranslationally modified amino acid residues) on the portion of the antigen-binding domain that specifically binds the antigen and (ii) all monomers (e.g. individual amino acid residues, sugar side chains, posttranslationally modified amino acid residues) on the portion of the antigen that is specifically bound by the antigen-binding domain. Paratopes can, e.g. consist of surface-accessible amino acid residues and may have specific three-dimensional structural characteristics, as well as specific charge characteristics. In some embodiments, a paratope refers to a portion of a full-length antigen-binding domain or a portion thereof that is defined by a three-dimensional structure (e.g., protein folding). In some embodiments, a paratope is defined by a discontinuous amino acid sequence that is brought together via protein folding. In some embodiments, an epitope is defined by a discontinuous amino acid sequence that is brought together by quaternary structure (e.g., a cleft formed by the

interaction of two different polypeptide chains). The amino acid sequences between the residues that define the paratope may not be critical to three-dimensional structure of the paratope. A paratope may comprise amino acid residues that are directly involved in the binding, and other amino acid residues, which are not directly involved in the binding.

Methods for identifying a paratope to which an antigen-binding domain specifically binds are known in the art, e.g., structure-based analysis (e.g., X-ray crystallography, NMR, and/or electron microscopy) (e.g. on the antigen-binding domain, and/or the antigen binding domain-antigen complex), and/or mutagenesis-based analysis (e.g., alanine scanning mutagenesis, glycine scanning mutagenesis, and homology scanning mutagenesis) wherein mutants are measured in a binding assay with a binding partner, many of which are known in the art.

The phrase "present on the surface of a mammalian cell" means (1) an antigen that physically attached to or at least partially embedded in the plasma membrane of a mammalian cell (e.g., a transmembrane protein, a peripheral membrane protein, a lipid-anchored protein (e.g., a GPI-anchor), an N-myristolyated protein, or a S-palmitoylated protein) or (2) an antigen that is stably bound to its cognate receptor, where the cognate receptor is physically attached to the plasma membrane of a mammalian cell (e.g., a ligand bound to its cognate receptor, where the cognate receptor is physically attached to the plasma membrane). Non-limiting methods for determining the presence of antigen on the surface of a mammalian cell include fluorescence-activated cell sorting (FACS), immunohistochemistry, cell-fractionation assays and Western blotting.

The phrase "control ABPC" or "control antigen-binding protein construct" means (i) an ABPC that is capable of specifically binding to LRRC15 or an epitope of LRRC15 presented on the surface of a mammalian cell (e.g., a target mammalian cell), where one or both of the following is true: (a) the dissociation rate of the first antigen-binding domain at a pH of about 4.0 to about 6.5 (e.g., any of the subranges of this range described herein) is no more than 3-fold (e.g., no more than 2.8-fold, no more than 2.6-fold, no more than 2.5-fold, no more than 2.4-fold, no more than 2.2-fold, no more than 2.0-fold, no more than 1.8-fold, no more than 1.6-fold, no more than 1.5-fold, no more than 1.4-fold, no more than 1.2-fold, no more than 1.0-fold, no more than 0.8-fold, no more than 0.6-fold, no more than 0.5-fold, no more than 0.4-fold, no more than 0.3-fold no more than 0.2-fold, or no more than 0.1-fold) faster than the dissociation rate at a pH of about 7.0 to about 8.0 (e.g., any of the subranges of this range described herein); or (b) the

dissociation constant (K_D) of the first antigen-binding domain at a pH of about 4.0 to about 6.5 (e.g., any of the subranges of this range described herein) is no more than 3-fold (e.g., no more than 2.8-fold, no more than 2.6-fold, no more than 2.5-fold, no more than 2.4-fold, no more than 2.2-fold, no more than 2.0-fold, no more than 1.8-fold, no more than 1.6-fold, no more than 1.5-fold, no more than 1.4-fold, no more than 1.2-fold, no more than 1.0-fold, no more than 0.8-fold, no more than 0.6-fold, no more than 0.5-fold, no more than 0.4-fold, no more than 0.3-fold no more than 0.2-fold, or no more than 0.1-fold) greater than the K_D at a pH of about 7.0 to about 8.0 (e.g., any of the subranges of this range described herein); (ii) samrotamab; (iii) hu139.10; (iv) huAD208.4.1 and/or (v) huAD208.12.1.

The term "extracellular space" means the liquid exterior to the plasma membrane of a mammalian cell. When a mammalian cell is *in vitro*, the extracellular space can be a liquid culture medium. When a mammalian cell is *in vivo*, the extracellular space can be, e.g., plasma, serum, blood, interstitial fluid, or lymph.

The term "endolysosomal space" means the fluid encapsulated by the vesicles and organelles that make-up the endosomal/lysosomal pathway in a mammalian cell.

The phrase "a reduced level" or "a decreased level" can be a reduction or decrease of at least a 1% (e.g., at least 2%, at least 4%, at least 6%, at least 8%, at least 10%, at least 12%, at least 14%, at least 16%, at least 18%, at least 20%, at least 22%, at least 24%, at least 26%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99%) reduction as compared to a reference level or value.

The term "cell killing potency" refers to the ability of an agent (e.g., any of the ABPCs described herein) to induce, directly or indirectly, the apoptosis and/or necrosis of a mammalian cell (e.g., a cancer cell), measured as a rate over time or at a relevant timepoint. Methods for determining the cell killing potency of a cell are known in the art (e.g., trypan blue staining, microscopy, fluorescence-assisted cell sorting, and assays to detect markers of apoptosis (e.g., Annexin V)). In non-limiting examples, cell killing potency can be measured, e.g., by cell killing at a single concentration of an agent, by the IC50 of the agent (i.e. the concentration of the agent whereby half the maximal cell killing potency is achieved), or by the ratio of an agent's dissociation constant KD on mammalian cells divided by its IC50. In some non-limiting examples, the IC50s and/or the KD ratios described herein are compared to those of a control

ABPC (as defined herein), and, optionally, demonstrate that the ABPCs described herein have a higher cell killing potency as compared to the control ABPC.

The term "toxin liberation" refers to the ability of a mammalian cell (e.g., a non-cancerous mammalian cell or a cancer cell) to internalize (e.g., via pinocytosis and/or receptor-mediated endocytosis) any of the ABPCs described herein (e.g., any of ABPCs or control ABPCs described herein) that are conjugated to a toxin, and subsequently release the toxin conjugated to the ABPC, measured as a rate over time or at a specific timepoint. Toxin liberation can be assessed using a variety of different exemplary assays, e.g., ELISA, immunofluorescence, cell killing assays, cell cycle arrest assays, DNA damage assays, mass spectrometry, HPLC, and/or an isotope-labeled toxin.

The phrase "target cell" or "target mammalian cell" or "mammalian target cell" means a mammalian cell that has at least one LRRC15 present on its surface. In some examples, a mammalian target cell can be a cancer cell. In some embodiments of a target mammalian cell can have a total of about 1 to about 10,000,000, about 1 to about 9,000,000, about 1 to about 8,000,000, about 1 to about 7,000,000, about 1 to about 6,000,000, about 1 to about 5,000,000, about 1 to about 4,000,000, about 1 to about 3,000,000, about 1 to about 2,000,000, about 1 to about 1,000,000, about 1 to about 800,000, about 1 to about 600,000, about 1 to about 400,000, about 1 to about 200,000, about 1 to about 100,000, about 1 to about 80,000, about 1 to about 80,000, about 1 to about 75,000, about 1 to about 70,000, about 1 to about 65,000, about 1 to about 60,000, about 1 to about 55,000, about 1 to about 50,000, about 1 to about 45,000, about 1 to about 40,000, about 1 to about 35,000, about 1 to about 30,000, about 1 to about 25,000, about 1 to about 20,000, about 1 to about 15,000, about 1 to about 10,000, about 1 to about 7,500, about 1 to about 5,000, about 1 to about 4,000, about 1 to about 3,000, about 1 to about 2,000, about 1 to about 1,000, about 1 to about 500, about 1 to about 100, about 1 to about 50, about 1 to about 10, about 10 to about 10,000,000, about 10 to about 9,000,000, about 10 to about 8,000,000, about 10 to about 7,000,000, about 10 to about 6,000,000, about 10 to about 5,000,000, about 10 to about 4,000,000, about 10 to about 3,000,000, about 10 to about 2,000,000, about 10 to about 1,000,000, about 10 to about 800,000, about 10 to about 600,000, about 10 to about 400,000, about 10 to about 200,000, about 10 to about 100,000, about 10 to about 80,000, about 10 to about 80,000, about 10 to about 75,000, about 10 to about 70,000, about 10 to about 65,000, about 10 to about 60,000, about 10 to about 55,000, about 10 to about

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about 600,000, about 100,000 to about 400,000, about 100,000 to about 200,000, about 200,000 to about 10,000,000, about 200,000 to about 9,000,000, about 200,000 to about 8,000,000, about 200,000 to about 7,000,000, about 200,000 to about 6,000,000, about 200,000 to about 5,000,000, about 200,000 to about 4,000,000, about 200,000 to about 3,000,000, about 200,000 to about 2,000,000, about 200,000 to about 1,000,000, about 200,000 to about 800,000, about 200,000 to about 600,000, about 200,000 to about 400,000, about 400,000 to about 10,000,000, about 400,000 to about 9,000,000, about 400,000 to about 8,000,000, about 400,000 to about 7,000,000, about 400,000 to about 6,000,000, about 400,000 to about 5,000,000, about 400,000 to about 4,000,000, about 400,000 to about 3,000,000, about 400,000 to about 2,000,000, about 400,000 to about 1,000,000, about 400,000 to about 800,000, about 400,000 to about 600,000, about 600,000 to about 10,000,000, about 600,000 to about 9,000,000, about 600,000 to about 8,000,000, about 600,000 to about 7,000,000, about 600,000 to about 6,000,000, about 600,000 to about 5,000,000, about 600,000 to about 4,000,000, about 600,000 to about 3,000,000, about 600,000 to about 2,000,000, about 600,000 to about 1,000,000, about 600,000 to about 800,000, about 800,000 to about 10,000,000, about 800,000 to about 9,000,000, about 800,000 to about 8,000,000, about 800,000 to about 7,000,000, about 800,000 to about 6,000,000, about 800,000 to about 5,000,000, about 800,000 to about 4,000,000, about 800,000 to about 3,000,000, about 800,000 to about 2,000,000, about 800,000 to about 1,000,000, about 1,000,000 to about 10,000,000, about 1,000,000 to about 9,000,000, about 1,000,000 to about 8,000,000, about 1,000,000 to about 7,000,000, about 1,000,000 to about 6,000,000, about 1,000,000 to about 5,000,000, about 1,000,000 to about 4,000,000, about 1,000,000 to about 3,000,000, about 1,000,000 to about 2,000,000, about 2,000,000 to about 10,000,000, about 2,000,000 to about 9,000,000, about 2,000,000 to about 8,000,000, about 2,000,000 to about 7,000,000, about 2,000,000 to about 6,000,000, about 2,000,000 to about 5,000,000, about 2,000,000 to about 4,000,000, about 2,000,000 to about 3,000,000, about 3,000,000 to about 10,000,000, about 3,000,000 to about 9,000,000, about 3,000,000 to about 8,000,000, about 3,000,000 to about 7,000,000, about 3,000,000 to about 6,000,000, about 3,000,000 to about 5,000,000, about 3,000,000 to about 4,000,000, about 4,000,000 to about 10,000,000, about 4,000,000 to about 9,000,000, about 4,000,000 to about 8,000,000, about 4,000,000 to about 7,000,000, about 4,000,000 to about 6,000,000, about 4,000,000 to about 5,000,000, about 5,000,000 to about 10,000,000, about 5,000,000 to about 9,000,000, about 5,000,000 to about 8,000,000, about

5,000,000 to about 7,000,000, about 5,000,000 to about 6,000,000, about 6,000,000 to about 10,000,000, about 6,000,000 to about 9,000,000, about 6,000,000 to about 8,000,000, about 6,000,000 to about 7,000,000, about 7,000,000 to about 10,000,000, about 7,000,000 to about 9,000,000, about 7,000,000 to about 8,000,000, about 8,000,000 to about 10,000,000, about 8,000,000 to about 9,000,000, or about 9,000,000 to about 10,000,000 of the LRRC15 on present on the plasma membrane of the target mammalian cell.

The phrase "antigen density" means the number of LRRC15 present on the surface of a target mammalian cell or the average number of LRRC15 on the surface of a population of particular type of target mammalian cells. It can be measured, e.g., using the Quantibright bead kit or radiolabel (e.g., BD Biosciences PE Phycoerythrin Fluorescence Quantitation Kit, catalog #340495).

The phrase "amino acid substituted with a histidine" means the substitution of an amino acid residue that is not histidine in a reference polypeptide sequence with a histidine. Non-limiting methods for substituting an amino acid residue in a reference polypeptide with a histidine are described herein. Additional methods for substituting an amino acid residue in a reference polypeptide with a histidine are known in the art.

The phrase "amino acid substituted with an alanine" means the substitution of an amino acid residue that is a histidine in a reference polypeptide sequence with an alanine. Non-limiting methods for substituting a histidine in a reference polypeptide with an alanine are described herein. Additional methods for substituting an histidine in a reference polypeptide with an alanine are known in the art.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Methods and materials are described herein for use in the present invention; other, suitable methods and materials known in the art can also be used. The materials, methods, and examples are illustrative only and not intended to be limiting. All publications, patent applications, patents, sequences, database entries, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control.

Other features and advantages of the invention will be apparent from the following detailed description and figures, and from the claims.

BRIEF DESCRIPTION OF DRAWINGS

Figure 1: SDS PAGE for SAMROTAMAB histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to confirm expression of SAMROTAMAB and histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT0963 is SAMROTAMAB and the rest of the lanes (MYT0964 – MYT1003) are SAMROTAMAB heavy chain histidine scanning and alanine scanning variants.

Figures 2a to 2ao: Binding of SAMROTAMAB starting ABPC and histidine scanning and alanine scanning variants to LRRC15 by biolayer interferometry. MYT0963 (SAMROTAMAB) and MYT0964 – MYT1003, heavy chain histidine scanning and alanine scanning variants, were captured on anti-human Fc biosensors and associated with LRRC15 at low pH or high pH, as specified in the figures.

Figure 3: Construct identifier to SEQ ID NO correspondence table. Constructs, heavy chain histidine scanning and alanine scanning variants, are listed in the first column of the table, SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figures 4: SDS PAGE for SAMROTAMAB histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to confirm expression of SAMROTAMAB and histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT2726 – MYT2752 are SAMROTAMAB light chain histidine scanning and alanine scanning variants.

Figures 5a to 5aa: Binding of SAMROTAMAB starting ABPC and histidine scanning and alanine scanning variants to LRRC15 by biolayer interferometry. MYT2726 – MYT2752, light chain histidine scanning and alanine scanning variants of SAMROTAMAB, were captured on anti-human Fc biosensors and associated with LRRC15 at low pH or high pH, as specified in the figures.

Figure 6: Construct identifier to SEQ ID NO correspondence table. Constructs, light chain histidine scanning and alanine scanning variants, are listed in the first column of the table,

SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figure 7: SDS PAGE for SAMROTAMAB histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to confirm expression of SAMROTAMAB histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT2722 – MYT2725 are SAMROTAMAB heavy chain combinations histidine scanning and alanine scanning variants.

Figures 8a to 8d: Binding of histidine scanning and alanine scanning variants of SAMROTAMAB to LRRC15 by biolayer interferometry. MYT2722 – MYT2725, heavy chain combination histidine scanning and alanine scanning variants of SAMROTAMAB, were captured on anti-human Fc biosensors and associated with LRRC15 at low pH or high pH, as specified in the figures.

Figure 9: Construct identifier to SEQ ID NO correspondence table. Constructs, heavy chain combinations histidine scanning and alanine scanning variants, are listed in the first column of the table, SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figures 10: SDS PAGE for hu139.10 histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to confirm expression of hu139.10 and histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT3252 is hu139.10 and the rest of the lanes (MYT3253 – MYT3292) are hu139.10 heavy chain histidine scanning and alanine scanning variants.

Figures 11a to 11ao: Binding of hu139.10 starting ABPC and histidine scanning and alanine scanning variants to LRRC15 by biolayer interferometry. MYT3252 (hu139.10) and MYT3253 – MYT3292, heavy chain histidine scanning and alanine scanning variants of hu139.10, were captured on anti-human Fc biosensors and associated with LRRC15 at low pH or high pH, as specified in the figures.

Figure 12: Construct identifier to SEQ ID NO correspondence table. Constructs, heavy chain histidine scanning and alanine scanning variants, are listed in the first column of the

table, SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figures 13: SDS PAGE for hu139.10 histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to confirm expression of hu139.10 and histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT3293 – MYT3324 are hu139.10 light chain histidine scanning and alanine scanning variants.

Figures 14a to 14af: Binding of hu139.10 starting ABPC and histidine scanning and alanine scanning variants to LRRC15 by biolayer interferometry. MYT3293 – MYT3324, light chain histidine scanning and alanine scanning variants of hu139.10, were captured on anti-human Fc biosensors and associated with LRRC15 at low pH or high pH, as specified in the figures.

Figure 15: Construct identifier to SEQ ID NO correspondence table. Constructs, light chain histidine scanning and alanine scanning variants, are listed in the first column of the table, SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figures 16: SDS PAGE for hu139.10 histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to confirm expression of hu139.10 histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT4161 – MYT4164 are hu139.10 heavy chain combinations histidine scanning and alanine scanning variants.

Figures 17a to 17d: Binding of histidine scanning and alanine scanning variants of hu139.10 to LRRC15 by biolayer interferometry. MYT4161 – MYT4164, heavy chain combination histidine scanning and alanine scanning variants, were captured on anti-human Fc biosensors and associated with LRRC15 at low pH or high pH, as specified in the figures.

Figure 18: Construct identifier to SEQ ID NO correspondence table. Constructs, heavy chain combinations histidine scanning and alanine scanning variants, are listed in the first column of the table, SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figures 19: SDS PAGE for hu139.10 histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to

confirm expression of hu139.10 histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT4165 – MYT4174 are hu139.10 light chain combinations histidine scanning and alanine scanning variants.

Figures 20a to 20j: Binding of histidine scanning and alanine scanning variants of hu139.10 to LRRC15 by biolayer interferometry. MYT4165 – MYT4174, light chain combination histidine scanning and alanine scanning variants, were captured on anti-human Fc biosensors and associated with LRRC15 at low pH or high pH, as specified in the figures.

Figure 21: Construct identifier to SEQ ID NO correspondence table. Constructs, light chain combinations histidine scanning and alanine scanning variants, are listed in the first column of the table, SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figures 22: SDS PAGE for huAD208.4.1 histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to confirm expression of huAD208.4.1 and histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT3325 is huAD208.4.1 and the rest of the lanes (MYT3326 – MYT3367) are huAD208.4.1 heavy chain histidine scanning and alanine scanning variants.

Figures 23a to 23aq: Binding of huAD208.4.1 starting ABPC and histidine scanning and alanine scanning variants to LRRC15 by biolayer interferometry. MYT3325 (huAD208.4.1) and MYT3326 – MYT3367, heavy chain histidine scanning and alanine scanning variants, were captured on anti-human Fc biosensors and associated with LRRC15 at low pH or high pH, as specified in the figures.

Figure 24: Construct identifier to SEQ ID NO correspondence table. Constructs, heavy chain histidine scanning and alanine scanning variants, are listed in the first column of the table, SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figures 25: SDS PAGE for huAD208.4.1 histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to confirm expression of huAD208.4.1 and histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT3369 – MYT3398 are huAD208.4.1 light chain histidine scanning and alanine scanning variants.

Figures 26a to 26ad: Binding of huAD208.4.1 starting ABPC and histidine scanning and alanine scanning variants to LRRC15 by biolayer interferometry. MYT3369 – MYT3398, light chain histidine scanning and alanine scanning variants of huAD208.4.1, were captured on anti-human Fc biosensors and associated with LRRC15 at low pH or high pH, as specified in the figures.

Figure 27: Construct identifier to SEQ ID NO correspondence table. Constructs, light chain histidine scanning and alanine scanning variants, are listed in the first column of the table, SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figures 28: SDS PAGE for huAD208.4.1 histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to confirm expression of huAD208.4.1 histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT4385 – MYT4388 are huAD208.4.1 heavy chain combinations histidine scanning and alanine scanning variants.

Figures 29a to 29d: Binding of histidine scanning and alanine scanning variants of huAD208.4.1 to LRRC15 by biolayer interferometry. MYT4385 – MYT4388, heavy chain combination histidine scanning and alanine scanning variants of huAD208.4.1, were captured on anti-human Fc biosensors and associated with LRRC15 at low pH or high pH, as specified in the figures.

Figure 30: Construct identifier to SEQ ID NO correspondence table. Constructs, heavy chain combinations histidine scanning and alanine scanning variants, are listed in the first column of the table, SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figures 31: SDS PAGE for huAD208.4.1 histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to confirm expression of huAD208.4.1 histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT4390 – MYT4399 are huAD208.4.1 light chain combinations histidine scanning and alanine scanning variants.

Figures 32a to 32j: Binding of histidine scanning and alanine scanning variants of huAD208.4.1 to LRRC15 by biolayer interferometry. MYT4390 – MYT4399, light chain combination histidine scanning and alanine scanning variants of huAD208.4.1, were captured on anti-human Fc biosensors and associated with LRRC15 at low pH or high pH, as specified in the figures.

Figure 33: Construct identifier to SEQ ID NO correspondence table. Constructs, light chain combinations histidine scanning and alanine scanning variants, are listed in the first column of the table, SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figures 34: SDS PAGE for huAD208.12.1 histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to confirm expression of huAD208.12.1 and histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT3179 is huAD208.12.1 and the rest of the lanes (MYT4090 – MYT4133) are huAD208.12.1 heavy chain histidine scanning and alanine scanning variants.

Figures 35a to 35as: Binding of huAD208.12.1 starting ABPC and histidine scanning and alanine scanning variants to LRRC15 by biolayer interferometry. MYT3179 (huAD208.12.1) and MYT4090 – MYT4133, heavy chain histidine scanning and alanine scanning variants, were captured on anti-human Fc biosensors and associated with LRRC15 at pH 7.4. Dissociation was at pH 7.4 (black trace) or pH 5.4 (grey trace).

Figure 36: Construct identifier to SEQ ID NO correspondence table. Constructs, heavy chain histidine scanning and alanine scanning variants, are listed in the first column of the table, SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figures 37: SDS PAGE for huAD208.12.1 histidine scanning and alanine scanning. Expi293 cell culture supernatants post-harvest were loaded on non-reduced SDS PAGE gels to confirm expression of huAD208.12.1 and histidine scanning and alanine scanning variants. Arrows show the corresponding size for an IgG on a non-reduced SDS PAGE gel. MYT4134 – MYT4160 are huAD208.12.1 light chain histidine scanning and alanine scanning variants.

Figures 38a to 38aa: Binding of huAD208.12.1 starting ABPC and histidine scanning and alanine scanning variants to LRRC15 by biolayer interferometry. MYT4134

– MYT4160, light chain histidine scanning and alanine scanning variants of huAD208.12.1, were captured on anti-human Fc biosensors and associated with LRRC15 at pH 7.4. Dissociation was at pH 7.4 (black trace) or pH 5.4 (grey trace).

Figure 39: Construct identifier to SEQ ID NO correspondence table. Constructs, light chain histidine scanning and alanine scanning variants, are listed in the first column of the table, SEQ ID NOs are listed and correspond to constructs on the left and the appropriate heavy chain and/or light chain categories along the top.

Figures 40a - 40b: Characterization of binding affinity for anti-LRRC15 mAbs. Anti-LRRC15 mAbs were assayed for their binding to U-87 MG (LRRC15+) cells. Figure 40a shows MYT0963 (samrotamab) with an IC50 of 0.228 nM, Figure 40b shows MYT0971 with an IC50 of 0.484 nM.

Figures 41a - 41g: Internalization of anti-LRRC15 mAbs in cells. Anti-LRRC15 pH engineered antibody variants, corresponding starting ABPC antibody, control IgG1 isotype control (BP0297, Bioxcell), along with a vehicle control, as specified in Figure 41 were assayed for internalization and endolysosomal delivery as measured by mean fluorescence intensity on cells, at 25nM after 24 hours. Error bars represent standard deviation where present. Numbers above the bars represent fold change over the corresponding starting ABPC.

Figure 42: Melting temperature of select anti-LRRC15 mAbs. Selected anti-LRRC15 mAbs listed in the table were assayed for their melting temperature by Differential Scanning Fluorimetry (DSF), and the resulting Sypro Orange signal was plotted as its first derivative. Melting temperature (Tm) was calculated as the local maxima of this graph and is shown in the table.

Figure 43: SDS PAGE for MYT0766. Purified MYT0766 was loaded as non-reduced (NR) and reduced (R) onto an SDS PAGE gel to confirm size and purity. Theoretical molecular weight of intact MYT0766 is approximately 109 kDa.

DETAILED DESCRIPTION

Provided herein are antigen-binding protein constructs (ABPCs) and antibodies that include: a first antigen-binding domain that is capable of specifically binding LRRC15 or an epitope of LRRC15 presented on the surface of a target mammalian cell, where: (a) the dissociation rate of the first antigen-binding domain at a pH of about 4.0 to about 6.5 is faster

than the dissociation rate at a pH of about 7.0 to about 8.0; and/or (b) the dissociation constant (K_D) of the first antigen-binding domain at a pH of about 4.0 to about 6.5 is greater than the K_D at a pH of about 7.0 to about 8.0. In some examples of these ABPCs, the ABPC is degraded in the target mammalian cell following internalization of the ABPC by the target mammalian cell. Some examples of any of the ABPCs described herein can further include a conjugated toxin, radioisotope, drug, or small molecule (e.g., a fluorophore or dye).

Also provided are antigen-binding protein constructs (ABPCs) and antibodies that include: a first antigen-binding domain that is capable of specifically binding LRRC15 or an epitope of LRRC15 presented on the surface of a target mammalian cell; and a conjugated toxin, radioisotope, drug, or small molecule, where: (a) the dissociation rate of the first antigen-binding domain at a pH of about 4.0 to about 6.5 is faster than the dissociation rate at a pH of about 7.0 to about 8.0; and/or the dissociation constant (K_D) of the first antigen-binding domain at a pH of about 4.0 to about 6.5 is greater than the K_D at a pH of about 7.0 to about 8.0; and (b) a composition including the ABPC provides for one or more (e.g., two or three) of: an increase (e.g., a detectable increase) in toxin liberation in the target mammalian cell as compared to a composition comprising the same amount of a control ABPC; an increase (e.g., a detectable increase) in target mammalian cell killing as compared to a composition comprising the same amount of a control ABPC; and an increase (e.g., a detectable increase) in endolysosomal delivery in the target mammalian cell as compared to a composition comprising the same amount of a control ABPC.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of samrotamab with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine. In some examples of any of the ABPCs described herein, the first antigen-binding domain includes a light chain variable domain of samrotamab with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine. In some examples of any of the ABPCs described herein, the first antigen-binding domain includes a heavy chain variable domain of samrotamab with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty)

amino acids substituted with a histidine; and a light chain variable domain of samrotamab with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine. In some examples of any of the ABPCs described herein, the heavy chain variable domain of samrotamab comprises SEQ ID NO: 1. In some examples of any of the ABPCs described herein, the light chain variable domain of samrotamab comprises SEQ ID NO: 2.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 3, SEQ ID NO: 4, and SEQ ID NO: 5, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 3-5 substituted with a histidine. In some examples of any of the ABPCs described herein, the first antigen-binding domain comprises a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 6, SEQ ID NO: 7, and SEQ ID NO: 8, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 6-8 substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes: a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 3, SEQ ID NO: 4, and SEQ ID NO: 5, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 3-5 substituted with a histidine; and a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 6, SEQ ID NO: 7, and SEQ ID NO: 8, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 6-8 substituted with a histidine.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 1 selected from the group consisting of: 33, 34, 50, 52, 57, 59, 100, 102, 103, 107, 108, or 109 . In some examples of any

of the ABPCs described herein, the first antigen-binding domain includes a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 2, where the light chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 2 selected from the group consisting of: 32, 34, 50, 51, 89, 90, 92, 93, 94, or 96. In some examples of any of the ABPCs and antibodies described herein the first antigen-binding domain includes: a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 1 selected from the group consisting of: 33, 34, 50, 52, 57, 59, 100, 102, 103, 107, 108, or 109, and a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 2, where the light chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 2 selected from the group consisting of: 32, 34, 50, 51, 89, 90, 92, 93, 94, or 96.

In some examples of any of the ABPCs and antibodies described herein, a heavy chain variable domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 1 listed in Table 1.

Table 1. Exemplary Combinations of Amino Acid Positions in SEQ ID NO: 1 that can be Substituted with Histidine

33 + 34, 33 + 50, 33 + 52, 33 + 57, 33 + 59, 33 + 100, 33 + 102, 33 + 103, 33 + 107, 33 + 108, 33 + 109, 34 + 50, 34 + 52, 34 + 57, 34 + 59, 34 + 100, 34 + 102, 34 + 103, 34 + 107, 34 + 108, 34 + 109, 50 + 52, 50 + 57, 50 + 59, 50 + 100, 50 + 102, 50 + 103, 50 + 107, 50 + 108,

50 + 109, 52 + 57, 52 + 59, 52 + 100, 52 + 102, 52 + 103, 52 + 107, 52 + 108, 52 + 109, 57 + 59, 57 + 100, 57 + 102, 57 + 103, 57 + 107, 57 + 108, 57 + 109, 59 + 100, 59 + 102, 59 + 103, 59 + 107, 59 + 108, 59 + 109, 100 + 102, 100 + 103, 100 + 107, 100 + 108, 100 + 109, 102 + 103, 102 + 107, 102 + 108, 102 + 109, 103 + 107, 103 + 108, 103 + 109, 107 + 108, 107 + 109, 108 + 109, 33 + 34 + 50, 33 + 34 + 52, 33 + 34 + 57, 33 + 34 + 59, 33 + 34 + 100, 33 + 34 + 102, 33 + 34 + 103, 33 + 34 + 107, 33 + 34 + 108, 33 + 34 + 109, 33 + 50 + 52, 33 + 50 + 57, 33 + 50 + 59, 33 + 50 + 100, 33 + 50 + 102, 33 + 50 + 103, 33 + 50 + 107, 33 + 50 + 108, 33 + 50 + 109, 34 + 50 + 52, 34 + 50 + 57, 34 + 50 + 59, 34 + 50 + 100, 34 + 50 + 102, 34 + 50 + 103, 34 + 50 + 107, 34 + 50 + 108, 34 + 50 + 109, 33 + 52 + 57, 33 + 52 + 59, 33 + 52 + 100, 33 + 52 + 102, 33 + 52 + 103, 33 + 52 + 107, 33 + 52 + 108, 33 + 52 + 109, 34 + 52 + 57, 34 + 52 + 59, 34 + 52 + 100, 34 + 52 + 102, 34 + 52 + 103, 34 + 52 + 107, 34 + 52 + 108, 34 + 52 + 109, 50 + 52 + 57, 50 + 52 + 59, 50 + 52 + 100, 50 + 52 + 102, 50 + 52 + 103, 50 + 52 + 107, 50 + 52 + 108, 50 + 52 + 109, 33 + 57 + 59, 33 + 57 + 100, 33 + 57 + 102, 33 + 57 + 103, 33 + 57 + 107, 33 + 57 + 108, 33 + 57 + 109, 34 + 57 + 59, 34 + 57 + 100, 34 + 57 + 102, 34 + 57 + 103, 34 + 57 + 107, 34 + 57 + 108, 34 + 57 + 109, 50 + 57 + 59, 50 + 57 + 100, 50 + 57 + 102, 50 + 57 + 103, 50 + 57 + 107, 50 + 57 + 108, 50 + 57 + 109, 52 + 57 + 59, 52 + 57 + 100, 52 + 57 + 102, 52 + 57 + 103, 52 + 57 + 107, 52 + 57 + 108, 52 + 57 + 109, 33 + 59 + 100, 33 + 59 + 102, 33 + 59 + 103, 33 + 59 + 107, 33 + 59 + 108, 33 + 59 + 109, 34 + 59 + 100, 34 + 59 + 102, 34 + 59 + 103, 34 + 59 + 107, 34 + 59 + 108, 34 + 59 + 109, 50 + 59 + 100, 50 + 59 + 102, 50 + 59 + 103, 50 + 59 + 107, 50 + 59 + 108, 50 + 59 + 109, 52 + 59 + 100, 52 + 59 + 102, 52 + 59 + 103, 52 + 59 + 107, 52 + 59 + 108, 52 + 59 + 109, 57 + 59 + 100, 57 + 59 + 102, 57 + 59 + 103, 57 + 59 + 107, 57 + 59 + 108, 57 + 59 + 109, 33 + 100 + 102, 33 + 100 + 103, 33 + 100 + 107, 33 + 100 + 108, 33 + 100 + 109, 34 + 100 + 102, 34 + 100 + 103, 34 + 100 + 107, 34 + 100 + 108, 34 + 100 + 109, 50 + 100 + 102, 50 + 100 + 103, 50 + 100 + 107, 50 + 100 + 108, 50 + 100 + 109, 52 + 100 + 102, 52 + 100 + 103, 52 + 100 + 107, 52 + 100 + 108, 52 + 100 + 109, 57 + 100 + 102, 57 + 100 + 103, 57 + 100 + 107, 57 + 100 + 108, 57 + 100 + 109, 59 + 100 + 102, 59 + 100 + 103, 59 + 100 + 107, 59 + 100 + 108, 59 + 100 + 109, 33 + 102 + 103, 33 + 102 + 107, 33 + 102 + 108, 33 + 102 + 109, 34 + 102 + 103, 34 + 102 + 107, 34 + 102 + 108, 34 + 102 + 109, 50 + 102 + 103, 50 + 102 + 107, 50 + 102 + 108, 50 + 102 + 109, 52 + 102 + 103, 52 + 102 + 107, 52 + 102 + 108, 52 + 102 + 109,

57 + 102 + 103, 57 + 102 + 107, 57 + 102 + 108, 57 + 102 + 109, 59 + 102 + 103, 59 + 102 + 107, 59 + 102 + 108, 59 + 102 + 109, 100 + 102 + 103, 100 + 102 + 107, 100 + 102 + 108, 100 + 102 + 109, 33 + 103 + 107, 33 + 103 + 108, 33 + 103 + 109, 34 + 103 + 107, 34 + 103 + 108, 34 + 103 + 109, 50 + 103 + 107, 50 + 103 + 108, 50 + 103 + 109, 52 + 103 + 107, 52 + 103 + 108, 52 + 103 + 109, 57 + 103 + 107, 57 + 103 + 108, 57 + 103 + 109, 59 + 103 + 107, 59 + 103 + 108, 59 + 103 + 109, 100 + 103 + 107, 100 + 103 + 108, 100 + 103 + 109, 102 + 103 + 107, 102 + 103 + 108, 102 + 103 + 109, 33 + 107 + 108, 33 + 107 + 109, 34 + 107 + 108, 34 + 107 + 109, 50 + 107 + 108, 50 + 107 + 109, 52 + 107 + 108, 52 + 107 + 109, 57 + 107 + 108, 57 + 107 + 109, 59 + 107 + 108, 59 + 107 + 109, 100 + 107 + 108, 100 + 107 + 109, 102 + 107 + 108, 102 + 107 + 109, 103 + 107 + 108, 103 + 107 + 109, 33 + 108 + 109, 34 + 108 + 109, 50 + 108 + 109, 52 + 108 + 109, 57 + 108 + 109, 59 + 108 + 109, 100 + 108 + 109, 102 + 108 + 109, 103 + 108 + 109, 107 + 108 + 109

In some examples of any of the ABPCs and antibodies described herein, a light chain variable domain includes a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 2, where the light chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 2 listed in Table 2.

Table 2. Exemplary Combinations of Amino Acid Positions in SEQ ID NO: 2 that can be Substituted with Histidine

32 + 34, 32 + 50, 32 + 51, 32 + 89, 32 + 90, 32 + 92, 32 + 93, 32 + 94, 32 + 96, 34 + 50, 34 + 51, 34 + 89, 34 + 90, 34 + 92, 34 + 93, 34 + 94, 34 + 96, 50 + 51, 50 + 89, 50 + 90, 50 + 92, 50 + 93, 50 + 94, 50 + 96, 51 + 89, 51 + 90, 51 + 92, 51 + 93, 51 + 94, 51 + 96, 89 + 90, 89 + 92, 89 + 93, 89 + 94, 89 + 96, 90 + 92, 90 + 93, 90 + 94, 90 + 96, 92 + 93, 92 + 94, 92 + 96, 93 + 94, 93 + 96, 94 + 96, 32 + 34 + 50, 32 + 34 + 51, 32 + 34 + 89, 32 + 34 + 90, 32 + 34 + 92, 32 + 34 + 93, 32 + 34 + 94, 32 + 34 + 96, 32 + 50 + 51, 32 + 50 + 89, 32 + 50 + 90, 32 + 50 + 92, 32 + 50 + 93, 32 + 50 + 94, 32 + 50 + 96, 32 + 51 + 89, 32 + 51 + 90, 32 + 51 + 92, 32 + 51 + 93, 32 + 51 + 94, 32 + 51 + 96, 32 + 89 + 90, 32 + 89 + 92, 32 + 89 + 93, 32 + 89 + 94, 32 + 89 + 96, 32 + 90 + 92, 32 + 90 + 93, 32 + 90 + 94, 32 + 90 + 96, 32 + 92 + 93, 32 +

92 + 94, 32 + 92 + 96, 32 + 93 + 94, 32 + 93 + 96, 32 + 94 + 96, 34 + 50 + 51, 34 + 50 + 89, 34 + 50 + 90, 34 + 50 + 92, 34 + 50 + 93, 34 + 50 + 94, 34 + 50 + 96, 34 + 51 + 89, 34 + 51 + 90, 34 + 51 + 92, 34 + 51 + 93, 34 + 51 + 94, 34 + 51 + 96, 34 + 89 + 90, 34 + 89 + 92, 34 + 89 + 93, 34 + 89 + 94, 34 + 89 + 96, 34 + 90 + 92, 34 + 90 + 93, 34 + 90 + 94, 34 + 90 + 96, 34 + 92 + 93, 34 + 92 + 94, 34 + 92 + 96, 34 + 93 + 94, 34 + 93 + 96, 34 + 94 + 96, 50 + 51 + 89, 50 + 51 + 90, 50 + 51 + 92, 50 + 51 + 93, 50 + 51 + 94, 50 + 51 + 96, 50 + 89 + 90, 50 + 89 + 92, 50 + 89 + 93, 50 + 89 + 94, 50 + 89 + 96, 50 + 90 + 92, 50 + 90 + 93, 50 + 90 + 94, 50 + 90 + 96, 50 + 92 + 93, 50 + 92 + 94, 50 + 92 + 96, 50 + 93 + 94, 50 + 93 + 96, 50 + 94 + 96, 51 + 89 + 90, 51 + 89 + 92, 51 + 89 + 93, 51 + 89 + 94, 51 + 89 + 96, 51 + 90 + 92, 51 + 90 + 93, 51 + 90 + 94, 51 + 90 + 96, 51 + 92 + 93, 51 + 92 + 94, 51 + 92 + 96, 51 + 93 + 94, 51 + 93 + 96, 51 + 94 + 96, 89 + 90 + 92, 89 + 90 + 93, 89 + 90 + 94, 89 + 90 + 96, 89 + 92 + 93, 89 + 92 + 94, 89 + 92 + 96, 89 + 93 + 94, 89 + 93 + 96, 89 + 94 + 96, 90 + 92 + 93, 90 + 92 + 94, 90 + 92 + 96, 90 + 93 + 94, 90 + 93 + 96, 90 + 94 + 96, 92 + 93 + 94, 92 + 93 + 96, 92 + 94 + 96, 93 + 94 + 96

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 1 listed in Table 1; and a light chain variable domain that that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 2, where the light chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 2 listed in Table 2.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain comprising SEQ ID NO: 2, and a heavy chain variable domain that is at least 90% identical (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more (e.g., two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NO: 1 listed in Table 1.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 2, wherein the light chain variable domain includes a histidine at position 32 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 1 listed in Table 1.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 2, wherein the light chain variable domain includes a histidine at position 34 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 1 listed in Table 1.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 2, wherein the light chain variable domain includes a histidine at position 50 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 1 listed in Table 1.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 2, wherein the light chain variable domain includes a histidine at position 51 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 1 listed in Table 1.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 2, wherein the light chain variable domain includes a histidine at position 89 in SEQ ID NO:

2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 1 listed in Table 1.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 2, wherein the light chain variable domain includes a histidine at position 90 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 1 listed in Table 1.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 2, wherein the light chain variable domain includes a histidine at position 92 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 1 listed in Table 1.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 2, wherein the light chain variable domain includes a histidine at position 93 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 1 listed in Table 1.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 2, wherein the light chain variable domain includes a histidine at position 94 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain

variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 1 listed in Table 1.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 2, wherein the light chain variable domain includes a histidine at position 96 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 1 listed in Table 1.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of samrotamab with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidine(s) substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain of samrotamab with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidine(s) substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of samrotamab with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidines substituted with an alanine; and a light chain variable domain of samrotamab with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidine(s) substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the heavy chain variable domain of samrotamab comprises SEQ ID NO: 1. In some examples of any of the ABPCs and antibodies described herein, the light chain variable domain of samrotamab comprises SEQ ID NO: 2.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 3, SEQ ID NO: 4, and SEQ ID NO: 5, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in

SEQ ID NOs: 3-5 substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 6, SEQ ID NO: 7, and SEQ ID NO: 8, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 6-8 substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes: a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 3, SEQ ID NO: 4, and SEQ ID NO: 5, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 3-5 substituted with an alanine; and a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 6, SEQ ID NO: 7, and SEQ ID NO: 8, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 6-8 substituted with an alanine.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a heavy chain variable domain of SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain of SEQ ID NO: 2, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, or SEQ ID NO: 79.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 2, and a heavy chain variable domain comprising: SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 53, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 54, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 55, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 56, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 57, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 58, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 59, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 60, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 61, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 62, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 63, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 64, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 65, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 66, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 67, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 68, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 69, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 70, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 71, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 72 and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 73, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 74, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 75, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 76, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 77, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 78, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 79, and a heavy chain variable domain comprising: SEQ ID NO: 1, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27, SEQ ID NO: 28, SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 39, SEQ ID NO: 40, SEQ ID NO: 41, SEQ ID NO: 42, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 47, SEQ ID NO: 48, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, or SEQ ID NO: 52.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, or SEQ ID NO: 83.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain comprising SEQ ID NO: 80, and a light chain variable domain comprising SEQ ID NO: 2, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, or SEQ ID NO: 79.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain comprising SEQ ID NO: 81, and a light chain variable domain comprising SEQ ID NO: 2, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, or SEQ ID NO: 79.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain comprising SEQ ID NO: 82, and a light

chain variable domain comprising SEQ ID NO: 2, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, or SEQ ID NO: 79.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain comprising SEQ ID NO: 83, and a light chain variable domain comprising SEQ ID NO: 2, SEQ ID NO: 53, SEQ ID NO: 54, SEQ ID NO: 55, SEQ ID NO: 56, SEQ ID NO: 57, SEQ ID NO: 58, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 61, SEQ ID NO: 62, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 66, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 78, or SEQ ID NO: 79.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of a hu139.10 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain of hu139.10 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of hu139.10 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine; and a light chain variable domain of hu139.10 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the heavy chain variable domain of hu139.10 comprises SEQ ID NO: 84. In

some examples of any of the ABPCs and antibodies described herein, the light chain variable domain of hu139.10 comprises SEQ ID NO: 85.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 86, SEQ ID NO: 87, and SEQ ID NO: 88, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 86-88 substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 89, SEQ ID NO: 90, and SEQ ID NO: 91, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 89-91 substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes: a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 86, SEQ ID NO: 87, and SEQ ID NO: 88, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 89-91 substituted with a histidine; and a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 89, SEQ ID NO: 90, and SEQ ID NO: 91, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 89-91 substituted with a histidine.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 84 selected from the group consisting of: 27, 29, 32, 50, 54, 58, 99, 100, 102, 104, or 105. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 85, where the light chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten,

eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 85 selected from the group of: 29, 31, 32, 34, 36, 37, 38, 40, 56, 60, 61, 95, 96, 97, or 100. In some examples of any of the ABPCs and antibodies described herein the first antigen-binding domain includes: a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 84 selected from the group consisting of: 27, 29, 32, 50, 54, 58, 99, 100, 102, 104, and 105, and a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 85, where the light chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 85 selected from the group consisting of: 29, 31, 32, 34, 36, 37, 38, 40, 56, 60, 61, 95, 96, 97, or 100.

In some examples of any of the ABPCs and antibodies described herein, a heavy chain variable domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 1, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes an alanine at position 35 in SEQ ID NO: 84.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes an alanine at position 98 in SEQ ID NO: 84.

In some examples of any of the ABPCs and antibodies described herein the first antigen-binding domain includes: a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84,

where the heavy chain variable domain includes an alanine at position 35 in SEQ ID NO: 84, and a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 85, where the light chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 85 selected from the group consisting of: 29, 31, 32, 34, 36, 37, 38, 40, 56, 60, 61, 95, 96, 97, or 100.

In some examples of any of the ABPCs and antibodies described herein the first antigen-binding domain includes: a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes an alanine at position 98 in SEQ ID NO: 84, and a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 85, where the light chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 85 selected from the group consisting of: 29, 31, 32, 34, 36, 37, 38, 40, 56, 60, 61, 95, 96, 97, or 100.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 84 selected from the group consisting of: 27, 29, 32, 50, 54, 58, 99, 100, 102, 104, or 105 and where the heavy chain variable domain includes an alanine at position 35 and/or 98 in SEQ ID NO: 84. In some examples of any of the ABPCs and antibodies described herein the first antigen-binding domain includes: a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 84 selected from the group consisting

of: 27, 29, 32, 50, 54, 58, 99, 100, 102, 104, or 105 and where the heavy chain variable domain includes an alanine at position 35 or 98 in SEQ ID NO: 84, and a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 85, where the light chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 85 selected from the group consisting of: 29, 31, 32, 34, 36, 37, 38, 40, 56, 60, 61, 95, 96, 97, or 100.

In some examples of any of the ABPCs and antibodies described herein, a heavy chain variable domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 1 and where the heavy chain variable domain includes an alanine at position 35 and/or 98 of SEQ ID NO: 84.

Table 3. Exemplary Combinations of Amino Acid Positions in SEQ ID NO: 84 that can be Substituted with Histidine

27 + 29, 27 + 32, 27 + 50, 27 + 54, 27 + 58, 27 + 99, 27 + 100, 27 + 102, 27 + 104, 27 + 105, 29 + 32, 29 + 50, 29 + 54, 29 + 58, 29 + 99, 29 + 100, 29 + 102, 29 + 104, 29 + 105, 32 + 50, 32 + 54, 32 + 58, 32 + 99, 32 + 100, 32 + 102, 32 + 104, 32 + 105, 50 + 54, 50 + 58, 50 + 99, 50 + 100, 50 + 102, 50 + 104, 50 + 105, 54 + 58, 54 + 99, 54 + 100, 54 + 102, 54 + 104, 54 + 105, 58 + 99, 58 + 100, 58 + 102, 58 + 104, 58 + 105, 99 + 100, 99 + 102, 99 + 104, 99 + 105, 100 + 102, 100 + 104, 100 + 105, 102 + 104, 102 + 105, 104 + 105, 27 + 29 + 32, 27 + 29 + 50, 27 + 29 + 54, 27 + 29 + 58, 27 + 29 + 99, 27 + 29 + 100, 27 + 29 + 102, 27 + 29 + 104, 27 + 29 + 105, 27 + 32 + 50, 27 + 32 + 54, 27 + 32 + 58, 27 + 32 + 99, 27 + 32 + 100, 27 + 32 + 102, 27 + 32 + 104, 27 + 32 + 105, 27 + 50 + 54, 27 + 50 + 58, 27 + 50 + 99, 27 + 50 + 100, 27 + 50 + 102, 27 + 50 + 104, 27 + 50 + 105, 27 + 54 + 58, 27 + 54 + 99, 27 + 54 + 100, 27 + 54 + 102, 27 + 54 + 104, 27 + 54 + 105, 27 + 58 + 99, 27 + 58 + 100, 27 + 58 + 102, 27 + 58 + 104, 27 + 58 + 105, 27 + 99 + 100, 27 + 99 + 102, 27 + 99 + 104, 27 + 99 + 105, 27 + 100 + 102, 27 + 100 + 104, 27 + 100 + 105, 27 + 102 + 104, 27 + 102 + 105, 27 + 104 + 105, 29 +

32 + 50, 29 + 32 + 54, 29 + 32 + 58, 29 + 32 + 99, 29 + 32 + 100, 29 + 32 + 102, 29 + 32 + 104, 29 + 32 + 105, 29 + 50 + 54, 29 + 50 + 58, 29 + 50 + 99, 29 + 50 + 100, 29 + 50 + 102, 29 + 50 + 104, 29 + 50 + 105, 29 + 54 + 58, 29 + 54 + 99, 29 + 54 + 100, 29 + 54 + 102, 29 + 54 + 104, 29 + 54 + 105, 29 + 58 + 99, 29 + 58 + 100, 29 + 58 + 102, 29 + 58 + 104, 29 + 58 + 105, 29 + 99 + 100, 29 + 99 + 102, 29 + 99 + 104, 29 + 99 + 105, 29 + 100 + 102, 29 + 100 + 104, 29 + 100 + 105, 29 + 102 + 104, 29 + 102 + 105, 29 + 104 + 105, 32 + 50 + 54, 32 + 50 + 58, 32 + 50 + 99, 32 + 50 + 100, 32 + 50 + 102, 32 + 50 + 104, 32 + 50 + 105, 32 + 54 + 58, 32 + 54 + 99, 32 + 54 + 100, 32 + 54 + 102, 32 + 54 + 104, 32 + 54 + 105, 32 + 58 + 99, 32 + 58 + 100, 32 + 58 + 102, 32 + 58 + 104, 32 + 58 + 105, 32 + 99 + 100, 32 + 99 + 102, 32 + 99 + 104, 32 + 99 + 105, 32 + 100 + 102, 32 + 100 + 104, 32 + 100 + 105, 32 + 102 + 104, 32 + 102 + 105, 32 + 104 + 105, 50 + 54 + 58, 50 + 54 + 99, 50 + 54 + 100, 50 + 54 + 102, 50 + 54 + 104, 50 + 54 + 105, 50 + 58 + 99, 50 + 58 + 100, 50 + 58 + 102, 50 + 58 + 104, 50 + 58 + 105, 50 + 99 + 100, 50 + 99 + 102, 50 + 99 + 104, 50 + 99 + 105, 50 + 100 + 102, 50 + 100 + 104, 50 + 100 + 105, 50 + 102 + 104, 50 + 102 + 105, 50 + 104 + 105, 54 + 58 + 99, 54 + 58 + 100, 54 + 58 + 102, 54 + 58 + 104, 54 + 58 + 105, 54 + 99 + 100, 54 + 99 + 102, 54 + 99 + 104, 54 + 99 + 105, 54 + 100 + 102, 54 + 100 + 104, 54 + 100 + 105, 54 + 102 + 104, 54 + 102 + 105, 54 + 104 + 105, 58 + 99 + 100, 58 + 99 + 102, 58 + 99 + 104, 58 + 99 + 105, 58 + 100 + 102, 58 + 100 + 104, 58 + 100 + 105, 58 + 102 + 104, 58 + 102 + 105, 58 + 104 + 105, 99 + 100 + 102, 99 + 100 + 104, 99 + 100 + 105, 99 + 102 + 104, 99 + 102 + 105, 99 + 104 + 105, 100 + 102 + 104, 100 + 102 + 105, 100 + 104 + 105, 102 + 104 + 105

In some examples of any of the ABPCs and antibodies described herein, a light chain variable domain includes a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 85, where the light chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 85 listed in Table 4.

Table 4. Exemplary Combinations of Amino Acid Positions in SEQ ID NO: 85 that can be Substituted with Histidine

29 + 31, 29 + 32, 29 + 34, 29 + 36, 29 + 37, 29 + 38, 29 + 40, 29 + 56, 29 + 60, 29 + 61, 29 + 95, 29 + 96, 29 + 97, 29 + 100, 31 + 32, 31 + 34, 31 + 36, 31 + 37, 31 + 38, 31 + 40, 31 + 56, 31 + 60, 31 + 61, 31 + 95, 31 + 96, 31 + 97, 31 + 100, 32 + 34, 32 + 36, 32 + 37, 32 + 38, 32 + 40, 32 + 56, 32 + 60, 32 + 61, 32 + 95, 32 + 96, 32 + 97, 32 + 100, 34 + 36, 34 + 37, 34 + 38, 34 + 40, 34 + 56, 34 + 60, 34 + 61, 34 + 95, 34 + 96, 34 + 97, 34 + 100, 36 + 37, 36 + 38, 36 + 40, 36 + 56, 36 + 60, 36 + 61, 36 + 95, 36 + 96, 36 + 97, 36 + 100, 37 + 38, 37 + 40, 37 + 56, 37 + 60, 37 + 61, 37 + 95, 37 + 96, 37 + 97, 37 + 100, 38 + 40, 38 + 56, 38 + 60, 38 + 61, 38 + 95, 38 + 96, 38 + 97, 38 + 100, 40 + 56, 40 + 60, 40 + 61, 40 + 95, 40 + 96, 40 + 97, 40 + 100, 56 + 60, 56 + 61, 56 + 95, 56 + 96, 56 + 97, 56 + 100, 60 + 61, 60 + 95, 60 + 96, 60 + 97, 60 + 100, 61 + 95, 61 + 96, 61 + 97, 61 + 100, 95 + 96, 95 + 97, 95 + 100, 96 + 97, 96 + 100, 97 + 100, 29 + 31 + 32, 29 + 31 + 34, 29 + 31 + 36, 29 + 31 + 37, 29 + 31 + 38, 29 + 31 + 40, 29 + 31 + 56, 29 + 31 + 60, 29 + 31 + 61, 29 + 31 + 95, 29 + 31 + 96, 29 + 31 + 97, 29 + 31 + 100, 29 + 32 + 34, 29 + 32 + 36, 29 + 32 + 37, 29 + 32 + 38, 29 + 32 + 40, 29 + 32 + 56, 29 + 32 + 60, 29 + 32 + 61, 29 + 32 + 95, 29 + 32 + 96, 29 + 32 + 97, 29 + 32 + 100, 29 + 34 + 36, 29 + 34 + 37, 29 + 34 + 38, 29 + 34 + 40, 29 + 34 + 56, 29 + 34 + 60, 29 + 34 + 61, 29 + 34 + 95, 29 + 34 + 96, 29 + 34 + 97, 29 + 34 + 100, 29 + 36 + 37, 29 + 36 + 38, 29 + 36 + 40, 29 + 36 + 56, 29 + 36 + 60, 29 + 36 + 61, 29 + 36 + 95, 29 + 36 + 96, 29 + 36 + 97, 29 + 36 + 100, 29 + 37 + 38, 29 + 37 + 40, 29 + 37 + 56, 29 + 37 + 60, 29 + 37 + 61, 29 + 37 + 95, 29 + 37 + 96, 29 + 37 + 97, 29 + 37 + 100, 29 + 38 + 40, 29 + 38 + 56, 29 + 38 + 60, 29 + 38 + 61, 29 + 38 + 95, 29 + 38 + 96, 29 + 38 + 97, 29 + 38 + 100, 29 + 40 + 56, 29 + 40 + 60, 29 + 40 + 61, 29 + 40 + 95, 29 + 40 + 96, 29 + 40 + 97, 29 + 40 + 100, 29 + 56 + 60, 29 + 56 + 61, 29 + 56 + 95, 29 + 56 + 96, 29 + 56 + 97, 29 + 56 + 100, 29 + 60 + 61, 29 + 60 + 95, 29 + 60 + 96, 29 + 60 + 97, 29 + 60 + 100, 29 + 61 + 95, 29 + 61 + 96, 29 + 61 + 97, 29 + 61 + 100, 29 + 95 + 96, 29 + 95 + 97, 29 + 95 + 100, 29 + 96 + 97, 29 + 96 + 100, 29 + 97 + 100, 31 + 32 + 34, 31 + 32 + 36, 31 + 32 + 37, 31 + 32 + 38, 31 + 32 + 40, 31 + 32 + 56, 31 + 32 + 60, 31 + 32 + 61, 31 + 32 + 95, 31 + 32 + 96, 31 + 32 + 97, 31 + 32 + 100, 31 + 34 + 36, 31 + 34 + 37, 31 + 34 + 38, 31 + 34 + 40, 31 + 34 + 56, 31 + 34 + 60, 31 + 34 + 61, 31 + 34 + 95, 31 + 34 + 96, 31 + 34 + 97, 31 + 34 + 100, 31 + 36 + 37, 31 + 36 + 38, 31 + 36 + 40, 31 + 36 + 56, 31 + 36 + 60,

31 + 36 + 61, 31 + 36 + 95, 31 + 36 + 96, 31 + 36 + 97, 31 + 36 + 100, 31 + 37 + 38, 31 + 37 + 40, 31 + 37 + 56, 31 + 37 + 60, 31 + 37 + 61, 31 + 37 + 95, 31 + 37 + 96, 31 + 37 + 97, 31 + 37 + 100, 31 + 38 + 40, 31 + 38 + 56, 31 + 38 + 60, 31 + 38 + 61, 31 + 38 + 95, 31 + 38 + 96, 31 + 38 + 97, 31 + 38 + 100, 31 + 40 + 56, 31 + 40 + 60, 31 + 40 + 61, 31 + 40 + 95, 31 + 40 + 96, 31 + 40 + 97, 31 + 40 + 100, 31 + 56 + 60, 31 + 56 + 61, 31 + 56 + 95, 31 + 56 + 96, 31 + 56 + 97, 31 + 56 + 100, 31 + 60 + 61, 31 + 60 + 95, 31 + 60 + 96, 31 + 60 + 97, 31 + 60 + 100, 31 + 61 + 95, 31 + 61 + 96, 31 + 61 + 97, 31 + 61 + 100, 31 + 95 + 96, 31 + 95 + 97, 31 + 95 + 100, 31 + 96 + 97, 31 + 96 + 100, 31 + 97 + 100, 32 + 34 + 36, 32 + 34 + 37, 32 + 34 + 38, 32 + 34 + 40, 32 + 34 + 56, 32 + 34 + 60, 32 + 34 + 61, 32 + 34 + 95, 32 + 34 + 96, 32 + 34 + 97, 32 + 34 + 100, 32 + 36 + 37, 32 + 36 + 38, 32 + 36 + 40, 32 + 36 + 56, 32 + 36 + 60, 32 + 36 + 61, 32 + 36 + 95, 32 + 36 + 96, 32 + 36 + 97, 32 + 36 + 100, 32 + 37 + 38, 32 + 37 + 40, 32 + 37 + 56, 32 + 37 + 60, 32 + 37 + 61, 32 + 37 + 95, 32 + 37 + 96, 32 + 37 + 97, 32 + 37 + 100, 32 + 38 + 40, 32 + 38 + 56, 32 + 38 + 60, 32 + 38 + 61, 32 + 38 + 95, 32 + 38 + 96, 32 + 38 + 97, 32 + 38 + 100, 32 + 40 + 56, 32 + 40 + 60, 32 + 40 + 61, 32 + 40 + 95, 32 + 40 + 96, 32 + 40 + 97, 32 + 40 + 100, 32 + 56 + 60, 32 + 56 + 61, 32 + 56 + 95, 32 + 56 + 96, 32 + 56 + 97, 32 + 56 + 100, 32 + 60 + 61, 32 + 60 + 95, 32 + 60 + 96, 32 + 60 + 97, 32 + 60 + 100, 32 + 61 + 95, 32 + 61 + 96, 32 + 61 + 97, 32 + 61 + 100, 32 + 95 + 96, 32 + 95 + 97, 32 + 95 + 100, 32 + 96 + 97, 32 + 96 + 100, 32 + 97 + 100, 34 + 36 + 37, 34 + 36 + 38, 34 + 36 + 40, 34 + 36 + 56, 34 + 36 + 60, 34 + 36 + 61, 34 + 36 + 95, 34 + 36 + 96, 34 + 36 + 97, 34 + 36 + 100, 34 + 37 + 38, 34 + 37 + 40, 34 + 37 + 56, 34 + 37 + 60, 34 + 37 + 61, 34 + 37 + 95, 34 + 37 + 96, 34 + 37 + 97, 34 + 37 + 100, 34 + 38 + 40, 34 + 38 + 56, 34 + 38 + 60, 34 + 38 + 61, 34 + 38 + 95, 34 + 38 + 96, 34 + 38 + 97, 34 + 38 + 100, 34 + 40 + 56, 34 + 40 + 60, 34 + 40 + 61, 34 + 40 + 95, 34 + 40 + 96, 34 + 40 + 97, 34 + 40 + 100, 34 + 56 + 60, 34 + 56 + 61, 34 + 56 + 95, 34 + 56 + 96, 34 + 56 + 97, 34 + 56 + 100, 34 + 60 + 61, 34 + 60 + 95, 34 + 60 + 96, 34 + 60 + 97, 34 + 60 + 100, 34 + 61 + 95, 34 + 61 + 96, 34 + 61 + 97, 34 + 61 + 100, 34 + 95 + 96, 34 + 95 + 97, 34 + 95 + 100, 34 + 96 + 97, 34 + 96 + 100, 34 + 97 + 100, 36 + 37 + 38, 36 + 37 + 40, 36 + 37 + 56, 36 + 37 + 60, 36 + 37 + 61, 36 + 37 + 95, 36 + 37 + 96, 36 + 37 + 97, 36 + 37 + 100, 36 + 38 + 40, 36 + 38 + 56, 36 + 38 + 60, 36 + 38 + 61, 36 + 38 + 95, 36 + 38 + 96, 36 + 38 + 97, 36 + 38 + 100, 36 + 40 + 56, 36 + 40 + 60, 36 + 40 + 61, 36 + 40 + 95, 36 + 40 + 96, 36 + 40 + 97, 36 + 40 + 100, 36 + 56 + 60, 36 + 56 + 61, 36 + 56

+ 95, 36 + 56 + 96, 36 + 56 + 97, 36 + 56 + 100, 36 + 60 + 61, 36 + 60 + 95, 36 + 60 + 96, 36 + 60 + 97, 36 + 60 + 100, 36 + 61 + 95, 36 + 61 + 96, 36 + 61 + 97, 36 + 61 + 100, 36 + 95 + 96, 36 + 95 + 97, 36 + 95 + 100, 36 + 96 + 97, 36 + 96 + 100, 36 + 97 + 100, 37 + 38 + 40, 37 + 38 + 56, 37 + 38 + 60, 37 + 38 + 61, 37 + 38 + 95, 37 + 38 + 96, 37 + 38 + 97, 37 + 38 + 100, 37 + 40 + 56, 37 + 40 + 60, 37 + 40 + 61, 37 + 40 + 95, 37 + 40 + 96, 37 + 40 + 97, 37 + 40 + 100, 37 + 56 + 60, 37 + 56 + 61, 37 + 56 + 95, 37 + 56 + 96, 37 + 56 + 97, 37 + 56 + 100, 37 + 60 + 61, 37 + 60 + 95, 37 + 60 + 96, 37 + 60 + 97, 37 + 60 + 100, 37 + 61 + 95, 37 + 61 + 96, 37 + 61 + 97, 37 + 61 + 100, 37 + 95 + 96, 37 + 95 + 97, 37 + 95 + 100, 37 + 96 + 97, 37 + 96 + 100, 37 + 97 + 100, 38 + 40 + 56, 38 + 40 + 60, 38 + 40 + 61, 38 + 40 + 95, 38 + 40 + 96, 38 + 40 + 97, 38 + 40 + 100, 38 + 56 + 60, 38 + 56 + 61, 38 + 56 + 95, 38 + 56 + 96, 38 + 56 + 97, 38 + 56 + 100, 38 + 60 + 61, 38 + 60 + 95, 38 + 60 + 96, 38 + 60 + 97, 38 + 60 + 100, 38 + 61 + 95, 38 + 61 + 96, 38 + 61 + 97, 38 + 61 + 100, 38 + 95 + 96, 38 + 95 + 97, 38 + 95 + 100, 38 + 96 + 97, 38 + 96 + 100, 38 + 97 + 100, 40 + 56 + 60, 40 + 56 + 61, 40 + 56 + 95, 40 + 56 + 96, 40 + 56 + 97, 40 + 56 + 100, 40 + 60 + 61, 40 + 60 + 95, 40 + 60 + 96, 40 + 60 + 97, 40 + 60 + 100, 40 + 61 + 95, 40 + 61 + 96, 40 + 61 + 97, 40 + 61 + 100, 40 + 95 + 96, 40 + 95 + 97, 40 + 95 + 100, 40 + 96 + 97, 40 + 96 + 100, 40 + 97 + 100, 56 + 60 + 61, 56 + 60 + 95, 56 + 60 + 96, 56 + 60 + 97, 56 + 60 + 100, 56 + 61 + 95, 56 + 61 + 96, 56 + 61 + 97, 56 + 61 + 100, 56 + 95 + 96, 56 + 95 + 97, 56 + 95 + 100, 56 + 96 + 97, 56 + 96 + 100, 56 + 97 + 100, 60 + 61 + 95, 60 + 61 + 96, 60 + 61 + 97, 60 + 61 + 100, 60 + 95 + 96, 60 + 95 + 97, 60 + 95 + 100, 60 + 96 + 97, 60 + 96 + 100, 60 + 97 + 100, 61 + 95 + 96, 61 + 95 + 97, 61 + 95 + 100, 61 + 96 + 97, 61 + 96 + 100, 61 + 97 + 100, 95 + 96 + 97, 95 + 96 + 100, 95 + 97 + 100, 96 + 97 + 100

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3; and a light chain variable domain that that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 85, where the light chain variable domain includes

a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 85 listed in Table 4.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3, and where the heavy chain variable domain includes an alanine at position 35 in SEQ ID NO: 84; and a light chain variable domain that that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 85, where the light chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 4.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3, and where the heavy chain variable domain includes an alanine at position 98 in SEQ ID NO: 84; and a light chain variable domain that that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 85, where the light chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 4.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain comprising SEQ ID NO: 85, and a heavy chain variable domain that is at least 90% identical (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more (e.g., two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID

NO: 85, wherein the light chain variable domain includes a histidine at position 29 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 31 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 32 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 34 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 36 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy

chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 37 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 38 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 40 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 56 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 60 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 61 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 95 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 96 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 97 in SEQ ID

NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at position 100 in SEQ ID NO: 85; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 84, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 84 listed in Table 3.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of hu139.10 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidine(s) substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain of hu139.10 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidine(s) substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of hu139.10 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidines substituted with an alanine; and a light chain variable domain of hu139.10 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidine(s) substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the heavy chain variable domain of hu139.10 comprises SEQ ID NO: 84. In some examples of any of the ABPCs and antibodies described herein, the light chain variable domain of hu139.10 comprises SEQ ID NO: 85.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a heavy chain variable domain comprising a CDR1, a CDR2, and a

CDR3 of SEQ ID NO: 86, SEQ ID NO: 87, and SEQ ID NO: 88, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 86-88 substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 89, SEQ ID NO: 90, and SEQ ID NO: 91, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 89-91 substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes: a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 86, SEQ ID NO: 87, and SEQ ID NO: 88, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 86-88 substituted with an alanine; and a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 89, SEQ ID NO: 90, and SEQ ID NO: 91, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 89-91 substituted with an alanine.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a heavy chain variable domain of SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain of SEQ ID NO: 85, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137, SEQ ID NO: 138, SEQ ID NO: 139, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 142, SEQ ID NO: 143, SEQ ID NO: 144, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 147, SEQ ID NO: 148, SEQ ID NO: 149, SEQ ID NO: 150, SEQ ID NO: 151, SEQ ID NO: 152, SEQ ID NO: 153,

SEQ ID NO: 154, SEQ ID NO: 155, SEQ ID NO: 156, SEQ ID NO: 157, SEQ ID NO: 158, SEQ ID NO: 159, SEQ ID NO: 160, SEQ ID NO: 161, SEQ ID NO: 162, or SEQ ID NO: 163.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 85, and a heavy chain variable domain comprising: SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 132, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 133, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120,

SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 134, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 135, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 136, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID

NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 137, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 138, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 139, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99,

SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 140, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 141, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 142, and a heavy

chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 143, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 144, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 145, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 146, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 147, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ

ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 148, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 149, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 150, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO:

115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 151, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 152, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 153, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ

ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 154, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 155, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 156, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID

NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 157, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 158, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 159, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 160, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 161, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ

ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 162, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 163, and a heavy chain variable domain comprising: SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, or SEQ ID NO: 131.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain comprising SEQ ID NO: 164, and a light chain variable domain comprising SEQ ID NO: 85, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137, SEQ ID NO: 138, SEQ ID NO:

139, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 142, SEQ ID NO: 143, SEQ ID NO: 144, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 147, SEQ ID NO: 148, SEQ ID NO: 149, SEQ ID NO: 150, SEQ ID NO: 151, SEQ ID NO: 152, SEQ ID NO: 153, SEQ ID NO: 154, SEQ ID NO: 155, SEQ ID NO: 156, SEQ ID NO: 157, SEQ ID NO: 158, SEQ ID NO: 159, SEQ ID NO: 160, SEQ ID NO: 161, SEQ ID NO: 162, or SEQ ID NO: 163.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain comprising SEQ ID NO: 165, and a light chain variable domain comprising SEQ ID NO: 85, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137, SEQ ID NO: 138, SEQ ID NO: 139, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 142, SEQ ID NO: 143, SEQ ID NO: 144, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 147, SEQ ID NO: 148, SEQ ID NO: 149, SEQ ID NO: 150, SEQ ID NO: 151, SEQ ID NO: 152, SEQ ID NO: 153, SEQ ID NO: 154, SEQ ID NO: 155, SEQ ID NO: 156, SEQ ID NO: 157, SEQ ID NO: 158, SEQ ID NO: 159, SEQ ID NO: 160, SEQ ID NO: 161, SEQ ID NO: 162, or SEQ ID NO: 163.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain comprising SEQ ID NO: 166, and a light chain variable domain comprising SEQ ID NO: 85, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137, SEQ ID NO: 138, SEQ ID NO: 139, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 142, SEQ ID NO: 143, SEQ ID NO: 144, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 147, SEQ ID NO: 148, SEQ ID NO: 149, SEQ ID NO: 150, SEQ ID NO: 151, SEQ ID NO: 152, SEQ ID NO: 153, SEQ ID NO: 154, SEQ ID NO: 155, SEQ ID NO: 156, SEQ ID NO: 157, SEQ ID NO: 158, SEQ ID NO: 159, SEQ ID NO: 160, SEQ ID NO: 161, SEQ ID NO: 162, or SEQ ID NO: 163.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain comprising SEQ ID NO: 167, and a light chain variable domain comprising SEQ ID NO: 85, SEQ ID NO: 132, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 136, SEQ ID NO: 137, SEQ ID NO: 138, SEQ ID NO: 139, SEQ ID NO: 140, SEQ ID NO: 141, SEQ ID NO: 142, SEQ ID NO: 143, SEQ ID NO: 144, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 147, SEQ ID NO: 148, SEQ ID NO: 149, SEQ ID NO: 150, SEQ ID NO: 151, SEQ ID NO: 152, SEQ ID NO: 153, SEQ ID NO: 154, SEQ ID

NO: 155, SEQ ID NO: 156, SEQ ID NO: 157, SEQ ID NO: 158, SEQ ID NO: 159, SEQ ID NO: 160, SEQ ID NO: 161, SEQ ID NO: 162, or SEQ ID NO: 163.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of SEQ ID NO: 168, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, or SEQ ID NO: 177.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 168, and a heavy chain variable domain comprising SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 169, and a heavy chain variable domain comprising SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 170, and a heavy chain variable domain comprising SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID

NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 171, and a heavy chain variable domain comprising SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 172, and a heavy chain variable domain comprising SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 173, and a heavy chain variable domain comprising SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 174, and a heavy chain variable domain comprising SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 175, and a heavy chain variable domain comprising SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ

ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 176, and a heavy chain variable domain comprising SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 177, and a heavy chain variable domain comprising SEQ ID NO: 84, SEQ ID NO: 92, SEQ ID NO: 93, SEQ ID NO: 94, SEQ ID NO: 95, SEQ ID NO: 96, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 100, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 105, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 112, SEQ ID NO: 113, SEQ ID NO: 114, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 123, SEQ ID NO: 124, SEQ ID NO: 125, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 164, SEQ ID NO: 165, SEQ ID NO: 166, or SEQ ID NO: 167.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of huAD208.4.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain of huAD208.4.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen,

seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of huAD208.4.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine; and a light chain variable domain of huAD208.4.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the heavy chain variable domain of huAD208.4.1 comprises SEQ ID NO: 178. In some examples of any of the ABPCs and antibodies described herein, the light chain variable domain of huAD208.4.1 comprises SEQ ID NO: 179.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 180, SEQ ID NO: 181, and SEQ ID NO: 182, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 180-182 substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 183, SEQ ID NO: 184, and SEQ ID NO: 185, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 183-185 substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes: a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 180, SEQ ID NO: 181, and SEQ ID NO: 182, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 180-182 substituted with a histidine; and a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 183, SEQ ID NO: 184, and SEQ ID NO: 185, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 183-185 substituted with a histidine.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at

least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 178 selected from the group of: 33, 52, 56, 57, or 106. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 179, where the light chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 179 selected from the group of: 25, 26, 28, 29, 31, 36, 37, 57, 59, 94, 95, 96, or 100. In some examples of any of the ABPCs and antibodies described herein the first antigen-binding domain includes: a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 178 selected from the group consisting of: 33, 52, 56, 57, or 106, and a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 179, where the light chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 179 selected from the group consisting of: 25, 26, 28, 29, 31, 36, 37, 57, 59, 94, 95, 96, or 100.

In some examples of any of the ABPCs and antibodies described herein, a heavy chain variable domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

Table 5. Exemplary Combinations of Amino Acid Positions in SEQ ID NO: 178 that can be Substituted with Histidine

33 + 52, 33 + 56, 33 + 57, 33 + 106, 52 + 56, 52 + 57, 52 + 106, 56 + 57, 56 + 106, 57 + 106, 33 + 52 + 56, 33 + 52 + 57, 33 + 52 + 106, 33 + 56 + 57, 33 + 56 + 106, 33 + 57 + 106, 52 + 56 + 57, 52 + 56 + 106, 52 + 57 + 106, 56 + 57 + 106

In some examples of any of the ABPCs and antibodies described herein, a light chain variable domain includes a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 179, where the light chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 179 listed in Table 6.

Table 6. Exemplary Combinations of Amino Acid Positions in SEQ ID NO: 179 that can be Substituted with Histidine

25 + 26, 25 + 28, 25 + 29, 25 + 31, 25 + 36, 25 + 37, 25 + 57, 25 + 59, 25 + 94, 25 + 95, 25 + 96, 25 + 100, 26 + 28, 26 + 29, 26 + 31, 26 + 36, 26 + 37, 26 + 57, 26 + 59, 26 + 94, 26 + 95, 26 + 96, 26 + 100, 28 + 29, 28 + 31, 28 + 36, 28 + 37, 28 + 57, 28 + 59, 28 + 94, 28 + 95, 28 + 96, 28 + 100, 29 + 31, 29 + 36, 29 + 37, 29 + 57, 29 + 59, 29 + 94, 29 + 95, 29 + 96, 29 + 100, 31 + 36, 31 + 37, 31 + 57, 31 + 59, 31 + 94, 31 + 95, 31 + 96, 31 + 100, 36 + 37, 36 + 57, 36 + 59, 36 + 94, 36 + 95, 36 + 96, 36 + 100, 37 + 57, 37 + 59, 37 + 94, 37 + 95, 37 + 96, 37 + 100, 57 + 59, 57 + 94, 57 + 95, 57 + 96, 57 + 100, 59 + 94, 59 + 95, 59 + 96, 59 + 100, 94 + 95, 94 + 96, 94 + 100, 95 + 96, 95 + 100, 96 + 100, 25 + 26 + 28, 25 + 26 + 29, 25 + 26 + 31, 25 + 26 + 36, 25 + 26 + 37, 25 + 26 + 57, 25 + 26 + 59, 25 + 26 + 94, 25 + 26 + 95, 25 + 26 + 96, 25 + 26 + 100, 25 + 28 + 29, 25 + 28 + 31, 25 + 28 + 36, 25 + 28 + 37, 25 + 28 + 57, 25 + 28 + 59, 25 + 28 + 94, 25 + 28 + 95, 25 + 28 + 96, 25 + 28 + 100, 25 + 29 + 31, 25 + 29 + 36, 25 + 29 + 37, 25 + 29 + 57, 25 + 29 + 59, 25 + 29 + 94, 25 + 29 + 95, 25 + 29 + 96, 25 + 29 + 100, 25 + 31 + 36, 25 + 31 + 37, 25 + 31 + 57, 25 + 31 + 59, 25 + 31 + 94, 25 + 31 + 95, 25 + 31 + 96, 25 + 31 + 100, 25 + 36 + 37, 25 + 36 + 57, 25 + 36 + 59, 25 + 36 + 94, 25 + 36 + 95, 25 + 36 + 96, 25 + 36 + 100, 25 + 37 + 57, 25 + 37 + 59, 25 + 37 + 94, 25 + 37 + 95, 25 + 37 + 96, 25 + 37 + 100, 25 + 57 + 59, 25 + 57 + 94, 25 + 57 + 95, 25 + 57 + 96, 25 + 57 + 100,

25 + 59 + 94, 25 + 59 + 95, 25 + 59 + 96, 25 + 59 + 100, 25 + 94 + 95, 25 + 94 + 96, 25 + 94 + 100, 25 + 95 + 96, 25 + 95 + 100, 25 + 96 + 100, 26 + 28 + 29, 26 + 28 + 31, 26 + 28 + 36, 26 + 28 + 37, 26 + 28 + 57, 26 + 28 + 59, 26 + 28 + 94, 26 + 28 + 95, 26 + 28 + 96, 26 + 28 + 100, 26 + 29 + 31, 26 + 29 + 36, 26 + 29 + 37, 26 + 29 + 57, 26 + 29 + 59, 26 + 29 + 94, 26 + 29 + 95, 26 + 29 + 96, 26 + 29 + 100, 26 + 31 + 36, 26 + 31 + 37, 26 + 31 + 57, 26 + 31 + 59, 26 + 31 + 94, 26 + 31 + 95, 26 + 31 + 96, 26 + 31 + 100, 26 + 36 + 37, 26 + 36 + 57, 26 + 36 + 59, 26 + 36 + 94, 26 + 36 + 95, 26 + 36 + 96, 26 + 36 + 100, 26 + 37 + 57, 26 + 37 + 59, 26 + 37 + 94, 26 + 37 + 95, 26 + 37 + 96, 26 + 37 + 100, 26 + 57 + 59, 26 + 57 + 94, 26 + 57 + 95, 26 + 57 + 96, 26 + 57 + 100, 26 + 59 + 94, 26 + 59 + 95, 26 + 59 + 96, 26 + 59 + 100, 26 + 94 + 95, 26 + 94 + 96, 26 + 94 + 100, 26 + 95 + 96, 26 + 95 + 100, 26 + 96 + 100, 28 + 29 + 31, 28 + 29 + 36, 28 + 29 + 37, 28 + 29 + 57, 28 + 29 + 59, 28 + 29 + 94, 28 + 29 + 95, 28 + 29 + 96, 28 + 29 + 100, 28 + 31 + 36, 28 + 31 + 37, 28 + 31 + 57, 28 + 31 + 59, 28 + 31 + 94, 28 + 31 + 95, 28 + 31 + 96, 28 + 31 + 100, 28 + 36 + 37, 28 + 36 + 57, 28 + 36 + 59, 28 + 36 + 94, 28 + 36 + 95, 28 + 36 + 96, 28 + 36 + 100, 28 + 37 + 57, 28 + 37 + 59, 28 + 37 + 94, 28 + 37 + 95, 28 + 37 + 96, 28 + 37 + 100, 28 + 57 + 59, 28 + 57 + 94, 28 + 57 + 95, 28 + 57 + 96, 28 + 57 + 100, 28 + 59 + 94, 28 + 59 + 95, 28 + 59 + 96, 28 + 59 + 100, 28 + 94 + 95, 28 + 94 + 96, 28 + 94 + 100, 28 + 95 + 96, 28 + 95 + 100, 28 + 96 + 100, 29 + 31 + 36, 29 + 31 + 37, 29 + 31 + 57, 29 + 31 + 59, 29 + 31 + 94, 29 + 31 + 95, 29 + 31 + 96, 29 + 31 + 100, 29 + 36 + 37, 29 + 36 + 57, 29 + 36 + 59, 29 + 36 + 94, 29 + 36 + 95, 29 + 36 + 96, 29 + 36 + 100, 29 + 37 + 57, 29 + 37 + 59, 29 + 37 + 94, 29 + 37 + 95, 29 + 37 + 96, 29 + 37 + 100, 29 + 57 + 59, 29 + 57 + 94, 29 + 57 + 95, 29 + 57 + 96, 29 + 57 + 100, 29 + 59 + 94, 29 + 59 + 95, 29 + 59 + 96, 29 + 59 + 100, 29 + 94 + 95, 29 + 94 + 96, 29 + 94 + 100, 29 + 95 + 96, 29 + 95 + 100, 29 + 96 + 100, 31 + 36 + 37, 31 + 36 + 57, 31 + 36 + 59, 31 + 36 + 94, 31 + 36 + 95, 31 + 36 + 96, 31 + 36 + 100, 31 + 37 + 57, 31 + 37 + 59, 31 + 37 + 94, 31 + 37 + 95, 31 + 37 + 96, 31 + 37 + 100, 31 + 57 + 59, 31 + 57 + 94, 31 + 57 + 95, 31 + 57 + 96, 31 + 57 + 100, 31 + 59 + 94, 31 + 59 + 95, 31 + 59 + 96, 31 + 59 + 100, 31 + 94 + 95, 31 + 94 + 96, 31 + 94 + 100, 31 + 95 + 96, 31 + 95 + 100, 31 + 96 + 100, 36 + 37 + 57, 36 + 37 + 59, 36 + 37 + 94, 36 + 37 + 95, 36 + 37 + 96, 36 + 37 + 100, 36 + 57 + 59, 36 + 57 + 94, 36 + 57 + 95, 36 + 57 + 96, 36 + 57 + 100, 36 + 59 + 94, 36 + 59 + 95, 36 + 59 + 96, 36 + 59 + 100, 36 + 94 + 95, 36 + 94 + 96, 36 + 94 + 100, 36 + 95 + 96, 36 + 95 + 100, 36 + 96 + 100, 37 + 57 + 59, 37 + 57 +

94, 37 + 57 + 95, 37 + 57 + 96, 37 + 57 + 100, 37 + 59 + 94, 37 + 59 + 95, 37 + 59 + 96, 37 + 59 + 100, 37 + 94 + 95, 37 + 94 + 96, 37 + 94 + 100, 37 + 95 + 96, 37 + 95 + 100, 37 + 96 + 100, 57 + 59 + 94, 57 + 59 + 95, 57 + 59 + 96, 57 + 59 + 100, 57 + 94 + 95, 57 + 94 + 96, 57 + 94 + 100, 57 + 95 + 96, 57 + 95 + 100, 57 + 96 + 100, 59 + 94 + 95, 59 + 94 + 96, 59 + 94 + 100, 59 + 95 + 96, 59 + 95 + 100, 59 + 96 + 100, 94 + 95 + 96, 94 + 95 + 100, 94 + 96 + 100, 95 + 96 + 100

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5; and a light chain variable domain that that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 179, where the light chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 179 listed in Table 6.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain comprising SEQ ID NO: 179, and a heavy chain variable domain that is at least 90% identical (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more (e.g., two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 25 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 26 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 28 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 29 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 31 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 36 in SEQ ID

NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 37 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 57 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 59 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 94 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy

chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 95 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 96 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at position 100 in SEQ ID NO: 2; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 178, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 178 listed in Table 5.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of huAD208.4.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidine(s) substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain of huAD208.4.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidine(s) substituted with an alanine. In some

examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of huAD208.4.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidines substituted with an alanine; and a light chain variable domain of huAD208.4.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidine(s) substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the heavy chain variable domain of huAD208.4.1 comprises SEQ ID NO: 178. In some examples of any of the ABPCs and antibodies described herein, the light chain variable domain of huAD208.4.1 comprises SEQ ID NO: 179.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 180, SEQ ID NO: 181, and SEQ ID NO: 182, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 180-182 substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 183, SEQ ID NO: 184, and SEQ ID NO: 185, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 183-185 substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes: a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 180, SEQ ID NO: 181, and SEQ ID NO: 182, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 180-182 substituted with an alanine; and a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 183, SEQ ID NO: 184, and SEQ ID NO: 185, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 183-185 substituted with an alanine.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a heavy chain variable domain of SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ

ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain of SEQ ID NO: 179, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 230, SEQ ID NO: 231, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 234, SEQ ID NO: 235, SEQ ID NO: 236, SEQ ID NO: 237, SEQ ID NO: 238, SEQ ID NO: 239, SEQ ID NO: 240, SEQ ID NO: 241, SEQ ID NO: 242, SEQ ID NO: 243, SEQ ID NO: 244, SEQ ID NO: 245, SEQ ID NO: 246, SEQ ID NO: 247, SEQ ID NO: 248, SEQ ID NO: 249, SEQ ID NO: 250, SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 253, SEQ ID NO: 254, SEQ ID NO: 255, SEQ ID NO: 256, or SEQ ID NO: 257.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 179, and a heavy chain variable domain comprising: SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 228, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO:

198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 229, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 230, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 231, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ

ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 232, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 233, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 234, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 235, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 236, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO:

219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 237, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 238, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 239, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ

ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 240, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 241, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 242, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO:

198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 243, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 244, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 245, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ

ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 246, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 247, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 248, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 249, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 250, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO:

219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 251, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 252, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 253, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ

ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 254, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 255, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 256, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO:

198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 257, and a heavy chain variable domain comprising: SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, or SEQ ID NO: 227.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain comprising SEQ ID NO: 258, and a light chain variable domain comprising SEQ ID NO: 179, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 230, SEQ ID NO: 231, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 234, SEQ ID NO: 235, SEQ ID NO: 236, SEQ ID NO: 237, SEQ ID NO: 238, SEQ ID NO: 239, SEQ ID NO: 240, SEQ ID NO: 241, SEQ ID NO: 242, SEQ ID NO: 243, SEQ ID NO: 244, SEQ ID NO: 245, SEQ ID NO: 246, SEQ ID NO: 247, SEQ ID NO: 248, SEQ ID NO: 249, SEQ ID NO: 250, SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 253, SEQ ID NO: 254, SEQ ID NO: 255, SEQ ID NO: 256, or SEQ ID NO: 257.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain comprising SEQ ID NO: 259, and a light

chain variable domain comprising SEQ ID NO: 179, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 230, SEQ ID NO: 231, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 234, SEQ ID NO: 235, SEQ ID NO: 236, SEQ ID NO: 237, SEQ ID NO: 238, SEQ ID NO: 239, SEQ ID NO: 240, SEQ ID NO: 241, SEQ ID NO: 242, SEQ ID NO: 243, SEQ ID NO: 244, SEQ ID NO: 245, SEQ ID NO: 246, SEQ ID NO: 247, SEQ ID NO: 248, SEQ ID NO: 249, SEQ ID NO: 250, SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 253, SEQ ID NO: 254, SEQ ID NO: 255, SEQ ID NO: 256, or SEQ ID NO: 257.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain comprising SEQ ID NO: 260, and a light chain variable domain comprising SEQ ID NO: 179, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 230, SEQ ID NO: 231, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 234, SEQ ID NO: 235, SEQ ID NO: 236, SEQ ID NO: 237, SEQ ID NO: 238, SEQ ID NO: 239, SEQ ID NO: 240, SEQ ID NO: 241, SEQ ID NO: 242, SEQ ID NO: 243, SEQ ID NO: 244, SEQ ID NO: 245, SEQ ID NO: 246, SEQ ID NO: 247, SEQ ID NO: 248, SEQ ID NO: 249, SEQ ID NO: 250, SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 253, SEQ ID NO: 254, SEQ ID NO: 255, SEQ ID NO: 256, or SEQ ID NO: 257.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain comprising SEQ ID NO: 261, and a light chain variable domain comprising SEQ ID NO: 179, SEQ ID NO: 228, SEQ ID NO: 229, SEQ ID NO: 230, SEQ ID NO: 231, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 234, SEQ ID NO: 235, SEQ ID NO: 236, SEQ ID NO: 237, SEQ ID NO: 238, SEQ ID NO: 239, SEQ ID NO: 240, SEQ ID NO: 241, SEQ ID NO: 242, SEQ ID NO: 243, SEQ ID NO: 244, SEQ ID NO: 245, SEQ ID NO: 246, SEQ ID NO: 247, SEQ ID NO: 248, SEQ ID NO: 249, SEQ ID NO: 250, SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 253, SEQ ID NO: 254, SEQ ID NO: 255, SEQ ID NO: 256, or SEQ ID NO: 257.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain of SEQ ID NO: 262, SEQ ID NO: 263, SEQ ID NO: 264, SEQ ID NO: 265, SEQ ID NO: 266, SEQ ID NO: 267, SEQ ID NO: 268, SEQ ID NO: 269, SEQ ID NO: 270, or SEQ ID NO: 271.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 262, and a heavy

chain variable domain comprising SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 263, and a heavy chain variable domain comprising SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 264, and a heavy chain variable domain comprising SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO:

219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 265, and a heavy chain variable domain comprising SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 266, and a heavy chain variable domain comprising SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 267, and a heavy chain variable domain comprising SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID

NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 268, and a heavy chain variable domain comprising SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 269, and a heavy chain variable domain comprising SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224,

SEQ ID NO: 225, SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 270, and a heavy chain variable domain comprising SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 271, and a heavy chain variable domain comprising SEQ ID NO: 178, SEQ ID NO: 186, SEQ ID NO: 187, SEQ ID NO: 188, SEQ ID NO: 189, SEQ ID NO: 190, SEQ ID NO: 191, SEQ ID NO: 192, SEQ ID NO: 193, SEQ ID NO: 194, SEQ ID NO: 195, SEQ ID NO: 196, SEQ ID NO: 197, SEQ ID NO: 198, SEQ ID NO: 199, SEQ ID NO: 200, SEQ ID NO: 201, SEQ ID NO: 202, SEQ ID NO: 203, SEQ ID NO: 204, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 207, SEQ ID NO: 208, SEQ ID NO: 209, SEQ ID NO: 210, SEQ ID NO: 211, SEQ ID NO: 212, SEQ ID NO: 213, SEQ ID NO: 214, SEQ ID NO: 215, SEQ ID NO: 216, SEQ ID NO: 217, SEQ ID NO: 218, SEQ ID NO: 219, SEQ ID NO: 220, SEQ ID NO: 221, SEQ ID NO: 222, SEQ ID NO: 223, SEQ ID NO: 224, SEQ ID NO: 225, SEQ ID NO: 226, SEQ ID NO: 227, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of huAD208.12.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first

antigen-binding domain includes a light chain variable domain of huAD208.12.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of huAD208.12.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine; and a light chain variable domain of huAD208.12.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acids substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the heavy chain variable domain of huAD208.12.1 comprises SEQ ID NO: 272. In some examples of any of the ABPCs and antibodies described herein, the light chain variable domain of huAD208.12.1 comprises SEQ ID NO: 273.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 274, SEQ ID NO: 275, and SEQ ID NO: 276, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 274-276 substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 277, SEQ ID NO: 278, and SEQ ID NO: 279, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 277-279 substituted with a histidine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes: a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 274, SEQ ID NO: 275, and SEQ ID NO: 276, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 274-276 substituted with a histidine; and a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 277, SEQ ID NO: 278, and SEQ ID NO: 279, respectively, with

collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NOs: 277-279 substituted with a histidine.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272, where the heavy chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 272 selected from the group of: 24, 27, 29, 62, 63, 98, or 108. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 273, where the light chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 273 selected from the group of: 27, 28, 29, 31, 32, 89, 92, or 93. In some examples of any of the ABPCs and antibodies described herein the first antigen-binding domain includes: a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272, where the heavy chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 272 selected from the group consisting of: 24, 27, 29, 62, 63, 98, or 108, and a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 273, where the light chain variable domain includes a histidine at one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) amino acid positions in SEQ ID NO: 273 is selected from the group consisting of: 27, 28, 29, 31, 32, 89, 92, or 93.

In some examples of any of the ABPCs and antibodies described herein, a heavy chain variable domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272,

where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 272 listed in Table 7.

Table 7. Exemplary Combinations of Amino Acid Positions in SEQ ID NO: 272 that can be Substituted with Histidine

24 + 27, 24 + 29, 24 + 62, 24 + 63, 24 + 98, 24 + 108, 27 + 29, 27 + 62, 27 + 63, 27 + 98, 27 + 108, 29 + 62, 29 + 63, 29 + 98, 29 + 108, 62 + 63, 62 + 98, 62 + 108, 63 + 98, 63 + 108, 98 + 108, 24 + 27 + 29, 24 + 27 + 62, 24 + 27 + 63, 24 + 27 + 98, 24 + 27 + 108, 24 + 29 + 62, 24 + 29 + 63, 24 + 29 + 98, 24 + 29 + 108, 24 + 62 + 63, 24 + 62 + 98, 24 + 62 + 108, 24 + 63 + 98, 24 + 63 + 108, 24 + 98 + 108, 27 + 29 + 62, 27 + 29 + 63, 27 + 29 + 98, 27 + 29 + 108, 27 + 62 + 63, 27 + 62 + 98, 27 + 62 + 108, 27 + 63 + 98, 27 + 63 + 108, 27 + 98 + 108, 29 + 62 + 63, 29 + 62 + 98, 29 + 62 + 108, 29 + 63 + 98, 29 + 63 + 108, 29 + 98 + 108, 62 + 63 + 98, 62 + 63 + 108, 62 + 98 + 108, 63 + 98 + 108

In some examples of any of the ABPCs and antibodies described herein, a light chain variable domain includes a light chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 273, where the light chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 273 listed in Table 8.

Table 8. Exemplary Combinations of Amino Acid Positions in SEQ ID NO: 273 that can be Substituted with Histidine

27 + 28, 27 + 29, 27 + 31, 27 + 32, 27 + 89, 27 + 92, 27 + 93, 28 + 29, 28 + 31, 28 + 32, 28 + 89, 28 + 92, 28 + 93, 29 + 31, 29 + 32, 29 + 89, 29 + 92, 29 + 93, 31 + 32, 31 + 89, 31 + 92, 31 + 93, 32 + 89, 32 + 92, 32 + 93, 89 + 92, 89 + 93, 92 + 93, 27 + 28 + 29, 27 + 28 + 31, 27 + 28 + 32, 27 + 28 + 89, 27 + 28 + 92, 27 + 28 + 93, 27 + 29 + 31, 27 + 29 + 32, 27 + 29 + 89, 27 + 29 + 92, 27 + 29 + 93, 27 + 31 + 32, 27 + 31 + 89, 27 + 31 + 92, 27 + 31 + 93, 27 + 32 + 89, 27 + 32 + 92, 27 + 32 + 93, 27 + 89 + 92, 27 + 89 + 93, 27 + 92 + 93, 28 + 29 + 31, 28 + 29 + 32, 28 + 29 + 89, 28 + 29 + 92, 28 + 29 + 93, 28 + 31 + 32, 28 + 31 + 89, 28 + 31 + 92, 28 + 31 + 93, 28 + 32 + 89, 28 + 32 + 92, 28 + 32 + 93, 28 + 89 + 92, 28 + 89 + 93, 28 + 92 +

93, 29 + 31 + 32, 29 + 31 + 89, 29 + 31 + 92, 29 + 31 + 93, 29 + 32 + 89, 29 + 32 + 92, 29 + 32 + 93, 29 + 89 + 92, 29 + 89 + 93, 29 + 92 + 93, 31 + 32 + 89, 31 + 32 + 92, 31 + 32 + 93, 31 + 89 + 92, 31 + 89 + 93, 31 + 92 + 93, 32 + 89 + 92, 32 + 89 + 93, 32 + 92 + 93, 89 + 92 + 93

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 272 listed in Table 7; and a light chain variable domain that that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 273, where the light chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 273 listed in Table 8.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain comprising SEQ ID NO: 273, and a heavy chain variable domain that is at least 90% identical (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more (e.g., two, three, four, five, six, seven, eight, nine, or ten) amino acid positions in SEQ ID NO: 272 listed in Table 7.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 273, wherein the light chain variable domain includes a histidine at position 27 in SEQ ID NO: 273; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 272 listed in Table 7.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 273, wherein the light chain variable domain includes a histidine at position 28 in SEQ ID

NO: 273; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 272 listed in Table 7.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 273, wherein the light chain variable domain includes a histidine at position 29 in SEQ ID NO: 273; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 272 listed in Table 7.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 273, wherein the light chain variable domain includes a histidine at position 31 in SEQ ID NO: 273; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 272 listed in Table 7.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 273, wherein the light chain variable domain includes a histidine at position 32 in SEQ ID NO: 273; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 272 listed in Table 7.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 273, wherein the light chain variable domain includes a histidine at position 89 in SEQ ID NO: 273; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272, where the heavy

chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 272 listed in Table 7.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 273, wherein the light chain variable domain includes a histidine at position 92 in SEQ ID NO: 273; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 272 listed in Table 7.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain that is at least 90% identical to SEQ ID NO: 273, wherein the light chain variable domain includes a histidine at position 93 in SEQ ID NO: 273; and a heavy chain variable domain that is at least 90% (e.g., at least 92%, at least 94%, at least 96%, at least 98%, at least 99%, or 100%) identical to SEQ ID NO: 272, where the heavy chain variable domain includes a histidine at any of the specific combinations of one or more amino acid positions in SEQ ID NO: 272 listed in Table 7.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of huAD208.12.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidine(s) substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain of huAD208.12.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidine(s) substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a heavy chain variable domain of huAD208.12.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidines substituted with an alanine; and a light chain variable domain of huAD208.12.1 with one or more (e.g., one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen, eighteen, nineteen, or twenty) histidine(s) substituted with an alanine. In some examples of any

of the ABPCs and antibodies described herein, the heavy chain variable domain of huAD208.12.1 comprises SEQ ID NO: 272. In some examples of any of the ABPCs and antibodies described herein, the light chain variable domain of huAD208.12.1 comprises SEQ ID NO: 273.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 274, SEQ ID NO: 275, and SEQ ID NO: 276, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 274-276 substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 277, SEQ ID NO: 278, and SEQ ID NO: 279, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 277-279 substituted with an alanine. In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes: a heavy chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 274, SEQ ID NO: 275, and SEQ ID NO: 276, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 274-276 substituted with an alanine; and a light chain variable domain comprising a CDR1, a CDR2, and a CDR3 of SEQ ID NO: 277, SEQ ID NO: 278, and SEQ ID NO: 279, respectively, with collectively a total of one or more (e.g., one, two, three, four, five, six, seven, eight, nine, or ten) histidine(s) in SEQ ID NOs: 277-279 substituted with an alanine.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain comprises a heavy chain variable domain of SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO:

317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain of SEQ ID NO: 273, SEQ ID NO: 324, SEQ ID NO: 325, SEQ ID NO: 326, SEQ ID NO: 327, SEQ ID NO: 328, SEQ ID NO: 329, SEQ ID NO: 330, SEQ ID NO: 331, SEQ ID NO: 332, SEQ ID NO: 333, SEQ ID NO: 334, SEQ ID NO: 335, SEQ ID NO: 336, SEQ ID NO: 337, SEQ ID NO: 338, SEQ ID NO: 339, SEQ ID NO: 340, SEQ ID NO: 341, SEQ ID NO: 342, SEQ ID NO: 343, SEQ ID NO: 344, SEQ ID NO: 345, SEQ ID NO: 346, SEQ ID NO: 347, SEQ ID NO: 348, SEQ ID NO: 349, or SEQ ID NO: 350.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 273, and a heavy chain variable domain comprising: SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 324, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 325, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 326, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 327, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO:

313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 328, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 329, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 330, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ

ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 331, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 332, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 333, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO:

292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 334, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 335, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 336, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ

ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 337, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 338, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 339, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 340, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 341, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO:

313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 342, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 343, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 344, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ

ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 345, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 346, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 347, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO:

292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 348, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 349, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

In some examples of any of the ABPCs and antibodies described herein, the first antigen-binding domain includes a light chain variable domain comprising SEQ ID NO: 350, and a heavy chain variable domain comprising: SEQ ID NO: 272, SEQ ID NO: 280, SEQ ID NO: 281, SEQ

ID NO: 282, SEQ ID NO: 283, SEQ ID NO: 284, SEQ ID NO: 285, SEQ ID NO: 286, SEQ ID NO: 287, SEQ ID NO: 288, SEQ ID NO: 289, SEQ ID NO: 290, SEQ ID NO: 291, SEQ ID NO: 292, SEQ ID NO: 293, SEQ ID NO: 294, SEQ ID NO: 295, SEQ ID NO: 296, SEQ ID NO: 297, SEQ ID NO: 298, SEQ ID NO: 299, SEQ ID NO: 300, SEQ ID NO: 301, SEQ ID NO: 302, SEQ ID NO: 303, SEQ ID NO: 304, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 307, SEQ ID NO: 308, SEQ ID NO: 309, SEQ ID NO: 310, SEQ ID NO: 311, SEQ ID NO: 312, SEQ ID NO: 313, SEQ ID NO: 314, SEQ ID NO: 315, SEQ ID NO: 316, SEQ ID NO: 317, SEQ ID NO: 318, SEQ ID NO: 319, SEQ ID NO: 320, SEQ ID NO: 321, SEQ ID NO: 322, or SEQ ID NO: 323.

Also provided herein are pharmaceutical compositions including any of the ABPCs and antibodies described herein. Also provided herein are methods of treating a subject in need thereof that include administering a therapeutically effective amount of any of the ABPCs and antibodies described herein to the subject.

In some examples of any of the ABPCs and antibodies described herein, a composition including the ABPC or antibody (e.g., any of the ABPCs and antibodies described herein) can provide for an increase (e.g., a detectable increase) (e.g., at least a 1% increase, at least a 2% increase, at least a 5% increase, at least a 10% increase, at least a 15% increase, at least a 20% increase, at least a 25% increase, at least a 30% increase, at least a 35% increase, at least a 40% increase, at least a 45% increase, at least a 50% increase, at least a 55% increase, at least a 60% increase, at least a 65% increase, at least a 70% increase, at least a 75% increase, at least a 80% increase, at least a 85% increase, at least a 90% increase, at least a 95% increase, at least a 100% increase, at least a 120% increase, at least a 140% increase, at least a 160% increase, at least a 180% increase, at least a 200% increase, at least a 250% increase, at least a 300% increase, at least a 350% increase, at least a 400% increase, at least a 450% increase, at least a 500% increase, at least a 1,000% increase, at least a 2,000% increase, at least a 3,000% increase, at least a 4,000% increase, at least a 5,000% increase, at least a 6,000% increase, at least a 7,000% increase, at least a 8,000% increase, at a least a 9,000% increase, or at least a 10,000% increase, or about a 1% increase to about 10,000% increase, about a 1% increase to about a 9,000% increase, about a 1% increase to about a 8,000% increase, about a 1% increase to about a 7,000% increase, about a 1% increase to about a 6,000% increase, about a 1% increase to about a 5,000% increase, about a 1% increase to about a 4,000% increase, about a 1% increase to about a 3,000% increase, about a 1% increase to about a 2,000% increase, about a 1% increase to about a

1,000% increase, about a 1% increase to about a 500% increase, about a 1% increase to about a 450% increase, about a 1% increase to about a 400% increase, about a 1% increase to about a 350% increase, about a 1% increase to about a 300% increase, about a 1% increase to about a 250% increase, about a 1% increase to about a 200% increase, about a 1% increase to about a 180% increase, about a 1% increase to about a 160% increase, about a 1% increase to about a 140% increase, about a 1% increase to about a 120% increase, about a 1% increase to about a 100% increase, about a 1% increase to about a 95% increase, about a 1% increase to about a 90% increase, about a 1% increase to about a 85% increase, about a 1% increase to about a 80% increase, about a 1% increase to about a 75% increase, about a 1% increase to about a 70% increase, about a 1% increase to about a 65% increase, about a 1% increase to about a 60% increase, about a 1% increase to about a 55% increase, about a 1% increase to about a 50% increase, about a 1% increase to about a 45% increase, about a 1% increase to about a 40% increase, about a 1% increase to about a 35% increase, about a 1% increase to about a 25% increase, about a 1% increase to about a 20% increase, about a 1% increase to about a 15% increase, about a 1% increase to about a 10% increase, about a 1% increase to about a 5% increase, about a 2% increase to about 10,000% increase, about a 2% increase to about a 9,000% increase, about a 2% increase to about a 8,000% increase, about a 2% increase to about a 7,000% increase, about a 2% increase to about a 6,000% increase, about a 2% increase to about a 5,000% increase, about a 2% increase to about a 4,000% increase, about a 2% increase to about a 3,000% increase, about a 2% increase to about a 2,000% increase, about a 2% increase to about a 1,000% increase, about a 2% increase to about a 500% increase, about a 2% increase to about a 450% increase, about a 2% increase to about a 400% increase, about a 2% increase to about a 350% increase, about a 2% increase to about a 300% increase, about a 2% increase to about a 250% increase, about a 2% increase to about a 200% increase, about a 2% increase to about a 180% increase, about a 2% increase to about a 160% increase, about a 2% increase to about a 140% increase, about a 2% increase to about a 120% increase, about a 2% increase to about a 100% increase, about a 2% increase to about a 95% increase, about a 2% increase to about a 90% increase, about a 2% increase to about a 85% increase, about a 2% increase to about a 80% increase, about a 2% increase to about a 75% increase, about a 2% increase to about a 70% increase, about a 2% increase to about a 65% increase, about a 2% increase to about a 60% increase, about a 2% increase to about a 55% increase, about a 2% increase to about a 50%

increase, about a 2% increase to about a 45% increase, about a 2% increase to about a 40% increase, about a 2% increase to about a 35% increase, about a 2% increase to about a 25% increase, about a 2% increase to about a 20% increase, about a 2% increase to about a 15% increase, about a 2% increase to about a 10% increase, about a 2% increase to about a 5% increase, about a 5% increase to about 10,000% increase, about a 5% increase to about a 9,000% increase, about a 5% increase to about a 8,000% increase, about a 5% increase to about a 7,000% increase, about a 5% increase to about a 6,000% increase, about a 5% increase to about a 5,000% increase, about a 5% increase to about a 4,000% increase, about a 5% increase to about a 3,000% increase, about a 5% increase to about a 2,000% increase, about a 5% increase to about a 1,000% increase, about a 5% increase to about a 500% increase, about a 5% increase to about a 450% increase, about a 5% increase to about a 400% increase, about a 5% increase to about a 350% increase, about a 5% increase to about a 300% increase, about a 5% increase to about a 250% increase, about a 5% increase to about a 200% increase, about a 5% increase to about a 180% increase, about a 5% increase to about a 160% increase, about a 5% increase to about a 140% increase, about a 5% increase to about a 120% increase, about a 5% increase to about a 100% increase, about a 5% increase to about a 95% increase, about a 5% increase to about a 90% increase, about a 5% increase to about a 85% increase, about a 5% increase to about a 80% increase, about a 5% increase to about a 75% increase, about a 5% increase to about a 70% increase, about a 5% increase to about a 65% increase, about a 5% increase to about a 60% increase, about a 5% increase to about a 55% increase, about a 5% increase to about a 50% increase, about a 5% increase to about a 45% increase, about a 5% increase to about a 40% increase, about a 5% increase to about a 35% increase, about a 5% increase to about a 25% increase, about a 5% increase to about a 20% increase, about a 5% increase to about a 15% increase, about a 5% increase to about a 10% increase, about a 10% increase to about 10,000% increase, about a 10% increase to about a 9,000% increase, about a 10% increase to about a 8,000% increase, about a 10% increase to about a 7,000% increase, about a 10% increase to about a 6,000% increase, about a 10% increase to about a 5,000% increase, about a 10% increase to about a 4,000% increase, about a 10% increase to about a 3,000% increase, about a 10% increase to about a 2,000% increase, about a 10% increase to about a 1,000% increase, about a 10% increase to about a 500% increase, about a 10% increase to about a 450% increase, about a 10% increase to about a 400% increase, about a 10% increase to about a 350% increase, about a

10% increase to about a 300% increase, about a 10% increase to about a 250% increase, about a 10% increase to about a 200% increase, about a 10% increase to about a 180% increase, about a 10% increase to about a 160% increase, about a 10% increase to about a 140% increase, about a 10% increase to about a 120% increase, about a 10% increase to about a 100% increase, about a 10% increase to about a 95% increase, about a 10% increase to about a 90% increase, about a 10% increase to about a 85% increase, about a 10% increase to about a 80% increase, about a 10% increase to about a 75% increase, about a 10% increase to about a 70% increase, about a 10% increase to about a 65% increase, about a 10% increase to about a 60% increase, about a 10% increase to about a 55% increase, about a 10% increase to about a 50% increase, about a 10% increase to about a 45% increase, about a 10% increase to about a 40% increase, about a 10% increase to about a 35% increase, about a 10% increase to about a 30% increase, about a 10% increase to about a 25% increase, about a 10% increase to about a 20% increase, about a 10% increase to about a 15% increase, about a 15% increase to about 10,000% increase, about a 15% increase to about a 9,000% increase, about a 15% increase to about a 8,000% increase, about a 15% increase to about a 7,000% increase, about a 15% increase to about a 6,000% increase, about a 15% increase to about a 5,000% increase, about a 15% increase to about a 4,000% increase, about a 15% increase to about a 3,000% increase, about a 15% increase to about a 2,000% increase, about a 15% increase to about a 1,000% increase, about a 15% increase to about a 500% increase, about a 15% increase to about a 450% increase, about a 15% increase to about a 400% increase, about a 15% increase to about a 350% increase, about a 15% increase to about a 300% increase, about a 15% increase to about a 250% increase, about a 15% increase to about a 200% increase, about a 15% increase to about a 180% increase, about a 15% increase to about a 160% increase, about a 15% increase to about a 140% increase, about a 15% increase to about a 120% increase, about a 15% increase to about a 100% increase, about a 15% increase to about a 95% increase, about a 15% increase to about a 90% increase, about a 15% increase to about a 85% increase, about a 15% increase to about a 80% increase, about a 15% increase to about a 75% increase, about a 15% increase to about a 70% increase, about a 15% increase to about a 65% increase, about a 15% increase to about a 60% increase, about a 15% increase to about a 55% increase, about a 15% increase to about a 50% increase, about a 15% increase to about a 45% increase, about a 15% increase to about a 40% increase, about a 15% increase to about a 35% increase, about a 15% increase to about a 30% increase, about a 15% increase to

about a 25% increase, about a 15% increase to about a 20% increase, about a 20% increase to about 10,000% increase, about a 20% increase to about a 9,000% increase, about a 20% increase to about a 8,000% increase, about a 20% increase to about a 7,000% increase, about a 20% increase to about a 6,000% increase, about a 20% increase to about a 5,000% increase, about a 20% increase to about a 4,000% increase, about a 20% increase to about a 3,000% increase, about a 20% increase to about a 2,000% increase, about a 20% increase to about a 1,000% increase, about a 20% increase to about a 500% increase, about a 20% increase to about a 450% increase, about a 20% increase to about a 400% increase, about a 20% increase to about a 350% increase, about a 20% increase to about a 300% increase, about a 20% increase to about a 250% increase, about a 20% increase to about a 200% increase, about a 20% increase to about a 180% increase, about a 20% increase to about a 160% increase, about a 20% increase to about a 140% increase, about a 20% increase to about a 120% increase, about a 20% increase to about a 100% increase, about a 20% increase to about a 95% increase, about a 20% increase to about a 90% increase, about a 20% increase to about a 85% increase, about a 20% increase to about a 80% increase, about a 20% increase to about a 75% increase, about a 20% increase to about a 70% increase, about a 20% increase to about a 65% increase, about a 20% increase to about a 60% increase, about a 20% increase to about a 55% increase, about a 20% increase to about a 50% increase, about a 20% increase to about a 45% increase, about a 20% increase to about a 40% increase, about a 20% increase to about a 35% increase, about a 20% increase to about a 30% increase, about a 20% increase to about a 25% increase, about a 25% increase to about 10,000% increase, about a 25% increase to about a 9,000% increase, about a 25% increase to about a 8,000% increase, about a 25% increase to about a 7,000% increase, about a 25% increase to about a 6,000% increase, about a 25% increase to about a 5,000% increase, about a 25% increase to about a 4,000% increase, about a 25% increase to about a 3,000% increase, about a 25% increase to about a 2,000% increase, about a 25% increase to about a 1,000% increase, about a 25% increase to about a 500% increase, about a 25% increase to about a 450% increase, about a 25% increase to about a 400% increase, about a 25% increase to about a 350% increase, about a 25% increase to about a 300% increase, about a 25% increase to about a 250% increase, about a 25% increase to about a 200% increase, about a 25% increase to about a 180% increase, about a 25% increase to about a 160% increase, about a 25% increase to about a 140% increase, about a 25% increase to about a 120% increase, about a 25% increase to about a 100% increase, about a

25% increase to about a 95% increase, about a 25% increase to about a 90% increase, about a 25% increase to about a 85% increase, about a 25% increase to about a 80% increase, about a 25% increase to about a 75% increase, about a 25% increase to about a 70% increase, about a 25% increase to about a 65% increase, about a 25% increase to about a 60% increase, about a 25% increase to about a 55% increase, about a 25% increase to about a 50% increase, about a 25% increase to about a 45% increase, about a 25% increase to about a 40% increase, about a 25% increase to about a 35% increase, about a 25% increase to about a 30% increase, about a 30% increase to about 10,000% increase, about a 30% increase to about a 9,000% increase, about a 30% increase to about a 8,000% increase, about a 30% increase to about a 7,000% increase, about a 30% increase to about a 6,000% increase, about a 30% increase to about a 5,000% increase, about a 30% increase to about a 4,000% increase, about a 30% increase to about a 3,000% increase, about a 30% increase to about a 2,000% increase, about a 30% increase to about a 1,000% increase, about a 30% increase to about a 500% increase, about a 30% increase to about a 450% increase, about a 30% increase to about a 400% increase, about a 30% increase to about a 350% increase, about a 30% increase to about a 300% increase, about a 30% increase to about a 250% increase, about a 30% increase to about a 200% increase, about a 30% increase to about a 180% increase, about a 30% increase to about a 160% increase, about a 30% increase to about a 140% increase, about a 30% increase to about a 120% increase, about a 30% increase to about a 100% increase, about a 30% increase to about a 95% increase, about a 30% increase to about a 90% increase, about a 30% increase to about a 85% increase, about a 30% increase to about a 80% increase, about a 30% increase to about a 75% increase, about a 30% increase to about a 70% increase, about a 30% increase to about a 65% increase, about a 30% increase to about a 60% increase, about a 30% increase to about a 55% increase, about a 30% increase to about a 50% increase, about a 30% increase to about a 45% increase, about a 30% increase to about a 40% increase, about a 30% increase to about a 35% increase, about a 35% increase to about 10,000% increase, about a 35% increase to about a 9,000% increase, about a 35% increase to about a 8,000% increase, about a 35% increase to about a 7,000% increase, about a 35% increase to about a 6,000% increase, about a 35% increase to about a 5,000% increase, about a 35% increase to about a 4,000% increase, about a 35% increase to about a 3,000% increase, about a 35% increase to about a 2,000% increase, about a 35% increase to about a 1,000% increase, about a 35% increase to about a 500% increase, about a 35% increase

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In some examples of any of the ABPCs and antibodies described herein, a composition including the ABPC or antibody (e.g., any of the ABPCs or antibodies described herein) can provide for an increase (e.g., a detectable increase) (e.g., at least a 0.1-fold increase, at least a 0.2-fold increase, at least a 0.3-fold increase, at least a 0.4-fold increase, at least a 0.5-fold increase, at least a 0.6-fold increase, at least a 0.7-fold increase, at least a 0.8-fold increase, at least a 0.9-fold increase, at least a 1.0-fold increase, at least a 1.2-fold increase, at least a 1.4-fold increase, at least a 1.5-fold increase, at least a 1.6-fold increase, at least a 1.8-fold increase, at least a 2.0-fold increase, at least a 2.2-fold increase, at least a 2.4-fold increase, at least a 2.5-fold increase, at least a 2.6-fold increase, at least a 2.8-fold increase, at least a 3.0-fold increase, at least a 3.5-fold increase, at least a 4.0-fold increase, at least a 4.5-fold increase, at least a 5.0-fold increase, at least a 5.5-fold increase, at least a 6.0-fold increase, at least a 6.5-fold increase, at least a 7.0-fold increase, at least a 7.5-fold increase, at least a 8.0-fold increase, at least a 8.5-fold increase, at least a 9.0-fold increase, at least a 9.5-fold increase, at least a 10-fold increase, at least a 15-fold increase, at least a 20-fold increase, at least a 25-fold increase, at least a 30-fold increase, at least a 35-fold increase, at least a 40-fold increase, at least a 45-fold increase, at least a 50-fold increase, at least a 55-fold increase, at least a 60-fold increase, at least a 65-fold increase, at least a 70-fold increase, at least a 75-fold increase, at least a 80-fold increase, at least a 85-fold increase, at least a 90-fold increase, at least a 95-fold increase, or at least a 100-fold increase, or about a 0.1-fold increase to about a 100-fold increase, about 0.1-fold increase to about a 90-fold increase, about 0.1-fold increase to about a 80-fold increase, about a 0.1-fold increase to about a 70-fold increase, about a 0.1-fold increase to about a 60-fold increase, about a 0.1-fold increase to about a 50-fold increase, about a 0.1-fold increase to about a 40-fold increase, about a 0.1-fold increase to about a 30-fold increase, about 0.1-fold increase to about 20-fold increase, about a 0.1-fold increase to about a 10-fold increase, about a 0.1-fold increase to about a 9.5-fold increase, about a 0.1-fold increase to about a 9.0-fold increase, about a 0.1-fold increase to about a 8.5-fold increase, about a 0.1-fold increase to about a 8.0-fold increase, about a 0.1-fold increase to about a 7.5-fold increase, about a 0.1-fold increase to about a 7.0-fold increase, about a 0.1-fold increase to about a 6.5-fold increase, about a 0.1-fold increase to about a 6.0-fold increase, about a 0.1-fold increase to about a 5.5-fold increase, about a 0.1-fold increase to about a 5.0-fold increase, about a 0.1-fold increase to about a 4.5-fold increase, about a 0.1-fold increase to about a 4.0-fold increase, about a 0.1-fold increase to about a 3.5-fold

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increase to about a 80-fold increase, about a 20-fold increase to about a 70-fold increase, about a 20-fold increase to about a 60-fold increase, about a 20-fold increase to about a 50-fold increase, about a 20-fold increase to about a 40-fold increase, about a 20-fold increase to about a 30-fold increase, about a 30-fold increase to about a 100-fold increase, about 30-fold increase to about a 90-fold increase, about 30-fold increase to about a 80-fold increase, about a 30-fold increase to about a 70-fold increase, about a 30-fold increase to about a 60-fold increase, about a 30-fold increase to about a 50-fold increase, about a 30-fold increase to about a 40-fold increase, about a 40-fold increase to about a 100-fold increase, about 40-fold increase to about a 90-fold increase, about 40-fold increase to about a 80-fold increase, about a 40-fold increase to about a 70-fold increase, about a 40-fold increase to about a 60-fold increase, about a 40-fold increase to about a 50-fold increase, about a 50-fold increase to about a 100-fold increase, about 50-fold increase to about a 90-fold increase, about 50-fold increase to about a 80-fold increase, about a 50-fold increase to about a 70-fold increase, about a 50-fold increase to about a 60-fold increase, about a 60-fold increase to about a 100-fold increase, about 60-fold increase to about a 90-fold increase, about 60-fold increase to about a 80-fold increase, about a 60-fold increase to about a 70-fold increase, about a 70-fold increase to about a 100-fold increase, about 70-fold increase to about a 90-fold increase, about 70-fold increase to about a 80-fold increase, about a 80-fold increase to about a 100-fold increase, about 80-fold increase to about a 90-fold increase, or about a 90-fold increase to about a 100-fold increase) in toxin liberation in the target mammalian cell (e.g., any of the target mammalian cells described herein) as compared to a composition including the same amount of a control ABPC or control antibody (e.g., any of the exemplary control ABPCs or control antibodies described herein).

In some examples of any of the ABPCs and antibodies described herein, a composition including the ABPC or antibody (e.g., any of the ABPCs or antibodies described herein) can provide for an increase (e.g., a detectable increase) (e.g., at least a 1% increase, at least a 2% increase, at least a 5% increase, at least a 10% increase, at least a 15% increase, at least a 20% increase, at least a 25% increase, at least a 30% increase, at least a 35% increase, at least a 40% increase, at least a 45% increase, at least a 50% increase, at least a 55% increase, at least a 60% increase, at least a 65% increase, at least a 70% increase, at least a 75% increase, at least a 80% increase, at least a 85% increase, at least a 90% increase, at least a 95% increase, at least a 100% increase, at least a 120% increase, at least a 140% increase, at least a 160% increase, at least a

180% increase, at least a 200% increase, at least a 250% increase, at least a 300% increase, at least a 350% increase, at least a 400% increase, at least a 450% increase, at least a 500% increase, at least a 1,000% increase, at least a 2,000% increase, at least a 3,000% increase, at least a 4,000% increase, at least a 5,000% increase, at least a 6,000% increase, at least a 7,000% increase, at least a 8,000% increase, at a least a 9,000% increase, or at least a 10,000% increase, or about a 1% increase to about a 10,000% increase (e.g., or any of the subranges of this range described herein)) in target mammalian cell killing (e.g., any of the exemplary target mammalian cells described herein) as compared to a composition including the same amount of a control ABPC or control antibody (e.g., any of the exemplary control ABPCs or control antibodies described herein).

In some examples of any of the ABPCs and antibodies described herein, a composition including the ABPC or antibody (e.g., any of the ABPCs or antibodies described herein) can provide for an increase (e.g., a detectable increase) (e.g., at least a 0.1-fold increase, at least a 0.2-fold increase, at least a 0.3-fold increase, at least a 0.4-fold increase, at least a 0.5-fold increase, at least a 0.6-fold increase, at least a 0.7-fold increase, at least a 0.8-fold increase, at least a 0.9-fold increase, at least a 1.0-fold increase, at least a 1.2-fold increase, at least a 1.4-fold increase, at least a 1.5-fold increase, at least a 1.6-fold increase, at least a 1.8-fold increase, at least a 2.0-fold increase, at least a 2.2-fold increase, at least a 2.4-fold increase, at least a 2.5-fold increase, at least a 2.6-fold increase, at least a 2.8-fold increase, at least a 3.0-fold increase, at least a 3.5-fold increase, at least a 4.0-fold increase, at least a 4.5-fold increase, at least a 5.0-fold increase, at least a 5.5-fold increase, at least a 6.0-fold increase, at least a 6.5-fold increase, at least a 7.0-fold increase, at least a 7.5-fold increase, at least a 8.0-fold increase, at least a 8.5-fold increase, at least a 9.0-fold increase, at least a 9.5-fold increase, at least a 10-fold increase, at least a 15-fold increase, at least a 20-fold increase, at least a 25-fold increase, at least a 30-fold increase, at least a 35-fold increase, at least a 40-fold increase, at least a 40-fold increase, at least a 45-fold increase, at least a 50-fold increase, at least a 55-fold increase, at least a 60-fold increase, at least a 65-fold increase, at least a 70-fold increase, at least a 80-fold increase, at least a 85-fold increase, at least a 90-fold increase, at least a 95-fold increase, or at least a 100-fold increase, or about a 0.1-fold increase to about a 100-fold increase (or any of the subranges of this range described herein)) in target mammalian cell killing (e.g., any of the exemplary target mammalian cells described herein) as compared to a composition including the same amount of a

control ABPC or control antibody (e.g., any of the exemplary control ABPCs or control antibodies described herein).

In some examples of any of the ABPCs and antibodies described herein, a composition including any of the ABPCs and antibodies described herein (e.g., upon contacting target mammalian cells presenting LRRC15 on their surface) results in decreased (e.g., at least a 1% decrease, at least a 5% decrease, at least a 10% decrease, at least a 15% decrease, at least a 20% decrease, at least a 25% decrease, at least a 30% decrease, at least a 35% decrease, at least a 40% decrease, at least a 45% decrease, at least a 50% decrease, at least a 55% decrease, at least a 60% decrease, at least a 65% decrease, at least a 70% decrease, at least a 75% decrease, at least a 80% decrease, at least a 85% decrease, at least a 90% decrease, at least a 95% decrease, or at least a 99% decrease, about a 1% decrease to about a 99% decrease, or any of the subranges of this range described herein) IC_{50} (for target mammalian cell killing) as compared to the IC_{50} for a composition including the same amount of a control ABPC or control antibody (e.g., any of the control ABPCs or control antibodies described herein) (e.g., upon contacting the same target mammalian cells).

In some examples of any of the ABPCs and antibodies described herein, a composition including any of the ABPCs or antibodies described herein (e.g., upon contacting target mammalian cells presenting LRRC15 on their surface) can provide for an increase (e.g., at least a 0.1-fold increase, at least a 0.2-fold increase, at least a 0.4-fold increase, at least a 0.6-fold increase, at least a 0.8-fold increase, at least a 1-fold increase, at least a 2-fold increase, at least a 5-fold increase, at least a 10-fold increase, at least a 15-fold increase, at least a 20-fold increase, at least a 25-fold increase, at least a 30-fold increase, at least a 35-fold increase, at least a 40-fold increase, at least a 45-fold increase, at least a 50-fold increase, at least a 55-fold increase, at least a 60-fold increase, at least a 65-fold increase, at least a 70-fold increase, at least a 75-fold increase, at least a 80-fold increase, at least a 85-fold increase, at least a 90-fold increase, at least a 95-fold increase, or at least a 100-fold increase, or about a 0.1-fold increase to about 500-fold increase (or any of the subranges of this range described herein) in the ratio of K_D on target mammalian cells presenting LRRC15 on their surface at a neutral pH (a pH of about 7.0 to about 8.0) to IC_{50} at the neutral pH on the same target cells, e.g., as compared to a control ABPC or control antibody (e.g., any of the exemplary control ABPCs or control antibodies described herein).

In some examples of any of the ABPCs and antibodies described herein, a composition including the ABPC or antibody (e.g., any of the ABPCs or antibodies described herein) can provide for an increase (e.g., a detectable increase) (e.g., at least a 1% increase, at least a 2% increase, at least a 5% increase, at least a 10% increase, at least a 15% increase, at least a 20% increase, at least a 25% increase, at least a 30% increase, at least a 35% increase, at least a 40% increase, at least a 45% increase, at least a 50% increase, at least a 55% increase, at least a 60% increase, at least a 65% increase, at least a 70% increase, at least a 75% increase, at least a 80% increase, at least a 85% increase, at least a 90% increase, at least a 95% increase, at least a 100% increase, at least a 120% increase, at least a 140% increase, at least a 160% increase, at least a 180% increase, at least a 200% increase, at least a 250% increase, at least a 300% increase, at least a 350% increase, at least a 400% increase, at least a 450% increase, at least a 500% increase, at least a 1,000% increase, at least a 2,000% increase, at least a 3,000% increase, at least a 4,000% increase, at least a 5,000% increase, at least a 6,000% increase, at least a 7,000% increase, at least a 8,000% increase, at least a 9,000% increase, or at least a 10,000% increase, or about a 1% increase to about a 10,000% increase (e.g., or any of the subranges of this range described herein)) in endolysosomal delivery in the target mammalian cell (e.g., any of the exemplary target mammalian cells described herein) as compared to a composition including the same amount of a control ABPC or control antibody (e.g., any of the exemplary control ABPCs or control antibodies described herein).

In some examples of any of the ABPCs and antibodies described herein, a composition including the ABPC or antibody (e.g., any of the ABPCs or antibodies described herein) can provide for an increase (e.g., a detectable increase) (e.g., at least a 0.1-fold increase, at least a 0.2-fold increase, at least a 0.3-fold increase, at least a 0.4-fold increase, at least a 0.5-fold increase, at least a 0.6-fold increase, at least a 0.7-fold increase, at least a 0.8-fold increase, at least a 0.9-fold increase, at least a 1.0-fold increase, at least a 1.2-fold increase, at least a 1.4-fold increase, at least a 1.5-fold increase, at least a 1.6-fold increase, at least a 1.8-fold increase, at least a 2.0-fold increase, at least a 2.2-fold increase, at least a 2.4-fold increase, at least a 2.5-fold increase, at least a 2.6-fold increase, at least a 2.8-fold increase, at least a 3.0-fold increase, at least a 3.5-fold increase, at least a 4.0-fold increase, at least a 4.5-fold increase, at least a 5.0-fold increase, at least a 5.5-fold increase, at least a 6.0-fold increase, at least a 6.5-fold increase, at least a 7.0-fold increase, at least a 7.5-fold increase, at least a 8.0-fold increase, at least a 8.5-fold

increase, at least a 9.0-fold increase, at least a 9.5-fold increase, at least a 10-fold increase, at least a 15-fold increase, at least a 20-fold increase, at least a 25-fold increase, at least a 30-fold increase, at least a 35-fold increase, at least a 40-fold increase, at least a 45-fold increase, at least a 50-fold increase, at least a 55-fold increase, at least a 60-fold increase, at least a 65-fold increase, at least a 70-fold increase, at least a 75-fold increase, at least a 80-fold increase, at least a 85-fold increase, at least a 90-fold increase, at least a 95-fold increase, or at least a 100-fold increase, or about a 0.1-fold increase to about a 100-fold increase (or any of the subranges of this range described herein)) in endolysosomal delivery in the target mammalian cell (e.g., any of the exemplary target mammalian cells described herein) as compared to a composition including the same amount of a control ABPC or control antibody (e.g., any of the exemplary control ABPCs or control antibodies described herein).

In examples of any of the ABPCs or antibodies described herein, the target mammalian cell does not express an FcRn receptor, or expresses a lower (e.g., a detectably lower) level (e.g., at least a 1% decreased, at least a 2% decreased, at least a 5% decreased, at least a 10% decrease, at least a 15% decreased, at least a 20% decreased, at least a 25% decreased, at least a 30% decreased, at least a 35% decreased, at least a 40% decreased, at least a 45% decreased, at least a 50% decreased, at least a 55% decreased, at least a 60% decreased, at least a 65% decreased, at least a 70% decreased, at least a 75% decreased, at least a 80% decreased, at least a 85% decreased, at least a 90% decreased, at least a 95% decreased, or at least a 99% decreased level) of FcRn receptor as compared to a FcRn expressing control cell (e.g., HUVEC – ThermoFisher #C0035C). In some examples of any of the ABPCs or antibodies described herein, the target mammalian cell is a cancer cell. In some examples of any of the ABPCs or antibodies described herein, the ABPC or antibody is cytotoxic or cytostatic to the target mammalian cell.

In some examples of any of the ABPCs or antibodies described herein, a composition including any of the ABPCs or antibodies described herein (e.g., upon administration to a subject) results in less (e.g., a 1% decrease to about a 99% decrease, or any of the subranges of this range described herein) of a reduction in the level of LRRC15 presented on the surface of the target cell as compared to a composition including the same amount of a control ABPC or a control antibody (e.g., any of the control ABPCs or control antibodies described herein). In some examples of any of the ABPCs or antibodies described herein, the composition does not

result in a detectable reduction in the level of the LRRC15 presented on the surface of the target mammalian cell.

In some examples of any of the ABPCs or antibodies described herein, the ABPC or antibody is cross-reactive with a non-human primate LRRC15 and a human LRRC15. In some examples of any of the ABPCs or antibodies described herein, the ABPC or antibody is cross-reactive with a non-human primate LRRC15, a human LRRC15, and one or both of rat LRRC15 and a mouse LRRC15. In some examples of any of the ABPCs or antibodies described herein, the ABPC or antibody is cross-reactive with a non-human primate LRRC15, a human LRRC15, a rat LRRC15, and a mouse LRRC15. In some examples of any of the ABPCs or antibodies described herein, the ABPC or antibody is cross-reactive with mouse LRRC15 and rat LRRC15. In some examples of any of the ABPCs or antibodies described herein, the antigen-binding domain binds to an epitope of LRRC15 that is present on the surface of cells from an Old World Monkey.

Some examples of any of the ABPCs or antibodies described herein can further include a second antigen-binding domain (e.g., any of the exemplary antigen-binding domains described herein).

Non-limiting aspects of these methods are described below, and can be used in any combination without limitation. Additional aspects of these methods are known in the art.

LRRC15 or Epitope of LRRC15

Leucine Rich Repeat Containing Protein 15 (LRRC15) is a tumor antigen that is known in the art, and is the target of therapeutic antibodies in oncology (Purcell et al (2018) "LRRC15 Is a Novel Mesenchymal Protein and Stromal Target for Antibody-Drug Conjugates" Cancer Res. 78(14):4059-4072). The sequence of the mature Human LRRC15 can be found in SEQ ID NO: 9. The sequence of the cDNA encoding the mature Human LRRC15 can be found in SEQ ID NO: 10. The sequence of the extracellular domain of LRRC15 can be found in SEQ ID NO: 11. The sequence of the cDNA encoding the extracellular domain of LRRC15 can be found in SEQ ID NO: 12.

Antigen-Binding Protein Constructs

Any of the antigen-binding protein constructs (ABPCs) described herein can be a single polypeptide, or can include two, three, four, five, six, seven, eight, nine, or ten (the same or different) polypeptides. In some embodiments where the ABPC is a single polypeptide, the ABPC can include a single antigen-binding domain or two antigen-binding domains. In some embodiments where the ABPC is a single polypeptide and includes two antigen-binding domains, the first and second antigen-binding domains can be identical or different from each other (and can specifically bind to the same or different antigens or epitopes).

In some embodiments where the ABPC is a single polypeptide, the first antigen-binding domain and the second antigen-binding domain (if present) can each be independently selected from the group of: a VH domain, a VHH domain, a VNAR domain, and a scFv. In some embodiments where the ABPC is a single polypeptide, the antigen-binding protein construct can be a BiTe, a (scFv)2, a nanobody, a nanobody-HSA, a DART, a TandAb, a scDiabody, a scDiabody-CH3, scFv-CH-CL-scFv, a HSAbody, scDiabody-HAS, a tandem-scFv, an Adnectin, a DARPin, a fibronectin, and a DEP conjugate. Additional examples of antigen-binding domains that can be used when the ABPC is a single polypeptide are known in the art.

A V_HH domain is a single monomeric variable antibody domain that can be found in camelids. A V_{NAR} domain is a single monomeric variable antibody domain that can be found in cartilaginous fish. Non-limiting aspects of V_HH domains and V_{NAR} domains are described in, e.g., Cromie et al., *Curr. Top. Med. Chem.* 15:2543-2557, 2016; De Genst et al., *Dev. Comp. Immunol.* 30:187-198, 2006; De Meyer et al., *Trends Biotechnol.* 32:263-270, 2014; Kijanka et al., *Nanomedicine* 10:161-174, 2015; Kovaleva et al., *Expert. Opin. Biol. Ther.* 14:1527-1539, 2014; Krah et al., *Immunopharmacol. Immunotoxicol.* 38:21-28, 2016; Mujic-Delic et al., *Trends Pharmacol. Sci.* 35:247-255, 2014; Muyldermans, *J. Biotechnol.* 74:277-302, 2001; Muyldermans et al., *Trends Biochem. Sci.* 26:230-235, 2001; Muyldermans, *Ann. Rev. Biochem.* 82:775-797, 2013; Rahbarizadeh et al., *Immunol. Invest.* 40:299-338, 2011; Van Audenhove et al., *EBioMedicine* 8:40-48, 2016; Van Bockstaele et al., *Curr. Opin. Investig. Drugs* 10:1212-1224, 2009; Vincke et al., *Methods Mol. Biol.* 911:15-26, 2012; and Wesolowski et al., *Med. Microbiol. Immunol.* 198:157-174, 2009.

In some embodiments where the ABPC is a single polypeptide and includes two antigen-binding domains, the first antigen-binding domain and the second antigen-binding domain can

both be VHH domains, or at least one antigen-binding domain can be a VHH domain. In some embodiments where the ABPC is a single polypeptide and includes two antigen-binding domains, the first antigen-binding domain and the second antigen-binding domain are both V_{NAR} domains, or at least one antigen-binding domain is a V_{NAR} domain. In some embodiments where the ABPC is a single polypeptide, the first antigen-binding domain is a scFv domain. In some embodiments where the ABPC is a single polypeptide and includes two antigen-binding domains, the first antigen-binding domain and the second antigen-binding domain can both be scFv domains, or at least one antigen-binding domain can be a scFv domain.

In some embodiments, the ABPC can include two or more polypeptides (e.g., two, three, four, five, six, seven, eight, nine, or ten polypeptides). In some embodiments where the ABPC includes two or more polypeptides, two, three, four, five or six of the polypeptides of the two or more polypeptides can be identical.

In some embodiments where the ABPC includes two or more polypeptides (e.g., two, three, four, five, six, seven, eight, nine, or ten polypeptides), two or more of the polypeptides of the ABPC can assemble (e.g., non-covalently assemble) to form one or more antigen-binding domains, e.g., an antigen-binding fragment of an antibody (e.g., any of the antigen-binding fragments of an antibody described herein), a VHH-scAb, a VHH-Fab, a Dual scFab, a F(ab')2, a diabody, a crossMab, a DAF (two-in-one), a DAF (four-in-one), a DutaMab, a DT-IgG, a knobs-in-holes common light chain, a knobs-in-holes assembly, a charge pair, a Fab-arm exchange, a SEEDbody, a LUZ-Y, a Fcab, a κλ-body, an orthogonal Fab, a DVD-IgG, a IgG(H)-scFv, a scFv-(H)IgG, IgG(L)-scFv, scFv-(L)IgG, IgG(L,H)-Fv, IgG(H)-V, V(H)-IgG, IgG(L)-V, V(L)-IgG, KIH IgG-scFab, 2scFv-IgG, IgG-2scFv, scFv4-Ig, Zybody, DVI-IgG, Diabody-CH3, a triple body, a miniantibody, a minibody, a TriBi minibody, scFv-CH3 KIH, Fab-scFv, a F(ab')2-scFv2, a scFv-KIH, a Fab-scFv-Fc, a tetravalent HCAb, a scDiabody-Fc, a Diabody-Fc, a tandem scFv-Fc, a VHH-Fc, a tandem VHH-Fc, a VHH-Fc KiH, a Fab-VHH-Fc, an Intrabody, a dock and lock, an ImmTAC, an IgG-IgG conjugate, a Cov-X-Body, a scFv1-PEG-scFv2, an Adnectin, a DARPin, a fibronectin, and a DEP conjugate. See, e.g., Spiess et al., *Mol. Immunol.* 67:95-106, 2015, incorporated in its entirety herewith, for a description of these elements. Non-limiting examples of an antigen-binding fragment of an antibody include an Fv fragment, a Fab fragment, a $F(ab')_2$ fragment, and a Fab' fragment. Additional examples of an antigen-binding fragment of an antibody is an antigen-binding fragment of an IgG (e.g., an antigen-binding

fragment of IgG1, IgG2, IgG3, or IgG4) (e.g., an antigen-binding fragment of a human or humanized IgG, e.g., human or humanized IgG1, IgG2, IgG3, or IgG4); an antigen-binding fragment of an IgA (e.g., an antigen-binding fragment of IgA1 or IgA2) (e.g., an antigen-binding fragment of a human or humanized IgA, e.g., a human or humanized IgA1 or IgA2); an antigen-binding fragment of an IgD (e.g., an antigen-binding fragment of a human or humanized IgD); an antigen-binding fragment of an IgE (e.g., an antigen-binding fragment of a human or humanized IgE); or an antigen-binding fragment of an IgM (e.g., an antigen-binding fragment of a human or humanized IgM).

A "Fv" fragment includes a non-covalently-linked dimer of one heavy chain variable domain and one light chain variable domain.

A "Fab" fragment includes, the constant domain of the light chain and the first constant domain (C_{H1}) of the heavy chain, in addition to the heavy and light chain variable domains of the Fv fragment.

A "F(ab')$_2$" fragment includes two Fab fragments joined, near the hinge region, by disulfide bonds.

A "dual variable domain immunoglobulin" or "DVD-Ig" refers to multivalent and multispecific binding proteins as described, e.g., in DiGiammarino et al., *Methods Mol. Biol.* 899:145-156, 2012; Jakob et al., *MABs* 5:358-363, 2013; and U.S. Patent Nos. 7,612,181; 8,258,268; 8,586,714; 8,716,450; 8,722,855; 8,735,546; and 8,822,645, each of which is incorporated by reference in its entirety.

DARTs are described in, e.g., Garber, *Nature Reviews Drug Discovery* 13:799-801, 2014.

Additional aspects of ABPCs are known in the art.

Exemplary Properties of Antigen-Binding Domains

In some embodiments of any of the antigen-binding protein constructs (ABPCs) or antibodies described herein, the dissociation rate of the first antigen-binding domain (and optionally the second antigen-binding domain, if present) at a pH of about 4.0 to about 6.5 (e.g., about 4.0 to about 6.4, about 4.0 to about 6.3, about 4.0 to about 6.2, about 4.0 to about 6.1, about 4.0 to about 6.0, about 4.0 to about 5.9, about 4.0 to about 5.8, about 4.0 to about 5.7, about 4.0 to about 5.6, about 4.0 to about 5.5, about 4.0 to about 5.4, about 4.0 to about 5.3, about 4.0 to about 5.2, about 4.0 to about 5.1, about 4.0 to about 5.0, about 4.0 to about 4.9,

about 4.0 to about 4.8, about 4.0 to about 4.7, about 4.0 to about 4.6, about 4.0 to about 4.5, about 4.0 to about 4.4, about 4.0 to about 4.3, about 4.0 to about 4.2, about 4.0 to about 4.1, about 4.1 to about 6.5, about 4.1 to about 6.4, about 4.1 to about 6.3, about 4.1 to about 6.2, about 4.1 to about 6.1, about 4.1 to about 6.0, about 4.1 to about 5.9, about 4.1 to about 5.8, about 4.1 to about 5.7, about 4.1 to about 5.6, about 4.1 to about 5.5, about 4.1 to about 5.4, about 4.1 to about 5.3, about 4.1 to about 5.2, about 4.1 to about 5.1, about 4.1 to about 5.0, about 4.1 to about 4.9, about 4.1 to about 4.8, about 4.1 to about 4.7, about 4.1 to about 4.6, about 4.1 to about 4.5, about 4.1 to about 4.4, about 4.1 to about 4.3, about 4.1 to about 4.2, about 4.2 to about 6.5, about 4.2 to about 6.4, about 4.2 to about 6.3, about 4.2 to about 6.2, about 4.2 to about 6.1, about 4.2 to about 6.0, about 4.2 to about 5.9, about 4.2 to about 5.8, about 4.2 to about 5.7, about 4.2 to about 5.6, about 4.2 to about 5.5, about 4.2 to about 5.4, about 4.2 to about 5.3, about 4.2 to about 5.2, about 4.2 to about 5.1, about 4.2 to about 5.0, about 4.2 to about 4.9, about 4.2 to about 4.8, about 4.2 to about 4.7, about 4.2 to about 4.6, about 4.2 to about 4.5, about 4.2 to about 4.4, about 4.2 to about 4.3, about 4.3 to about 6.5, about 4.3 to about 6.4, about 4.3 to about 6.3, about 4.3 to about 6.2, about 4.3 to about 6.1, about 4.3 to about 6.0, about 4.3 to about 5.9, about 4.3 to about 5.8, about 4.3 to about 5.7, about 4.3 to about 5.6, about 4.3 to about 5.5, about 4.3 to about 5.4, about 4.3 to about 5.3, about 4.3 to about 5.2, about 4.3 to about 5.1, about 4.3 to about 5.0, about 4.3 to about 4.9, about 4.3 to about 4.8, about 4.3 to about 4.7, about 4.3 to about 4.6, about 4.3 to about 4.5, about 4.3 to about 4.4, about 4.4 to about 6.5, about 4.4 to about 6.4, about 4.4 to about 6.3, about 4.4 to about 6.2, about 4.4 to about 6.1, about 4.4 to about 6.0, about 4.4 to about 5.9, about 4.4 to about 5.8, about 4.4 to about 5.7, about 4.4 to about 5.6, about 4.4 to about 5.5, about 4.4 to about 5.4, about 4.4 to about 5.3, about 4.4 to about 5.2, about 4.4 to about 5.1, about 4.4 to about 5.0, about 4.4 to about 4.9, about 4.4 to about 4.8, about 4.4 to about 4.7, about 4.4 to about 4.6, about 4.4 to about 4.5, about 4.5 to about 6.5, about 4.5 to about 6.4, about 4.5 to about 6.3, about 4.5 to about 6.2, about 4.5 to about 6.1, about 4.5 to about 6.0, about 4.5 to about 5.9, about 4.5 to about 5.8, about 4.5 to about 5.7, about 4.5 to about 5.6, about 4.5 to about 5.5, about 4.5 to about 5.4, about 4.5 to about 5.3, about 4.5 to about 5.2, about 4.5 to about 5.1, about 4.5 to about 5.0, about 4.5 to about 4.9, about 4.5 to about 4.8, about 4.5 to about 4.7, about 4.5 to about 4.6, about 4.6 to about 6.5, about 4.6 to about 6.4, about 4.6 to about 6.3, about 4.6 to about 6.2, about 4.6 to about 6.1, about 4.6 to about 6.0,

about 4.6 to about 5.9, about 4.6 to about 5.8, about 4.6 to about 5.7, about 4.6 to about 5.6, about 4.6 to about 5.5, about 4.6 to about 5.4, about 4.6 to about 5.3, about 4.6 to about 5.2, about 4.6 to about 5.1, about 4.6 to about 5.0, about 4.6 to about 4.9, about 4.6 to about 4.8, about 4.6 to about 4.7, about 4.7 to about 6.5, about 4.7 to about 6.4, about 4.7 to about 6.3, about 4.7 to about 6.2, about 4.7 to about 6.1, about 4.7 to about 6.0, about 4.7 to about 5.9, about 4.7 to about 5.8, about 4.7 to about 5.7, about 4.7 to about 5.6, about 4.7 to about 5.5, about 4.7 to about 5.4, about 4.7 to about 5.3, about 4.7 to about 5.2, about 4.7 to about 5.1, about 4.7 to about 5.0, about 4.7 to about 4.9, about 4.7 to about 4.8, about 4.8 to about 6.5, about 4.8 to about 6.4, about 4.8 to about 6.3, about 4.8 to about 6.2, about 4.8 to about 6.1, about 4.8 to about 6.0, about 4.8 to about 5.9, about 4.8 to about 5.8, about 4.8 to about 5.7, about 4.8 to about 5.6, about 4.8 to about 5.5, about 4.8 to about 5.4, about 4.8 to about 5.3, about 4.8 to about 5.2, about 4.8 to about 5.1, about 4.8 to about 5.0, about 4.8 to about 4.9, about 4.9 to about 6.5, about 4.9 to about 6.4, about 4.9 to about 6.3, about 4.9 to about 6.2, about 4.9 to about 6.1, about 4.9 to about 6.0, about 4.9 to about 5.9, about 4.9 to about 5.8, about 4.9 to about 5.7, about 4.9 to about 5.6, about 4.9 to about 5.5, about 4.9 to about 5.4, about 4.9 to about 5.3, about 4.9 to about 5.2, about 4.9 to about 5.1, about 4.9 to about 5.0, about 5.0 to about 6.5, about 5.0 to about 6.4, about 5.0 to about 6.3, about 5.0 to about 6.2, about 5.0 to about 6.1, about 5.0 to about 6.0, about 5.0 to about 5.9, about 5.0 to about 5.8, about 5.0 to about 5.7, about 5.0 to about 5.6, about 5.0 to about 5.5, about 5.0 to about 5.4, about 5.0 to about 5.3, about 5.0 to about 5.2, about 5.0 to about 5.1, about 5.1 to about 6.5, about 5.1 to about 6.4, about 5.1 to about 6.3, about 5.1 to about 6.2, about 5.1 to about 6.1, about 5.1 to about 6.0, about 5.1 to about 5.9, about 5.1 to about 5.8, about 5.1 to about 5.7, about 5.1 to about 5.6, about 5.1 to about 5.5, about 5.1 to about 5.4, about 5.1 to about 5.3, about 5.1 to about 5.2, about 5.2 to about 6.5, about 5.2 to about 6.4, about 5.2 to about 6.3, about 5.2 to about 6.2, about 5.2 to about 6.1, about 5.2 to about 6.0, about 5.2 to about 5.9, about 5.2 to about 5.8, about 5.2 to about 5.7, about 5.2 to about 5.6, about 5.2 to about 5.5, about 5.2 to about 5.4, about 5.2 to about 5.3, about 5.3 to about 6.5, about 5.3 to about 6.4, about 5.3 to about 6.3, about 5.3 to about 6.2, about 5.3 to about 6.1, about 5.3 to about 6.0, about 5.3 to about 5.9, about 5.3 to about 5.8, about 5.3 to about 5.7, about 5.3 to about 5.6, about 5.3 to about 5.5, about 5.3 to about 5.4, about 5.4 to about 6.5, about 5.4 to about 6.4, about 5.4 to about 6.3, about 5.4 to about 6.2, about 5.4 to about 6.1, about 5.4 to about 6.0,

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In some embodiments of any of the antigen-binding protein constructs (ABPCs) or antibodies described herein, the dissociation constant (K_D) of the first antigen-binding domain (and optionally the second antigen-binding domain, if present) at a pH of about 4.0 to about 6.5 (e.g., any of the subranges of this range described herein) is greater (e.g., detectably greater) (e.g., at least 5% greater, at least 10% greater, at least 15% greater, at least 20% greater, at least 25% greater, at least 30% greater, at least 35% greater, at least 40% greater, at least 45% greater, at least 50% greater, at least 55% greater, at least 60% greater, at least 65% greater, at least 70% greater, at least 80% greater, at least 85% greater, at least 90% greater, at least 95% greater, at least 100% greater, at least 120% greater, at least 140% greater, at least 160% greater, at least 180% greater, at least 200% greater, at least 220% greater, at least 240% greater, at least 260% greater, at least 280% greater, at least 300% greater, at least 320% greater, at least 340% greater, at least 360% greater, at least 380% greater, at least 400% greater, at least 420% greater, at least 440% greater, at least 460% greater, at least 480% greater, at least 500% greater, at least 1,000% greater, at least 2,000% greater, at least 3,000% greater, at least 4,000% greater, at least 5,000% greater, at least 6,000% greater, at least 7,000% greater, at least 8,000% greater, at least 9,000% greater, or at least 10,000% greater, or about 5% greater to about 10,000% greater, about 5% greater to about 9,000% greater, about 5% greater to about 8,000% greater, about 5% greater to about 7,000% greater, about 5% greater to about 6,000% greater, about 5% greater to about 5,000% greater, about 5% greater to about 4,000% greater, about 5% greater to about 3,000% greater, about 5% greater to about 2,000% greater, about 5% greater to about 1,000% greater, about 5% greater to about 500% greater, about 5% greater to about 480% greater, about 5% greater to about 460% greater, about 5% greater to about 440% greater, about 5% greater to about 420% greater, about 5% greater to about 400% greater, about 5% greater to about 380% greater, about 5% greater to about 360% greater, about 5% greater to about 340% greater, about 5% greater to about 320% greater, about 5% greater to about 300% greater, about 5% greater to about 280% greater, about 5% greater to about 260% greater, about 5% greater to about 240%

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In some embodiments of any of the antigen-binding protein constructs (ABPCs) or antibodies described herein, the dissociation rate of the first antigen-binding domain (and optionally the second antigen-binding domain, if present) at a pH of about 4.0 to about 6.5 (e.g., any of the subranges of this range described herein) is faster (e.g., at least 0.2-fold faster, at least 0.3-fold, at least 0.4-fold, at least 0.5-fold, at least 0.6-fold, at least 0.7-fold, at least 0.8-fold, at

least 0.9-fold, at least 1.0-fold, at least 1.5-fold, at least 2.0-fold, at least 2.5-fold, at least 3.0 fold, at least 3.5-fold, at least 4.0-fold, at least 4.5-fold, at least 5.0-fold, at least 5.5-fold, at least 6.0-fold, at least 6.5-fold, at least 7.0-fold, at least 7.5-fold, at least 8.0-fold, at least 8.5-fold, at least 9.0-fold, at least 9.5-fold, at least 10.0-fold, at least 10.5-fold, at least 11.0-fold, at least 11.5-fold, at least 12.0-fold, at least 12.5-fold, at least 13.0-fold, at least 13.5-fold, at least 14.0-fold, at least 14.5-fold, at least 15.0-fold, at least 15.5-fold, at least 16.0-fold, at least 16.5-fold, at least 17.0-fold, at least 17.5-fold, at least 18.0-fold, at least 18.5-fold, at least 19.0-fold, at least 19.5-fold, at least 20-fold, at least 25-fold, at least 30-fold, at least 35-fold, at least 40-fold, at least 45-fold, at least 50-fold, at least 55-fold, at least 60-fold, at least 65-fold, at least 70-fold, at least 75-fold, at least 80-fold, at least 85-fold, at least 90-fold, at least 95-fold, or at least 100-fold faster or about 0.2-fold to about 100-fold faster, about 0.2-fold to about 90-fold faster, about 0.2-fold to about 80-fold faster, about 0.2-fold to about 70-fold faster, about 0.2-fold to about 60-fold faster, about 0.2-fold to about 50-fold faster, about 0.2-fold to about 40-fold faster, about 0.2-fold to about 30-fold faster, about 0.2-fold to about 20-fold faster, about 0.2-fold to about 15-fold faster, about 0.2-fold to about 10-fold faster, about 0.2-fold to about 5-fold, about 0.2-fold to about 2-fold faster, about 0.2-fold to about 1-fold faster, about 0.2-fold to about 0.5-fold faster, about 0.5-fold to about 100-fold faster, about 0.5-fold to about 90-fold faster, about 0.5-fold to about 80-fold faster, about 0.5-fold to about 70-fold faster, about 0.5-fold to about 60-fold faster, about 0.5-fold to about 50-fold faster, about 0.5-fold to about 40-fold faster, about 0.5-fold to about 30-fold faster, about 0.5-fold to about 20-fold faster, about 0.5-fold to about 15-fold faster, about 0.5-fold to about 10-fold faster, about 0.5-fold to about 5-fold, about 0.5-fold to about 2-fold faster, about 0.5-fold to about 1-fold faster, about 1-fold to about 100-fold faster, about 1-fold to about 90-fold faster, about 1-fold to about 80-fold faster, about 1-fold to about 70-fold faster, about 1-fold to about 60-fold faster, about 1-fold to about 50-fold faster, about 1-fold to about 40-fold faster, about 1-fold to about 30-fold faster, about 1-fold to about 20-fold faster, about 1-fold to about 15-fold faster, about 1-fold to about 10-fold faster, about 1-fold to about 5-fold, about 1-fold to about 2-fold faster, about 2-fold to about 100-fold faster, about 2-fold to about 90-fold faster, about 2-fold to about 80-fold faster, about 2-fold to about 70-fold faster, about 2-fold to about 60-fold faster, about 2-fold to about 50-fold faster, about 2-fold to about 40-fold faster, about 2-fold to about 30-fold faster, about 2-fold to about 20-fold faster, about 2-fold to about 15-fold faster, about 2-fold to about 10-fold faster, about 2-fold to about 5-fold,

about 5-fold to about 100-fold faster, about 5-fold to about 90-fold faster, about 5-fold to about 80-fold faster, about 5-fold to about 70-fold faster, about 5-fold to about 60-fold faster, about 5-fold to about 50-fold faster, about 5-fold to about 40-fold faster, about 5-fold to about 30-fold faster, about 5-fold to about 20-fold faster, about 5-fold to about 15-fold faster, about 5-fold to about 10-fold faster, about 10-fold to about 100-fold faster, about 10-fold to about 90-fold faster, about 10-fold to about 80-fold faster, about 10-fold to about 70-fold faster, about 10-fold to about 60-fold faster, about 10-fold to about 50-fold faster, about 10-fold to about 40-fold faster, about 10-fold to about 30-fold faster, about 10-fold to about 20-fold faster, about 10-fold to about 15-fold faster, about 15-fold to about 100-fold faster, about 15-fold to about 90-fold faster, about 15-fold to about 80-fold faster, about 15-fold to about 70-fold faster, about 15-fold to about 60-fold faster, about 15-fold to about 50-fold faster, about 15-fold to about 40-fold faster, about 15-fold to about 30-fold faster, about 15-fold to about 20-fold faster, about 20-fold to about 100-fold faster, about 20-fold to about 90-fold faster, about 20-fold to about 80-fold faster, about 20-fold to about 70-fold faster, about 20-fold to about 60-fold faster, about 20-fold to about 50-fold faster, about 20-fold to about 40-fold faster, about 20-fold to about 30-fold faster, about 30-fold to about 100-fold faster, about 30-fold to about 90-fold faster, about 30-fold to about 80-fold faster, about 30-fold to about 70-fold faster, about 30-fold to about 60-fold faster, about 30-fold to about 50-fold faster, about 30-fold to about 40-fold faster, about 40-fold to about 100-fold faster, about 40-fold to about 90-fold faster, about 40-fold to about 80-fold faster, about 40-fold to about 70-fold faster, about 40-fold to about 60-fold faster, about 40-fold to about 50-fold faster, about 50-fold to about 100-fold faster, about 50-fold to about 90-fold faster, about 50-fold to about 80-fold faster, about 50-fold to about 70-fold faster, about 50-fold to about 60-fold faster, about 60-fold to about 100-fold faster, about 60-fold to about 90-fold faster, about 60-fold to about 80-fold faster, about 60-fold to about 70-fold faster, about 70-fold to about 100-fold faster, about 70-fold to about 90-fold faster, about 70-fold to about 80-fold faster, about 80-fold to about 100-fold faster, about 80-fold to about 90-fold faster, or about 90-fold to about 100-fold faster) than the dissociation rate at a pH of about 7.0 to about 8.0 (e.g., or any of the subranges of this range described herein).

In some embodiments of any of the antigen-binding protein constructs (ABPCs) or antibodies described herein, the dissociation constant (K_D) of the first antigen-binding domain (and optionally the second antigen-binding domain, if present) at a pH of about 4.0 to about 6.5

(e.g., any of the subranges of this range described herein) is greater (e.g., detectably greater) (e.g., at least 0.2-fold greater, at least 0.3-fold, at least 0.4-fold, at least 0.5-fold, at least 0.6-fold, at least 0.7-fold, at least 0.8-fold, at least 0.9-fold, at least 1.0-fold, at least 1.5-fold, at least 2.0-fold, at least 2.5-fold, at least 3.0 fold, at least 3.5-fold, at least 4.0-fold, at least 4.5-fold, at least 5.0-fold, at least 5.5-fold, at least 6.0-fold, at least 6.5-fold, at least 7.0-fold, at least 7.5-fold, at least 8.0-fold, at least 8.5-fold, at least 9.0-fold, at least 9.5-fold, at least 10.0-fold, at least 10.5-fold, at least 11.0-fold, at least 11.5-fold, at least 12.0-fold, at least 12.5-fold, at least 13.0-fold, at least 13.5-fold, at least 14.0-fold, at least 14.5-fold, at least 15.0-fold, at least 15.5-fold, at least 16.0-fold, at least 16.5-fold, at least 17.0-fold, at least 17.5-fold, at least 18.0-fold, at least 18.5-fold, at least 19.0-fold, at least 19.5-fold, at least 20-fold greater, at least 25-fold greater, at least 30-fold greater, at least 35-fold greater, at least 40-fold greater, at least 45-fold greater, at least 50-fold greater, at least 55-fold greater, at least 60-fold greater, at least 65-fold greater, at least 70-fold greater, at least 75-fold greater, at least 80-fold greater, at least 85-fold greater, at least 90-fold greater, at least 95-fold greater, or at least 100-fold greater, or about 0.2-fold to about 100-fold greater, about 0.2-fold to about 90-fold greater, about 0.2-fold to about 80-fold greater, about 0.2-fold to about 70-fold greater, about 0.2-fold to about 60-fold greater, about 0.2-fold to about 50-fold greater, about 0.2-fold to about 40-fold greater, about 0.2-fold to about 30-fold greater, about 0.2-fold to about 25-fold greater, about 0.2-fold to about 20-fold greater, about 0.2-fold to about 15-fold greater, about 0.2-fold to about 10-fold greater, about 0.2-fold to about 8-fold greater, about 0.2-fold to about 5-fold greater, about 0.2-fold to about 2-fold greater, about 0.2-fold to about 1-fold greater, about 0.2-fold to about 0.5-fold greater, about 0.5-fold to about 100-fold greater, about 0.5-fold to about 90-fold greater, about 0.5-fold to about 80-fold greater, about 0.5-fold to about 70-fold greater, about 0.5-fold to about 60-fold greater, about 0.5-fold to about 50-fold greater, about 0.5-fold to about 40-fold greater, about 0.5-fold to about 30-fold greater, about 0.5-fold to about 25-fold greater, about 0.5-fold to about 20-fold greater, about 0.5-fold to about 15-fold greater, about 0.5-fold to about 10-fold greater, about 0.5-fold to about 8-fold greater, about 0.5-fold to about 5-fold greater, about 0.5-fold to about 2-fold greater, about 0.5-fold to about 1-fold greater, about 1-fold to about 100-fold greater, about 1-fold to about 90-fold greater, about 1-fold to about 80-fold greater, about 1-fold to about 70-fold greater, about 1-fold to about 60-fold greater, about 1-fold to about 50-fold greater, about 1-fold to about 40-fold greater, about 1-fold to about 30-fold greater, about 1-fold to about 25-fold greater, about

1-fold to about 20-fold greater, about 1-fold to about 15-fold greater, about 1-fold to about 10-fold greater, about 1-fold to about 8-fold greater, about 1-fold to about 5-fold greater, about 1-fold to about 2-fold greater, about 2-fold to about 100-fold greater, about 2-fold to about 90-fold greater, about 2-fold to about 80-fold greater, about 2-fold to about 70-fold greater, about 2-fold to about 60-fold greater, about 2-fold to about 50-fold greater, about 2-fold to about 40-fold greater, about 2-fold to about 30-fold greater, about 2-fold to about 25-fold greater, about 2-fold to about 20-fold greater, about 2-fold to about 15-fold greater, about 2-fold to about 10-fold greater, about 2-fold to about 8-fold greater, about 2-fold to about 5-fold greater, about 5-fold to about 100-fold greater, about 5-fold to about 90-fold greater, about 5-fold to about 80-fold greater, about 5-fold to about 70-fold greater, about 5-fold to about 60-fold greater, about 5-fold to about 50-fold greater, about 5-fold to about 40-fold greater, about 5-fold to about 30-fold greater, about 5-fold to about 25-fold greater, about 5-fold to about 20-fold greater, about 5-fold to about 15-fold greater, about 5-fold to about 10-fold greater, about 5-fold to about 8-fold greater, about 8-fold to about 100-fold greater, about 8-fold to about 90-fold greater, about 8-fold to about 80-fold greater, about 8-fold to about 70-fold greater, about 8-fold to about 60-fold greater, about 8-fold to about 50-fold greater, about 8-fold to about 40-fold greater, about 8-fold to about 30-fold greater, about 8-fold to about 25-fold greater, about 8-fold to about 20-fold greater, about 8-fold to about 15-fold greater, about 8-fold to about 10-fold greater, about 10-fold to about 100-fold greater, about 10-fold to about 90-fold greater, about 10-fold to about 80-fold greater, about 10-fold to about 70-fold greater, about 10-fold to about 60-fold greater, about 10-fold to about 50-fold greater, about 10-fold to about 40-fold greater, about 10-fold to about 30-fold greater, about 10-fold to about 25-fold greater, about 10-fold to about 20-fold greater, about 10-fold to about 15-fold greater, about 15-fold to about 100-fold greater, about 15-fold to about 90-fold greater, about 15-fold to about 80-fold greater, about 15-fold to about 70-fold greater, about 15-fold to about 60-fold greater, about 15-fold to about 50-fold greater, about 15-fold to about 40-fold greater, about 15-fold to about 30-fold greater, about 15-fold to about 25-fold greater, about 15-fold to about 20-fold greater, about 20-fold to about 100-fold greater, about 20-fold to about 90-fold greater, about 20-fold to about 80-fold greater, about 20-fold to about 70-fold greater, about 20-fold to about 60-fold greater, about 20-fold to about 50-fold greater, about 20-fold to about 40-fold greater, about 20-fold to about 30-fold greater, about 20-fold to about 25-fold greater, about 25-fold to about 100-fold greater, about 25-fold to about 90-fold greater,

about 25-fold to about 80-fold greater, about 25-fold to about 70-fold greater, about 25-fold to about 60-fold greater, about 25-fold to about 50-fold greater, about 25-fold to about 40-fold greater, about 25-fold to about 30-fold greater, about 30-fold to about 100-fold greater, about 30-fold to about 90-fold greater, about 30-fold to about 80-fold greater, about 30-fold to about 70-fold greater, about 30-fold to about 60-fold greater, about 30-fold to about 50-fold greater, about 30-fold to about 40-fold greater, about 40-fold to about 100-fold greater, about 40-fold to about 90-fold greater, about 40-fold to about 80-fold greater, about 40-fold to about 70-fold greater, about 40-fold to about 60-fold greater, about 40-fold to about 50-fold greater, about 50-fold to about 100-fold greater, about 50-fold to about 90-fold greater, about 50-fold to about 80-fold greater, about 50-fold to about 70-fold greater, about 50-fold to about 60-fold greater, about 60-fold to about 100-fold greater, about 60-fold to about 90-fold greater, about 60-fold to about 80-fold greater, about 60-fold to about 70-fold greater, about 70-fold to about 100-fold greater, about 70-fold to about 90-fold greater, about 70-fold to about 80-fold greater, about 80-fold to about 100-fold greater, about 80-fold to about 90-fold greater, or about 90-fold to about 100-fold greater), than the K_D at a pH of about 7.0 to about 8.0 (e.g., any of the subranges of this range described herein).

In some embodiments of the ABPCs that include a first antigen-binding domain and a second antigen-binding domain, the first and second antigen-binding domains are identical or are at least 80% identical (e.g., at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% identical) in amino acid sequence to each other. In some embodiments, the ABPCs that include a first antigen-binding domain and a second antigen-binding domain, the first antigen-binding domain and the second antigen-binding domain have a sequence that is less than 80% identical (e.g., less than 75% identical, less than 70% identical, less than 65% identical, less than 60% identical, less than 55% identical, less than 50% identical, less than 45% identical, less than 40% identical, less than 35% identical, less than 30% identical, less than 25% identical, less than 20% identical, less than 15% identical, less than 10% identical, or less than 5% identical) to each other. In some embodiments of ABPCs that include a first and a second antigen-binding domain, the first and second antigen-binding domain binds two different epitopes (e.g., two different epitopes on LRRC15 or the first antigen-binding domain

binding specifically to LRRC15 and the second antigen-binding domain binding to an antigen other than LRRC15).

In some embodiments of any of the ABPCs or antibodies described herein, the K_D of the first antigen-binding domain (and optionally, the second antigen-binding domain if present) at a pH of about 7.0 to about 8.0 (e.g., any of the subranges of this range described herein) is between about 1 pM to about 5 μM (e.g., about 1 pM to about 2 μM, about 1 pM to about 1 μM, about 1 pM to about 500 nM, about 1 pM to about 250 nM, about 1 pM to about 240 nM, about 1 pM to about 230 nM, about 1 pM to about 220 nM, about 1 pM to about 210 nM, about 1 pM to about 200 nM, about 1 pM to about 190 nM, about 1 pM to about 180 nM, about 1 pM to about 170 nM, about 1 pM to about 160 nM, about 1 pM to about 150 nM, about 1 pM to about 140 nM, about 1 pM to about 130 nM, about 1 pM to about 120 nM, about 1 pM to about 110 nM, about 1 pM to about 100 nM, about 1 pM to about 95 nM, about 1 pM to about 90 nM, about 1 pM to about 85 nM, about 1 pM to about 80 nM, about 1 pM to about 75 nM, about 1 pM to about 70 nM, about 1 pM to about 65 nM, about 1 pM to about 60 nM, about 1 pM to about 55 nM, about 1 pM to about 50 nM, about 1 pM to about 45 nM, about 1 pM to about 40 nM, about 1 pM to about 35 nM, about 1 pM to about 30 nM, about 1 pM to about 25 nM, about 1 pM to about 20 nM, about 1 pM to about 15 nM, about 1 pM to about 10 nM, about 1 pM to about 5 nM, about 1 pM to about 2 nM, about 1 pM to about 1 nM, about 1 pM to about 950 pM, about 1 pM to about 900 pM, about 1 pM to about 850 pM, about 1 pM to about 800 pM, about 1 pM to about 750 pM, about 1 pM to about 700 pM, about 1 pM to about 650 pM, about 1 pM to about 600 pM, about 1 pM to about 550 pM, about 1 pM to about 500 pM, about 1 pM to about 450 pM, about 1 pM to about 400 pM, about 1 pM to about 350 pM, about 1 pM to about 300 pM, about 1 pM to about 250 pM, about 1 pM to about 200 pM, about 1 pM to about 150 pM, about 1 pM to about 100 pM, about 1 pM to about 90 pM, about 1 pM to about 80 pM, about 1 pM to about 70 pM, about 1 pM to about 60 pM, about 1 pM to about 50 pM, about 1 pM to about 40 pM, about 1 pM to about 30 pM, about 1 pM to about 20 pM, about 1 pM to about 10 pM, about 1 pM to about 5 pM, about 1 pM to about 4 pM, about 1 pM to about 3 pM, about 1 pM to about 2 pM, about 2 pM to about 5 μM, about 2 pM to about 2 μM, about 2 pM to about 1 μM, about 2 pM to about 500 nM, about 2 pM to about 250 nM, about 2 pM to about 240 nM, about 2 pM to about 230 nM, about 2 pM to about 220 nM, about 2 pM to about 210 nM, about 2 pM to about 200 nM, about 2 pM to about 190 nM, about 2 pM to about 180 nM, about 2 pM to about 170 nM,

about 2 pM to about 160 nM, about 2 pM to about 150 nM, about 2 pM to about 140 nM, about 2 pM to about 130 nM, about 2 pM to about 120 nM, about 2 pM to about 110 nM, about 2 pM to about 100 nM, about 2 pM to about 95 nM, about 2 pM to about 90 nM, about 2 pM to about 85 nM, about 2 pM to about 80 nM, about 2 pM to about 75 nM, about 2 pM to about 70 nM, about 2 pM to about 65 nM, about 2 pM to about 60 nM, about 2 pM to about 55 nM, about 2 pM to about 50 nM, about 2 pM to about 45 nM, about 2 pM to about 40 nM, about 2 pM to about 35 nM, about 2 pM to about 30 nM, about 2 pM to about 25 nM, about 2 pM to about 20 nM, about 2 pM to about 15 nM, about 2 pM to about 10 nM, about 2 pM to about 5 nM, about 2 pM to about 2 nM, about 2 pM to about 1 nM, about 2 pM to about 950 pM, about 2 pM to about 900 pM, about 2 pM to about 850 pM, about 2 pM to about 800 pM, about 2 pM to about 750 pM, about 2 pM to about 700 pM, about 2 pM to about 650 pM, about 2 pM to about 600 pM, about 2 pM to about 550 pM, about 2 pM to about 500 pM, about 2 pM to about 450 pM, about 2 pM to about 400 pM, about 2 pM to about 350 pM, about 2 pM to about 300 pM, about 2 pM to about 250 pM, about 2 pM to about 200 pM, about 2 pM to about 150 pM, about 2 pM to about 100 pM, about 2 pM to about 90 pM, about 2 pM to about 80 pM, about 2 pM to about 70 pM, about 2 pM to about 60 pM, about 2 pM to about 50 pM, about 2 pM to about 40 pM, about 2 pM to about 30 pM, about 2 pM to about 20 pM, about 2 pM to about 10 pM, about 2 pM to about 5 pM, about 2 pM to about 4 pM, about 2 pM to about 3 pM, about 5 pM to about 5 μM, about 5 pM to about 2 μM, about 5 pM to about 1 μM, about 5 pM to about 500 nM, about 5 pM to about 250 nM, about 5 pM to about 240 nM, about 5 pM to about 230 nM, about 5 pM to about 220 nM, about 5 pM to about 210 nM, about 5 pM to about 200 nM, about 5 pM to about 190 nM, about 5 pM to about 180 nM, about 5 pM to about 170 nM, about 5 pM to about 160 nM, about 5 pM to about 150 nM, about 5 pM to about 140 nM, about 5 pM to about 130 nM, about 5 pM to about 120 nM, about 5 pM to about 110 nM, about 5 pM to about 100 nM, about 5 pM to about 95 nM, about 5 pM to about 90 nM, about 5 pM to about 85 nM, about 5 pM to about 80 nM, about 5 pM to about 75 nM, about 5 pM to about 70 nM, about 5 pM to about 65 nM, about 5 pM to about 60 nM, about 5 pM to about 55 nM, about 5 pM to about 50 nM, about 5 pM to about 45 nM, about 5 pM to about 40 nM, about 5 pM to about 35 nM, about 5 pM to about 30 nM, about 5 pM to about 25 nM, about 5 pM to about 20 nM, about 5 pM to about 15 nM, about 5 pM to about 10 nM, about 5 pM to about 5 nM, about 5 pM to about 2 nM, about 5 pM to about 1 nM, about 5 pM to about 950 pM, about 5 pM to about 900 pM, about 5 pM to about 850

pM, about 5 pM to about 800 pM, about 5 pM to about 750 pM, about 5 pM to about 700 pM, about 5 pM to about 650 pM, about 5 pM to about 600 pM, about 5 pM to about 550 pM, about 5 pM to about 500 pM, about 5 pM to about 450 pM, about 5 pM to about 400 pM, about 5 pM to about 350 pM, about 5 pM to about 300 pM, about 5 pM to about 250 pM, about 5 pM to about 200 pM, about 5 pM to about 150 pM, about 5 pM to about 100 pM, about 5 pM to about 90 pM, about 5 pM to about 80 pM, about 5 pM to about 70 pM, about 5 pM to about 60 pM, about 5 pM to about 50 pM, about 5 pM to about 40 pM, about 5 pM to about 30 pM, about 5 pM to about 20 pM, about 5 pM to about 10 pM, about 10 pM to about 5 μM, about 10 pM to about 2 μM, about 10 pM to about 1 μM, about 10 pM to about 500 nM, about 10 pM to about 250 nM, about 10 pM to about 240 nM, about 10 pM to about 230 nM, about 10 pM to about 220 nM, about 10 pM to about 210 nM, about 10 pM to about 200 nM, about 10 pM to about 190 nM, about 10 pM to about 180 nM, about 10 pM to about 170 nM, about 10 pM to about 160 nM, about 10 pM to about 150 nM, about 10 pM to about 140 nM, about 10 pM to about 130 nM, about 10 pM to about 120 nM, about 10 pM to about 110 nM, about 10 pM to about 100 nM, about 10 pM to about 95 nM, about 10 pM to about 90 nM, about 10 pM to about 85 nM, about 10 pM to about 80 nM, about 10 pM to about 75 nM, about 10 pM to about 70 nM, about 10 pM to about 65 nM, about 10 pM to about 60 nM, about 10 pM to about 55 nM, about 10 pM to about 50 nM, about 10 pM to about 45 nM, about 10 pM to about 40 nM, about 10 pM to about 35 nM, about 10 pM to about 30 nM, about 10 pM to about 25 nM, about 10 pM to about 20 nM, about 10 pM to about 15 nM, about 10 pM to about 10 nM, about 10 pM to about 5 nM, about 10 pM to about 2 nM, about 10 pM to about 1 nM, about 10 pM to about 950 pM, about 10 pM to about 900 pM, about 10 pM to about 850 pM, about 10 pM to about 800 pM, about 10 pM to about 750 pM, about 10 pM to about 700 pM, about 10 pM to about 650 pM, about 10 pM to about 600 pM, about 10 pM to about 550 pM, about 10 pM to about 500 pM, about 10 pM to about 450 pM, about 10 pM to about 400 pM, about 10 pM to about 350 pM, about 10 pM to about 300 pM, about 10 pM to about 250 pM, about 10 pM to about 200 pM, about 10 pM to about 150 pM, about 10 pM to about 100 pM, about 10 pM to about 90 pM, about 10 pM to about 80 pM, about 10 pM to about 70 pM, about 10 pM to about 60 pM, about 10 pM to about 50 pM, about 10 pM to about 40 pM, about 10 pM to about 30 pM, about 10 pM to about 20 pM, about 15 pM to about 5 μM, about 15 pM to about 2 μM, about 15 pM to about 1 μM, about 15 pM to about 500 nM, about 15 pM to about 250 nM, about 15 pM to about 240 nM, about 15 pM

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In some embodiments of any of the ABPCs or antibodies described herein, the K_D of the first antigen-binding domain (and optionally, the second antigen-binding domain, if present) at a pH of about 4.0 to about 6.5 (e.g., any of the subranges of this range described herein) can be greater than 1 nM (e.g., between about 1 nM to about 1 mM, about 1 nM to about 900 μM, about 1 nM to about 800 μM, about 1 nM to about 700 μM, about 1 nM to about 600 μM, about 1 nM to about 500 μM, about 1 nM to about 400 μM, about 1 nM to about 300 μM, about 1 nM to about 200 μM, about 1 nM to about 100 μM, about 1 nM to about 90 μM, about 1 nM to about 80 μM, about 1 nM to about 70 μM, about 1 nM to about 60 μM, about 1 nM to about 50 μM, about 1 nM to about 40 μM, about 1 nM to about 30 μM, about 1 nM to about 20 μM, about 1 nM to about 10 μM, about 1 nM to about 5 μM, about 1 nM to about 4 μM, about 1 nM to about 2 μM, about 1 nM to about 1 μM, about 1 nM to about 900 nM, about 1 nM to about 800 nM, about 1 nM to about 700 nM, about 1 nM to about 600 nM, about 1 nM to about 500 nM, about 1 nM to about 400 nM, about 1 nM to about 300 nM, about 1 nM to about 200 nM, about 1 nM to about 100 nM, about 1 nM to about 90 nM, about 1 nM to about 80 nM, about 1 nM to about 70 nM, about 1 nM to about 60 nM, about 1 nM to about 50 nM, about 1 nM to about 40 nM, about 1 nM to about 30 nM, about 2 nM to about 1 mM, about 2 nM to about 900 μM, about 2 nM to about 800 μM, about 2 nM to about 700 μM, about 2 nM to about 600 μM, about 2 nM to about 500 μM, about 2 nM to about 400 μM, about 2 nM to about 300 μM, about 2 nM to about 200 μM, about 2 nM to about 100 μM, about 2 nM to about 90 μM, about 2 nM to about 80 μM, about 2 nM to about 70 μM, about 2 nM to about 60 μM, about 2 nM to about 50 μM, about 2 nM to about 40 μM, about 2 nM to about 30 μM, about 2 nM to about 20 μM, about 2 nM to about 10 μM, about 2 nM to about 5 μM, about 2 nM to about 4 μM, about 2 nM to about 2 μM, about 2 nM to about 1 μM, about 2 nM to about 900 nM, about 2 nM to about 800 nM, about 2 nM to about 700 nM, about 2 nM to about 600 nM, about 2 nM to about 500 nM, about 2 nM to

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A variety of different methods known in the art can be used to determine the K_D values of any of the antigen-binding protein constructs described herein (e.g., an electrophoretic mobility shift assay, a filter binding assay, surface plasmon resonance, a biomolecular binding kinetics assay, in vitro binding assay on antigen-expressing cells, etc.).

In some embodiments, the half-life of any of the antibodies described herein, the half-life of the antibody in vivo is increased (e.g., a detectable increase) relatively to a control antibody (e.g., the same antibody but not including the amino acid substitutions or insertions in the CH1-CH2-CH3 of the heavy chain or any the amino acid substitutions in the C_L domain). In some

embodiments, one or more amino acid substitutions can increase the half-life of any of the antibodies described herein. Non-limiting examples of amino acid substitutions that can increase the half-life of the antibody in vivo include a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317 of SEQ ID NO: 351 or SEQ ID NO: 352 and/or a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139 of SEQ ID NO: 351 or SEQ ID NO: 352. In some embodiments, the half-life of the antibody in vivo is increased (e.g., a detectable increase) (e.g., at least a 1% increase, at least a 5% increase, at least a 10% increase, at least a 15% increase, at least a 20% increase, at least a 25% increase, at least a 30% increase, at least a 35% increase, at least a 40% increase, at least a 45% increase, at least a 50% increase, at least a 55% increase, at least a 60% increase, at least a 65% increase, at least a 70% increase, at least a 75% increase, at least a 80% increase, at least a 85% increase, at least a 90% increase, at least a 95% increase, or at least a 99% increase, or about a 1% increase to about a 99% increase, about a 1% increase to about a 95% increase, about a 1% increase to about a 90% increase, about a 1% increase to about a 85% increase, about a 1% increase to about a 80% increase, about a 1% increase to about a 75% increase, about a 1% increase to about a 70% increase, about a 1% increase to about a 65% increase, about a 1% increase to about a 60% increase, about a 1% increase to about a 55% increase, about a 1% increase to about a 50% increase, about a 1% increase to about a 45% increase, about a 1% increase to about a 40% increase, about a 1% increase to about a 35% increase, about a 1% increase to about a 30% increase, about a 1% increase to about a 25% increase, about a 1% increase to about a 20% increase, about a 1% increase to about a 15% increase, about a 1% increase to about a 10% increase, about a 1% increase to about a 5% increase, about a 5% increase to about a 99% increase, about a 5% increase to about a 95% increase, about a 5% increase to about a 90% increase, about a 5% increase to about a 85% increase, about a 5% increase to about a 80% increase, about a 5% increase to about a 75% increase, about a 5% increase to about a 70% increase, about a 5% increase to about a 65% increase, about a 5% increase to about a 60% increase, about a 5% increase to about a 55% increase, about a 5% increase to about a 50% increase, about a 5% increase to about a 45% increase, about a 5% increase to about a 40% increase, about a 5% increase to about a 35% increase, about a 5% increase to about a 30% increase, about a 5% increase to about a 25%

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In some examples of any of the ABPCs or antibodies described herein, the half-life of the ABPC *in vivo* is decreased (e.g., a detectable decrease) (e.g., at least a 1% decrease, at least a 5% decrease, at least a 10% decrease, at least a 15% decrease, at least a 20% decrease, at least a 25%

decrease, at least a 30% decrease, at least a 35% decrease, at least a 40% decrease, at least a 45% decrease, at least a 50% decrease, at least a 55% decrease, at least a 60% decrease, at least a 65% decrease, at least a 70% decrease, at least a 75% decrease, at least a 80% decrease, at least a 85% decrease, at least a 90% decrease, at least a 95% decrease, or at least a 99% decrease, or about a 1% decrease to about a 99% decrease, about a 1% decrease to about a 95% decrease, about a 1% decrease to about a 90% decrease, about a 1% decrease to about a 85% decrease, about a 1% decrease to about a 80% decrease, about a 1% decrease to about a 75% decrease, about a 1% decrease to about a 70% decrease, about a 1% decrease to about a 65% decrease, about a 1% decrease to about a 60% decrease, about a 1% decrease to about a 55% decrease, about a 1% decrease to about a 50% decrease, about a 1% decrease to about a 45% decrease, about a 1% decrease to about a 40% decrease, about a 1% decrease to about a 35% decrease, about a 1% decrease to about a 30% decrease, about a 1% decrease to about a 25% decrease, about a 1% decrease to about a 20% decrease, about a 1% decrease to about a 15% decrease, about a 1% decrease to about a 10% decrease, about a 1% decrease to about a 5% decrease, about a 5% decrease to about a 99% decrease, about a 5% decrease to about a 95% decrease, about a 5% decrease to about a 90% decrease, about a 5% decrease to about a 85% decrease, about a 5% decrease to about a 80% decrease, about a 5% decrease to about a 75% decrease, about a 5% decrease to about a 70% decrease, about a 5% decrease to about a 65% decrease, about a 5% decrease to about a 60% decrease, about a 5% decrease to about a 55% decrease, about a 5% decrease to about a 50% decrease, about a 5% decrease to about a 45% decrease, about a 5% decrease to about a 40% decrease, about a 5% decrease to about a 35% decrease, about a 5% decrease to about a 30% decrease, about a 5% decrease to about a 25% decrease, about a 5% decrease to about a 20% decrease, about a 5% decrease to about a 15% decrease, about a 5% decrease to about a 10% decrease, about a 10% decrease to about a 99% decrease, about a 10% decrease to about a 95% decrease, about a 10% decrease to about a 90% decrease, about a 10% decrease to about a 85% decrease, about a 10% decrease to about a 80% decrease, about a 10% decrease to about a 75% decrease, about a 10% decrease to about a 70% decrease, about a 10% decrease to about a 65% decrease, about a 10% decrease to about a 60% decrease, about a 10% decrease to about a 55% decrease, about a 10% decrease to about a 50% decrease, about a 10% decrease to about a 45% decrease, about a 10% decrease to about a 40% decrease, about a 10% decrease to about a 35% decrease, about a 10% decrease to about a 30% decrease, about a 10%

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Conjugation

In some embodiments, the ABPCs or antibodies provided herein can be conjugated to a drug (e.g., a chemotherapeutic drug, a small molecule), a toxin, or a radioisotope. Non-limiting examples of drugs, toxins, and radioisotopes (e.g., known to be useful for the treatment of cancer) are known in the art.

In some embodiments, at least one polypeptide of any of the ABPCs or antibodies described herein is conjugated to the toxin, the radioisotope, or the drug via a cleavable linker. In some embodiments, the cleavable linker includes a protease cleavage site. In some embodiments, the cleavable linker is cleaved on the ABPC or antibody once it is transported to the lysosome or late endosome by the target mammalian cell. In some embodiments, cleavage of the linker functionally activates the drug or toxin.

In some embodiments, at least one polypeptide of any of the ABPCs or antibodies described herein is conjugated to the toxin, the radioisotope, or the drug via a non-cleavable linker. In some embodiments, the conjugated toxin, radioisotope, or drug is released during lysosomal and/or late endosomal degradation of the ABPC or antibody.

Non-limiting examples of cleavable linkers include: hydrazone linkers, peptide linkers, disulfide linkers, and thioether linkers. See, e.g., Carter et al., *Cancer J.* 14(3):154-169, 2008; Sanderson et al., *Clin. Cancer Res.* 11(2 Pt1):843-852, 2005; Chari et al., *Acc. Chem. Res.* 41(1):98-107, 2008; Oflazoglu et al., *Clin. Cancer Res.* 14(19): 6171-6180, 2008; and Lu et al., *Int. J. Mol. Sci.* 17(4): 561, 2016.

Non-limiting examples of non-cleavable linkers include: maleimide alkane-linkers and meleimide cyclohexane linker (MMC) (see, e.g., those described in McCombs et al., *AAPS J.* 17(2):339-351, 2015).

In some embodiments, any of the ABPCs or antibodies described herein is cytotoxic or cytostatic to the target mammalian cell.

In some embodiments, the antibodies provided herein can comprise one or more amino acid substitutions to provide a conjugation site (e.g., conjugated to a drug, a toxin, a radioisotope). In some embodiments, the antibodies provided herein can have one conjugation site. In some embodiments, the antibodies described herein can have two conjugation sites. In some embodiments, the antibodies provided herein can have three or more conjugation sites. A non-limiting example of an amino acid substitution to produce a conjugation site (e.g., "a triple hinge" conjugation site) is described in U.S. Patent Application No. 2017/0348429, which is incorporated herein by reference in its entirety. For example, a lysine to cysteine substitution at amino acid position 105 and deletion of a threonine at amino acid positions 106 and 108 of SEQ ID NO: 351 or SEQ ID NO: 352 can provide a "triple hinge" conjugation site in any of the antibodies described herein. In some embodiments, an alanine to a cysteine substitution at amino acid position 1 of SEQ ID NO: 351 or SEQ ID NO: 352 can provide a conjugation site for any of the antibodies described herein. In some embodiments, a valine to cysteine substitution at amino acid position 98 of SEQ ID NO: 353 can provide a conjugation site for any of the antibodies described herein.

Naturally-occurring cysteine amino acids can also provide a conjugation (e.g., conjugated to a drug, a toxin, a radioisotope.). In some embodiments, the antibodies provided herein can

have a drug, a toxin, or a radioisotope conjugated at one or more (e.g., one, two, three, or four) naturally-occurring conjugation sites. In some embodiments, the cysteine at amino acid position 103 of SEQ ID NO: 351 or 352 is a naturally occurring conjugation site. In some embodiments, the cysteine at amino acid position 109 of SEQ ID NO: 351 or 352 is a naturally occurring conjugation site. In some embodiments, the cysteine at amino acid position 112 of SEQ ID NO: 5 or SEQ 6 is a naturally-occurring conjugation site. In some embodiments, the cysteine at amino acid position 107 of SEQ ID NO: 353 is a naturally-occurring conjugation site.

In some embodiments, the antibodies provided herein can have a drug, a toxin, or a radioisotope conjugated at one or more (e.g., two, three, or four) naturally occurring conjugation sites, e.g., the cysteine at amino acid position 103, the cysteine at cysteine at amino acid position 109, and/or the cysteine at amino acid position 112 of SEQ ID NO: 351 or SEQ ID NO: 352, and/or the cysteine at amino acid position 107 of SEQ ID NO: 353. In some embodiments, the antibodies provided herein can have a drug, a toxin, or a radioisotope conjugated at one or more (e.g., two, three, or four) naturally occurring conjugation sites and one or more (e.g., two, or three) engineered conjugation sites (e.g., engineered by amino acid substitutions, deletions, additions, etc.).

Conjugation through engineered cysteines is achieved by methods known in the art. Briefly, engineered cysteine-containing antibody is prepared for conjugation by treatment with a reducing agent, for example, tris (2-carboxyethyl) phosphine (TCEP), Dithiothreitol (DTT), or 2-Mercaptoethanol (BME). In the reduction reaction the reducing reagent with disulfide bonds in the antibody, breaking interchain disulfides and removing disulfide caps from the engineered cysteines. An optional reoxidation step, achieved by exposure of the solution to air, or an oxidizing agent such as dehydroascorbic acid, allows reformation of the interchain disulfide bonds, leaving the engineered cysteines with a thiolate reactive group. Conjugation with a maleimide functionality on the linker-payload, maleimide-vc-MMAE, is achieved by reaction with the payload in buffered solution, containing cosolvent such as ethanol, dimethylacetamide (DMA), or dimethyl sulfoxide (DMSO). The crude conjugated antibody solution is purified by size exclusion chromatography, or selective filtration methods, such as tangential flow filtration. In this step, residual unreacted payload, reducing agent and oxidizing agents are removed from the reaction mixture, and the conjugated ADC product may be transferred into a desirable formulation buffer.

Conjugation through hinge cysteines is achieved by similar methods, using antibodies with, or without, additional engineered cysteine conjugation sites. Briefly, the antibody is prepared for conjugation by treatment with a reducing agent, for example, tris (2-carboxyethyl) phosphine (TCEP) or Dithiothreitol (DTT). The reducing strength and concentration of the reducing agent are selected such that some or all of the interchain disulfide bonds are reduced leaving free cysteines for conjugation. The solution may be directly conjugated in the presence of excess reducing agent. Conjugation with a maleimide functionality on the linker-payload, maleimide-vc-MMAE, is achieved by reaction with the payload in buffered solution, containing cosolvent such as ethanol, dimethylacetamide (DMA), or dimethyl sulfoxide (DMSO). Unreacted linker-payload may be rendered non-reactive by addition of a sacrificial thiolate molecule such as acetyl-cysteine. The crude conjugated antibody solution may be further purified by methods known in the art, including hydrophobic interaction chromatography, ion-exchange chromatography, or mixed-mode chromatography such as ceramic hydroxyapatite chromatography. Isolation of chromatography fractions allows selection of the desired antibody to payload ratio and removal of unreacted antibody, protein aggregates and fragments, and payload-related reaction side products. The purified antibody drug conjugate may be further purified and by size exclusion chromatography, or selective filtration methods, such as tangential flow filtration. In this step the conjugated ADC product may also be transferred into a desirable formulation buffer.

In some examples, an antibody conjugate can be made comprising an antibody linked to monomethyl auristatin E (MMAE) via a valine-citrulline (vc) linker (hereafter, LRRC15-IgG-DC). Conjugation of the antibody with vcMMAE begins with a partial reduction of the LRRC15-IgG followed by reaction with maleimidocaproyl-Val-Cit-PABC-MMAE (vcMMAE). The LRRC15-IgG (10 mg/mL) is partially reduced by addition of TCEP (molar equivalents of TCEP:mAb is 2:1) followed by incubation at 4° C overnight. The reduction reaction is then warmed to 25° C. To conjugate all of the thiols, vcMMAE is added to a final vcMMAE:reduced Cys molar ratio of 1:10. The conjugation reaction is carried out in the presence of 10% v/v of Dimethylacetamide (DMA) and allowed to proceed at 25° C for 60 minutes.

In some examples, an antibody conjugate (ADC) is made comprising the LRRC15-binding IgG (hereafter, LRRC15-IgG) described herein linked to monomethyl auristatin E

(MMAE) via a valine-citrulline (vc) linker (hereafter, LRRC15-IgG-DC). Conjugation of the antibody with vcMMAE begins with a partial reduction of the LRRC15-IgG followed by reaction with maleimidocaproyl-Val-Cit-PABC-MMAE (vcMMAE). The LRRC15-IgG (10 mg/mL) is reduced by addition of DTT (molar equivalents of DTT:mAb is 100:1) followed by incubation at 25° C overnight. The reduced LRRC15-IgG (10 mg/mL) is then re-oxidized by exposure to DHAA (molar equivalents of DHAA:mAb is 10:1) followed by incubation at 25° C for 2 hours. To conjugate all of the thiols, vcMMAE is added to a final vcMMAE:mAb molar ratio of 4:1. The conjugation reaction is carried out in the presence of 10% v/v of DMA and allowed to proceed at 25° C for 3 hours.

Expression of an Antigen-Binding Protein Construct or Antibody in a Cell

Also provided herein are methods of generating a recombinant cell that expresses an ABPC or an antibody (e.g., any of the ABPCs or antibodies described herein) that include: introducing into a cell a nucleic acid encoding the ABPC or antibody to produce a recombinant cell; and culturing the recombinant cell under conditions sufficient for the expression of the ABPC or antibody. In some embodiments, the introducing step includes introducing into a cell an expression vector including a nucleic acid encoding the ABPC or antibody to produce a recombinant cell.

Any of the ABPCs or antibodies described herein can be produced by any cell, e.g., a eukaryotic cell or a prokaryotic cell. As used herein, the term "eukaryotic cell" refers to a cell having a distinct, membrane-bound nucleus. Such cells may include, for example, mammalian (e.g., rodent, non-human primate, or human), insect, fungal, or plant cells. In some embodiments, the eukaryotic cell is a yeast cell, such as *Saccharomyces cerevisiae*. In some embodiments, the eukaryotic cell is a higher eukaryote, such as mammalian, avian, plant, or insect cells. As used herein, the term "prokaryotic cell" refers to a cell that does not have a distinct, membrane-bound nucleus. In some embodiments, the prokaryotic cell is a bacterial cell.

Methods of culturing cells are well known in the art. Cells can be maintained *in vitro* under conditions that favor proliferation, differentiation, and growth. Briefly, cells can be cultured by contacting a cell (e.g., any cell) with a cell culture medium that includes the necessary growth factors and supplements to support cell viability and growth.

Methods of introducing nucleic acids and expression vectors into a cell (e.g., a eukaryotic cell) are known in the art. Non-limiting examples of methods that can be used to introduce a nucleic acid into a cell include lipofection, transfection, electroporation, microinjection, calcium phosphate transfection, dendrimer-based transfection, cationic polymer transfection, cell squeezing, sonoporation, optical transfection, impalection, hydrodynamic delivery, magnetofection, viral transduction (e.g., adenoviral and lentiviral transduction), and nanoparticle transfection.

Provided herein are methods that further include isolation of the ABPCs from a cell (e.g., a eukaryotic cell) using techniques well-known in the art (e.g., ammonium sulfate precipitation, polyethylene glycol precipitation, ion-exchange chromatography (anion or cation), chromatography based on hydrophobic interaction, metal-affinity chromatography, ligand-affinity chromatography, and size exclusion chromatography).

Avidity

Antibodies and antigens binding fragment thereof are multivalent, and thus comprise more than one binding site. Generally, the measure of total binding strength of an antibody at its binding site is termed avidity. Generally, the terms "fold avidity" and "selectivity" can refer to the fold-difference between the affinity of an antibody and the avidity of an antibody, for example as seen when measuring the total binding strength of an antibody on a cell line with high target expression (avidity; e.g. a cancer cell, e.g. SAOS-2 cells) as compared to the total binding strength of an antibody on a cell line with low target expression (affinity, e.g. a non-cancer cell, e.g. G-292 cells). Generally, avidity is determined by four factors: the binding affinity (e.g., the strength of the binding at an individual binding site); valency (e.g., the total number of binding sites); structural arrangement (e.g., the structure of the antigen and antibody); and antigen density (e.g., the number of antigens per cell).

Provided herein are methods of decreasing the risk of developing a metastasis or decreasing the risk of developing an additional metastasis in a subject having a cancer, where the cancer is characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface the method comprising, administering a therapeutically effective amount of any of the antibodies described herein or any of the pharmaceutical

compositions described herein to a subject identified as having a cancer characterized by having the population of cancer cells. In some embodiments, the antibodies described herein can have at least new at least 5%, at least 10%, at least 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 100%, at least 105%, at least 110%, at least 115%, at least 120%, at least 125%, at least 130%, at least 135%, at least 140%, at least 145%, at least 150%, at least 155%, at least 160%, at least 165%, at least 170%, at least 175%, at least 180%, at least 185%, at least 190%, at least 195%, or at least 200% at least 205%, at least 210%, at least 215%, at least 220%, at least 225%, at least 230%, at least 235%, at least 240%, at least 245%, at least 250%, at least 255%, at least 260%, at least 265%, at least 270%, at least 275%, at least 280%, at least 285%, at least 290%, at least 295%, at least 300%, at least 305%, at least 310%, at least 315%, at least 320%, at least 325%, at least 330%, at least 335%, at least 340%, at least 345%, at least 350%, at least 355%, at least 360%, at least 365%, at least 370%, at least 375%, at least 380%, at least 385%, at least 390%, at least 395%, or at least 400%, increase in selectivity for a cancer cell as compared to a non-cancer cell.

Methods of Treatment

Provided herein are methods of treating a cancer characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface, that include: administering a therapeutically effective amount of any of the pharmaceutical compositions described herein or any of the ABPCs or antibodies described herein to a subject identified as having a cancer characterized by having the population of cancer cells.

Also provided herein are methods of reducing the volume of a tumor in a subject, wherein the tumor is characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface, that include: administering a therapeutically effective amount of any of the pharmaceutical compositions described herein or any of the ABPCs or antibodies described herein to a subject identified as having a cancer characterized by having the population of cancer cells. In some embodiments of any of the methods described herein, the volume of at least one (e.g., 1, 2, 3, 4, or 5) tumor (e.g., solid tumor) or tumor location (e.g., a site of metastasis) is reduced (e.g., a detectable reduction) by at least 1%, at least 2%, at least 3%, at least 4%, at least 5%, at least 6%, at least 8%, at least 10%, at least 12%, at

least 14%, at least 16%, at least 18%, at least 20%, at least 22%, at least 24%, at least 26%, at least 28%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99%) reduced as compared to the size of the at least one tumor (e.g., solid tumor) before administration of the ABPC or antibody.

Also provided herein are methods of inducing cell death in a cancer cell in a subject, wherein the cancer cell has LRRC15 or an epitope of LRRC15 presented on its surface, that include: administering a therapeutically effective amount of any of the pharmaceutical compositions of described herein or any of the ABPCs or antibodies described herein to a subject identified as having a cancer characterized as having the population of cancer cells. In some embodiments, the cell death that is induced is necrosis. In some embodiments, the cell death that is induced is apoptosis.

In some embodiments of any of the methods described herein, the cancer is a primary tumor.

In some embodiments of any of the methods described herein, the cancer is a metastasis.

In some embodiments of any of the methods described herein, the cancer is a non-T-cell-infiltrating tumor. In some embodiments of any of the methods described herein, the cancer is a T-cell-infiltrating tumor.

Provided herein are methods of decreasing the risk of developing a metastasis or decreasing the risk of developing an additional metastasis in a subject having a cancer, wherein the cancer is characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface, that include: administering a therapeutically effective amount of any of the pharmaceutical compositions of described herein or any of the ABPCs or antibodies described herein to a subject identified as having a cancer characterized as having the population of cancer cells. In some embodiments, the risk of developing a metastasis or the risk of developing an additional metastasis is decreased (e.g., a detectable decrease) by at least 1%, by at least 2%, at least 3%, at least 4%, at least 5%, at least 6%, at least 8%, at least 10%, at least 12%, at least 14%, at least 16%, at least 18%, at least 20%, at least 25%, at least 30%, at least 35%, at least 40%, at least 45%, at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, or at least 99% in the subject as compared to the risk of a subject having a similar cancer, but administered

no treatment or a treatment that does not include the administration of any of the ABPCs or antibodies described herein.

In some embodiments of any of the methods described herein, the cancer is a non-T-cell-infiltrating tumor. In some embodiments of any of the methods described herein, the cancer is a T-cell-infiltrating tumor. In some embodiments of any of the methods described herein, the cellular compartment is part of the endosomal/lysosomal pathway. In some embodiments of any of the methods described herein, the cellular compartment is an endosome.

The term "subject" refers to any mammal. In some embodiments, the subject or "subject suitable for treatment" may be a canine (e.g., a dog), feline (e.g., a cat), equine (e.g., a horse), ovine, bovine, porcine, caprine, primate, e.g., a simian (e.g., a monkey (e.g., marmoset, baboon), or an ape (e.g., a gorilla, chimpanzee, orangutan, or gibbon) or a human; or rodent (e.g., a mouse, a guinea pig, a hamster, or a rat). In some embodiments, the subject or "subject suitable for treatment" may be a non-human mammal, especially mammals that are conventionally used as models for demonstrating therapeutic efficacy in humans (e.g., murine, lapine, porcine, canine or primate animals) may be employed.

As used herein, treating includes reducing the number, frequency, or severity of one or more (e.g., two, three, four, or five) signs or symptoms of a cancer in a patient having a cancer (e.g., any of the cancers described herein). For example, treatment can reducing cancer progression, reduce the severity of a cancer, or reduce the risk of re-occurrence of a cancer in a subject having the cancer.

Provided herein are methods of inhibiting the growth of a solid tumor in a subject (e.g., any of the subjects described herein) that include administering to the subject a therapeutically effective amount of any of the ABPCs or antibodies described herein or any of the pharmaceutical compositions described herein (e.g., as compared to the growth of the solid tumor in the subject prior to treatment or the growth of a similar solid tumor in a different subject receiving a different treatment or receiving no treatment).

In some embodiments of any of the methods described herein, the growth of a solid tumor is primary growth of a solid tumor. In some embodiments of any of the methods described herein, the growth of a solid tumor is recurrent growth of a solid tumor. In some embodiments of any of the methods described herein, the growth of a solid tumor is metastatic growth of a solid tumor. In some embodiments, treatment results in about a 1% decrease to about 99%

decrease (or any of the subranges of this range described herein) in the growth of a solid tumor in the subject (e.g., as compared to the growth of the solid tumor in the subject prior to treatment or the growth of a similar solid tumor in a different subject receiving a different treatment or receiving no treatment). The growth of a solid tumor in a subject can be assessed by a variety of different imaging methods, e.g., positron emission tomography, X-ray computed tomography, computed axial tomography, and magnetic resonance imaging.

Also provided herein are methods of decreasing the risk of developing a metastasis or developing an additional metastasis over a period of time in a subject identified as having a cancer (e.g., any of the exemplary cancers described herein) that include administering to the subject a therapeutically effective amount of any of the proteins described herein or any of the pharmaceutical compositions described herein (e.g., as compared to a subject having a similar cancer and receiving a different treatment or receiving no treatment). In some embodiments of any of the methods described herein, the metastasis or additional metastasis is one or more to a bone, lymph nodes, brain, lung, liver, skin, chest wall including bone, cartilage and soft tissue, abdominal cavity, contralateral breast, soft tissue, muscle, bone marrow, ovaries, adrenal glands, and pancreas.

In some embodiments of any of the methods described herein, the period of time is about 1 month to about 3 years (e.g., about 1 month to about 2.5 years, about 1 month to about 2 years, about 2 months to about 1.5 years, about 1 month to about 1 year, about 1 month to about 10 months, about 1 month to about 8 months, about 1 month to about 6 months, about 1 month to about 5 months, about 1 month to about 4 months, about 1 month to about 3 months, about 1 month to about 2 months, about 2 months to about 3 years, about 2 months to about 2.5 years, about 2 months to about 2 years, about 2 months to about 1.5 years, about 2 months to about 1 year, about 2 months to about 10 months, about 2 months to about 8 months, about 2 months to about 6 months, about 2 months to about 5 months, about 2 months to about 4 months, about 2 months to about 3 months, about 3 months to about 3 years, about 3 months to about 2.5 years, about 3 months to about 2 years, about 3 months to about 1.5 years, about 3 months to about 1 year, about 3 months to about 10 months, about 3 months to about 8 months, about 3 months to about 6 months, about 3 months to about 5 months, about 3 months to about 4 months, about 4 months to about 3 years, about 4 months to about 2.5 years, about 4 months to about 2 years, about 4 months to about 1.5 years, about 4 months to about 1 year, about 4 months to about 10

months, about 4 months to about 8 months, about 4 months to about 6 months, about 4 months to about 5 months, about 5 months to about 3 years, about 5 months to about 2.5 years, about 5 months to about 2 years, about 5 months to about 1.5 years, about 5 months to about 1 year, about 5 months to about 10 months, about 5 months to about 8 months, about 5 months to about 6 months, about 6 months to about 3 years, about 6 months to about 2.5 years, about 6 months to about 2 years, about 6 months to about 1.5 years, about 6 months to about 1 year, about 6 months to about 10 months, about 6 months to about 8 months, about 8 months to about 3 years, about 8 months to about 2.5 years, about 8 months to about 2 years, about 8 months to about 1.5 years, about 8 months to about 1 year, about 8 months to about 10 months, about 10 months to about 3 years, about 10 months to about 2.5 years, about 10 months to about 2 years, about 10 months to about 1.5 years, about 10 months to about 1 year, about 1 year to about 3 years, about 1 year to about 2.5 years, about 1 year to about 2 years, about 1 year to about 1.5 years, about 1.5 years to about 3 years, about 1.5 years to about 2.5 years, about 1.5 years to about 2 years, about 2 years to about 3 years, about 2 years to about 2.5 years, or about 2.5 years to about 3 years).

In some embodiments, the risk of developing a metastasis or developing an additional metastasis over a period of time in a subject identified as having a cancer is decreased by about 1% to about 99% (e.g., or any of the subranges of this range described herein), e.g., as compared to the risk in a subject having a similar cancer receiving a different treatment or receiving no treatment.

Non-limiting examples of cancer include: acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), adrenocortical carcinoma, anal cancer, appendix cancer, astrocytoma, basal cell carcinoma, brain tumor, bile duct cancer, bladder cancer, bone cancer, breast cancer, bronchial tumor, Burkitt Lymphoma, carcinoma of unknown primary origin, cardiac tumor, cervical cancer, chordoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloproliferative neoplasm, colon cancer, colorectal cancer, craniopharyngioma, cutaneous T-cell lymphoma, ductal carcinoma, embryonal tumor, endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, fibrous histiocytoma, Ewing sarcoma, eye cancer, germ cell tumor, gallbladder cancer, gastric cancer, gastrointestinal carcinoid tumor, gastrointestinal stromal tumor, gestational trophoblastic disease, glioma, head and neck cancer, hairy cell leukemia, hepatocellular cancer, histiocytosis, Hodgkin lymphoma, hypopharyngeal cancer, intraocular melanoma, islet cell tumor, Kaposi sarcoma,

kidney cancer, Langerhans cell histiocytosis, laryngeal cancer, leukemia, lip and oral cavity cancer, liver cancer, lobular carcinoma in situ, lung cancer, lymphoma, macroglobulinemia, malignant fibrous histiocytoma, melanoma, Merkel cell carcinoma, mesothelioma, metastatic squamous neck cancer with occult primary, midline tract carcinoma involving NUT gene, mouth cancer, multiple endocrine neoplasia syndrome, multiple myeloma, mycosis fungoides, myelodysplastic syndrome, myelodysplastic/myeloproliferative neoplasm, nasal cavity and para-nasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-Hodgkin lymphoma, non-small cell lung cancer, oropharyngeal cancer, osteosarcoma, ovarian cancer, pancreatic cancer, papillomatosis, paraganglioma, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytomas, pituitary tumor, pleuropulmonary blastoma, primary central nervous system lymphoma, prostate cancer, rectal cancer, renal cell cancer, renal pelvis and ureter cancer, retinoblastoma, rhabdoid tumor, salivary gland cancer, Sezary syndrome, skin cancer, small cell lung cancer, small intestine cancer, soft tissue sarcoma, spinal cord tumor, stomach cancer, T-cell lymphoma, teratoid tumor, testicular cancer, throat cancer, thymoma and thymic carcinoma, thyroid cancer, urethral cancer, uterine cancer, vaginal cancer, vulvar cancer, and Wilms' tumor. Additional examples of cancer are known in the art.

In some embodiments, the patient is further administered one or more additional therapeutic agents (e.g., one or more of a chemotherapeutic agent, a recombinant cytokine or interleukin protein, a kinase inhibitor, and a checkpoint inhibitor). In some embodiments, the one or more additional therapeutic agents is administered to the patient at approximately the same time as any of the ABPCs or antibodies described herein are administered to the patient. In some embodiments, the one or more additional therapeutic agents are administered to the patient after the administration of any of the ABPCs or antibodies described herein to the patient. In some embodiments, the one or more additional therapeutic agents are administered to the patient before the administration of any of the ABPCs or antibodies described herein to the patient.

In some embodiments of any of the methods described herein, the cancer is a solid cancer (e.g., breast cancer, prostate cancer, or non-small cell lung cancer).

Compositions

Also provided herein are compositions (e.g., pharmaceutical compositions) that include at least one of any of the ABPCs or antibodies described herein. In some embodiments, the

compositions (e.g., pharmaceutical compositions) can be disposed in a sterile vial or a pre-loaded syringe.

In some embodiments, the compositions (e.g., pharmaceutical compositions) are formulated for different routes of administration (e.g., intravenous, subcutaneous, intramuscular, or intratumoral). In some embodiments, the compositions (e.g., pharmaceutical compositions) can include a pharmaceutically acceptable carrier (e.g., phosphate buffered saline). Single or multiple administrations of any of the pharmaceutical compositions described herein can be given to a subject depending on, for example: the dosage and frequency as required and tolerated by the patient. A dosage of the pharmaceutical composition should provide a sufficient quantity of the ABPC or antibody to effectively treat or ameliorate conditions, diseases, or symptoms. Also provided herein are methods of treating a subject having a cancer (e.g., any of the cancers described herein) that include administering a therapeutically effective amount of at least one of any of the compositions or pharmaceutical compositions provided herein.

Kits

Also provided herein are kits that include any of the ABPCs or antibodies described herein, any of the compositions described herein, or any of the pharmaceutical compositions described herein. In some embodiments, the kits can include instructions for performing any of the methods described herein. In some embodiments, the kits can include at least one dose of any of the compositions (e.g., pharmaceutical compositions) described herein. In some embodiments, the kits can provide a syringe for administering any of the pharmaceutical compositions described herein.

Protein Constructs

Also provided are protein constructs (PCs) that include: a first antigen-binding domain that is capable of specifically binding LRRC15 or an epitope of LRRC15 presented on the surface of a target mammalian cell, where: (a) the dissociation rate of the first antigen-binding domain at a pH of about 7.0 to about 8.0 (or any of the subranges of this range described herein) is faster than the dissociation rate at a pH of about 4.0 to about 6.5 (or any of the subranges of this range described herein); and/or (b) the dissociation constant (K_D) of the first antigen-binding

domain at a pH of about 7.0 to about 8.0 (or any of the subranges of this range) is greater than the K_D at a pH of about 4.0 to about 6.5.

Also provided herein are pharmaceutical compositions including any of the PCs described herein. Also provided herein are methods of treating a subject in need thereof that include administering a therapeutically effective amount of any of the PCs described herein to the subject.

Methods of Improving pH Dependence of an Antigen-Binding Protein Construct

Also provided herein are methods of improving pH dependence of an antigen-binding protein construct, the method comprises providing a starting antigen-binding protein construct comprising an antigen-binding domain and introducing one or more histidine amino acid substitutions into one or more CDRs of the antigen-binding domain in the starting antigen-binding protein construct, wherein the method results in the generation of an antigen-binding protein construct having one or both of: (a) an increased (e.g., at least a 0.1-fold increase to about a 100-fold increase, or any of the subranges of this range described herein) ratio of the dissociation rate of the antigen-binding domain at a pH of about 4.0 to about 6.5 to the dissociation rate at a pH of about 7.0 to about 8.0, as compared to the starting antigen-binding protein construct, and (b) an increased (e.g., at least a 0.1-fold increase to about a 100-fold increase, or any of the subranges of this range described herein) ratio the dissociation constant (K_D) of the antigen-binding domain at a pH of about 4.0 to about 6.5 to the K_D at a pH of about 7.0 to about 8.0, as compared to the starting antigen-binding protein construct.

The invention is further described in the following examples, which do not limit the scope of the invention described in the claims.

EXAMPLES

Example 1. Generation of LRRC15 binders and engineering of pH binding dependence

pH-engineered ABPCs specific for LRRC15 are generated using two methods. In the first approach, published monoclonal antibodies against LRRC15 are used as a starting template for introduction of additional mutations that allow engineering of pH-dependent binding to

LRRC15 and i) enhanced endolysosomal accumulation of a conjugated toxin, as well as ii) enhanced LRRC15 recycling to the cell surface. The second approach involves discovery of de novo ABPCs specific for LRRC15 via antibody display methods from naive libraries or libraries with defined CDR compositions and screening under conditions designed for selection of pH-engineered ABPCs specific for LRRC15. In either case, histidine residues play an important role in engineering pH-dependent binding proteins.

Histidine residues are at least partially protonated at a pH below 6.5 owing to its pKa of 6.0. Therefore, if a histidine side chain in an antigen-binding domain participates in an electrostatic binding interaction with its antigen it will start to turn positively charged at a pH at or below 6.5. This could either weaken or enhance the binding affinity of the interaction at a pH below 6.5, based on the corresponding charge of and interactions with the antigen epitope. Thus, systematic introduction of histidines into antibody complementarity determining regions (CDRs) in an antibody or other binder library (e.g., an scFv library) can be used to identify substitutions that will affect an antigen-binding domain's interaction with an antigen at lower pH values. The first approach therefore involves histidine-scanning of variable region sequences of published monoclonal antibodies to identify pH-dependent variants.

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding Purcell et. al., LRRC15 Is a Novel Mesenchymal Protein and Stromal Target for Antibody-Drug Conjugates, Cancer Res. 78(14):4059-4072 (2018). Briefly, for a subset of the antibody sequences, CDRs in each chain are identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest (DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To engineer pH-dependent sequence variants, individual amino acid residues within the heavy chain and/or light chain CDRs are systematically substituted with a histidine, one at a time. In cases where the starting CDR residue is a histidine, it is mutated to an alanine. Antibody variants with only one histidine or alanine mutation in a heavy/light chain CDR are generated by co-transfection of Expi293 cells with a) one heavy chain or light chain sequence variant, and b) the corresponding starting ABPC (e.g., the starting LRRC15-binding monoclonal antibody) light chain or heavy chain,

respectively, using methods known to the art. After allowing for a period of protein expression, cell culture supernatants are collected, quantified, and the pH dependence of the variant is evaluated using biolayer interferometry (BLI) or other methods known to the art. Briefly, cell culture supernatants are normalized to an antibody expression level of 50 μg/mL, and captured on an anti-human Fc sensor (Forte Bio). A baseline is established using 1X kinetics buffer (Forte Bio), and the sensor is associated with 100 nM of LRRC15 in 1X PBS at pH 7.4 for 300 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor is exposed to 1X PBS at either pH 5.5 or pH 7.4 for 300-500 sec. Association and dissociation phase curves are examined for the starting ABPC antibody and each corresponding antibody variant at pH 5.5 and pH 7.4 to inform on two criteria: a) enhanced dissociation (i.e., higher koff values) at pH 5.5 due to histidine or alanine substitution compared to the starting ABPC, and b) reduced dissociation at pH 7.4 (i.e., lower koff values) compared to pH 5.5 in the antibody variant itself and with the starting ABPC. Variants that show either enhanced dissociation at pH 5.5 or reduced dissociation at pH 7.4 or both are selected for further analysis. It is also noted that while some histidine and alanine mutations obliterate LRRC15 binding, others are tolerated with little (e.g., less than 1-fold change in KD or dissociation rate) or no change in LRRC15 binding kinetics. Especially because histidine is a large, positively charged amino acid, these histidine variants and alanine variants with no change are noted as positions that may tolerate a wide range of mutations and lead to antibodies with different sequence but similar binding properties, a designation that is not otherwise apparent. The variants selected for further analysis are expressed at a larger scale and purified using protein A affinity chromatography. Binding kinetics (kon and koff) of the purified starting ABPC and variant antibodies are measured at pH 5.5 and pH 7.4 using Biacore (GE Healthcare). The ratio of the antibody's rate of dissociation (koff at pH 7.4 divided by koff at pH 5.5) is also used as a quantitative assessment of pH-dependent binding; similarly, the dissociation constant KD is calculated at both pH 5.5 and pH 7.4 as koff divided by kon and the ratio of the antibody's dissociation constant (KD at pH 7.4 divided by KD at pH 5.5) is also used as a quantitative assessment of pH-dependent binding. Antibodies with a rate of dissociation ratio less than that of the starting ABPC and/or a dissociation constant ratio less than that of the starting ABPC are selected for further assessment of combinatorial substitutions. Favorable histidine and/or alanine amino acid positions can also be combined to enhance pH dependence; this can be done by, e.g.,

combinatorially or rationally combining histidine and/or alanine substitutions on a given heavy or light chain that individually improve pH dependence, by, e.g., combinatorially or rationally combining modified heavy and light chains such that histidine and/or alanine substitutions are present on both chains, or combinations thereof. Such combinatorial variants are generated and tested/analyzed for differential pH dependence using the methods and protocols described herein, or others known to the art. Antibody variants that have the lowest rate of dissociation ratios and/or dissociation constant ratios are selected as candidates for further analysis (hereafter referred to as "pH-engineered ABPCs specific for LRRC15").

The second method for selection of pH-engineered ABPCs specific for LRRC15 involves either screening libraries to identify de novo pH-dependent ABPCs specific for LRRC15 or ABPCs that could serve as templates for engineering pH-dependent binding as described herein. Two types of libraries can be used for these selections: naive phage/yeast display antibody libraries (e.g., Fab, scFv, VHH, VL, or others known to the art) or phage/yeast display libraries where CDRs have been mutated to express a subset of amino acid residues. Libraries are screened against soluble recombinant LRRC15 extracellular domains using methods known to the art with positive selection for variants that bind weakly (e.g., are eluted from beads) at pH 5.0 and bind strongly (e.g., are bound to beads) at pH 7.4. Three rounds of selections are performed. The final round of binders are screened using ELISA for binding to human LRRC15 and cyno LRRC15 and mouse LRRC15 or via mean fluorescence intensity in flow cytometric analysis. If more binders with cyno or murine cross-reactivity are desired, the final selection round can instead be performed on cyno LRRC15 or murine LRRC15. Selected binding proteins are subcloned into mammalian expression vectors and expressed as either full IgG proteins or Fc fusions in Expi293 cells. BLI analysis is performed as described herein for selection of pH-dependent binder variants and confirmed using Biacore.

Example 2. In vitro demonstration of pH-dependent binding to LRRC15, pH-dependent release of LRRC15, enhanced endolysosomal delivery in LRRC15+ cells, and increased LRRC15 antigen density in LRRC15+ cells after exposure to pH-engineered ABPCs specific for LRRC15 as compared to control ABPCs specific for LRRC15.

As discussed herein, pH-engineered ABPCs specific for LRRC15 exhibit the desirable property of decreased LRRC15 binding at acidic pH (e.g., pH 5.0, pH 5.5), but enhanced binding

at higher pH (e.g., pH 7.4), which enhances their accumulation in endolysosomes under physiological conditions.

pH-dependent binding to LRRC15 on cells

To demonstrate that pH-engineered ABPCs specific for LRRC15 binds cell surface LRRC15 at neutral pH, a cell surface binding assay is performed. A panel of human cells that are LRRC15+ is assembled (e.g., ATCC: U118-MG Cat#HTB-15, ATCC: PANC-1 Cat#CRL-1469, ATCC: RPMI-7951 Cat#HTB-66). Methods of identifying and quantifying gene expression (e.g., LRRC15) for a given cell line are known to the art, and include, e.g., consulting the Cancer Cell Line Encyclopedia (CCLE; https://portals.broadinstitute.org/ccle) to ascertain the expression level and/or mutation status of a given gene in a tumor cell line), rtPCR, microarray, or RNA-Seq analysis, or cell staining with antibodies known in the art (e.g. (Recombinant Anti-LRRC15 antibody, abcam Cat# ab150376 clone EPR8188(2); Hi-Affi™ Recombinant Rabbit Anti-LRRC15 Monoclonal Antibody, Creative Biolabs Cat#MOR-2090 Clone#DS2090AB for LRRC15). Cells are seeded at approximately 5-10,000 per well in 150 µL of pH 7.4 culture medium and incubated at 37 °C for 5 minutes at several doses (e.g., a two-fold dilution series) from 1 pM to 1 µM with one of the following antibodies: a known, control ABPC specific for LRRC15 (e.g., an antibody, samrotamab, hu139.10, huAD208.4.1, huAD208.12.1, 1-13C3, or 1-19G12), the pH-engineered ABPC specific for LRRC15, and an appropriate negative isotype control mAb (e.g., Biolegend Purified Human IgG1 Isotype Control Recombinant Antibody, Cat#403501). Prior to the onset of the experiment, the binding properties of all antibodies are validated using methods known to the art. Following the 5 minute incubation, cells are fixed with 4% formaldehyde (20 min at room temperature) and incubated with an appropriate fluorophore-labeled secondary antibody (e.g., ThermoFisher Mouse anti-Human IgG1 Fc Secondary Antibody, Alexa Fluor 488, Cat#A-10631) for 60 minutes. Unbound reagents are washed with a series of PBS washes, and the cell panels are imaged using confocal microscopy. Upon analysis of the images, significant fluorescence can be observed on the surface of cells bound with the known, control ABPC specific for LRRC15 as well as the pH-engineered ABPC specific for LRRC15, but little surface binding can be observed for the isotype negative control. To isolate the effect of pH on surface binding, the same experiment is repeated twice, with the primary antibody incubation taking place at sequentially lower pH (e.g., pH 6.5

and 5.5 and 5.0). Analysis of the resulting confocal microscopy images can show significant fluorescence on the surface of cells bound with all mAbs tested, excepting the isotype negative control, and that this fluorescence decreases for the pH-engineered ABPC specific for LRRC15 as the pH decreases. Alternatively, cells are analyzed for mean fluorescent intensity by flow cytometry using methods known in the art. A dissociation constant KD on cells at neutral pH of the antibodies analyzed is determined by nonlinear regression methods known in the art (e.g., a Scatchard plot). Taken together, the results can show that the pH engineering process results in the creation of a pH-engineered ABPC specific for LRRC15 that is pH-dependent in its binding properties and that it more effectively binds at neutral pH as compared to more acidic pH. Other methods of assessing the pH dependence of the pH-engineered ABPCs specific for LRRC15 are known in the art and include, e.g., using flow cytometry to measure ABPC surface binding.

pH-dependent release of LRRC15 on cells

To demonstrate that pH-engineered ABPCs specific for LRRC15 are capable of releasing LRRC15 at low pH after binding at a neutral pH, a variant of the cell surface binding assay described above is performed using methods known to the art (e.g., as generally described in Gera N. (2012) PLoS ONE 7(11): e48928). Briefly, an appropriate LRRC15+ cell line (passage number less than 25) is harvested and 50,000 cells per well are plated in a U-Bottomed 96-well microplate. Three conditions are tested; binding and secondary staining at pH 7.4, binding and secondary staining at pH 5.0, and binding at pH 7.4 followed by release at pH 5.0 for 30 minutes and secondary staining at pH 7.4. Both pH-engineered ABPCs specific for LRRC15 as well as a control ABPC specific for LRRC15 are tested. The cells are washed two times with 200 µL of FACS buffer (1x PBS containing 3% Fetal Bovine Serum) at either pH 7.4 or 5.0 depending on the condition being tested. The purified protein samples are diluted into FACS buffer of the appropriate pH and added to the cells and allowed to bind for one hour on ice. After incubation with the primary antibodies the pH 7.4 and pH 5.0 conditions are washed twice as before, and then 100 µl of secondary rat anti-human Fc AF488 (BioLegend 410706) or other appropriate antibody, diluted 1:50, or anti Myc-Tag mouse mAb-AF488 (Cell Signaling Technologies 2279S) diluted 1:50 is added in FACS buffer of the appropriate pH, and incubated for 30 minutes on ice. The pH 5.0 release condition is washed twice with FACS buffer pH 7.4 and then resuspended in 100 µl of FACS buffer pH 5.0 and incubated on ice for 30 minutes, followed by

secondary staining in FACS buffer pH 7.4 as described for the other conditions. The plates are washed twice as before and resuspended in 1% paraformaldehyde in the appropriate FACS buffer to fix them for flow cytometry analysis. All conditions are read on a flow cytometer (Accuri C6, BD Biosciences). Binding is observed as a shift in the FLl signal (as a mean fluorescence intensity) versus secondary alone. Upon analysis of the data, it can be determined that both the pH-engineered ABPC specific for LRRC15 as well as the control ABPC specific for LRRC15 effectively bind the surface of LRRC15+ cells at neutral pH, but the pH-engineered ABPC specific for LRRC15 binds poorly at pH 5.0; similarly, it can be determined that the pH-engineered ABPC specific for LRRC15 binds effectively at pH 7.4, but then releases/unbinds LRRC15 at pH 5.0.

Enhanced endolysosomal delivery in LRRC15+ cells of pH-engineered ABPCs specific for LRRC15 as compared to control ABPCs specific for LRRC15 (pHrodo)

To verify and demonstrate that ABPCs specific for LRRC15 achieve endolysosomal localization following cellular uptake, an internalization assay is performed using methods known to the art (e.g., Mahmutefendic et al., Int. J. Biochem. Cell Bio., 2011). Briefly, as described herein, a panel of human cells that express LRRC15 highly is assembled using methods known to the art. Cells are plated, washed three times with PBS, and incubated at 37 degrees C for 60 minutes in media at neutral pH, with added concentrations of 2 micrograms per milliliter of a known, control ABPC specific for LRRC15 (e.g., as described herein), the pH-engineered ABPC specific for LRRC15, and an appropriate negative isotype control mAb (e.g., as described herein). In a subset of cells, validation of antibody internalization and endosomal localization is performed using methods known to the art; e.g., cells are fixed in 4% formaldehyde as described herein, permeabilized using TWEEN 20 or other methods known to the art (Jamur MC et al (2010) Permeabilization of cell membranes, Methods Mol Biol. 588:63-6), additionally stained with an endosomal marker, e.g., a fluorescent RAB11 antibody (RAB11 Antibody, Alexa Fluor 488, 3H18L5, ABfinity™ Rabbit Monoclonal), stained with an appropriate fluorescently labeled anti-human secondary antibody (e.g., as described herein), and imaged using confocal fluorescence microscopy, as described herein. Analysis of the confocal images can be used to show that both the pH-engineered ABPC specific for LRRC15 as well as the control ABPC specific for LRRC15 are internalized and accumulate in the endolysosomes.

To demonstrate that pH-engineered ABPCs specific for LRRC15 achieve enhanced endolysosomal accumulation relative to a control ABPC specific for LRRC15, a pHrodo-based internalization assay is performed using both a known, control ABPC specific for LRRC15 (e.g., as described herein) as well as the pH-engineered ABPC specific for LRRC15. The assay makes use of pHrodo™ iFL (P36014, ThermoFisher), a dye whose fluorescence increases with decreasing pH, such that its level of fluorescence outside the cell at neutral pH is lower than its level of fluorescence inside the acidic pH environment of endolysosomes. Briefly, an appropriate LRRC15+ cell line (less than passage 25) is suspended in its recommended media (e.g., by cell banks or cell bank databases ATCC, DSMZ, or ExPASy Cellosaurus) and plated in a 24-well plate at a density of 2,000,000 cells/mL, 1 mL per well. While keeping the cells on ice, 1 mL of 2x pHrodo iFL-labeled antibody (prepared in accordance with the manufacturer's instructions) is added to each well, the well is pipetted/mixed five times, and the plate is incubated in a light-protected environment for 45 minutes, on ice. An identical but separate plate is also incubated on ice that is meant as a no-internalization negative control. Following this incubation, the experimental plate is moved to a 37 degree C incubator, the negative control plate is kept on ice to slow or block internalization, and samples are taken at designated time points to create an internalization time course. Samples are placed into a U-bottom 96-well plate, and internalization is quenched via addition of 200 µL/well of ice-cold FACS buffer. The plates are spun down at 2000xg for 2 minutes, resuspended in 200 µL ice-cold FACS buffer, spun down again, and resuspended in FACS buffer a second time. Finally, the samples are loaded into a flow cytometer for read-out of cellular pHrodo fluorescence using excitation and emission wavelengths consistent with the excitation and emission maxima of the pHrodo iFL Red dye (566 nm and 590 nm, respectively). Upon completion of the flow cytometry experiment and analysis of the data, it can be observed that cells treated with the pH-engineered ABPC specific for LRRC15 have a higher pHrodo iFL signal relative to a known, control ABPC specific for LRRC15, indicating that pH-engineered ABPCs specific for LRRC15 achieve enhanced endolysosomal accumulation relative to a control ABPC specific for LRRC15.

Alternatively, to demonstrate that pH-engineered ABPCs specific for LRRC15 achieve enhanced endolysosomal accumulation relative to a control ABPC specific for LRRC15, a variation of the above-described experiment is performed. LRRC15+ cells are plated, washed three times with PBS, and incubated at 37 degrees C for 60 minutes in media at neutral pH with

added concentrations of 2 μg/mL of either pH-engineered ABPC specific for LRRC15 or control ABPC specific for LRRC15. Following incubation, cells are washed three times with PBS, fixed and permeabilized, and stained with a panel of appropriately selected antibodies that bind late endosomal markers as well as lysosomes (e.g., RAB7, and LAMP1; Cell Signaling Technology, Endosomal Marker Antibody Sampler Kit #12666; AbCam, Anti-LAMP2 antibody [GL2A7], ab13524). After primary antibody staining, cells are stained with an appropriate mixture of fluorescently labeled secondary antibodies (e.g., Goat Anti-Human IgG (H&L) Secondary Antibody (Alexa Fluor 647)Cat#A-21445, and Abcam Goat Anti-Rabbit IgG H&L (Alexa Fluor 488), Cat#ab150077), imaged using confocal fluorescence microscopy, and regions of co-localization of signal from LRRC15-specific antibodies and endosomal markers are visualized and quantified. Upon analysis of the data, it can be revealed that there is increased co-localization of endolysosomal and LRRC15-specific antibody signal in wells treated with the pH-engineered ABPCs specific for LRRC15 as compared to wells treated with control ABPC specific for LRRC15, and can thereby demonstrate that pH-engineered ABPCs specific for LRRC15 achieve enhanced endolysosomal accumulation relative to control ABPC specific for LRRC15.

Increased LRRC15 antigen density in LRRC15+ cells after exposure to pH-engineered ABPCs specific for LRRC15 as compared to control ABPCs specific for LRRC15

To demonstrate that treatment of cells with the pH-engineered ABPCs specific for LRRC15 does not result in a detectable reduction of the level of LRRC15 on the surface of cells exposed to the pH-engineered ABPCs specific for LRRC15, or that said treatment results in less of a reduction of the level of LRRC15 on the surface of cells exposed to the pH-engineered ABPC specific for LRRC15 versus a control ABPC specific for LRRC15, an antigen density study is performed using flow cytometry. Briefly, 4.0x10^5 cells that express LRRC15 are plated per well in a 96-well plate in 100 μL media. Cells are treated with a titration from 1 pM to 1 μM of i) pH-engineered ABPCs specific for LRRC15, ii) a first control ABPC specific for LRRC15, iii) an appropriate isotype control, and iv) an untreated control. Cells are incubated for 2 hours at 37 °C, at which point all cells are incubated with 200 nM of a fluorophore-labeled second control ABPC specific for LRRC15 (e.g., as described herein) which has a different epitope (as determined by, e.g., competitive binding studies on cells) than either the first control ABPC

specific for LRRC15 or the pH-engineered ABPCs specific for LRRC15 for 30 minutes at 4 °C. Following this 30-minute incubation, the mean fluorescence intensity (MFI) of all cells is read out using, e.g., flow cytometry, using methods known to one of ordinary skill in the art. In parallel, a quantitative standard curve that can be used to quantify the presence of LRRC15 on the surface of treated cells as a function of MFI is generated using a commercially available quantification kit (e.g., BD Biosciences PE Phycoerythrin Fluorescence Quantitation Kit, catalog #340495); the quantitative standard curve is created by following the manufacturer's instructions. Other methods of determining the absolute number of LRRC15 on the cell surface are known in the art and include, e.g., use of radioisotopically labeled reagents. Upon analysis of the data, it can be revealed that at least one antibody concentration, cells treated with a control ABPC specific for LRRC15 experience a reduction of the level of LRRC15 on their surface, whereas cells treated with pH-engineered ABPCs specific for LRRC15 experience a significantly smaller reduction or no reduction at all, both relative to the isotype and untreated controls.

Example 3. Conjugation of pH-engineered and control ABPCs specific for LRRC15 to cytotoxic drugs

An antigen-binding protein construct conjugate (ADC) is made comprising the LRRC15-binding IgG (hereafter, LRRC15-IgG) described herein linked to monomethyl auristatin E (MMAE) via a valine-citrulline (vc) linker (hereafter, LRRC15-IgG-DC). Conjugation of the antigen-binding protein construct with vcMMAE begins with a partial reduction of the LRRC15-IgG followed by reaction with maleimidocaproyl-Val-Cit-PABC-MMAE (vcMMAE). The LRRC15-IgG (20 mg/mL) is partially reduced by addition of TCEP (molar equivalents of TCEP:mAb is 2:1) followed by incubation at 0° C overnight. The reduction reaction is then warmed to 20° C. To conjugate all of the thiols, vcMMAE is added to a final vcMMAE:reduced Cys molar ratio of 1:15. The conjugation reaction is carried out in the presence of 10% v/v of DMSO and allowed to proceed at 20° C for 60 minutes.

After the conjugation reaction, excess free N(acetyl)-Cysteine (2 equivalents vs. vcMMAE charge) is added to quench unreacted vcMMAE to produce the Cys-Val-Cit-MMAE adduct. The Cys quenching reaction is allowed to proceed at 20° C for approximately 30 minutes. The Cys-quenched reaction mixture is purified as per below. The above conjugation

method can also be used to conjugate maleimidocaproyl monomethylauristatin F (mcMMAF) to an antigen-binding protein construct.

The LRRC15-IgG-DC is purified using a batch purification method. The reaction mixture is treated with the appropriate amount of water washed Bu-HIC resin (ToyoPearl; Tosoh Biosciences), i.e., seven weights of resin is added to the mixture. The resin/reaction mixture is stirred for the appropriate time, and monitored by analytical hydrophobic interaction chromatography for removal of drug conjugate products, filtered through a coarse polypropylene filter, and washed by two bed volumes of a buffer (0.28 M sodium chloride, 7 mM potassium phosphate, pH 7). The combined filtrate and rinses are combined and analyzed for product profile by HIC HPLC. The combined filtrate and rinses are buffer exchanged by ultrafiltration/diafiltration (UF/DF) to 15 mM histidine, pH 6 with 10 diavolumes 15 nM histidine buffer.

A similar protocol can be used to conjugate DNA toxins such as SG3249 and SGD-1910 to LRRC15-IgG (see Tiberghien AC et al (2016) Design and Synthesis of Tesirine, a Clinical Antibody−Drug Conjugate Pyrrolobenzodiazepine Dimer Payload, ACS Med Chem Lett 7:983−987). Briefly, for SG3249, LRRC15-IgG (15 mg, 100 nanomoles) is diluted into 13.5 mL of a reduction buffer containing 10 mM sodium borate pH 8.4, 2.5 mM EDTA and a final antibody concentration of 1.11 mg/mL. A 10 mM solution of TCEP is added (1.5 molar equivalent/antibody, 150 nanomoles, 15 microliters) and the reduction mixture is heated at +37 °C for 1.5 hours in an incubator. After cooling down to room temperature, SG3249 is added as a DMSO solution (5 molar equivalent/antibody, 500 nanomoles, in 1.5 mL DMSO). The solution is mixed for 1.25 hours at room temperature, then the conjugation is quenched by addition of N-acetyl cysteine (1 micromole, 100 microliters at 10 mM), and injected into an AKTA™ Pure FPLC using a GE Healthcare HiLoadTM 26/600 column packed with Superdex 200 PG, and eluted with 2.6 mL/min of sterile-filtered phosphate-buffered saline (PBS). Fractions corresponding to the LRRC15-IgG-DC monomer peak are pooled, concentrated using a 15mL Amicon Ultracell 50KDa MWCO spin filter, analysed and sterile-filtered. UHPLC analysis on a Shimadzu Prominence system using a Phenomenex Aeris 3.6u XB-C18 150 x 2.1 mm column eluting with a gradient of water and acetonitrile on a reduced sample of LRRC15-IgG-DC at 280 nm and 330 nm (SG3249 specific) can show a mixture of light and heavy chains attached to several molecules of SG3249, consistent with a drug-per-antibody ratio (DAR) of 1 to 4

molecules of SG3249 per antibody. UHPLC analysis on a Shimadzu Prominence system using a Phenomenex Yarra 3u SEC-3000 300 mm x 4.60 mm column eluting with sterile-filtered SEC buffer containing 200 mM potassium phosphate pH 6.95, 250 mM potassium chloride and 10% isopropanol (v/v) on a sample of LRRC15-IgG-DC at 280 nm can show a monomer purity of over 90% with no impurity detected. UHPLC SEC analysis allows determination of final LRRC15-IgG-DC yield of greater than 30%.

Alternatively, methods to conjugate toxins to antibodies via lysine residues are known in the art (e.g., see Catcott KC et al (2016) Microscale screening of antibody libraries as maytansinoid antibody-drug conjugates, MAbs 8:513-23). In addition, similar methods to the above can be used to conjugate drugs and toxins to non-IgG formats with disulfide bonds, such as Vh-Fcs.

Example 4. Demonstration of enhanced cytotoxicity of pH-engineered ABPC ADCs specific for LRRC15 in LRRC15+ cells as compared to a control ABPC ADC specific for LRRC15

The cytotoxic activity of both pH-engineered ADCs specific for LRRC15 (e.g., a pH-engineered LRRC15-IgG-DC) and control ABPC ADCs specific for LRRC15 (e.g., a control ABPC LRRC15-IgG-DC) are separately evaluated on a panel of LRRC15+ cell lines expressing a variety of antigen densities (e.g., as described herein) and a LRRC15- cell line (e.g., ATCC: HCT116 Cat#CLL-247EMT), selected using the methods described herein, and, optionally, cells expressing transgenic LRRC15, e.g., HEK293 cells transfected with LRRC15 using methods known in the art (e.g., Expi293™ Expression System Kit ThermoFisher Catalog number: A14635). For purposes of validation, prior to use, all cell lines are tested for expression of LRRC15 using methods known to the art, e.g., qPCR, flow cytometry, mRNA RPKM, and antibody staining using anti-LRRC15 antibodies known to the art (e.g., as described herein) followed by visualization of the stain using fluorescence microscopy, immunohistochemistry, flow cytometry, ELISA, or other methods known to the art. To evaluate the cytotoxicity of compounds, cells are seeded at approximately 10-40,000 per well in 150 microliters of culture medium, then treated with graded doses of compounds from 1pM to 1 μM in quadruplicates at the initiation of the assay. Cytotoxicity assays are carried out for 96 hours after addition of test compounds. Fifty microliters of resazurin dye are added to each well during the last 4 to 6 hours

of the incubation to assess viable cells at the end of culture. Dye reduction is determined by fluorescence spectrometry using the excitation and emission wavelengths of 535 nm and 590 nm, respectively. For analysis, the extent of resazurin reduction by the treated cells is compared to that of untreated control cells, and percent cytotoxicity is determined. Alternatively, a WST-8 kit is used to measure cytotoxicity per the manufacturer's instructions (e.g., Dojindo Molecular Technologies Catalog# CCK-8). IC50, the concentration at which half-maximal killing is observed, is calculated using curve-fitting methods known in the art. Upon analysis of the data, it can be determined that pH-engineered and control ABPC ADCs specific for LRRC15 are substantially cytotoxic to one or more LRRC15+ cell line, but less toxic to LRRC15- cells. It also can be determined that pH-engineered ADCs specific for LRRC15 are more cytotoxic to one or more LRRC15+ cell lines than control ABPC ADCs specific for LRRC15 because: a) they show greater depth of killing at one or more concentrations or, b) they show lower IC50 or, c) they show a greater ratio of their dissociation constant KD on cells at neutral pH (as described herein) divided by their IC50 on those same cells.

Additionally, the cytotoxic activity of ABPCs specific for LRRC15 can be measured in a secondary ADC assay. Secondary ADC assays are known in the art (e.g., Moradec Cat# αHFc-NC-MMAF and Cat# αHFc-CL-MMAE, and associated manufacturer's instructions). Briefly, the assay is carried out as in the previous paragraph, except the ABPC specific for LRRC15 is substituted for the ADC specific for LRRC15, and to evaluate the cytotoxicity of compounds, cells are seeded at approximately 10-40,000 per well in 150 microliters of culture medium, then treated with graded doses of ABPC specific for LRRC15 from 1pM to 1 μM (final concentration in culture medium, having been pre-mixed with 100nM, final concentration in culture medium, of Moradec Cat# αHFc-NC-MMAF secondary ADC reagent and pre-incubated at 37°C for 30min before addition of the mixture to the culture medium) in quadruplicates at the initiation of the assay.

The cytotoxic activity of pH-engineered ADCs specific for LRRC15 and control ABPC ADCs specific for LRRC15 conjugates, as well as ABPCs specific for LRRC15 in a secondary ADC assay, are additionally measured by a cell proliferation assay employing the following protocol (Promega Corp. Technical Bulletin TB288; Mendoza et al., Cancer Res. 62:5485-5488, 2002):

1. An aliquot of 100 microliters of cell culture containing about 104 cells (e.g., LRRC15+ cells as described herein) in medium is deposited in each well of a 96-well, opaque-walled plate.
2. Control wells are prepared containing medium and without cells.
3. ADC specific for LRRC15 is added to the experimental wells at a range of concentrations from 1pM-1uM and incubated for 1-5 days. Alternatively, in a secondary ADC assay, 100nM secondary ADC reagent (final concentration in culture medium, Moradec Cat# αHFc-NC-MMAF) and ABPC specific for LRRC15 at a range of concentrations from 1pM-1uM (final concentration in culture medium) are pre-mixed and pre-incubated at 37°C for 30min before addition of the mixture to the culture medium, and incubated for 1-5 days.
4. The plates are equilibrated to room temperature for approximately 30 minutes.
5. A volume of CellTiter-Glo Reagent equal to the volume of cell culture medium present in each well is added.
6. The contents are mixed for 2 minutes on an orbital shaker to induce cell lysis.
7. The plate is incubated at room temperature for 10 minutes to stabilize the luminescence signal.
8. Luminescence is recorded and reported in graphs as RLU = relative luminescence units.

Example 5. Demonstration of enhanced toxin liberation of pH-engineered ABPC ADCs specific for LRRC15 in LRRC15+ cells as compared to a control ABPC ADC specific for LRRC15

The pH-engineered ADCs specific for LRRC15 (e.g., a pH-engineered LRRC15-IgG-DC) can also demonstrate increased toxin liberation in LRRC15+ cells as compared to a control ABPC ADC specific for LRRC15 (e.g., a control ABPC LRRC15-IgG-DC). After treatment of LRRC15+ cells with pH-engineered and control ABPC ADCs specific for LRRC15 as described herein, an LC-MS/MS method is used to quantify unconjugated (i.e., liberated) MMAE in treated LRRC15+ cells (Singh, A.P. and Shah, D.K. Drug Metabolism and Disposition 45.11 (2017): 1120-1132.) An LC-MS/MS system with electrospray interphase and triple quadrupole mass spectrometer is used. For the detection of MMAE, a XBridge BEH Amide column (Waters, Milford, MA) is used with mobile phase A as water (with 5 mM ammonium formate and 0.1% formic acid) and mobile phase B as 95:5 acetonitrile/water (with 0.1% formic acid and 1 mM ammonium formate), using a gradient at a flow rate of 0.25 mL/min at 40 °C. The total duration

of the chromatographic run is 12 minutes, where two MRM scans (718.5/686.5 and 718.5/152.1 amu) are monitored. Deuterated (d8) MMAE (MCE MedChem Express, Monmouth Junction, NJ) is used as an internal standard. First, an equation for quantifying unconjugated MMAE in a biological sample is derived by dividing the peak area for each drug standard by the peak area obtained for the internal standard. The resultant peak area ratios are then plotted as a function of the standard concentrations, and data points are fitted to the curve using linear regression. Three QC samples are included in the low, middle, and upper ranges of the standard curve to assess the predictive capability of the developed standard curve. The standard curves obtained are then used to deduce the observed concentrations of MMAE in a biologic sample. For measurement of MMAE concentration, treated cell samples are pelleted and reconstituted in fresh media to a final concentration of 0.25 million cells/100 µL. Samples are spiked with d8-MMAE (1 ng/mL) before performing cell lysis by the addition of a 2-fold volume of ice-cold methanol followed by freeze-thaw cycle of 45 minutes at -20 °C. The final cell lysate is obtained by centrifuging the samples at 13,000 rpm for 15 minutes at 4 °C followed by collection of supernatant. For the preparation of standards and QC samples, a fresh cell suspension (0.25 million/100 µl) is spiked with known concentrations of MMAE and internal standard (d8-MMAE) before a procedure similar to the cell lysis mentioned above. The resulting cell lysates are then evaporated and reconstituted in mobile phase B before injection into LC-MS/MS. The concentration of unconjugated MMAE in lysates of LRRC15+ cells treated with pH-engineered ADCs specific for LRRC15 is observed to be greater than that in LRRC15+ cells treated with control ABPC ADC specific for LRRC15.

For tubulin-inhibiting toxins, toxin liberation is also assessed by monitoring of cell viability and cell cycle phase. ~2.0x10^5 LRRC15+ cells are plated in a 96-well flat bottom plate and treated with pH-engineered and control ABPC ADCs specific for LRRC15 as described herein. After treatment, cells are transferred to a 96-round bottom plate, and the plate is centrifuged at 400 rcf for 2 min to decant supernatant. Decanted cells are stained with Live/Dead eFluor 660. Cells are then centrifuged and washed with FACS buffer (PBS with 2% FBS), after which cell cycle distribution is analyzed with a BD Cycletest™ Plus DNA Kit (cat # 340242). Briefly, cells are re-suspended in 76 ul Solution A and incubated for 10 min at room temperature. 61 µL Solution B is then added, and cells are incubated for another 10 min at room temperature. Finally, 61 µL of cold Solution C is added, and cells are again incubated for 10 min at room temp. Immediately after the last incubation step, cells are analyzed by flow cytometry (without

washing) at a flow rate of 10 μL/sec. Increased G2/M-phase arrest can be observed with exposure to pH-engineered ADCs specific for LRRC15 as compared to control ABPC ADC specific for LRRC15.

For DNA-damaging toxins (e.g., pyrrolobenzodiazepine or "PBD"), DNA damage is assessed by measuring the phosphorylated histone H2AX (γH2AX). H2AX is normally phosphorylated in response to double-strand breaks in DNA; however, increased levels γH2AX may also be observed as a result of treatment with DNA-cross-linking toxins such as PBD or cisplatin (Huang, X. et al. 2004, Cytometry Part A 58A, 99–110). LRRC15+ cells are treated with pH-engineered and control ABPC ADCs specific for LRRC15 as described herein. After treatment, cells are rinsed with PBS, and then fixed in suspension in 1% methanol-free formaldehyde (Polysciences, Warrington, PA) in PBS at 0 °C for 15 min. Cells are resuspended in 70% ethanol for at least 2 h at -20°C. Cells are then washed twice in PBS and suspended in 0.2% Triton X-100 (Sigma) in a 1% (w/v) solution of BSA (Sigma) in PBS for 30 min to suppress nonspecific Ab binding. Cells are centrifuged again (200 g, 5 min) and the cell pellet is suspended in 100 μL of 1% BSA containing 1:800 diluted anti-histone γH2AX polyclonal Ab (Trevigen, Gaithersburg, MD). The cells are then incubated overnight at 4 °C, washed twice with PBS, and resuspended in 100 μL of 1:30 diluted FITC-conjugated F(ab')2 fragment of swine anti-rabbit immunoglobulin (DAKO, Carpinteria, CA) for 30 min at room temperature in the dark. The cells are then counterstained with 5 μg/mL of PI (Molecular Probes, Eugene, OR) dissolved in PBS containing 100 μg/mL of DNase-free RNase A (Sigma), for 20 min at room temperature. Cellular fluorescence of the FITC γH2AX signal and the PI counterstain are measured using flow cytometry using methods known in the art. When comparing cells within the same stage of the cell cycle (based on total DNA content), treated LRRC15+ cells can be observed to have an increased FITC γH2AX signal relative to untreated LRRC15+ cells (which serve as a baseline). Furthermore, LRRC15+ cells treated with pH-engineered ADCs specific for LRRC15 can be observed to have a greater increase in levels of γH2AX over baseline than cells treated with a control ABPC ADC specific for LRRC15. In addition to the γH2AX assay, DNA cross-linking can be more directly assessed with a Comet assay (Chandna, S. (2004) Cytometry 61A, 127–133).

In addition, as disclosed herein, pH-engineered and control ABPCs can be assayed using the methods in this example without direct conjugation by performing a secondary ADC assay instead of using primary conjugated ADCs.

Example 6. Demonstration of decreased half-life of pH-engineered ABPCs specific for LRRC15 as compared to a control ABPC specific for LRRC15 in tumor-bearing animals

One of the surprising aspects of the pH-engineered ABPCs specific for LRRC15 described by the invention can be their ability to facilitate increased dissociation of ABPCs from the LRRC15 within the endosome or lysosome resulting in a decreased serum half-life relative to control ABPCs specific for LRRC15 or ABPCs that are not specific for LRRC15 in tumor-bearing animals. To demonstrate these properties, a series of animal studies in mice and/or monkeys is performed using pH-engineered ABPC specific for LRRC15 and control ABPC specific for LRRC15 using methods known to the art (e.g., Gupta, P., et al. (2016), mAbs, 8:5, 991-997). Briefly, to conduct mouse studies, a single intravenous bolus (e.g., 5 mg/kg) of either pH-engineered ABPC specific for LRRC15 or control ABPC specific for LRRC15 is administered via tail vein to two groups of NOD SCID mice (e.g. Jackson Labs NOD.CB17-Prkdcscid/J Stock No: 001303) xenografted with a LRRC15+ cell line (e.g., as described herein). Xenografted mice are prepared by growing 1-5 million LRRC15+ cells in vitro and inoculating subcutaneously into the right flank of the mouse. Tumors are size matched at 300 mm3. Measurements of the length (L) and width (W) of the tumors are taken via electronic caliper and the volume is calculated according to the following equation: V=L×W^2/2. Blood samples are collected via retro-orbital bleeds from each group at each of the following time points: 15m, 30m, 1h, 8h, 24h, and 3d, 7d, 10d, 14d, 17d, 21d, and 28d. Samples are processed to collect serum, and antibody concentrations are quantified using ELISA or other methods known to the art (e.g., PAC assay or MAC assay; Fischer, S.K. et al. (2012), mAbs, 4:5, 623-631, utilizing, e.g., anti-human Fc antibody Jackson ImmunoResearch Labs, Cat# 109–006–006). Antibody concentrations of pH-engineered ABPC specific for LRRC15 and control ABPC specific for LRRC15 are plotted as a function of time. Upon analysis of the data, it can be observed that the pH-engineered ABPC specific for LRRC15 has a significantly shorter serum half-life relative to control ABPC specific for LRRC15, thereby demonstrating the ability of the pH-engineered ABPC specific for LRRC15's pH dependence to facilitate an enhanced

dissociation within the endosome or lysosome relative to other, similar binders (e.g., control ABPC specific for LRRC15) that bind the same antigen but that differ in their pH dependence. If the pH-engineered and control ABPCs specific for LRRC15 are cross-reactive with the mouse homolog of LRRC15, a similar experiment can be repeated with non-xenografted mice.

In addition, the half-life of pH-engineered and control ABPC ADCs specific for LRRC15 can be assessed using the above methods by substituting pH-engineered and control ABPC ADCs specific for LRRC15 for the pH-engineered and control ABPCs specific for LRRC15 (i.e., studying the ABPCs after conjugation to a drug or toxin, as described herein).

Example 7. Increased potency of pH-engineered ADCs specific for LRRC15 vs. a control ABPC ADC specific for LRRC15 in mouse xenograft models

The enhanced anti-tumor activity of the pH-engineered ADCs specific for LRRC15 against LRRC15+ tumors can be demonstrated in a subcutaneous xenograft model of LRRC15+ cells. For the experiments, 1-5 million LRRC15+ cells are grown in vitro and inoculated subcutaneously per mouse into the right flank of female immunodeficient (e.g., SCID-Beige or NOD scid) mice. Tumors are size matched at 100-200 mm3, and dosed intraperitoneally (IP) (1 dose given every ~4-7 days for a total of ~2-6 doses). Measurements of the length (L) and width (W) of the tumors are taken via electronic caliper and the volume is calculated according to the following equation: V=L×W^2/2. A bolus (e.g., 5 mg/kg) of either pH-engineered ADC specific for LRRC15 or control ABPC ADC specific for LRRC15 is administered via tail vein. Tumor growth inhibition (TGI) and tumor growth delay (TGD) and survival are significantly improved with administration of pH-engineered ADC specific for LRRC15 compared to administration of control ABPC ADC specific for LRRC15 at the same regimen.

Optionally, spread of tumor cells into the various tissues is determined in sacrificed animals. Metastasis is measured according to Schneider, T., et al., Clin. Exp. Metas. 19 (2002) 571-582. Briefly, tissues are harvested and human Alu sequences are quantified by real-time PCR. Higher human DNA levels, quantified by real-time PCR, correspond to higher levels of metastasis. Levels of human Alu sequences (correlating to invasion of tumor cells into secondary tissue) are significantly lower in animals treated with pH-engineered ADC specific for LRRC15, corresponding to reduced metastasis, compared to mice treated with control ABPC ADC specific

for LRRC15 at the same regimen. Alternatively, the enhanced anti-tumor activity of the pH-engineered ADC specific for LRRC15 can be shown in LRRC15+ patient-derived xenograft models (e.g., available from Charles River Laboratories).

Example 8. Creation of a pH-engineered bispecific LRRC15 bispecific ABPC and demonstration of exemplary properties as compared to a control bispecific ABPC

To create a pH-engineered ABPC specific for LRRC15 with modified toxicity and internalization properties, a bispecific antibody that binds two different epitopes on LRRC15 is constructed. It is known in the art that biparatopic antibodies can show increased antigen-dependent internalization, and are therefore useful for applications such as antibody-drug conjugates (e.g., see Li et al (2016) A Biparatopic HER2-Targeting Antibody-Drug Conjugate Induces Tumor Regression in Primary Models Refractory to or Ineligible for HER2-Targeted Therapy, Cancer Cell 29:117-29). Briefly, a pH-engineered LRRC15 x LRRC15 bispecific, biparatopic ABPC specific for LRRC15 is assembled using light chain/heavy chain pairs from two different pH-engineered ABPCs specific for LRRC15, each of which binds a distinct epitope on LRRC15 that does not overlap with the other epitope. A set of pH-engineered ABPCs specific for LRRC15 that bind non-overlapping epitopes are discovered, e.g., using the methods described herein, or others known to one of ordinary skill in the art. Briefly, two binders are selected on the basis that they bind substantially different epitopes on LRRC15, as determined by, e.g., a binding competition assay as in Abdiche YN et al (2009) Exploring blocking assays using Octet, ProteOn, and Biacore biosensors, Anal Biochem 386:172-80. Alternatively, briefly, as described herein, cell culture supernatants of cells transfected with a first ABPC specific for LRRC15 are normalized to an antibody expression level of 50 μg/mL, and captured on an anti-human Fc sensor (Forte Bio). A baseline is established using 1X kinetics buffer (Forte Bio), and the sensor is associated with 50 nM of LRRC15 in 1X PBS (that has been mixed and pre-incubated for 30 min at 37 degrees C with a second ABPC specific for LRRC15 transfection supernatant or the first ABPC specific for LRRC15 transfection supernatant, both normalized to 50ug/mL) at pH 7.4 for 300 sec to generate an association curve. If the association rate in the presence of the second ABPC specific for LRRC15 is significantly faster (as calculated by the instrument software, or as seen by an elevated level of association over time) than the association rate in the presence of the first ABPC specific for LRRC15, then the second ABPC specific for

LRRC15 is deemed to bind a non-overlapping epitope of LRRC15. Optionally, each antibody is screened for its internalization properties when bound to its epitope on a cell expressing LRRC15, and well-internalizing antibodies are selected. Assays for determining the internalization rate of a molecule present on the surface of a cell are known to the art. See, e.g., Wiley et al. (1991) J. Biol. Chem. 266: 11083-11094; and Sorkin and Duex (2010) Curr. Protoc. Cell Biol. Chapter, Unit-15.14; Vainshtein et al. (2015) Pharm Res. 32: 286-299. Once selected, heavy and light chain constructs with engineered mutations for heavy and light chain pairing (Spiess et al., "Alternative molecular formats and therapeutic applications of bispecific antibodies," 2015) are synthesized for both arms. Bispecific ABPCs specific for LRRC15 are produced by co-expression of corresponding heavy and light chain plasmids in, e.g., Expi293 cells. Cell culture supernatants are harvested and subjected to Protein A purification. Heterodimeric ABPCs specific for LRRC15 are separated from homodimeric species via additional purification steps such as ion exchange chromatography, hydrophobic interaction chromatography, and mixed mode chromatography. The purified pH-engineered LRRC15 x LRRC15 bispecific, biparatopic ABPCs specific for LRRC15 are characterized via mass spectrometry to confirm the purity and absence of homodimeric species and size exclusion chromatography to confirm the presence of monomeric antigen-binding protein construct species. For the product antibody, binding to the LRRC15 is confirmed via Biacore analysis. Other methods of bispecific antibody production are known to the art and could also be used to create a bispecific antibody, e.g., the LRRC15 x LRRC15 bispecific, biparatopic ABPCs specific for LRRC15 described herein (e.g., Labrijn et al (2014) "Controlled Fab-arm exchange for the generation of stable bispecific IgG1" Nature Protcols 9:2450–2463, accessed at http://www.nature.com/nprot/journal/v9/n10/abs/nprot.2014.169.html), as would be apparent to one of ordinary skill in the art. Alternatively, instead of a LRRC15 x LRRC15 ABPC specific for LRRC15, a pH-engineered LRRC15 x BINDER ABPC specific for LRRC15 can be constructed using similar methods apparent to one skilled in the art, where BINDER is any antibody that has been published in the art or discovered using methods like those herein or those known in the art (e.g., display-based or immunization-based methods).

Next, exemplary properties of pH-engineered LRRC15 x LRRC15 ABPCs specific for LRRC15 can be demonstrated using the methods described herein, with the appropriate control being a control ABPC monospecific or bispecific ABPC specific for LRRC15. Briefly, it can be

shown that, as compared to a control, the pH-engineered LRRC15 x LRRC15 ABPCs specific for LRRC15: a) bind in a pH-dependent manner to cells, e.g., bind at a neutral pH but not an acidic pH and b) release from cells in a pH-dependent manner, e.g. bind at a neutral pH and release at an acidic pH and c) show enhanced endolysosomal accumulation in LRRC15+ cells and d) show increased LRRC15 antigen density after exposure to LRRC15+ cells and e) when conjugated to a toxin, show increased cytotoxicity to LRRC15+ cells and f) when conjugated to a toxin, show increased toxin liberation when incubated with LRRC15+ cells and g) show decreased half-life when exposed to LRRC15 antigen in a relevant animal model and h) when conjugated to a toxin, show increased efficacy in a mouse xenograft model of LRRC15+ cells. Similarly, the exemplary properties of pH-engineered LRRC15 x BINDER ABPCs specific for LRRC15 can be demonstrated using the methods described herein, with the appropriate control being a control ABPC LRRC15 x BINDER bispecific ABPC specific for LRRC15.

Example 9. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Purcell et. al., LRRC15 Is a Novel Mesenchymal Protein and Stromal Target for Antibody-Drug Conjugates, Cancer Res., 78(14):4059-4072 (2018)). We selected samrotamab (Heavy chain SEQ ID NO: 1, Light chain SEQ ID NO: 2) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the heavy chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-dependent sequence variants, individual amino acid residues within the heavy chain CDRs were systematically substituted with a histidine, one at a time (MYT0964 - MYT1003). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with only one histidine or alanine mutation in a heavy chain CDR were generated by co-transfection of Expi293 cells with a) one heavy chain sequence variant, and b) the corresponding starting ABPC light chain using methods known to the art. After

allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 1), and the pH dependence of the variant was evaluated using biolayer interferometry (BLI) on an Octet RED 384 instrument. Briefly, 5µL of cell culture supernatant was diluted into 195µL of 1x PBST pH 7.4. This resulted in a high concentration of 16.4 µg/mL, a low concertation of 3.1 µg/mL, and an average concentration of 9.6 µg/mL. The resulting diluted supernatants were then captured on an anti-human Fc sensor (Forte Bio). A baseline was established using 1X PBST (50mM Potassium Phosphate Buffer + 150mM NaCl + 0.05% Tween 20) pH 7.4, and the sensor was associated with 50 nM of LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST pH 7.4 for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor was exposed to 1X PBST pH 7.4 for 180 sec. Baseline, association, and dissociation were repeated using 1X PBST pH 5.4 throughout in a separate condition. Association and dissociation phase curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (i.e., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC, (with no substitutions), and b) reduced dissociation at pH 7.4 (i.e., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Heavy chain variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to starting ABPC) as shown in Figure 2 were selected for further analysis (e.g., MYT0971, MYT0972, MYT0974, MYT0976, MYT0981, MYT0983, MYT0994, MYT0996, MYT0997, MYT1001, MYT1002, MYT1003). It was also noted that while some histidine and alanine mutations obliterated LRRC15 binding (e.g., MYT0973, MYT0991, MYT0993, MYT0995, MYT0998, MYT0999, MYT1000), others were tolerated with little (e.g., less than 1-fold change in dissociation constant KD or dissociation rate) or no change in LRRC15 binding kinetics (e.g., MYT0964, MYT0965, MYT0966, MYT0967, MYT0968, MYT0969, MYT0970, MYT0975, MYT0977, MYT0978, MYT0979, MYT0980, MYT0982, MYT0984, MYT0985, MYT0986, MYT0987, MYT0988, MYT0989, MYT0990).

Especially because histidine is a large, positively charged amino acid, these variants with no change were noted as positions in the heavy chain that may tolerate a wide range of mutations

and lead to antibodies with different sequence but similar binding properties, a designation that is not otherwise apparent.

The previously referenced absolute antibody antigen was generated by transfection of cells using methods known to the art. After allowing adequate protein expression, the cell culture supernatants were collected, quantified by analysis of SDS-PAGE (Figure 43) chromatography, and purified by sequential Protein A affinity chromatography, cation exchange chromatography, and size exclusion chromatography. The absolute antibody antigen was a bispecific Fc-fusion protein of LRRC15 with one chain containing a knobs-in-holes mouse Fc region, whereas the second chain was the complimentary knobs-in-holes mouse Fc region fused to LRCC15, creating an overall antigen with monovalent LRRC15 fused to mouse Fc.

Example 10. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Purcell et. al., LRRC15 Is a Novel Mesenchymal Protein and Stromal Target for Antibody-Drug Conjugates, Cancer Res., 78(14):4059-4072 (2018)). We selected samrotamab (Heavy chain SEQ ID NO: 1, Light chain SEQ ID NO: 2) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the light chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-dependent sequence variants, individual amino acid residues within the light chain CDRs were systematically substituted with a histidine, one at a time (MYT2726 - MYT2752). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with only one histidine or alanine mutation in a light chain CDR were generated by co-transfection of Expi293 cells with a) one light chain sequence variant, and b) the corresponding starting ABPC heavy chain using methods known to the art. After allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 4), and the pH dependence of the variant was evaluated using biolayer interferometry (BLI) on an Octet RED 96e instrument. Briefly, cell culture supernatants were

diluted based on qualitative expression level of the variant determined by visual examination of SDS-PAGE gels, 5 µL of cell culture supernatant was diluted into 195 µL of 1x PBST, pH 7.4 for high expressors, 25 µL of cell culture supernatant was diluted into 175 µL of 1x PBST, pH 7.4 for medium expressors and 100 µL of cell culture supernatant was diluted into 100 µL of 1x PBST, pH 7.4 for low expressors for loading onto the sensor tips. Diluted supernatants were then captured on an anti-human Fc sensor (Forte Bio). A baseline was established using 1X PBST (50mM Potassium Phosphate Buffer + 150mM NaCl + 0.05% Tween 20) pH 7.4, and the sensor was associated with 50 nM of LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST pH 7.4 for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor was exposed to 1X PBST pH 7.4 for 300-600 sec. Baseline, association, and dissociation were repeated using 1xPBST pH 5.4 throughout in a separate condition. Association and dissociation phase curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (i.e., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC (with no substitutions), and b) reduced dissociation at pH 7.4 (i.e., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Light chain variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to the starting ABPC), as shown in Figure 5 were selected for further analysis (e.g,MYT2734, MYT2736, MYT2737, MYT2738, MYT2744, MYT2745, MYT2747, MYT2748, MYT2749, and MYT2751). It was also noted that while some histidine and alanine mutations obliterated LRRC15 binding (e.g., MYT2746), others were tolerated with little (e.g., less than 1-fold change in dissociation constant KD or dissociation rate) or no change in LRRC15 binding kinetics (e.g., MYT2726, MYT2727, MYT2728, MYT2729, MYT2730, MYT2731, MYT2732, MYT2733, MYT2735, MYT2739, MYT2740, MYT2741, MYT2742, MYT2743, MYT2750, and MYT2752).

Especially because histidine is a large, positively charged amino acid, these variants with no change were noted as positions in the light chain that may tolerate a wide range of mutations and lead to antibodies with different sequence but similar binding properties, a designation that is not otherwise apparent.

Example 11. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Purcell et. al., LRRC15 Is a Novel Mesenchymal Protein and Stromal Target for Antibody-Drug Conjugates, Cancer Res., 78(14):4059-4072 (2018)). We selected samrotamab (Heavy chain SEQ ID NO: 1, Light chain SEQ ID NO: 2) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the heavy chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-dependent sequence variants, individual amino acid mutations within the heavy chain CDRs that had been previously selected for further analysis in Example 9 were systematically combined two or more at a time (MYT2722 - MYT2725). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with two or more histidine or alanine mutations in the heavy chain CDRs were generated by co-transfection of Expi293 cells with a) one heavy chain combinations sequence variant, and b) the corresponding starting ABPC light chain using methods known to the art. After allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 7), and the pH dependence of the variant was evaluated using biolayer interferometry (BLI) on an Octet RED 96e instrument. Briefly, cell culture supernatants were diluted based on qualitative expression level of the variant determined by visual examination of SDS-PAGE gels, 5 µL of cell culture supernatant was diluted into 195 µL of 1x PBST, pH 7.4 for high expressors, 25 µL of cell culture supernatant was diluted into 175 µL of 1x PBST, pH 7.4 for medium expressors and 100 µL of cell culture supernatant was diluted into 100 µL of 1x PBST, pH 7.4 for low expressors for loading onto the sensor tips. Diluted supernatants were then captured on an anti-human Fc sensor (Forte Bio). A baseline was established using 1X PBST (50mM Potassium Phosphate Buffer + 150mM NaCl + 0.05% Tween 20) pH 7.4, and the sensor was associated with 50 nM of LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST pH 7.4 for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the

sensor was exposed to 1X PBST pH 7.4 for 300-600 sec. Baseline, association, and dissociation were repeated using 1xPBST pH 5.4 throughout in a separate condition. Association and dissociation phase curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (i.e., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC (with no substitutions), and b) reduced dissociation at pH 7.4 (i.e., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Heavy chain combinations variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to the starting ABPC), as shown in Figure 8 were selected for further analysis (e.g., MYT2722, MYT2723, MYT2724, and MYT2725).

Example 12. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Gish K et al. "Anti-huLRRC15 Antibody Drug Conjugates and Methods for their Use" US Patent 10,195,209 B2 (2019)). We selected hu139.10 (Heavy chain SEQ ID NO: 84, Light chain SEQ ID NO: 85) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the heavy chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-dependent sequence variants, individual amino acid residues within the heavy chain CDRs were systematically substituted with a histidine, one at a time (MYT3253 - MYT3292). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with only one histidine or alanine mutation in a heavy chain CDR were generated by co-transfection of Expi293 cells with a) one heavy chain sequence variant, and b) the corresponding starting ABPC light chain using methods known to the art. After allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 10), and the pH dependence of the variant was evaluated using biolayer interferometry

(BLI) on an Octet RED e96 instrument. Briefly, cell culture supernatants were diluted based on qualitative expression level of the variant determined by visual examination of SDS-PAGE gels, 5 µL of cell culture supernatant was diluted into 195 µL of 1x PBST, pH 7.4 for high expressors, 25 µL of cell culture supernatant was diluted into 175 µL of 1x PBST, pH 7.4 for medium expressors and 100 µL of cell culture supernatant was diluted into 100 µL of 1x PBST, pH 7.4 for low expressors for loading onto the sensor tips. A baseline was established using 1X PBST (50mM Potassium Phosphate Buffer + 150mM NaCl + 0.05% Tween 20) pH 7.4, and the sensor was associated with 50 nM of LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST pH 7.4 for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor was exposed to 1X PBST pH 7.4 for 300sec. Baseline, association, and dissociation were repeated using 1X PBST pH 5.4 throughout in a separate condition. Association and dissociation phase curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (i.e., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC, (with no substitutions), and b) reduced dissociation at pH 7.4 (i.e., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Heavy chain variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to starting ABPC) as shown in Figure 11 were selected for further analysis (e.g., MYT3254, MYT3256, MYT3259, MYT3262, MYT3263, MYT3267, MYT3271, MYT3281, MYT3282, MYT3283, MYT3285, MYT3287, and MYT3288). It was also noted that while some histidine and alanine mutations obliterated LRRC15 binding (e.g., MYT3284), others were tolerated with little (e.g., less than 1-fold change in dissociation constant KD or dissociation rate) or no change in LRRC15 binding kinetics (e.g., MYT3253, MYT3255, MYT3257, MYT3258, MYT3264, MYT3268, MYT3270, MYT3272, MYT3273, MYT3274, MYT3275, MYT3276, MYT3277, MYT3278, and MYT3292).

Especially because histidine is a large, positively charged amino acid, these variants with no change were noted as positions in the heavy chain that may tolerate a wide range of mutations and lead to antibodies with different sequence but similar binding properties, a designation that is not otherwise apparent.

Example 13. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Gish K et al. "Anti-huLRRC15 Antibody Drug Conjugates and Methods for their Use" US Patent 10,195,209 B2 (2019)). We selected hu139.10 (Heavy chain SEQ ID NO: 84, Light chain SEQ ID NO: 85) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the light chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-dependent sequence variants, individual amino acid residues within the light chain CDRs were systematically substituted with a histidine, one at a time (MYT3293 - MYT3324). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with only one histidine or alanine mutation in a light chain CDR were generated by co-transfection of Expi293 cells with a) one light chain sequence variant, and b) the corresponding starting ABPC heavy chain using methods known to the art. After allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 13), and the pH dependence of the variant was evaluated using biolayer interferometry (BLI) on an Octet RED 96e instrument. Briefly, cell culture supernatants were diluted based on qualitative expression level of the variant determined by visual examination of SDS-PAGE gels, 5 µL of cell culture supernatant was diluted into 195 µL of 1x PBST, pH 7.4 for high expressors, 25 µL of cell culture supernatant was diluted into 175 µL of 1x PBST, pH 7.4 for medium expressors and 100 µL of cell culture supernatant was diluted into 100 µL of 1x PBST, pH 7.4 for low expressors for loading onto the sensor tips. Diluted supernatants were then captured on an anti-human Fc sensor (Forte Bio). A baseline was established using 1X PBST (50mM Potassium Phosphate Buffer + 150mM NaCl + 0.05% Tween 20) pH 7.4, and the sensor was associated with 50 nM of LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST pH 7.4 for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor was exposed to 1X PBST pH 7.4 for 300-600 sec. Baseline, association, and dissociation were

repeated using 1xPBST pH 5.4 throughout in a separate condition. Association and dissociation phase curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (i.e., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC (with no substitutions), and b) reduced dissociation at pH 7.4 (i.e., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Light chain variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to the starting ABPC), as shown in Figure 14 were selected for further analysis (e.g., MYT3298, MYT3300, MYT3301, MYT3303, MYT3305, MYT3306, MYT3307, MYT3309, MYT3310, MYT3314, MYT3315, MYT3317, MYT3318, MYT3319, and MYT3322). It was also noted that some histidine and alanine mutations were tolerated with little (e.g., less than 1-fold change in dissociation constant KD or dissociation rate) or no change in LRRC15 binding kinetics (e.g., MYT3293, MYT3294, MYT3295, MYT3296, MYT3297, MYT3299, MYT3302, MYT3304, MYT3308, MYT3311, MYT3312, MYT3313, MYT3316, MYT3320, MYT3321, and MYT3324).

Especially because histidine is a large, positively charged amino acid, these variants with no change were noted as positions in the light chain that may tolerate a wide range of mutations and lead to antibodies with different sequence but similar binding properties, a designation that is not otherwise apparent.

Example 14. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Gish K et al. "Anti-huLRRC15 Antibody Drug Conjugates and Methods for their Use" US Patent 10,195,209 B2 (2019)). We selected hu139.10 (Heavy chain SEQ ID NO: 84, Light chain SEQ ID NO: 85) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the heavy chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-

dependent sequence variants, individual amino acid mutations within the heavy chain CDRs that had been previously selected for further analysis in Example 12 were systematically combined two or more at a time (MYT4161 - MYT4164). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with two or more histidine or alanine mutations in the heavy chain CDRs were generated by co-transfection of Expi293 cells with a) one heavy chain combinations sequence variant, and b) the corresponding starting ABPC light chain using methods known to the art. After allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 16), and the pH dependence of the variant was evaluated using biolayer interferometry (BLI) on an Octet RED 96e instrument. Briefly, cell culture supernatants were diluted based on qualitative expression level of the variant determined by visual examination of SDS-PAGE gels, 5 µL of cell culture supernatant was diluted into 195 µL of 1x PBST, pH 7.4 for high expressors, 25 µL of cell culture supernatant was diluted into 175 µL of 1x PBST, pH 7.4 for medium expressors and 100 µL of cell culture supernatant was diluted into 100 µL of 1x PBST, pH 7.4 for low expressors for loading onto the sensor tips. Diluted supernatants were then captured on an anti-human Fc sensor (Forte Bio). A baseline was established using 1X PBST (50mM Potassium Phosphate Buffer + 150mM NaCl + 0.05% Tween 20) pH 7.4, and the sensor was associated with 50 nM of LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST pH 7.4 for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor was exposed to 1X PBST pH 7.4 for 300-600 sec. Baseline, association, and dissociation were repeated using 1xPBST pH 5.4 throughout in a separate condition. Association and dissociation phase curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (i.e., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC (with no substitutions), and b) reduced dissociation at pH 7.4 (i.e., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Heavy chain combinations variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to the starting ABPC), as shown in Figure 17 were selected for further analysis (e.g., MYT4163).

Example 15. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Gish K et al. "Anti-huLRRC15 Antibody Drug Conjugates and Methods for their Use" US Patent 10,195,209 B2 (2019)). We selected hu139.10 (Heavy chain SEQ ID NO: 84, Light chain SEQ ID NO: 85) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the light chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-dependent sequence variants, individual amino acid mutations within the light chain CDRs that had been previously selected for further analysis in Example 13 were systematically combined two or more at a time (MYT4165 - MYT4174). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with two or more histidine or alanine mutations in the light chain CDRs were generated by co-transfection of Expi293 cells with a) one light chain combinations sequence variant, and b) the corresponding starting ABPC heavy chain using methods known to the art. After allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 19), and the pH dependence of the variant was evaluated using biolayer interferometry (BLI) on an Octet RED 96e instrument. Briefly, cell culture supernatants were diluted based on qualitative expression level of the variant determined by visual examination of SDS-PAGE gels, 5 µL of cell culture supernatant was diluted into 195 µL of 1x PBST, pH 7.4 for high expressors, 25 µL of cell culture supernatant was diluted into 175 µL of 1x PBST, pH 7.4 for medium expressors and 100 µL of cell culture supernatant was diluted into 100 µL of 1x PBST, pH 7.4 for low expressors for loading onto the sensor tips. Diluted supernatants were then captured on an anti-human Fc sensor (Forte Bio). A baseline was established using 1X PBST (50 mM Potassium Phosphate Buffer + 150 mM NaCl + 0.05% Tween 20), pH 7.4, and the sensor was associated with 50nM LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST, pH 7.4, for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor was exposed to 1X PBST, pH

7.4, for 300-600 sec. Baseline, association, and dissociation were repeated using 1xPBST, pH 5.4, throughout in a separate condition. Association and dissociation phase curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (e.g., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC (with no substitutions), and b) reduced dissociation at pH 7.4 (e.g., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Light chain combinations variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to the starting ABPC), as shown in Figure 20 were selected for further analysis (e.g., MYT4166, MYT4167, MYT4168, MYT4169, MYT4170, MYT4171, MYT4172, MYT4173, and MYT4174).

Example 16. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Gish K et al. "Anti-huLRRC15 Antibody Drug Conjugates and Methods for their Use" US Patent 10,195,209 B2 (2019)). We selected huAD208.4.1 (Heavy chain SEQ ID NO: 178, Light chain SEQ ID NO: 179) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the heavy chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-dependent sequence variants, individual amino acid residues within the heavy chain CDRs were systematically substituted with a histidine, one at a time (MYT3326 - MYT3367). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with only one histidine or alanine mutation in a heavy chain CDR were generated by co-transfection of Expi293 cells with a) one heavy chain sequence variant, and b) the corresponding starting ABPC light chain using methods known to the art. After allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 22), and the pH dependence of the variant was evaluated using biolayer interferometry

(BLI) on an Octet RED 96e instrument. Briefly, cell culture supernatants were diluted based on qualitative expression level of the variant determined by visual examination of SDS-PAGE gels, 5 µL of cell culture supernatant was diluted into 195 µL of 1x PBST, pH 7.4 for high expressors, 25 µL of cell culture supernatant was diluted into 175 µL of 1x PBST, pH 7.4 for medium expressors and 100 µL of cell culture supernatant was diluted into 100 µL of 1x PBST, pH 7.4 for low expressors for loading onto the sensor tips. A baseline was established using 1X PBST (50mM Potassium Phosphate Buffer + 150mM NaCl + 0.05% Tween 20) pH 7.4, and the sensor was associated with 50 nM of LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST pH 7.4 for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor was exposed to 1X PBST pH 7.4 for 300sec. Baseline, association, and dissociation were repeated using 1X PBST pH 5.4 throughout in a separate condition. Association and dissociation phase curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (i.e., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC, (with no substitutions), and b) reduced dissociation at pH 7.4 (i.e., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Heavy chain variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to starting ABPC) as shown in Figure 23 were selected for further analysis (e.g., MYT3336, MYT3341, MYT3345, MYT3346, and MYT3365). It was also noted that some histidine and alanine mutations were tolerated with little (e.g., less than 1-fold change in dissociation constant KD or dissociation rate) or no change in LRRC15 binding kinetics (e.g., MYT3326, MYT3327, MYT3328, MYT3329, MYT3330, MYT3331, MYT3332, MYT3333, MYT3334, MYT3335, MYT3337, MYT3338, MYT3339, MYT3340, MYT3342, MYT3343, MYT3344, MYT3347, MYT3348, MYT3349, MYT3350, MYT3351, MYT3352, MYT3353, MYT3354, MYT3355, MYT3356, MYT3357, MYT3358, MYT3359, MYT3360, MYT3361, MYT3362, and MYT3364).

Especially because histidine is a large, positively charged amino acid, these variants with no change were noted as positions in the heavy chain that may tolerate a wide range of mutations and lead to antibodies with different sequence but similar binding properties, a designation that is not otherwise apparent.

Example 17. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Gish K et al. "Anti-huLRRC15 Antibody Drug Conjugates and Methods for their Use" US Patent 10,195,209 B2 (2019)). We selected huAD208.4.1 (Heavy chain SEQ ID NO: 178, Light chain SEQ ID NO: 179) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the light chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-dependent sequence variants, individual amino acid residues within the light chain CDRs were systematically substituted with a histidine, one at a time (MYT3369 - MYT3398). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with only one histidine or alanine mutation in a light chain CDR were generated by co-transfection of Expi293 cells with a) one light chain sequence variant, and b) the corresponding starting ABPC heavy chain using methods known to the art. After allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 25), and the pH dependence of the variant was evaluated using biolayer interferometry (BLI) on an Octet RED 96e instrument. Briefly, cell culture supernatants were diluted based on qualitative expression level of the variant determined by visual examination of SDS-PAGE gels, 5 µL of cell culture supernatant was diluted into 195 µL of 1x PBST, pH 7.4 for high expressors, 25 µL of cell culture supernatant was diluted into 175 µL of 1x PBST, pH 7.4 for medium expressors and 100 µL of cell culture supernatant was diluted into 100 µL of 1x PBST, pH 7.4 for low expressors for loading onto the sensor tips. Diluted supernatants were then captured on an anti-human Fc sensor (Forte Bio). A baseline was established using 1X PBST (50mM Potassium Phosphate Buffer + 150mM NaCl + 0.05% Tween 20) pH 7.4, and the sensor was associated with 50 nM of LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST pH 7.4 for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor was exposed to 1X PBST pH 7.4 for 300-600 sec. Baseline, association, and dissociation were

repeated using 1xPBST pH 5.4 throughout in a separate condition. Association and dissociation phase curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (i.e., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC (with no substitutions), and b) reduced dissociation at pH 7.4 (i.e., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Light chain variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to the starting ABPC), as shown in Figure 26 were selected for further analysis (e.g., MYT3370, MYT3371, MYT3373, MYT3374, MYT3376, MYT3381, MYT3382, MYT3387, MYT3389, MYT3392, MYT3393, MYT3394, and MYT3398). It was also noted that some histidine and alanine mutations were tolerated with little (e.g., less than 1-fold change in dissociation constant KD or dissociation rate) or no change in LRRC15 binding kinetics (e.g., MYT3369, MYT3372, MYT3375, MYT3377, MYT3378, MYT3379, MYT3380, MYT3383, MYT3384, MYT3385, MYT3386, MYT3388, MYT3390, MYT3391, MYT3395, MYT3396, and MYT3397).

Especially because histidine is a large, positively charged amino acid, these variants with no change were noted as positions in the light chain that may tolerate a wide range of mutations and lead to antibodies with different sequence but similar binding properties, a designation that is not otherwise apparent.

Example 18. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Gish K et al. "Anti-huLRRC15 Antibody Drug Conjugates and Methods for their Use" US Patent 10,195,209 B2 (2019)). We selected huAD208.4.1 (Heavy chain SEQ ID NO: 178, Light chain SEQ ID NO: 179) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the heavy chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-

dependent sequence variants, individual amino acid mutations within the heavy chain CDRs that had been previously selected for further analysis in Example 16 were systematically combined two or more at a time (MYT4385 - MYT4388). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with two or more histidine or alanine mutations in the heavy chain CDRs were generated by co-transfection of Expi293 cells with a) one heavy chain combinations sequence variant, and b) the corresponding starting ABPC light chain using methods known to the art. After allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 28), and the pH dependence of the variant was evaluated using biolayer interferometry (BLI) on an Octet RED 96e instrument. Briefly, cell culture supernatants were diluted based on qualitative expression level of the variant determined by visual examination of SDS-PAGE gels, 5 µL of cell culture supernatant was diluted into 195 µL of 1x PBST, pH 7.4 for high expressors, 25 µL of cell culture supernatant was diluted into 175 µL of 1x PBST, pH 7.4 for medium expressors and 100 µL of cell culture supernatant was diluted into 100 µL of 1x PBST, pH 7.4 for low expressors for loading onto the sensor tips. Diluted supernatants were then captured on an anti-human Fc sensor (Forte Bio). A baseline was established using 1X PBST (50mM Potassium Phosphate Buffer + 150mM NaCl + 0.05% Tween 20) pH 7.4, and the sensor was associated with 50 nM of LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST pH 7.4 for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor was exposed to 1X PBST pH 7.4 for 300-600 sec. Baseline, association, and dissociation were repeated using 1xPBST pH 5.4 throughout in a separate condition. Association and dissociation phase curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (i.e., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC (with no substitutions), and b) reduced dissociation at pH 7.4 (i.e., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Heavy chain combinations variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to the starting ABPC), as shown in Figure 29 were selected for further analysis (e.g., MYT4385, MYT4386, MYT4387, MYT4388).

Example 19. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Gish K et al. "Anti-huLRRC15 Antibody Drug Conjugates and Methods for their Use" US Patent 10,195,209 B2 (2019)). We selected huAD208.4.1 (Heavy chain SEQ ID NO: 178, Light chain SEQ ID NO: 179) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the light chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-dependent sequence variants, individual amino acid mutations within the light chain CDRs that had been previously selected for further analysis in Example 17 were systematically combined two or more at a time (MYT4390 - MYT4399). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with two or more histidine or alanine mutations in the light chain CDRs were generated by co-transfection of Expi293 cells with a) one light chain combinations sequence variant, and b) the corresponding starting ABPC heavy chain using methods known to the art. After allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 31), and the pH dependence of the variant was evaluated using biolayer interferometry (BLI) on an Octet RED 96e instrument. Briefly, cell culture supernatants were diluted based on qualitative expression level of the variant determined by visual examination of SDS-PAGE gels, 5 µL of cell culture supernatant was diluted into 195 µL of 1x PBST, pH 7.4 for high expressors, 25 µL of cell culture supernatant was diluted into 175 µL of 1x PBST, pH 7.4 for medium expressors and 100 µL of cell culture supernatant was diluted into 100 µL of 1x PBST, pH 7.4 for low expressors for loading onto the sensor tips. Diluted supernatants were then captured on an anti-human Fc sensor (Forte Bio). A baseline was established using 1X PBST (50 mM Potassium Phosphate Buffer + 150 mM NaCl + 0.05% Tween 20), pH 7.4, and the sensor was associated with 50nM LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST, pH 7.4, for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor was exposed to 1X PBST, pH

7.4, for 300-600 sec. Baseline, association, and dissociation were repeated using 1xPBST, pH 5.4, throughout in a separate condition. Association and dissociation phase curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (e.g., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC (with no substitutions), and b) reduced dissociation at pH 7.4 (e.g., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Light chain combinations variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to the starting ABPC), as shown in Figure 32 were selected for further analysis (e.g., MYT4391, MYT4392, MYT4396, MYT4397, MYT4398, and MYT4399).

Example 20. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Gish K et al. "Anti-huLRRC15 Antibody Drug Conjugates and Methods for their Use" US Patent 10,195,209 B2 (2019)). We selected huAD208.12.1 (Heavy chain SEQ ID NO: 272, Light chain SEQ ID NO: 273) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the heavy chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-dependent sequence variants, individual amino acid residues within the heavy chain CDRs were systematically substituted with a histidine, one at a time (MYT4090 - MYT4133). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with only one histidine or alanine mutation in a heavy chain CDR were generated by co-transfection of Expi293 cells with a) one heavy chain sequence variant, and b) the corresponding starting ABPC light chain using methods known to the art. After allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 34), and the pH dependence of the variant was evaluated using biolayer interferometry

(BLI) on an Octet RED 96e instrument. Briefly, cell culture supernatants were diluted based on qualitative expression level of the variant determined by visual examination of SDS-PAGE gels, 5 µL of cell culture supernatant was diluted into 195 µL of 1x PBST, pH 7.4 for high expressors, 25 µL of cell culture supernatant was diluted into 175 µL of 1x PBST, pH 7.4 for medium expressors and 100 µL of cell culture supernatant was diluted into 100 µL of 1x PBST, pH 7.4 for low expressors for loading onto the sensor tips. A baseline was established using 1X PBST (50mM Potassium Phosphate Buffer + 150mM NaCl + 0.05% Tween 20) pH 7.4, and the sensor was associated with 50 nM of LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST pH 7.4 for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor was exposed to 1X PBST pH 7.4 or pH 5.4, for 300-600sec. Association and dissociation phase curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (i.e., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC, (with no substitutions), and b) reduced dissociation at pH 7.4 (i.e., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Heavy chain variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to starting ABPC) as shown in Figure 35 were selected for further analysis (e.g., MYT4091, MYT4094, MYT4096, MYT4115, MYT4116, MYT4121, and MYT4131). It was also noted that while some histidine and alanine mutations obliterated LRRC15 binding (e.g., MYT4102, MYT4103, MYT4120, MYT4122, MYT4123, MYT4125, MYT4126, MYT4127, MYT4128, MYT4129, MYT4130, and MYT4132), others were tolerated with little (e.g., less than 1-fold change in dissociation constant KD or dissociation rate) or no change in LRRC15 binding kinetics (e.g., MYT4090, MYT4092, MYT4093, MYT4095, MYT4097, MYT4098, MYT4099, MYT4100, MYT4101, MYT4104, MYT4105, MYT4106, MYT4107, MYT4108, MYT4109, MYT4110, MYT4111, MYT4112, MYT4113, MYT4114, MYT4124, and MYT4133).

Especially because histidine is a large, positively charged amino acid, these variants with no change were noted as positions in the heavy chain that may tolerate a wide range of mutations and lead to antibodies with different sequence but similar binding properties, a designation that is not otherwise apparent.

Example 21. Construction and screening of pH-engineered LRRC15 ABPCs

Multiple LRRC15-binding monoclonal antibodies have been described in the literature and can be used as a template for engineering pH-dependent binding (Gish K et al. "Anti-huLRRC15 Antibody Drug Conjugates and Methods for their Use" US Patent 10,195,209 B2 (2019)). We selected huAD208.12.1 (Heavy chain SEQ ID NO: 272, Light chain SEQ ID NO: 273) as a LRRC15-binding monoclonal antibody for pH engineering via histidine scanning. Briefly, CDRs in the light chain were identified using the methods described by Kabat et al (Kabat et al. (1992) Sequences of Proteins of Immunological Interest, DIANE publishing) and IMGT (Lefranc MP (1999) "The IMGT unique numbering for Immunoglobulins, T cell receptors and Ig-like domains" The Immunologist 7, 132-136), and for each CDR, residues falling under either or both Kabat and IMGT CDR definitions were called as CDR residues. To generate pH-dependent sequence variants, individual amino acid residues within the light chain CDRs were systematically substituted with a histidine, one at a time (MYT4134 - MYT4160). In cases where the starting CDR residue was a histidine, it was mutated to an alanine. Antibody variants with only one histidine or alanine mutation in a light chain CDR were generated by co-transfection of Expi293 cells with a) one light chain sequence variant, and b) the corresponding starting ABPC heavy chain using methods known to the art. After allowing for four days of protein expression, cell culture supernatants were collected, quantified by SDS-PAGE analysis (Figure 37), and the pH dependence of the variant was evaluated using biolayer interferometry (BLI) on an Octet RED 96e instrument. Briefly, cell culture supernatants were diluted based on qualitative expression level of the variant determined by visual examination of SDS-PAGE gels, 5 µL of cell culture supernatant was diluted into 195 µL of 1x PBST, pH 7.4 for high expressors, 25 µL of cell culture supernatant was diluted into 175 µL of 1x PBST, pH 7.4 for medium expressors and 100 µL of cell culture supernatant was diluted into 100 µL of 1x PBST, pH 7.4 for low expressors for loading onto the sensor tips. Diluted supernatants were then captured on an anti-human Fc sensor (Forte Bio). A baseline was established using 1X PBST (50mM Potassium Phosphate Buffer + 150mM NaCl + 0.05% Tween 20) pH 7.4, and the sensor was associated with 50 nM of LRRC15 (Recombinant LRRC-15 heterodimeric mouse Fc fusion, Absolute Antibody Pr00374, Lot No. T1931B03) in 1X PBST pH 7.4 for 120 sec to generate an association curve. In the dissociation phase, the antibody-antigen complex on the sensor was exposed to 1X PBST pH 7.4 or pH 5.4 for 300-600 sec. Association and dissociation phase

curves were examined for the starting ABPC antibody (with no substitutions) and each corresponding antibody variant at pH 5.4 and pH 7.4 to inform on two criteria: a) enhanced dissociation (i.e., higher koff values) at pH 5.4 due to histidine or alanine substitution compared to the starting ABPC (with no substitutions), and b) reduced dissociation at pH 7.4 (i.e., lower koff values) compared to pH 5.4 in the antibody variant itself and with the starting ABPC (with no substitutions). Light chain variants that showed either enhanced dissociation at pH 5.4 or reduced dissociation at pH 7.4 or both (as compared to the starting ABPC), as shown in Figure 38 were selected for further analysis (e.g., MYT4137, MYT4138, MYT4139, MYT4141, MYT4142, MYT4152, MYT4155, and MYT4156). It was also noted that while some histidine and alanine mutations obliterated LRRC15 binding (e.g., MYT4143, MYT4145, MYT4154, MYT4157, MYT4158, MYT4159, and MYT4160), others were tolerated with little (e.g., less than 1-fold change in dissociation constant KD or dissociation rate) or no change in LRRC15 binding kinetics (e.g., MYT4134, MYT4135, MYT4136, MYT4140, MYT4144, MYT4146, MYT4147, MYT4148, MYT4149, MYT4150, MYT4151, and MYT4153).

Especially because histidine is a large, positively charged amino acid, these variants with no change were noted as positions in the light chain that may tolerate a wide range of mutations and lead to antibodies with different sequence but similar binding properties, a designation that is not otherwise apparent.

Example 22. Characterization of binding affinity for anti-LRRC15 mAbs

Binding affinity of selected LRRC15 pH engineered antibody variants from Example 9 were measured on U-87 MG (LRRC15+) cells. 100,000 U-87 MG cells (ATCC HTB-14) were seeded per well in a 96 well deep well plate. Samrotamab and a pH engineered antibody variant were serially diluted at a 1:3 dilution in ice cold FC buffer (phosphate buffered saline (PBS), pH 7.4 + 2mM ethylenediaminetetraacetic acid (EDTA) + 2% (v/v) HI FBS). The plates were spun at 2,000 RPM for 2 minutes, the supernatant was removed, and 100 µL of diluted antibody was added to each well with final concentration ranging from 60 nM to 1 pM and incubated for 2 hours at 4°C. Post incubation, the cells were spun at 2000 rpm for 2 min and supernatant was discarded. Cells were washed twice with 500 µL of ice-cold FC buffer and resuspended with 100 µL of FC buffer. The cells were then transferred from the deep well plate to 96 well round bottom plate, spun at 2000 rpm for 2 min and incubated with 100 µL of 10µg/mL Alexa Fluor

488 conjugated goat anti-human IgG secondary antibody (ThermoFisher Scientific, A11013) for 30 min. Post incubation, cells were washed with FC buffer and resuspended in 100 µL of FC buffer to read on a BD Accuri C6 flow cytometer. Mean fluorescence intensity at each concentration per sample was background subtracted and plotted as shown in Figure 40. Binding affinity was measured as a dissociation constant KD by GraphPad Prism assuming Michaelis-Menten binding kinetics. MYT0971 shows high affinity binding to cell surface LRRC15 on U-87 MG cells in the pM range confirming that variants created through pH engineering can retain functionally appropriate affinities as compared to their corresponding starting ABPCs (e.g., samrotamab). Variants with dissociation constants KD less than 100nM were selected for further analysis.

Example 23. Characterization of cellular internalization and endolysosomal delivery of pH engineered anti-LRRC15 ABPCs

Selected anti-LRRC15 pH engineered antibody variants from Examples 9, 10, 13, 16, 17, 20 and 21 were analyzed for internalization and endolysosomal delivery in U-87 MG cells (LRRC15+). U-87 MG cells (ATCC HTB-14) were collected and resuspended in EMEM medium (ATCC 30-2003) plus 10% GenClone heat inactivated fetal bovine serum (HI FBS) (Genesee Scientific; 25-514H). Cell counts were determined using trypan blue staining and the Countess II FL Automated Cell Counter (Thermofisher; AMQAF1000). Cells were then diluted to 2,000,000 cells/mL and 50µl/well was seeded into 96-well flat bottom cell culture plates (Genesee Scientific; 25-109). Anti-LRRC15 pH engineered antibody variants, starting ABPC antibodies, control IgG1 isotype control (BP0297, Bioxcell), and vehicle control were diluted in native culture media, and then mixed 1:1 with a 3x molar ratio Zenon pHrodo iFL Human IgG Labeling Reagent (ThermoFisher; Z25611). The mixture was incubated for 20 minutes at room temperature, followed by a 1:1 addition of cells for a final volume of 100 µL. The mixture of cells, anti-LRRC15 antibody variants, and Zenon pHrodo iFL Human IgG Labeling Reagent was incubated at 37 °C, 5% CO2 for 24 hours. Following incubation, 100 µL of ice cold Flow Cytometry (FC) buffer (phosphate buffered saline (PBS), pH 7.4 + 2mM ethylenediaminetetraacetic acid (EDTA) + 2% (v/v) HI FBS is added to each well. Cells were then spun down at 4°C for 2 min at 2000 rpm, washed with 200 µL ice cold FC buffer and resuspended in 100 µL ice cold FC buffer. Mean green fluorescence intensity was detected using

a BD Accuri C6 flow cytometer. Data was analyzed using Flowjo analysis software. pHrodo green is a pH sensitive dye that fluoresces in the low pH environment of the endosomes and lysosomes and therefore can be used to quantify antibody internalization and endolysosomal delivery. Internalization and endolysosomal delivery of anti-LRRC15 starting ABPC's and variants at 25nM in U-87 MG (LRRC15+) cells is shown in Figure 41 as measured by pHrodo green mean fluorescence intensity. Several pH engineered anti-LRRC15 antibody variants showed increased mean fluorescence intensity relative to their corresponding starting ABPC antibodies demonstrating that increased dissociation at lower pH leads to enhanced internalization and endolysosomal delivery inside cells as shown by increased fluorescence or increased fluorescence as compared to IgG1 isotype control. Increased endolysosomal delivery is quantitated for each pH engineered anti-LRRC15 antibody variant on the top of each bar as a ratio of: the variant's mean fluorescence intensity minus the mean fluorescence intensity of the IgG control, then all divided by the variant's corresponding starting ABPC's mean fluorescence intensity minus the mean fluorescence intensity of the IgG control. For example MYT0971, MYT0983, MYT0997, and MYT2737, antibody variants of samrotamab, showed increased internalization and endolysosomal delivery relative to samrotamab (MYT0963). For example MYT3310, MYT3315, and MYT3322, antibody variants of hu139.10, showed increased internalization and endolysosomal delivery relative to hu139.10 (MYT3252). For example MYT3336, MYT3370, MYT3376, and MYT3381, antibody variants of huAD208.4.1, showed increased internalization and endolysosomal delivery relative to huAD208.4.1 (MYT3325). For example MYT4095, MYT4099, MYT4115, MYT4133, MYT4137, MYT4140, and MYT4155, antibody variants of huAD208.12.1, showed increased internalization and endolysosomal delivery relative to huAD208.12.1 (MYT3179).

Such pH engineered anti-MET antibody variants with increased mean fluorescence intensity relative to their starting ABPC antibodies were selected for further analysis

Example 24. Thermal stability of anti-LRRC15 mAbs

Protein melting temperature (Tm) was measured through the use of Differential Scanning Flourimetry (DSF). DSF visualizes protein unfolding by measuring the fluorescent signal from the molecule Sypro Orange (Thermo Scientific cat. no. S6650) as a protein unfolds due to heating. As a protein unfolds it exposes more hydrophilic regions to the Sypro Orange dye,

which in turns binds to these hydrophilic regions resulting in increase in signal. The Tm for a protein is calculated as the half-maximal of the unfolding transition and can be visualized by plotting the first derivative of the Sypro Orange signal and finding a local maximum of this derivative plot. 20 µL of protein samples in 1xPBS, pH 7.4, was mixed with 5 µL of 25X Sypro Orange master mix, yielding a final concentration of 5x Sypro Orange. The samples were added to 96-well PCR plates (Thermo Scientific Cat. No. AB-2400/W) and sealed with optical covers (Thermo Scientific Cat. No. 4360954). The PCR plate was inserted into a real-time PCR machine (Thermo Scientific Quant Studio 3) and the plate temperature was stabilized for 3 minutes at 25 °C before ramping to 95 °C by 0.2 °C increments, stabilizing for 1 second before the Sypro Orange signal was measured. The melting temperature (Tm) values for select anti-LRRC15 starting ABPC and variant from Example 9 are shown in Figure 42. The variant shows similar melting temperature values to the starting ABPC confirming that variants created through pH engineering can retain functionally appropriate thermal stabilities as compared to their corresponding starting ABPC. Variants that had melting temperatures greater than or equal to the melting temperature of their corresponding starting ABPC (e.g., samrotamab) minus 10 °C and so were selected for further analysis.

The discoveries herein are in contrast to similar engineering on other antigens such as CLEC12a and two other targets wherein multiple variants per target showed enhanced dissociation at low pH, however, despite the favorable pH-dependent binding properties of these variants (which specifically bound CLEC12a and the two other targets), they had less than 10% increase in cell internalization and endolysosomal delivery as compared to the corresponding starting ABPC (e.g., the starting antibody). These variants (which specifically bound CLEC12a and the two other targets) also had similar biophysical characteristics (e.g., antibody expression, thermal stability, affinity at pH 7.4 etc.) to the corresponding starting ABPC (e.g., the starting antibody) confirming that this was not specific to the biophysical properties of the tested variant (i.e. the biophysical properties unrelated to enhanced dissociation at pH 5.4).

Example 25. Improvement in selective binding affinity of pH Engineered antibodies

Measurement of the affinity of pH-engineered antibodies specific for LRRC15 is performed by FACS analysis on cell lines with ranges of LRRC15 expression; SAOS-2, U118-MG, G-292. Cell lines selected for this study are obtained from commercial sources and cultured

using manufacturer recommended conditions. All cell lines are cultured upon receipt, expanded and cryopreserved at a similar passage number for use in the affinity experiments. Briefly, 1.0x10^5 cells that express LRRC15 are plated per well in a 96-well plate in 100 µL media. The cells are washed two times with 200 µL of FACS buffer (1x PBS containing 3% Fetal Bovine Serum) at pH 7.4. The purified protein samples are diluted into FACS buffer at pH 7.4, for a titration from 100 nM to 1 pM, and added to the cells and allowed to bind for 2 hours on ice. After incubation with the primary antibodies, cells are washed twice as before, and then 100 µl of secondary goat anti-Human AF488 (IgG Cross-Adsorbed polyclonal secondary antibody), diluted 1:200, is added in FACS buffer pH 7.4, and incubated for 1 hour on ice. The plates are washed twice. Binding is read on a flow cytometer (Accuri C6, BD Biosciences). Binding is observed as a shift in the FLl signal (as a mean fluorescence intensity) versus secondary alone.

Parent antibodies binding to SAOS-2 cells, expressing high levels of LRRC15, and G-292 cells, expressing lower levels of LRRC15 (e.g., lower levels than SAOS-2 cells), showed similar affinity. Select pH-engineered antibodies specific for LRRC15 may bind more strongly to target cells with higher LRRC15 expression levels, SAOS-2, than to target cells with lower LRRC15 expression, G-292 cells. The pH engineered antibody constructs may therefore be differentiated from the parent compounds in their avidity, which may be expected to translate to increased selectivity to high expressing target cells in the treatment of LRRC15 overexpressing malignancies, with reduced binding to normal tissues for the selected antibodies.

Example 26. Increased half-life of pH-engineered ADCs specific for LRRC15 as compared to a control ADCs specific for LRRC15 in non-tumor bearing animals

Another aspect of the pH-engineered ADCs specific for LRRC15 described herein can be their ability to facilitate increased serum half-life relative to control antibody ADCs specific for LRRC15 in non-tumor bearing animals. To demonstrate these properties, a series of animal studies in cynomolgus monkeys is performed using pH-engineered ADC specific for LRRC15 and control antibody ADC specific for LRRC15 using methods known to the art (e.g., Gupta, P., et al. (2016), mAbs, 8:5, 991-997). Female monkeys (3 per test article) are administered a bolus of either pH-engineered ADC specific for LRRC15 or control antibody ADC specific for LRRC15 at a dose of 2 to 5 mg/kg via saphenous vein injection. Alternatively, several different doses of LRRC15-binding protein are administered across a group of several monkeys. Blood

samples are collected via the peripheral vein or femoral vein at the following time points: pre-dose, 15 minutes, 12 hours, 2 days, 3 days, 4 days, 7 days, 10 days, 14 days, 17 days, 21 days and 28 days post-dose. Blood samples are analyzed for the presence of either pH-engineered ADC specific for LRRC15 or control antibody ADC specific for LRRC15 using methods known to the art (e.g., ELISA).

Antibody concentrations of pH-engineered ADC specific for LRRC15 and control antibody ADC specific for LRRC15 are plotted as a function of time. Upon analysis of the data, it can be observed that the pH-engineered ADC specific for LRRC15 has a significantly longer serum half-life relative to control antibody ADC specific for LRRC15, thereby demonstrating the improved serum stability and exposure profile.

OTHER EMBODIMENTS

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

SEQUENCE APPENDIX

>Heavy Chain of samrotamab IgG (SEQ ID NO: 1)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL VTVSS

>Light Chain of samrotamab IgG (SEQ ID NO: 2)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Heavy Chain CDR1 of samrotamab (SEQ ID NO: 3)

GYKFSSYWIE

>Heavy Chain CDR2 of samrotamab (SEQ ID NO: 4)

EILPGSDTTNYNEKFKD

>Heavy Chain CDR3 of samrotamab (SEQ ID NO: 5)

ARDRGNYRAWFGY

>Light Chain CDR1 of samrotamab (SEQ ID NO: 6)

RASQDISNYLN

>Light Chain CDR2 of samrotamab (SEQ ID NO: 7)

YTSRLHS

>Light Chain CDR3 of samrotamab (SEQ ID NO: 8)

QQGEALPWT

>Mature Human LRRC15 (SEQ ID NO: 9)

MPLKHYLLLLVGCQAWGAGLAYHGCPSECTCSRASQVECTGARIVAVPTPLPWNAMSL
QILNTHITELNESPFLNISALIALRIEKNELSRITPGAFRNLGSLRYLSLANNKLQVLPIGLF
QGLDSLESLLLSSNQLLQIQPAHFSQCSNLKELQLHGNHLEYIPDGAFDHLVGLTKLNLG
KNSLTHISPRVFQHLGNLQVLRLYENRLTDIPMGTFDGLVNLQELALQQNQIGLLSPGLF
HNNHNLQRLYLSNNHISQLPPSVFMQLPQLNRLTLFGNSLKELSPGIFGPMPNLRELWLY
DNHISSLPDNVFSNLRQLQVLILSRNQISFISPGAFNGLTELRELSLHTNALQDLDGNVFR
MLANLQNISLQNNRLRQLPGNIFANVNGLMAIQLQNNQLENLPLGIFDHLGKLCELRLY
DNPWRCDSDILPLRNWLLLNQPRLGTDTVPVCFSPANVRGQSLIIINVNVAVPSVHVPEV
PSYPETPWYPDTPSYPDTTSVSSTTELTSPVEDYTDLTTIQVTDDRSVWGMTQAQSGLAI
AAIVIGIVALACSLAACVGCCCCKKRSQAVLMQMKAPNEC

>cDNA Encoding Mature Human LRRC15 (SEQ ID NO: 10)

ATGCCACTGAAGCATTATCTCCTTTTGCTGGTGGGCTGCCAAGCCTGGGGTGCAGGG
TTGGCCTACCATGGCTGCCCTAGCGAGTGTACCTGCTCCAGGGCCTCCCAGGTGGAG
TGCACCGGGGCACGCATTGTGGCAGTGCCCACCCCTCTGCCCTGGAACGCCATGAGC
CTGCAGATCCTCAACACGCACATCACTGAACTCAATGAGTCCCCGTTCCTCAATATC
TCAGCCCTCATCGCCCTGAGGATTGAGAAGAATGAGCTGTCGCGCATCACGCCTGG
GGCCTTCCGAAACCTGGGCTCGCTGCGCTATCTCAGCCTCGCCAACAACAAGCTGCA
GGTTCTGCCCATCGGCCTCTTCCAGGGCCTGGACAGCCTCGAGTCTCTCCTTCTGTCC
AGTAACCAGCTGTTGCAGATCCAGCCGGCCCACTTCTCCCAGTGCAGCAACCTCAAG
GAGCTGCAGTTGCACGGCAACCACCTGGAATACATCCCTGACGGAGCCTTCGACCA
CCTGGTAGGACTCACGAAGCTCAATCTGGGCAAGAATAGCCTCACCCACATCTCACC
CAGGGTCTTCCAGCACCTGGGCAACCTCCAGGTCCTCCGGCTGTATGAGAACAGGCT

CACGGATATCCCCATGGGCACTTTTGATGGGCTTGTTAACCTGCAGGAACTGGCTCT
GCAGCAGAACCAGATTGGACTGCTCTCCCCTGGTCTCTTCCACAACAACCACAACCT
CCAGAGACTCTACCTGTCCAACAACCACATCTCCCAGCTGCCACCCAGCGTCTTCAT
GCAGCTGCCCCAGCTCAACCGTCTTACTCTCTTTGGGAATTCCCTGAAGGAGCTCTC
TCCGGGGATCTTCGGGCCCATGCCCAACCTGCGGGAGCTTTGGCTCTATGACAACCA
CATCTCTTCTCTACCCGACAATGTCTTCAGCAACCTCCGCCAGTTGCAGGTCCTGATT
CTTAGCCGCAATCAGATCAGCTTCATCTCCCCGGGTGCCTTCAACGGGCTAACGGAG
CTTCGGGAGCTGTCCCTCCACACCAACGCACTGCAGGACCTGGACGGGAACGTCTTC
CGCATGTTGGCCAACCTGCAGAACATCTCCCTGCAGAACAACCGCCTCAGACAGCTC
CCAGGGAATATCTTCGCCAACGTCAATGGCCTCATGGCCATCCAGCTGCAGAACAA
CCAGCTGGAGAACTTGCCCCTCGGCATCTTCGATCACCTGGGGAAACTGTGTGAGCT
GCGGCTGTATGACAATCCCTGGAGGTGTGACTCAGACATCCTTCCGCTCCGCAACTG
GCTCCTGCTCAACCAGCCTAGGTTAGGGACGGACACTGTACCTGTGTGTTTCAGCCC
AGCCAATGTCCGAGGCCAGTCCCTCATTATCATCAATGTCAACGTTGCTGTTCCAAG
CGTCCATGTCCCCGAGGTGCCTAGTTACCCAGAAACACCATGGTACCCAGACACACC
CAGTTACCCTGACACCACATCCGTCTCTTCTACCACTGAGCTAACCAGCCCTGTGGA
AGACTACACTGATCTGACTACCATTCAGGTCACTGATGACCGCAGCGTTTGGGGCAT
GACCCAGGCCCAGAGCGGGCTGGCCATTGCCGCCATTGTAATTGGCATTGTCGCCCT
GGCCTGCTCCCTGGCTGCCTGCGTCGGCTGTTGCTGCTGCAAGAAGAGGAGCCAAGC
TGTCCTGATGCAGATGAAGGCACCCAATGAGTGT

>Extracellular Domain of LRRC15 (SEQ ID NO: 11)

YHGCPSECTCSRASQVECTGARIVAVPTPLPWNAMSLQILNTHITELNESPFLNISALIAL
RIEKNELSRITPGAFRNLGSLRYLSLANNKLQVLPIGLFQGLDSLESLLLSSNQLLQIQPAH
FSQCSNLKELQLHGNHLEYIPDGAFDHLVGLTKLNLGKNSLTHISPRVFQHLGNLQVLRL
YENRLTDIPMGTFDGLVNLQELALQQNQIGLLSPGLFHNNHNLQRLYLSNNHISQLPPSV
FMQLPQLNRLTLFGNSLKELSPGIFGPMPNLRELWLYDNHISSLPDNVFSNLRQLQVLILS
RNQISFISPGAFNGLTELRELSLHTNALQDLDGNVFRMLANLQNISLQNNRLRQLPGNIF
ANVNGLMAIQLQNNQLENLPLGIFDHLGKLCELRLYDNPWRCDSDILPLRNWLLLNQPR
LGTDTVPVCFSPANVRGQSLIIINVNVAVPSVHVPEVPSYPETPWYPDTPSYPDTTSVSST
TELTSPVEDYTDLTTIQVTDDRSVWGMTQAQSG

>cDNA Encoding Extracellular Domain of LRRC15 (SEQ ID NO: 12)

TACCATGGCTGCCCTAGCGAGTGTACCTGCTCCAGGGCCTCCCAGGTGGAGTGCACC
GGGGCACGCATTGTGGCAGTGCCCACCCCTCTGCCCTGGAACGCCATGAGCCTGCA
GATCCTCAACACGCACATCACTGAACTCAATGAGTCCCCGTTCCTCAATATCTCAGC
CCTCATCGCCCTGAGGATTGAGAAGAATGAGCTGTCGCGCATCACGCCTGGGGCCTT
CCGAAACCTGGGCTCGCTGCGCTATCTCAGCCTCGCCAACAACAAGCTGCAGGTTCT
GCCCATCGGCCTCTTCCAGGGCCTGGACAGCCTCGAGTCTCTCCTTCTGTCCAGTAA
CCAGCTGTTGCAGATCCAGCCGGCCCACTTCTCCCAGTGCAGCAACCTCAAGGAGCT
GCAGTTGCACGGCAACCACCTGGAATACATCCCTGACGGAGCCTTCGACCACCTGGT
AGGACTCACGAAGCTCAATCTGGGCAAGAATAGCCTCACCCACATCTCACCCAGGG
TCTTCCAGCACCTGGGCAACCTCCAGGTCCTCCGGCTGTATGAGAACAGGCTCACGG
ATATCCCCATGGGCACTTTTGATGGGCTTGTTAACCTGCAGGAACTGGCTCTGCAGC
AGAACCAGATTGGACTGCTCTCCCCTGGTCTCTTCCACAACAACCACAACCTCCAGA
GACTCTACCTGTCCAACAACCACATCTCCCAGCTGCCACCCAGCGTCTTCATGCAGC
TGCCCCAGCTCAACCGTCTTACTCTCTTTGGGAATTCCCTGAAGGAGCTCTCTCCGG
GGATCTTCGGGCCCATGCCCAACCTGCGGGAGCTTTGGCTCTATGACAACCACATCT
CTTCTCTACCCGACAATGTCTTCAGCAACCTCCGCCAGTTGCAGGTCCTGATTCTTAG
CCGCAATCAGATCAGCTTCATCTCCCCGGGTGCCTTCAACGGGCTAACGGAGCTTCG
GGAGCTGTCCCTCCACACCAACGCACTGCAGGACCTGGACGGGAACGTCTTCCGCA
TGTTGGCCAACCTGCAGAACATCTCCCTGCAGAACAACCGCCTCAGACAGCTCCCAG
GGAATATCTTCGCCAACGTCAATGGCCTCATGGCCATCCAGCTGCAGAACAACCAG
CTGGAGAACTTGCCCCTCGGCATCTTCGATCACCTGGGGAAACTGTGTGAGCTGCGG
CTGTATGACAATCCCTGGAGGTGTGACTCAGACATCCTTCCGCTCCGCAACTGGCTC
CTGCTCAACCAGCCTAGGTTAGGGACGGACACTGTACCTGTGTGTTTCAGCCCAGCC
AATGTCCGAGGCCAGTCCCTCATTATCATCAATGTCAACGTTGCTGTTCCAAGCGTC
CATGTCCCCGAGGTGCCTAGTTACCCAGAAACACCATGGTACCCAGACACACCCAG
TTACCCTGACACCACATCCGTCTCTTCTACCACTGAGCTAACCAGCCCTGTGGAAGA
CTACACTGATCTGACTACCATTCAGGTCACTGATGACCGCAGCGTTTGGGGCATGAC
CCAGGCCCAGAGCGGG

>Heavy Chain of samrotamab IgG histidine scanning variant #1 (SEQ ID NO: 13)

EVQLVQSGAEVKKPGASVKVSCKASHYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #2 (SEQ ID NO: 14)

EVQLVQSGAEVKKPGASVKVSCKASGHKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #3 (SEQ ID NO: 15)

EVQLVQSGAEVKKPGASVKVSCKASGYHFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #4 (SEQ ID NO: 16)

EVQLVQSGAEVKKPGASVKVSCKASGYKHSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #5 (SEQ ID NO: 17)

EVQLVQSGAEVKKPGASVKVSCKASGYKFHSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #6 (SEQ ID NO: 18)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSHYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #7 (SEQ ID NO: 19)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSHWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #8 (SEQ ID NO: 20)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYHIEWVKQAPGQGLEWIGEILPGSDTTN
YNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTLV
TVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #9 (SEQ ID NO: 21)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWHEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #10 (SEQ ID NO: 22)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIHWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #11 (SEQ ID NO: 23)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGHILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #12 (SEQ ID NO: 24)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEHLPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #13 (SEQ ID NO: 25)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEIHPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #14 (SEQ ID NO: 26)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILHGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #15 (SEQ ID NO: 27)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPHSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #16 (SEQ ID NO: 28)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGHDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #17 (SEQ ID NO: 29)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSHTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #18 (SEQ ID NO: 30)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDHT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #19 (SEQ ID NO: 31)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTH
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #20 (SEQ ID NO: 32)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
HYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #21 (SEQ ID NO: 33)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NHNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #22 (SEQ ID NO: 34)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYHEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #23 (SEQ ID NO: 35)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNHKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #24 (SEQ ID NO: 36)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEHFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #25 (SEQ ID NO: 37)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKHKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #26 (SEQ ID NO: 38)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFHDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #27 (SEQ ID NO: 39)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKHRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #28 (SEQ ID NO: 40)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCHRDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #29 (SEQ ID NO: 41)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCAHDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #30 (SEQ ID NO: 42)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARHRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #31 (SEQ ID NO: 43)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDHGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #32 (SEQ ID NO: 44)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRHNYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #33 (SEQ ID NO: 45)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGHYRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #34 (SEQ ID NO: 46)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNHRAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #35 (SEQ ID NO: 47)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYHAWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #36 (SEQ ID NO: 48)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRHWFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #37 (SEQ ID NO: 49)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAHFGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #38 (SEQ ID NO: 50)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWHGYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #39 (SEQ ID NO: 51)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFHYWGQGTL
VTVSS

>Heavy Chain of samrotamab IgG histidine scanning variant #40 (SEQ ID NO: 52)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGHWGQGTL
VTVSS

>Light Chain of samrotamab IgG histidine scanning variant #1 (SEQ ID NO: 53)

DIQMTQSPSSLSASVGDRVTITCHASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #2 (SEQ ID NO: 54)

DIQMTQSPSSLSASVGDRVTITCRHSQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #3 (SEQ ID NO: 55)

DIQMTQSPSSLSASVGDRVTITCRAHQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #4 (SEQ ID NO: 56)

DIQMTQSPSSLSASVGDRVTITCRASHDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #5 (SEQ ID NO: 57)

DIQMTQSPSSLSASVGDRVTITCRASQHISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #6 (SEQ ID NO: 58)

DIQMTQSPSSLSASVGDRVTITCRASQDHSNYLNWYQQKPGGAVKFLIYYTSRLHSGVP
SRFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #7 (SEQ ID NO: 59)

DIQMTQSPSSLSASVGDRVTITCRASQDIHNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #8 (SEQ ID NO: 60)

DIQMTQSPSSLSASVGDRVTITCRASQDISHYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #9 (SEQ ID NO: 61)

DIQMTQSPSSLSASVGDRVTITCRASQDISNHLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #10 (SEQ ID NO: 62)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYHNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #11 (SEQ ID NO: 63)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLHWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #12 (SEQ ID NO: 64)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYHTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #13 (SEQ ID NO: 65)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYHSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #14 (SEQ ID NO: 66)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTHRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #15 (SEQ ID NO: 67)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSHLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #16 (SEQ ID NO: 68)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRHHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #17 (SEQ ID NO: 69)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLASGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #18 (SEQ ID NO: 70)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHHGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #19 (SEQ ID NO: 71)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCHQGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #20 (SEQ ID NO: 72)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQHGEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #21 (SEQ ID NO: 73)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQHEALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #22 (SEQ ID NO: 74)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGHALPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #23 (SEQ ID NO: 75)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEHLPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #24 (SEQ ID NO: 76)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEAHPWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #25 (SEQ ID NO: 77)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALHWTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #26 (SEQ ID NO: 78)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPHTFGGGTKVEIK

>Light Chain of samrotamab IgG histidine scanning variant #27 (SEQ ID NO: 79)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWHFGGGTKVEIK

>Heavy Chain Combinations of samrotamab IgG histidine scanning variant #1 (SEQ ID NO: 80)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWHEWVKQAPGQGLEWIGEILPGSDTT
HYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSS

>Heavy Chain Combinations of samrotamab IgG histidine scanning variant #2 (SEQ ID NO: 81)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWHEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNHRAWFGYWGQGTL
VTVSS

>Heavy Chain Combinations of samrotamab IgG histidine scanning variant #3 (SEQ ID NO: 82)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
HYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNHRAWFGYWGQGTL
VTVSS

>Heavy Chain Combinations of samrotamab IgG histidine scanning variant #4 (SEQ ID NO: 83)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWHEWVKQAPGQGLEWIGEILPGSDTT
HYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNHRAWFGYWGQGTL
VTVSS

>Heavy Chain of hu139.10 IgG (SEQ ID NO: 84)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Light Chain of hu139.10 IgG (SEQ ID NO: 85)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Heavy Chain CDR1 of hu139.10 (SEQ ID NO: 86)

GFSLTSYGVH

>Heavy Chain CDR2 of hu139.10 (SEQ ID NO: 87)

VIWAGGSTNYNSALMS

>Heavy Chain CDR3 of hu139.10 (SEQ ID NO: 88)

ATHMITEDYYGMDY

>Light Chain CDR1 of hu139.10 (SEQ ID NO: 89)

KSSQSLLNSRTRKNYLA

>Light Chain CDR2 of hu139.10 (SEQ ID NO: 90)

WASTRES

>Light Chain CDR3 of hu139.10 (SEQ ID NO: 91)

KQSYNLPT

>Heavy Chain of hu139.10 IgG histidine scanning variant #1 (SEQ ID NO: 92)

EVQLVESGGGLVQPGGSLRLSCAVSHFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #2 (SEQ ID NO: 93)

EVQLVESGGGLVQPGGSLRLSCAVSGHSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #3 (SEQ ID NO: 94)

EVQLVESGGGLVQPGGSLRLSCAVSGFHLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #4 (SEQ ID NO: 95)

EVQLVESGGGLVQPGGSLRLSCAVSGFSHTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #5 (SEQ ID NO: 96)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLHSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #6 (SEQ ID NO: 97)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTHYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #7 (SEQ ID NO: 98)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSHGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #8 (SEQ ID NO: 99)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYHVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #9 (SEQ ID NO: 100)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGHHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #10 (SEQ ID NO: 101)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVAWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #11 (SEQ ID NO: 102)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGHIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #12 (SEQ ID NO: 103)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVHWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #13 (SEQ ID NO: 104)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIHAGGSTN
YNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQGTT
VTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #14 (SEQ ID NO: 105)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWHGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #15 (SEQ ID NO: 106)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAHGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #16 (SEQ ID NO: 107)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGHST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #17 (SEQ ID NO: 108)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGHT
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #18 (SEQ ID NO: 109)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGSH
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #19 (SEQ ID NO: 110)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
HYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #20 (SEQ ID NO: 111)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NHNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #21 (SEQ ID NO: 112)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYHSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #22 (SEQ ID NO: 113)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNHALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #23 (SEQ ID NO: 114)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSHLMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #24 (SEQ ID NO: 115)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSAHMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #25 (SEQ ID NO: 116)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALHSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQGT
TVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #26 (SEQ ID NO: 117)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMHRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #27 (SEQ ID NO: 118)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCHTHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #28 (SEQ ID NO: 119)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCAHHMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #29 (SEQ ID NO: 120)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATAMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #30 (SEQ ID NO: 121)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHHITEDYYGMDYWGQGT
TVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #31 (SEQ ID NO: 122)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMHTEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #32 (SEQ ID NO: 123)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMIHEDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #33 (SEQ ID NO: 124)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITHDYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #34 (SEQ ID NO: 125)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEHYYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #35 (SEQ ID NO: 126)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDHYGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #36 (SEQ ID NO: 127)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYHGMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #37 (SEQ ID NO: 128)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYHMDYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #38 (SEQ ID NO: 129)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGHDYWGQGT
TVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #39 (SEQ ID NO: 130)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMHYWGQG
TTVTVSS

>Heavy Chain of hu139.10 IgG histidine scanning variant #40 (SEQ ID NO: 131)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDHWGQG
TTVTVSS

>Light Chain of hu139.10 IgG histidine scanning variant #1 (SEQ ID NO: 132)

DIVMTQSPDSLAVSLGERATINCHSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #2 (SEQ ID NO: 133)

DIVMTQSPDSLAVSLGERATINCKHSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #3 (SEQ ID NO: 134)

DIVMTQSPDSLAVSLGERATINCKSHQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #4 (SEQ ID NO: 135)

DIVMTQSPDSLAVSLGERATINCKSSHSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #5 (SEQ ID NO: 136)

DIVMTQSPDSLAVSLGERATINCKSSQHLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #6 (SEQ ID NO: 137)

DIVMTQSPDSLAVSLGERATINCKSSQSHLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #7 (SEQ ID NO: 138)

DIVMTQSPDSLAVSLGERATINCKSSQSLHNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #8 (SEQ ID NO: 139)

DIVMTQSPDSLAVSLGERATINCKSSQSLLHSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #9 (SEQ ID NO: 140)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNHRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #10 (SEQ ID NO: 141)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSHTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #11 (SEQ ID NO: 142)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRHRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #12 (SEQ ID NO: 143)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTHKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #13 (SEQ ID NO: 144)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRHNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #14 (SEQ ID NO: 145)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKHYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #15 (SEQ ID NO: 146)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNHLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #16 (SEQ ID NO: 147)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYHAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #17 (SEQ ID NO: 148)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLHWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #18 (SEQ ID NO: 149)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYHASTR
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #19 (SEQ ID NO: 150)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWHST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #20 (SEQ ID NO: 151)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAHT
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #21 (SEQ ID NO: 152)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWASH
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #22 (SEQ ID NO: 153)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
HESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #23 (SEQ ID NO: 154)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RHSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #24 (SEQ ID NO: 155)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
REHGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #25 (SEQ ID NO: 156)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCHQSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #26 (SEQ ID NO: 157)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKHSYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #27 (SEQ ID NO: 158)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQHYNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #28 (SEQ ID NO: 159)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSHNLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #29 (SEQ ID NO: 160)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYHLPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #30 (SEQ ID NO: 161)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNHPTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #31 (SEQ ID NO: 162)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLHTFGGGTKVEIK

>Light Chain of hu139.10 IgG histidine scanning variant #32 (SEQ ID NO: 163)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPHFGGGTKVEIK

>Heavy Chain Combinations of hu139.10 IgG histidine scanning variant #1 (SEQ ID NO: 164)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGHT
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATAMITEDYYGMDYWGQG
TTVTVSS

>Heavy Chain Combinations of hu139.10 IgG histidine scanning variant #2 (SEQ ID NO: 165)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGHT
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDHYGMDYWGQG
TTVTVSS

>Heavy Chain Combinations of hu139.10 IgG histidine scanning variant #3 (SEQ ID NO: 166)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATAMITEDHYGMDYWGQG
TTVTVSS

>Heavy Chain Combinations of hu139.10 IgG histidine scanning variant #4 (SEQ ID NO: 167)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGHT
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATAMITEDHYGMDYWGQG
TTVTVSS

>Light Chain Combinations of hu139.10 IgG histidine scanning variant #1 (SEQ ID NO: 168)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLHWYQQKPGQSPKLLIYHASTR
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain Combinations of hu139.10 IgG histidine scanning variant #2 (SEQ ID NO: 169)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLHWYQQKPGQSPKLLIYWAST
RHSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain Combinations of hu139.10 IgG histidine scanning variant #3 (SEQ ID NO: 170)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLHWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNHPTFGGGTKVEIK

>Light Chain Combinations of hu139.10 IgG histidine scanning variant #4 (SEQ ID NO: 171)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYHASTR
HSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain Combinations of hu139.10 IgG histidine scanning variant #5 (SEQ ID NO: 172)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYHASTR
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNHPTFGGGTKVEIK

>Light Chain Combinations of hu139.10 IgG histidine scanning variant #6 (SEQ ID NO: 173)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RHSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNHPTFGGGTKVEIK

>Light Chain Combinations of hu139.10 IgG histidine scanning variant #7 (SEQ ID NO: 174)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLHWYQQKPGQSPKLLIYHASTR
HSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIK

>Light Chain Combinations of hu139.10 IgG histidine scanning variant #8 (SEQ ID NO: 175)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLHWYQQKPGQSPKLLIYHASTR
ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNHPTFGGGTKVEIK

>Light Chain Combinations of hu139.10 IgG histidine scanning variant #9 (SEQ ID NO: 176)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLHWYQQKPGQSPKLLIYWAST
RHSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNHPTFGGGTKVEIK

>Light Chain Combinations of hu139.10 IgG histidine scanning variant #10 (SEQ ID NO: 177)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYHASTR
HSGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNHPTFGGGTKVEIK

>Heavy Chain of huAD208.4.1 IgG (SEQ ID NO: 178)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Light Chain of huAD208.4.1 IgG (SEQ ID NO: 179)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Heavy Chain CDR1 of huAD208.4.1 (SEQ ID NO: 180)

KASGFTFTDYYIH

>Heavy Chain CDR2 of huAD208.4.1 (SEQ ID NO: 181)

LVYPYIGGTNYNQKFKG

>Heavy Chain CDR3 of huAD208.4.1 (SEQ ID NO: 182)

ARGDNKYDAMDY

>Light Chain CDR1 of huAD208.4.1 (SEQ ID NO: 183)

RASQSVSTSSYSYMH

>Light Chain CDR2 of huAD208.4.1 (SEQ ID NO: 184)

YASSLES

>Light Chain CDR3 of huAD208.4.1 (SEQ ID NO: 185)

EQSWEIRT

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #1 (SEQ ID NO: 186)

EVQLVQSGAEVKKPGSSVKVSCHASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #2 (SEQ ID NO: 187)

EVQLVQSGAEVKKPGSSVKVSCKHSGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #3 (SEQ ID NO: 188)

EVQLVQSGAEVKKPGSSVKVSCKAHGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #4 (SEQ ID NO: 189)

EVQLVQSGAEVKKPGSSVKVSCKASHFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #5 (SEQ ID NO: 190)

EVQLVQSGAEVKKPGSSVKVSCKASGHTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #6 (SEQ ID NO: 191)

EVQLVQSGAEVKKPGSSVKVSCKASGFHFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #7 (SEQ ID NO: 192)

EVQLVQSGAEVKKPGSSVKVSCKASGFTHTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #8 (SEQ ID NO: 193)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFHDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #9 (SEQ ID NO: 194)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTHYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #10 (SEQ ID NO: 195)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDHYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #11 (SEQ ID NO: 196)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYHIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #12 (SEQ ID NO: 197)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYHHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #13 (SEQ ID NO: 198)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIAWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #14 (SEQ ID NO: 199)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGHVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #15 (SEQ ID NO: 200)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLHYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #16 (SEQ ID NO: 201)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVHPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #17 (SEQ ID NO: 202)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYHYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #18 (SEQ ID NO: 203)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPHIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #19 (SEQ ID NO: 204)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYHGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #20 (SEQ ID NO: 205)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIHGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #21 (SEQ ID NO: 206)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGHT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #22 (SEQ ID NO: 207)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGH
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #23 (SEQ ID NO: 208)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
HYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #24 (SEQ ID NO: 209)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NHNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #25 (SEQ ID NO: 210)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYHQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #26 (SEQ ID NO: 211)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNHKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #27 (SEQ ID NO: 212)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQHFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #28 (SEQ ID NO: 213)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKHKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #29 (SEQ ID NO: 214)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFHGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #30 (SEQ ID NO: 215)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKHKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #31 (SEQ ID NO: 216)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCHRGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #32 (SEQ ID NO: 217)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCAHGDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #33 (SEQ ID NO: 218)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARHDNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #34 (SEQ ID NO: 219)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGHNKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #35 (SEQ ID NO: 220)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDHKYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #36 (SEQ ID NO: 221)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNHYDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #37 (SEQ ID NO: 222)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKHDAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #38 (SEQ ID NO: 223)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYHAMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #39 (SEQ ID NO: 224)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDHMDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #40 (SEQ ID NO: 225)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAHDYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #41 (SEQ ID NO: 226)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMHYWGQGTT
VTVSS

>Heavy Chain of huAD208.4.1 IgG histidine scanning variant #42 (SEQ ID NO: 227)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDHWGQGTT
VTVSS

>Light Chain of huAD208.4.1 IgG histidine scanning variant #1 (SEQ ID NO: 228)

DIVLTQSPDSLAVSLGERATINCHASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #2 (SEQ ID NO: 229)

DIVLTQSPDSLAVSLGERATINCRHSQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #3 (SEQ ID NO: 230)

DIVLTQSPDSLAVSLGERATINCRAHQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #4 (SEQ ID NO: 231)

DIVLTQSPDSLAVSLGERATINCRASHSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #5 (SEQ ID NO: 232)

DIVLTQSPDSLAVSLGERATINCRASQHVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #6 (SEQ ID NO: 233)

DIVLTQSPDSLAVSLGERATINCRASQSHSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #7 (SEQ ID NO: 234)

DIVLTQSPDSLAVSLGERATINCRASQSVHTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #8 (SEQ ID NO: 235)

DIVLTQSPDSLAVSLGERATINCRASQSVSHSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #9 (SEQ ID NO: 236)

DIVLTQSPDSLAVSLGERATINCRASQSVSTHSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #10 (SEQ ID NO: 237)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSHYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #11 (SEQ ID NO: 238)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSHSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #12 (SEQ ID NO: 239)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYHYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #13 (SEQ ID NO: 240)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSHMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #14 (SEQ ID NO: 241)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYHHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #15 (SEQ ID NO: 242)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMAWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #16 (SEQ ID NO: 243)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKHASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #17 (SEQ ID NO: 244)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYHSSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #18 (SEQ ID NO: 245)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYAHSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #19 (SEQ ID NO: 246)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASHLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #20 (SEQ ID NO: 247)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSHES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #21 (SEQ ID NO: 248)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLHS
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #22 (SEQ ID NO: 249)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLEH
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #23 (SEQ ID NO: 250)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCHQSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #24 (SEQ ID NO: 251)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEHSWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #25 (SEQ ID NO: 252)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQHWEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #26 (SEQ ID NO: 253)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSHEIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #27 (SEQ ID NO: 254)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWHIRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #28 (SEQ ID NO: 255)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEHRTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #29 (SEQ ID NO: 256)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIHTFGGGTKVEIK

>Light Chain of huAD208.4.1 IgG histidine scanning variant #30 (SEQ ID NO: 257)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRHFGGGTKVEIK

>Heavy Chain Combinations of huAD208.4.1 IgG histidine scanning variant #1 (SEQ ID NO: 258)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYHIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKHDAMDYWGQGTT
VTVSS

>Heavy Chain Combinations of huAD208.4.1 IgG histidine scanning variant #2 (SEQ ID NO: 259)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYHIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAHDYWGQGTT
VTVSS

>Heavy Chain Combinations of huAD208.4.1 IgG histidine scanning variant #3 (SEQ ID NO: 260)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKHDAHDYWGQGTT
VTVSS

>Heavy Chain Combinations of huAD208.4.1 IgG histidine scanning variant #4 (SEQ ID NO: 261)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYHIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKHDAHDYWGQGTT
VTVSS

>Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #1 (SEQ ID NO: 262)

DIVLTQSPDSLAVSLGERATINCRHHQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #2 (SEQ ID NO: 263)

DIVLTQSPDSLAVSLGERATINCRHSQSVSHSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #3 (SEQ ID NO: 264)

DIVLTQSPDSLAVSLGERATINCRHSQSVSTSSYSHMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #4 (SEQ ID NO: 265)

DIVLTQSPDSLAVSLGERATINCRAHQSVSHSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #5 (SEQ ID NO: 266)

DIVLTQSPDSLAVSLGERATINCRAHQSVSTSSYSHMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #6 (SEQ ID NO: 267)

DIVLTQSPDSLAVSLGERATINCRASQSVSHSSYSHMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #7 (SEQ ID NO: 268)

DIVLTQSPDSLAVSLGERATINCRHHQSVSHSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #8 (SEQ ID NO: 269)

DIVLTQSPDSLAVSLGERATINCRHHQSVSTSSYSHMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #9 (SEQ ID NO: 270)

DIVLTQSPDSLAVSLGERATINCRHSQSVSHSSYSHMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #10 (SEQ ID NO: 271)

DIVLTQSPDSLAVSLGERATINCRAHQSVSHSSYSHMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIK

>Heavy Chain of huAD208.12.1 IgG (SEQ ID NO: 272)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Light Chain of huAD208.12.1 IgG (SEQ ID NO: 273)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Heavy Chain CDR1 of huAD208.12.1 (SEQ ID NO: 274)

KASGYTFTNYWMH

>Heavy Chain CDR2 of huAD208.12.1 (SEQ ID NO: 275)

MIHPNSGSTKHNEKFRG

>Heavy Chain CDR3 of huAD208.12.1 (SEQ ID NO: 276)

ARSDFGNYRWYFDV

>Light Chain CDR1 of huAD208.12.1 (SEQ ID NO: 277)

RASQSSSNNLH

>Light Chain CDR2 of huAD208.12.1 (SEQ ID NO: 278)

YVSQSIS

>Light Chain CDR3 of huAD208.12.1 (SEQ ID NO: 279)

QQSNSWPFT

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #1 (SEQ ID NO: 280)

EVQLVQSGAEVKKPGSSVKVSCHASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #2 (SEQ ID NO: 281)

EVQLVQSGAEVKKPGSSVKVSCKHSGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #3 (SEQ ID NO: 282)

EVQLVQSGAEVKKPGSSVKVSCKAHGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #4 (SEQ ID NO: 283)

EVQLVQSGAEVKKPGSSVKVSCKASHYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #5 (SEQ ID NO: 284)

EVQLVQSGAEVKKPGSSVKVSCKASGHTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #6 (SEQ ID NO: 285)

EVQLVQSGAEVKKPGSSVKVSCKASGYHFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #7 (SEQ ID NO: 286)

EVQLVQSGAEVKKPGSSVKVSCKASGYTHTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #8 (SEQ ID NO: 287)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFHNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #9 (SEQ ID NO: 288)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTHYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #10 (SEQ ID NO: 289)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNHWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #11 (SEQ ID NO: 290)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYHMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #12 (SEQ ID NO: 291)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWHHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #13 (SEQ ID NO: 292)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMAWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #14 (SEQ ID NO: 293)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGHIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #15 (SEQ ID NO: 294)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMHHPNSG
STKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQ
GTTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #16 (SEQ ID NO: 295)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIAPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #17 (SEQ ID NO: 296)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHHNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #18 (SEQ ID NO: 297)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPHSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #19 (SEQ ID NO: 298)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNHGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #20 (SEQ ID NO: 299)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSHS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #21 (SEQ ID NO: 300)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGH
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #22 (SEQ ID NO: 301)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
HKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #23 (SEQ ID NO: 302)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
THHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #24 (SEQ ID NO: 303)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKANEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #25 (SEQ ID NO: 304)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHHEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #26 (SEQ ID NO: 305)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNHKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #27 (SEQ ID NO: 306)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEHFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #28 (SEQ ID NO: 307)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKHRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #29 (SEQ ID NO: 308)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFHGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #30 (SEQ ID NO: 309)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRHKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #31 (SEQ ID NO: 310)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCHRSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #32 (SEQ ID NO: 311)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCAHSDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #33 (SEQ ID NO: 312)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARHDFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #34 (SEQ ID NO: 313)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSHFGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #35 (SEQ ID NO: 314)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDHGNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #36 (SEQ ID NO: 315)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFHNYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #37 (SEQ ID NO: 316)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGHYRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #38 (SEQ ID NO: 317)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNHRWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #39 (SEQ ID NO: 318)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYHWYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #40 (SEQ ID NO: 319)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRHYFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #41 (SEQ ID NO: 320)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWHFDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #42 (SEQ ID NO: 321)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYHDVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #43 (SEQ ID NO: 322)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFHVWGQG
TTVTVSS

>Heavy Chain of huAD208.12.1 IgG histidine scanning variant #44 (SEQ ID NO: 323)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDHWGQG
TTVTVSS

>Light Chain of huAD208.12.1 IgG histidine scanning variant #1 (SEQ ID NO: 324)

EIVLTQSPATLSLSPGERATLSCHASQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #2 (SEQ ID NO: 325)

EIVLTQSPATLSLSPGERATLSCRHSQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #3 (SEQ ID NO: 326)

EIVLTQSPATLSLSPGERATLSCRAHQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #4 (SEQ ID NO: 327)

EIVLTQSPATLSLSPGERATLSCRASHSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #5 (SEQ ID NO: 328)

EIVLTQSPATLSLSPGERATLSCRASQHSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #6 (SEQ ID NO: 329)

EIVLTQSPATLSLSPGERATLSCRASQSHSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #7 (SEQ ID NO: 330)

EIVLTQSPATLSLSPGERATLSCRASQSSHNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #8 (SEQ ID NO: 331)

EIVLTQSPATLSLSPGERATLSCRASQSSSHNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #9 (SEQ ID NO: 332)

EIVLTQSPATLSLSPGERATLSCRASQSSSNHLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #10 (SEQ ID NO: 333)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNHHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #11 (SEQ ID NO: 334)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLAWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #12 (SEQ ID NO: 335)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKHVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #13 (SEQ ID NO: 336)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYHSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #14 (SEQ ID NO: 337)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVHQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #15 (SEQ ID NO: 338)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSHSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #16 (SEQ ID NO: 339)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQHISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #17 (SEQ ID NO: 340)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSHSGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #18 (SEQ ID NO: 341)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSIHGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #19 (SEQ ID NO: 342)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCHQSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #20 (SEQ ID NO: 343)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQHSNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #21 (SEQ ID NO: 344)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQHNSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #22 (SEQ ID NO: 345)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSHSWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #23 (SEQ ID NO: 346)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNHWPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #24 (SEQ ID NO: 347)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSHPFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #25 (SEQ ID NO: 348)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWHFTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #26 (SEQ ID NO: 349)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPHTFGQGTKLEIK

>Light Chain of huAD208.12.1 IgG histidine scanning variant #27 (SEQ ID NO: 350)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFHFGQGTKLEIK

>Heavy Chain Constant Domain (SEQ ID NO: 351)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Heavy Chain Constant Domain (SEQ ID NO: 352)

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPELLGG
PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY
NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
DELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Light Chain Constant Domain (SEQ ID NO: 353)

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQ
DSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC**

>Heavy Chain of samrotamab IgG + LS mutation (SEQ ID NO: 354)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPG**

>Heavy Chain of samrotamab IgG + YTE mutation (SEQ ID NO: 355)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Heavy Chain of samrotamab IgG + A118C (SEQ ID NO: 356)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Heavy Chain of samrotamab IgG + A118C + LS mutation (SEQ ID NO: 357)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPG**

>Heavy Chain of samrotamab IgG + A118C + YTE (SEQ ID NO: 358)

EVQLVQSGAEVKKPGASVKVSCKASGYKFSSYWIEWVKQAPGQGLEWIGEILPGSDTT
NYNEKFKDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTL
VTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Light Chain of samrotamab IgG + V205C (SEQ ID NO: 359)

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPS
RFSGSGSGTDYTLTISSLQPEDFATYFCQQGEALPWTFGGGTKVEIKRTVAAPSVFIFPPS

DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL
TLSKADYEKHKVYACEVTHQGLSSPCTKSFNRGEC**

>Heavy Chain of hu139.10 IgG + LS Mutation (SEQ ID NO: 360)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPG**

>Heavy Chain of hu139.10 IgG + YTE Mutation (SEQ ID NO: 361)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Heavy Chain of hu139.10 IgG + A118C Mutation (SEQ ID NO: 362)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ

VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Heavy Chain of hu139.10 IgG + A118C + LS Mutation (SEQ ID NO: 363)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPG**

>Heavy Chain of hu139.10 IgG + A118C + YTE Mutation (SEQ ID NO: 364)

EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQATGKGLEWLGVIWAGGST
NYNSALMSRLTISKENAKSSVYLQMNSLRAGDTAMYYCATHMITEDYYGMDYWGQG
TTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Light Chain of hy139.10 IgG + V205 (SEQ ID NO: 365)

DIVMTQSPDSLAVSLGERATINCKSSQSLLNSRTRKNYLAWYQQKPGQSPKLLIYWAST
RESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCKQSYNLPTFGGGTKVEIKRTVAAPS
VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTY
SLSSTLTLSKADYEKHKVYACEVTHQGLSSPCTKSFNRGEC**

>Heavy Chain of huAD208.4.1 IgG + LS Mutation (SEQ ID NO: 366)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPG**

>Heavy Chain of huAD208.4.1 IgG + YTE Mutation (SEQ ID NO: 367)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Heavy Chain of huAD208.4.1 IgG + A118C Mutation (SEQ ID NO: 368)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Heavy Chain of huAD208.4.1 IgG + A118C + LS Mutation (SEQ ID NO: 369)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPG**

>Heavy Chain of huAD208.4.1 IgG + A118C + YTE Mutation (SEQ ID NO: 370)

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGT
NYNQKFKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTT
VTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
ELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Light Chain of huAD208.4.1 IgG + V205C (SEQ ID NO: 371)

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLES
GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCEQSWEIRTFGGGTKVEIKRTVAAPSVFIF

PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS
TLTLSKADYEKHKVYACEVTHQGLSSPCTKSFNRGEC**

>Heavy Chain of huAD208.12.1 IgG + LS Mutation (SEQ ID NO: 372)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPG**

>Heavy Chain of huAD208.12.1 IgG + YTE Mutation (SEQ ID NO: 373)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Heavy Chain of huAD208.12.1 IgG + A118C Mutation (SEQ ID NO: 374)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Heavy Chain variable domain of huAD208.12.1 IgG + A118C Mutation + LS Mutation (SEQ ID NO: 375)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
SKLTVDKSRWQQGNVFSCSVLHEALHSHYTQKSLSLSPG**

>Heavy Chain variable domain of huAD208.12.1 IgG + A118C Mutation + YTE Mutation (SEQ ID NO: 376)

EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQAPGQGLEWIGMIHPNSGS
TKHNEKFRGKATLTVDESTTTAYMELSSLRSEDTAVYYCARSDFGNYRWYFDVWGQG
TTVTVSSCSTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF
PAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP
APELLGGPSVFLFPPKPKDTLYITREPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFL
YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG**

>Light Chain of huAD208.12.1 IgG + V205C (SEQ ID NO: 377)

EIVLTQSPATLSLSPGERATLSCRASQSSSNNLHWYQQKPGQAPRVLIKYVSQSISGIPAR
FSGSGSGTDFTLTISSLEPEDFAVYFCQQSNSWPFTFGQGTKLEIKRTVAAPSVFIFPPSDE
QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLS
KADYEKHKVYACEVTHQGLSSPCTKSFNRGEC**

WHAT IS CLAIMED IS:

1. An antibody, wherein the antibody comprises:

(a) a heavy chain variable domain and a light chain variable domain selected from the group of:

(i) a heavy chain variable domain that is at least 90% identical to SEQ ID NO: 1 and wherein the heavy chain variable domain includes a histidine at one or more positions in SEQ ID NO: 1 selected from the group consisting of: 33, 34, 50, 52, 57, 59, 100, 102, 103, 107, 108, and 109; and/or
a light chain variable domain that is at least 90% identical to SEQ ID NO: 2, wherein the light chain variable domain includes a histidine at one or more positions in SEQ ID NO: 2 selected from the group consisting of: 32, 34, 50, 51, 89, 90, 92, 93, 94, and 96;

(ii) a heavy chain variable domain that is at least 90% identical to SEQ ID NO: 84, wherein the heavy chain variable domain includes a histidine at one or more positions in SEQ ID NO: 84 selected from the group consisting of: 27, 29, 32, 50, 54, 58, 99, 100, 102, 104, and 105; and/or
a light chain variable domain that is at least 90% identical to SEQ ID NO: 85, wherein the light chain variable domain includes a histidine at one or more positions in SEQ ID NO: 85 selected from the group consisting of: 29, 31, 32, 34, 36, 37, 38, 40, 56, 60, 61, 95, 96, 97, and 100;

(iii) a heavy chain variable domain that is at least 90% identical to SEQ ID NO: 178, wherein the heavy chain variable domain includes a histidine at one or more positions in SEQ ID NO: 178 selected from the group consisting of: 33, 52, 56, 57, or 106; and/or
a light chain variable domain that is at least 90% identical to SEQ ID NO: 179, wherein the light chain variable domain includes a histidine at one or more positions in SEQ ID NO: 179 selected from the group consisting of 25, 26, 28, 29, 31, 36, 37, 57, 59, 94, 95, 96, and 100; and

(iv) a heavy chain variable domain that is at least 90% identical to SEQ ID NO: 272, wherein the heavy chain variable domain includes a histidine at one or

more positions in SEQ ID NO: 272 selected from the group consisting of: 24, 27, 29, 62, 63, 98, and 108; and/or

a light chain variable domain that is at least 90% identical to SEQ ID NO: 273, wherein the light chain variable domain includes a histidine at one or more positions in SEQ ID NO: 273 selected from the group consisting of 27, 28, 29, 31, 32, 89, 92, and 93;

(b) a heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprising one or more of the following:

(i) a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139;

(ii) a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317; and

(iii) an alanine to a cysteine substitution at amino acid position 1;

and/or

a light chain C_L sequence of SEQ ID NO: 353 comprising a valine to cysteine substitution at amino acid position 98.

2. The antibody of claim 1, wherein the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317.

3. The antibody of claim 2, wherein the antibody comprises heavy chain and light chain sequences selected from the group of:

(i) SEQ ID NO: 354 and SEQ ID NO: 2, respectively;

(ii) SEQ ID NO: 360 and SEQ ID NO: 85, respectively;

(iii) SEQ ID NO: 366 and SEQ ID NO: 179, respectively; and

(iv) SEQ ID NO: 372 and SEQ ID NO: 273, respectively.

4. The antibody of claim 1, wherein the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139.

5. The antibody of claim 4, wherein the antibody comprises heavy chain and light chain sequences selected from the group of:

(i) SEQ ID NO: 355 and SEQ ID NO: 2, respectively;

(ii) SEQ ID NO: 361 and SEQ ID NO: 85, respectively;

(iii) SEQ ID NO: 367 and SEQ ID NO: 179, respectively; and

(iv) SEQ ID NO: 373 and SEQ ID NO: 273, respectively.

6. The antibody of claim 1, wherein the antibody wherein:

the light chain C_L sequence of SEQ ID NO: 353 comprises a valine to cysteine substitution at amino acid position 98.

7. The antibody of claim 6, wherein the antibody comprises heavy chain and light chain sequences selected from the group of:

(i) SEQ ID NO: 1 and SEQ ID NO: 359, respectively;

(ii) SEQ ID NO: 84 and SEQ ID NO: 365, respectively;

(iii) SEQ ID NO: 178 and SEQ ID NO: 371, respectively; and

(iv) SEQ ID NO: 272 and SEQ ID NO: 377, respectively.

8. The antibody of claim 1, wherein:

the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317; and

the light chain C_L sequence of SEQ ID NO: 353 comprises a valine to cysteine substitution at amino acid position 98.

9. The antibody of claim 8, wherein the antibody comprises heavy chain and light chain sequences selected from the group of:

(i) SEQ ID NO: 354 and SEQ ID NO: 359, respectively;

(ii) SEQ ID NO: 360 and SEQ ID NO: 365, respectively;

(iii) SEQ ID NO: 366 and SEQ ID NO: 371, respectively; and

(iv) SEQ ID NO: 372 and SEQ ID NO: 377, respectively;

10. The antibody of claim 1, wherein:

the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139; and

the light chain C_L sequence of SEQ ID NO: 353 comprises a valine to cysteine substitution at amino acid position 98.

11. The antibody of claim 10, wherein the antibody comprises heavy chain and light chain sequences selected from the group of:

(i) SEQ ID NO: 355 and SEQ ID NO: 359, respectively;

(ii) SEQ ID NO: 361 and SEQ ID NO: 365, respectively;

(iii) SEQ ID NO: 367 and SEQ ID NO: 371, respectively; and

(iv) SEQ ID NO: 373 and SEQ ID NO: 377, respectively.

12. The antibody of claim 1, wherein the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

an alanine to a cysteine substitution at amino acid position 1.

13. The antibody of claim 12, wherein the antibody comprises heavy chain and light chain sequences selected from the group of:

(i) SEQ ID NO: 356 and SEQ ID NO: 2, respectively;

(ii) SEQ ID NO: 362 and SEQ ID NO: 85, respectively;

(iii) SEQ ID NO: 368 and SEQ ID NO: 179, respectively; and

(iv) SEQ ID NO: 374 and SEQ ID NO: 273, respectively.

14. The antibody of claim 1, wherein the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317; and

an alanine to a cysteine substitution at amino acid position 1.

15. The antibody of claim 16, wherein the antibody comprises a heavy chain and a light chain sequence selected from the group of:

(i) SEQ ID NO: 357 and SEQ ID NO: 2, respectively;

(ii) SEQ ID NO: 363 and SEQ ID NO: 85, respectively;

(iii) SEQ ID NO: 369 and SEQ ID NO: 179, respectively; and

(iv) SEQ ID NO: 375 and SEQ ID NO: 273, respectively.

16. The antibody of claim 1, wherein the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139; and

an alanine to a cysteine substitution at amino acid position 1.

17. The antibody of claim 18, wherein the antibody comprises a heavy chain and a light chain sequence selected from the group of:

(i) SEQ ID NO: 358 and SEQ ID NO: 2, respectively;

(ii) SEQ ID NO: 364 and SEQ ID NO: 85, respectively;

(iii) SEQ ID NO: 370 and SEQ ID NO: 179, respectively; and

(iv) SEQ ID NO: 376 and SEQ ID NO: 273, respectively.

18. The antibody of any one of claims 1-17, wherein the antibody further comprises a cytotoxic drug conjugated to one or more of the following:

(a) a heavy chain CH1-CH2-CH3 of SEQ ID NO: 351 or SEQ ID NO: 352 comprising one or more of the following:

(i) the cysteine at amino acid position 103;

(ii) the cysteine at amino acid position 109;

(iii) the cysteine at amino acid position 112; and/or

(b) the cysteine at amino acid position 107 of SEQ ID NO: 353.

19. The antibody of any one of claims 6-11 and 18, wherein the antibody further comprises a cytotoxic or cytostatic agent is conjugated to the cysteine at position 98 of SEQ ID NO: 353.

20. The antibody of any one of claims 12-18, wherein the antibody further comprises a cytotoxic or cytostatic agent is conjugated to the cysteine at position 1 of SEQ ID NO: 351 or SEQ ID NO: 352.

21. The antibody of any one of claims 18-20, wherein the cytotoxic or cytostatic agent is a conjugated toxin, a radioisotope, drug, or a small molecule.

22. The antibody of any one of claims 1-21,

wherein:

(a) the dissociation rate of the antibody at a pH of about 4.0 to about 6.5 is faster than the dissociation rate at a pH of about 7.0 to about 8.0; or

(b) the dissociation constant (K_D) of the antibody at a pH of about 4.0 to about 6.5 is greater than the K_D at a pH of about 7.0 to about 8.0.

23. The antibody of any one of claims 18-22, wherein a composition comprising the antibody:

provides for one or more of:

an increase in toxin liberation in a target mammalian cell as compared to a composition comprising the same amount of a control antibody;

an increase in target mammalian cell killing as compared to a composition comprising the same amount of a control antibody; and

an increase in endolysosomal delivery in the target mammalian cell as compared to a composition comprising the same amount of a control antibody.

24. The antibody of any one of claims 1-23, wherein a composition comprising the antibody:

results in a less of a reduction in the level of LRRC15presented on the surface of a target mammalian cell as compared to a composition comprising the same amount of a control antibody; or

does not result in a detectable reduction in the level of LRRC15presented on the surface of the target mammalian cell.

25. The antibody of claim 23 or 24, wherein the antibody is degraded in a target mammalian cell following internalization of the antibody by a target mammalian cell.

26. The antibody of any one of claims 23-25, wherein the target mammalian cell is a cancer cell.

27. The antibody of any one of claims 23-26, wherein the antibody is cytotoxic or cytostatic to the target mammalian cell.

28. The antibody of any one of claims 1-27, wherein the antibody has an avidity that results in increased selectivity for cancer cells over non-cancerous cells.

29. The antibody of any one of claims 1-28, wherein the antibody is:

cross-reactive with a non-human primate LRRC15 and human LRRC15; or

cross-reactive with a non-human primate LRRC15, a human LRRC15, and one or both of rat LRRC15 and a mouse LRRC15.

30. The antibody of any one of claims 1-29, wherein the half-life of the antibody in vivo is increased as compared to the half-life of a control antibody in vivo.

31. A pharmaceutical composition comprising an effective amount of any one of the antibodies of claims 1-30 wherein the first antigen-binding domain comprises one of (a) through (d):

(a) a light chain variable domain of SEQ ID NO: 2, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 71, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 75, SEQ ID NO: 76, or SEQ ID NO: 78 and/or

a heavy chain variable domain of SEQ ID NO: 1, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 52, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 82, or SEQ ID NO: 83,

wherein the first antigen-binding domain does not comprise (i) a light chain variable domain of SEQ ID NO: 2 and a heavy chain variable domain of SEQ ID NO: 1; (ii) a light chain variable domain of SEQ ID NO: 2 and heavy chain variable domain that is not one of SEQ ID NOs: 20, 21, 23, 25, 30, 32, 43, 45, 46, 50-52, or 80-83; or (iii) a heavy chain variable domain of SEQ ID NO: 1 and a light chain variable domain that is not one of SEQ ID NOs: 61, 63-65, 71, 72, 74-76, or 78;

(b) a light chain variable domain of SEQ ID NO: 85, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 145, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 149, SEQ ID NO: 153, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 157, SEQ ID NO: 158, SEQ ID NO: 161, SEQ ID NO: 169, SEQ ID NO: 170, SEQ ID NO: 171, SEQ ID NO: 172, SEQ ID NO: 173, SEQ ID NO: 174, SEQ ID NO: 175, SEQ ID NO: 176, or SEQ ID NO: 177, and/or

a heavy chain variable domain of SEQ ID NO: 84, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 98, SEQ ID NO: 101, SEQ ID NO: 102, SEQ ID NO: 106, SEQ ID NO: 110, SEQ ID NO: 120, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, or SEQ ID NO: 166,

wherein the first antigen-binding domain does not comprise (i) a light chain variable domain of SEQ ID NO: 85 and a heavy chain variable domain of SEQ ID NO: 84; (ii) a light

chain variable domain of SEQ ID NO: 85 and heavy chain variable domain that is not one of SEQ ID NOs: 93, 95, 98, 101, 102, 106, 110, 120-122, 124, 126, 127, or 166; or (iii) a heavy chain variable domain of SEQ ID NO: 84 and a light chain variable domain that is not one of SEQ ID NOs: 137, 139, 140, 142, 144-146, 148, 149, 153, 154, 156-158, 161, or 169-177;

(c) a light chain variable domain of SEQ ID NO: 179, SEQ ID NO: 229, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 240, SEQ ID NO: 241, SEQ ID NO: 246, SEQ ID NO: 248 SEQ ID NO: 251, SEQ ID NO: 252, SEQ ID NO: 253, SEQ ID NO: 257, SEQ ID NO: 263, SEQ ID NO: 264, SEQ ID NO: 268, SEQ ID NO: 269, SEQ ID NO: 270, or SEQ ID NO: 271, and/or

a heavy chain variable domain of SEQ ID NO: 178, SEQ ID NO: 196, SEQ ID NO: 201, SEQ ID NO: 205, SEQ ID NO: 206, SEQ ID NO: 225, SEQ ID NO: 258, SEQ ID NO: 259, SEQ ID NO: 260, or SEQ ID NO: 261,

wherein the first antigen-binding domain does not comprise (i) a light chain variable domain of SEQ ID NO: 179 and a heavy chain variable domain of SEQ ID NO: 178; (ii) a light chain variable domain of SEQ ID NO: 179 and heavy chain variable domain that is not one of SEQ ID NOs: 196, 201, 205, 206, 225, or 258-261; or (iii) a heavy chain variable domain of SEQ ID NO: 178 and a light chain variable domain that is not one of SEQ ID NOs: 229, 230, 232, 233, 235, 240, 241, 246, 248, 251-253, 257, 263, 264, or 268-271; and

(d) a light chain variable domain of SEQ ID NO: 273, SEQ ID NO: 327, SEQ ID NO: 328, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 332, SEQ ID NO: 342, SEQ ID NO: 345, or SEQ ID NO: 346 and/or

a heavy chain variable domain of SEQ ID NO: 272, SEQ ID NO: 281, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 305, SEQ ID NO: 306, SEQ ID NO: 311, or SEQ ID NO: 321,

wherein the first antigen-binding domain does not comprise (i) a light chain variable domain of SEQ ID NO: 273 and a heavy chain variable domain of SEQ ID NO: 272; (ii) a light chain variable domain of SEQ ID NO: 273 and heavy chain variable domain that is not one of SEQ ID NOs: 281, 284, 286, 305, 306, 311, or 321; or (iii) a heavy chain variable domain of SEQ ID NO: 272 and a light chain variable domain that is not one of SEQ ID NOs: 327-329, 331, 332, 342, 345, or 346.

32. A kit comprising at least one dose of the antibody of any one of claims 1-30 or the pharmaceutical composition of claim 31.

33. A method of treating a cancer characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface, the method comprising:

administering a therapeutically effective amount of the antibody of any one of claims 1-30 or the pharmaceutical composition of claim 31 to a subject identified as having a cancer characterized by having the population of cancer cells.

34. A method of reducing the volume of a tumor in a subject, wherein the tumor is characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface, the method comprising:

administering a therapeutically effective amount of the antibody of any one of claims 1-30 or the pharmaceutical composition of claim 31 to a subject identified as having a cancer characterized by having the population of cancer cells.

35. A method of inducing cell death in a cancer cell in a subject, wherein the cancer cell has LRRC15 or an epitope of LRRC15 presented on its surface, wherein the method comprises:

administering a therapeutically effective amount of the antibody of any one of claims 1-30 or the pharmaceutical composition of claim 31 to a subject identified as having a cancer characterized by having a population of the cancer cells.

36. A method of decreasing the risk of developing a metastasis or decreasing the risk of developing an additional metastasis in a subject having a cancer, wherein the cancer is characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface the method comprising:

administering a therapeutically effective amount of the antibody of any one of claims 1-30 or the pharmaceutical composition of claim 31 to a subject identified as having a cancer characterized by having the population of cancer cells.

37. An antibody, wherein the antibody comprises:

(a) heavy chain variable domain and a light chain variable domain selected from the group consisting of:

(i) SEQ ID NO: 1 and SEQ ID NO: 2, respectively;

(ii) SEQ ID NO: 84 and SEQ ID NO: 85, respectively;

(iii) SEQ ID NO: 178 and SEQ ID NO: 179, respectively; and

(iv) SEQ ID NO: 272 and SEQ ID NO: 273, respectively;

(b) a heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprising one or more of the following substitution(s):

(i) a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139;

(ii) a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317; and

(iii) an alanine to cysteine substitution at amino acid position 1;

and/or

a light chain C_L sequence of SEQ ID NO: 353 comprising a valine to cysteine substitution at position 98.

38. The antibody of claim 37, wherein the heavy CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317.

39. The antibody of claim 38, wherein the antibody comprises heavy chain and light chain sequences selected from the group of:

(i) SEQ ID NO: 354 and SEQ ID NO: 2, respectively;

(ii) SEQ ID NO: 360 and SEQ ID NO: 85, respectively;

(iii) SEQ ID NO: 366 and SEQ ID NO: 179, respectively; and

(iv) SEQ ID NO: 372 and SEQ ID NO: 273, respectively.

40. The antibody of claim 37, wherein the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139.

41. The antibody of claim 40, wherein the antibody comprises a heavy chain and a light chain sequence selected from the group of:

(i) SEQ ID NO: 355 and SEQ ID NO: 2, respectively;

(ii) SEQ ID NO: 361 and SEQ ID NO: 85, respectively;

(iii) SEQ ID NO: 367 and SEQ ID NO: 179, respectively; and

(iv) SEQ ID NO: 373 and SEQ ID NO: 273, respectively.

42. The antibody of claim 37, wherein:

the light chain C_L sequence of SEQ ID NO: 353 comprises a valine to cysteine substitution at amino acid position 98.

43. The antibody of claim 42, wherein the antibody comprises heavy chain and light chain sequences selected from the group of:

(i) SEQ ID NO: 1 and SEQ ID NO: 359, respectively;

(ii) SEQ ID NO: 84 and SEQ ID NO: 365, respectively;

(iii) SEQ ID NO: 178 and SEQ ID NO: 371, respectively; and

(iv) SEQ ID NO: 272 and SEQ ID NO: 377, respectively.

44. The antibody of claim 37, wherein:

the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317; and

the light chain C_L sequence of SEQ ID NO: 353 comprises a valine to cysteine substitution at amino acid position 98.

45. The antibody of claim 44, wherein the antibody comprises heavy chain and light chain sequences selected from the group of:

(i) SEQ ID NO: 354 and SEQ ID NO: 359, respectively;

(ii) SEQ ID NO: 360 and SEQ ID NO: 365, respectively;

(iii) SEQ ID NO: 366 and SEQ ID NO: 371, respectively; and

(iv) SEQ ID NO: 372 and SEQ ID NO: 377, respectively.

46. The antibody of claim 37, wherein:

the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139; and

the light chain C_L sequence of SEQ ID NO: 353 comprises a valine to cysteine substitution at amino acid position 98.

47. The antibody of claim 46, wherein the antibody comprises heavy chain and light chain sequences selected from the group of:

(i) SEQ ID NO: 355 and SEQ ID NO: 359, respectively;

(ii) SEQ ID NO: 361 and SEQ ID NO: 365, respectively;

(iii) SEQ ID NO: 367 and SEQ ID NO: 371, respectively; and

(iv) SEQ ID NO: 373 and SEQ ID NO: 377, respectively.

48. The antibody of claim 37, wherein the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

an alanine to a cysteine substitution at amino acid position 1.

49. The antibody of claim 48, wherein the antibody comprises heavy chain and light chain sequences selected from the group of:

(i) SEQ ID NO: 356 and SEQ ID NO: 2, respectively;

(ii) SEQ ID NO: 362 and SEQ ID NO: 85, respectively;

(iii) SEQ ID NO: 368 and SEQ ID NO: 179, respectively; and

(iv) SEQ ID NO: 374 and SEQ ID NO: 273, respectively.

50. The antibody of claim 37, wherein the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

a methionine to leucine substitution at amino acid position 311 and an asparagine to serine substitution at amino acid position 317; and

an alanine to a cysteine substitution at amino acid position 1.

51. The antibody of claim 50, wherein the antibody comprises a heavy chain and a light chain sequence selected from the group of:

(i) SEQ ID NO: 357 and SEQ ID NO: 2, respectively;

(ii) SEQ ID NO: 363 and SEQ ID NO: 85, respectively;

(iii) SEQ ID NO: 369 and SEQ ID NO: 179, respectively; and

(iv) SEQ ID NO: 375 and SEQ ID NO: 273, respectively.

52. The antibody of claim 37, wherein the heavy chain CH1-CH2-CH3 sequence of SEQ ID NO: 351 or SEQ ID NO: 352 comprises:

a methionine to tyrosine substitution at amino acid position 135, a serine to threonine substitution at amino acid position 137, and a threonine to glutamic acid substitution at amino acid position 139; and

an alanine to a cysteine substitution at amino acid position 1.

53. The antibody of claim 52, wherein the antibody comprises heavy chain and light chain sequences selected from the group of:

(i) SEQ ID NO: 358 and SEQ ID NO: 2, respectively;

(ii) SEQ ID NO: 364 and SEQ ID NO: 85, respectively;

(iii) SEQ ID NO: 370 and SEQ ID NO: 179, respectively; and

(iv) SEQ ID NO: 376 and SEQ ID NO: 273, respectively.

54. The antibody of any one of claims 37-53, wherein the antibody further comprises a cytotoxic drug conjugated to one or more of the following:

(a) a heavy chain CH1-CH2-CH3 of SEQ ID NO: 351 or SEQ ID NO: 352 comprising one or more of the following:

(i) the cysteine at amino acid position 103;

(ii) the cysteine at amino acid position 109; and

(iii) the cysteine at amino acid position 112; and/or

(b) the cysteine at amino acid position 107 of SEQ ID NO: 353.

55. The antibody of any one of claims 42-47 and 54, wherein the antibody further comprises a cytotoxic or cytostatic agent is conjugated to the cysteine at position 98 of SEQ ID NO: 353.

56. The antibody of any one of claims 48-55, wherein the antibody further comprises a cytotoxic or cytostatic agent is conjugated to the cysteine at position 1 of SEQ ID NO: 351 or SEQ ID NO: 352.

57. The antibody of any one of claims 54-56, wherein the cytostatic or cytotoxic agent is a conjugated toxin, a radioisotope, drug, or a small molecule.

58. The antibody of any one of claims 54-57, wherein the antibody is cytotoxic or cytostatic to a target mammalian cell.

59. The antibody of claim 58, wherein the antibody is degraded in the target mammalian cell following internalization of the antibody by the target mammalian cell.

60. The antibody of claim 58 or 59, wherein the target mammalian cell is a cancer cell.

61. The antibody of any one of claims 37-60, wherein the antibody has an avidity that results in increased selectivity for cancer cells over non-cancerous cells.

62. The antibody of any one of claims 37-61, wherein the antibody is:

cross-reactive with a non-human primate LRRC15 and human LRRC15; or

cross-reactive with a non-human primate LRRC15, a human LRRC15, and one or both of rat LRRC15 and a mouse LRRC15.

63. The antibody of any one of claims 37-62, wherein the half-life of the antibody in vivo is increased as compared to the half-life of a control antibody in vivo.

64. The antibody of any one of claims 58-60, wherein the target mammalian cell is a cancer cell.

65. A pharmaceutical composition comprising an effective amount of any one of the antibodies of claims 37-64.

66. A kit comprising at least one dose of the antibody of any one of claims 37-64 or the pharmaceutical composition claim 65.

67. A method of treating a cancer characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface, the method comprising:

administering a therapeutically effective amount of the antibody of any one of claims 37-64 or the pharmaceutical composition of claim 65 to a subject identified as having a cancer characterized by having the population of cancer cells.

68. A method of reducing the volume of a tumor in a subject, wherein the tumor is characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface, the method comprising:

administering a therapeutically effective amount of the antibody of any one of claims 37-64 or the pharmaceutical composition of claim 65 to a subject identified as having a cancer characterized by having the population of cancer cells.

69. A method of inducing cell death in a cancer cell in a subject, wherein the cancer cell has LRRC15 or an epitope of LRRC15presented on its surface, wherein the method comprises:

administering a therapeutically effective amount of the antibody of any one of claims 37-64 or the pharmaceutical composition of claim 65 to a subject identified as having a cancer characterized by having a population of the cancer cells.

70. A method of decreasing the risk of developing a metastasis or decreasing the risk of developing an additional metastasis in a subject having a cancer, wherein the cancer is characterized by having a population of cancer cells that have LRRC15 or an epitope of LRRC15 presented on their surface the method comprising:

administering a therapeutically effective amount of the antibody of any one of claims 37-64 or the pharmaceutical composition of claim 65 to a subject identified as having a cancer characterized by having the population of cancer cells.

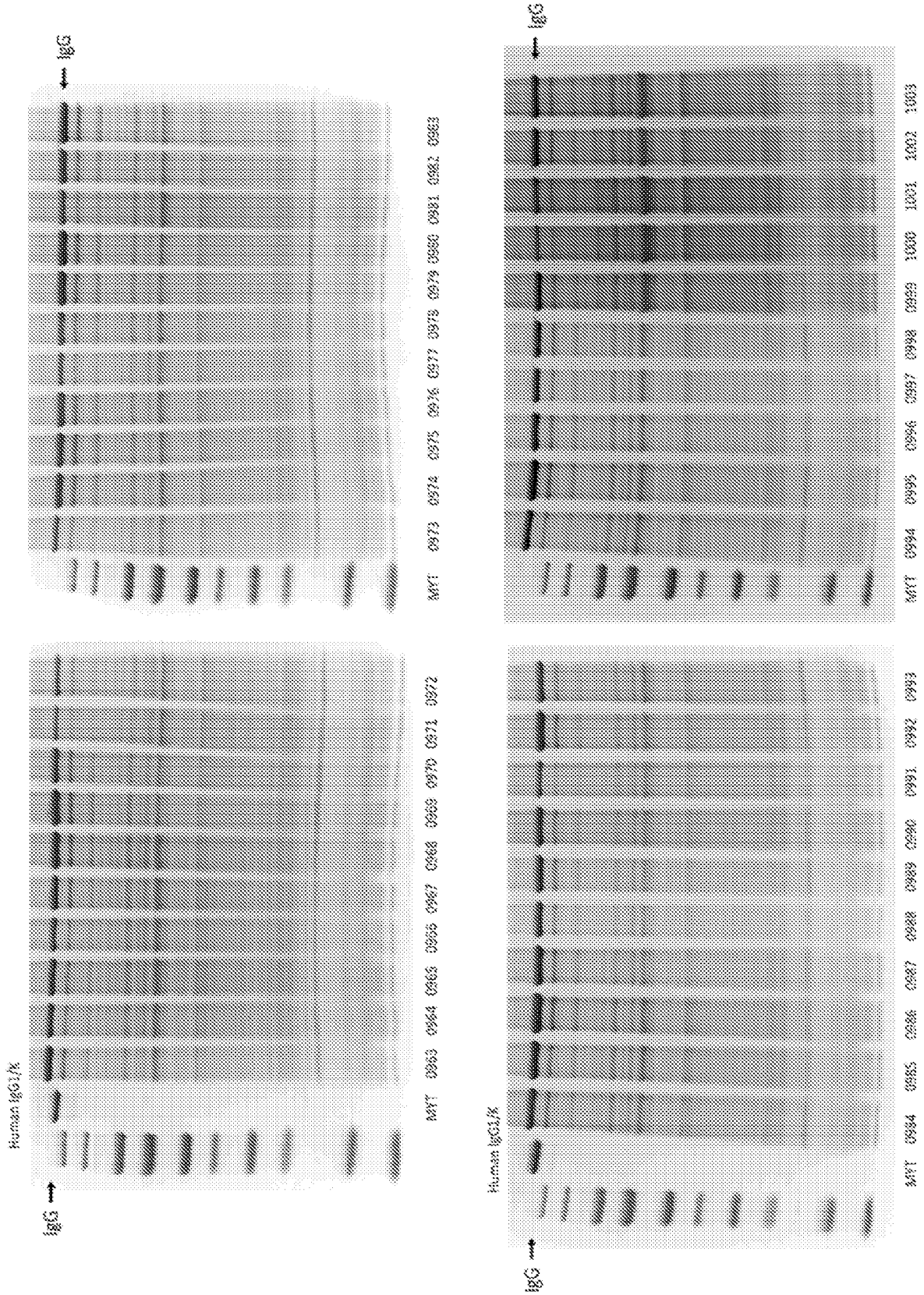

IgG
Human IgG1/k
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MYT 0973 0974 0975 0976 0977 0978 0979 0980 0981 0982 0983
IgG
Human IgG1/k
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MYT 0994 0995 0996 0997 0998 0999 1000 1001 1002 1003

FIG. 1

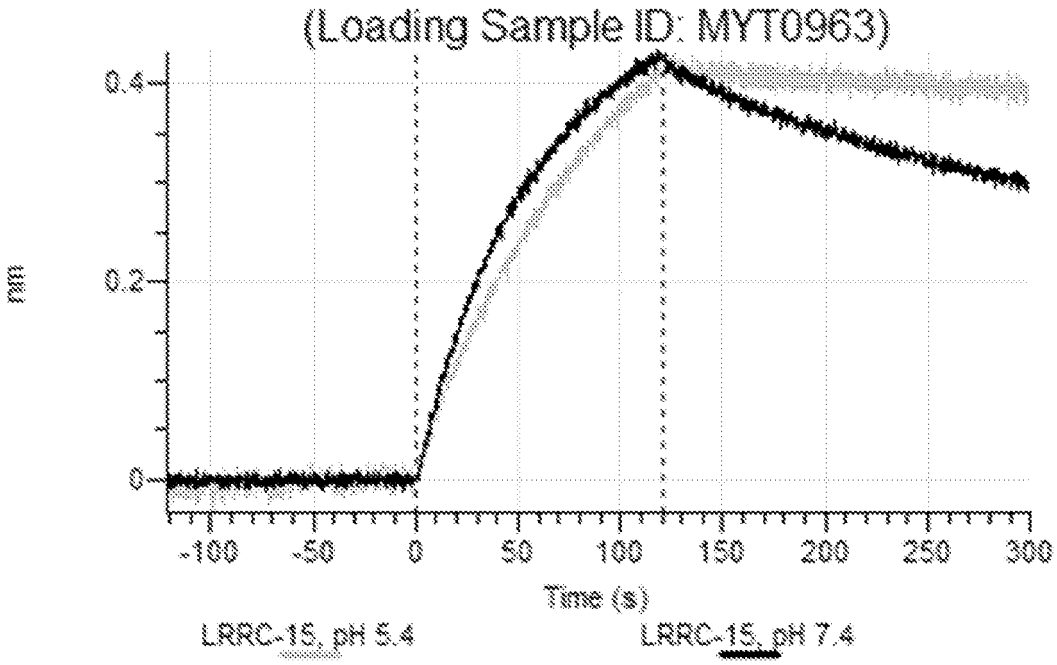

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200
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Time (s)
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LRRC-15, pH 7.4

FIG. 2A

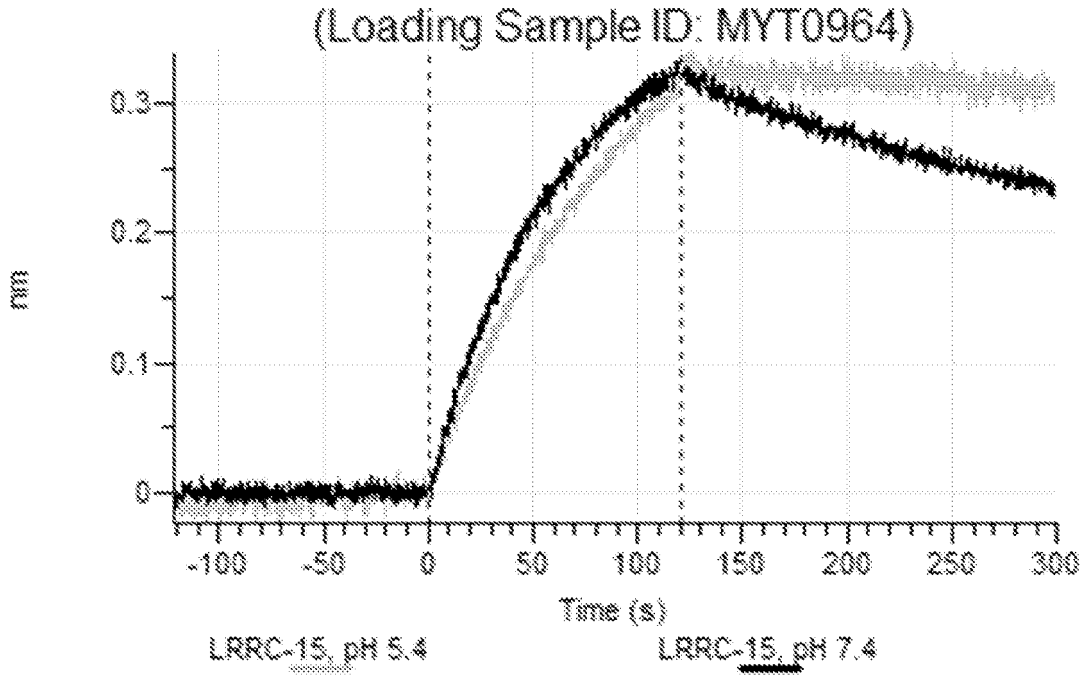

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Time (s)
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LRRC-15, pH 7.4

FIG. 2B

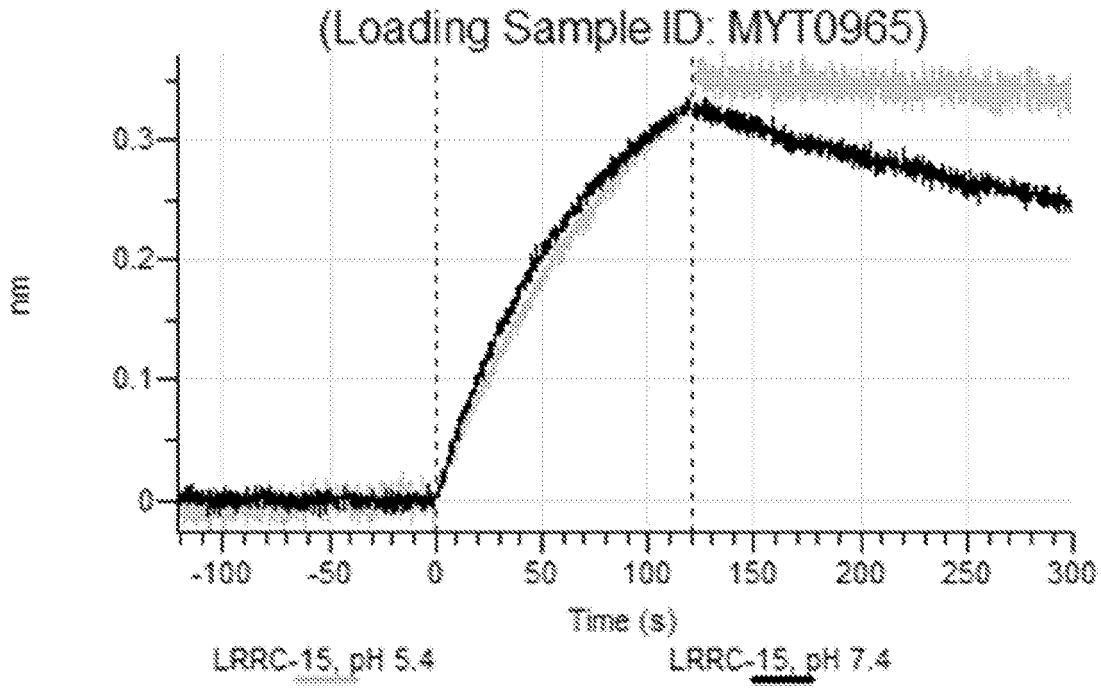

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LRRC-15, pH 7.4

FIG. 2C

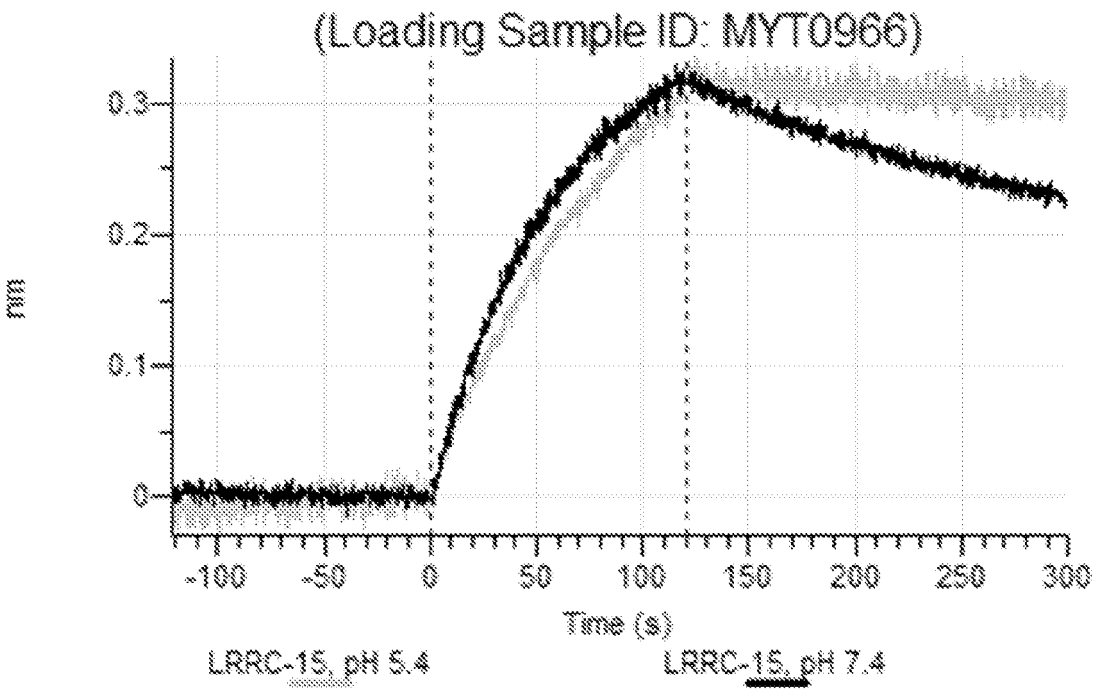

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Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2D

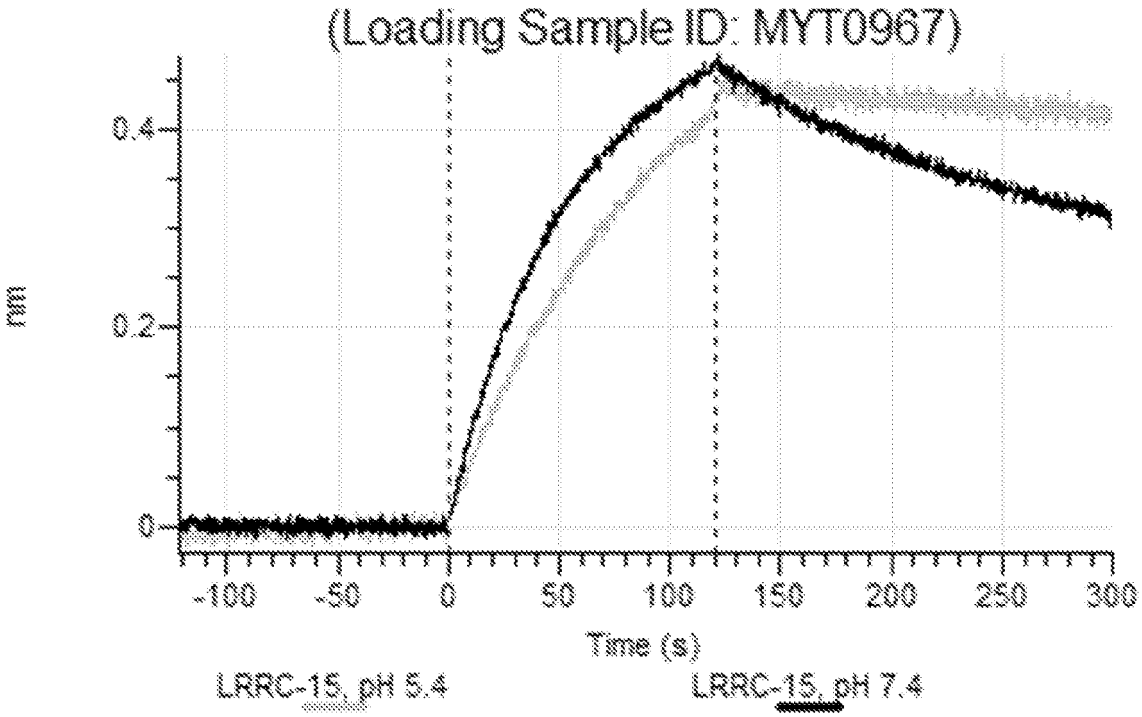

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300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2E

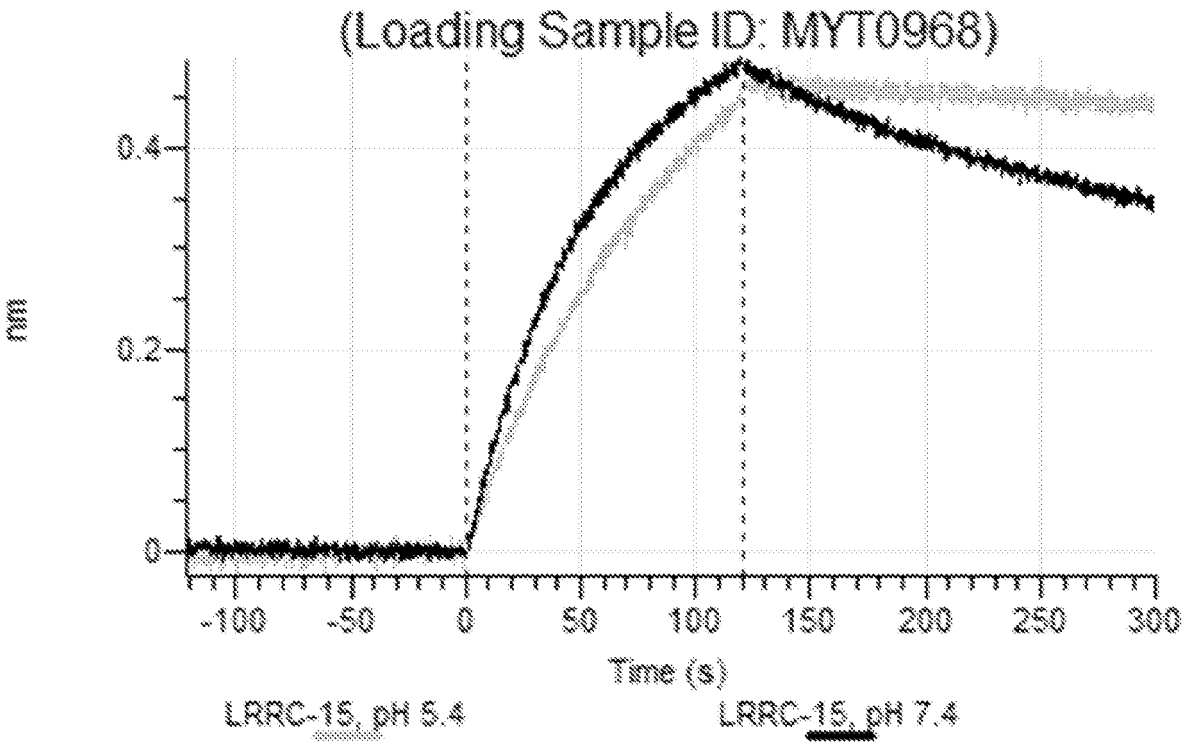

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Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2F

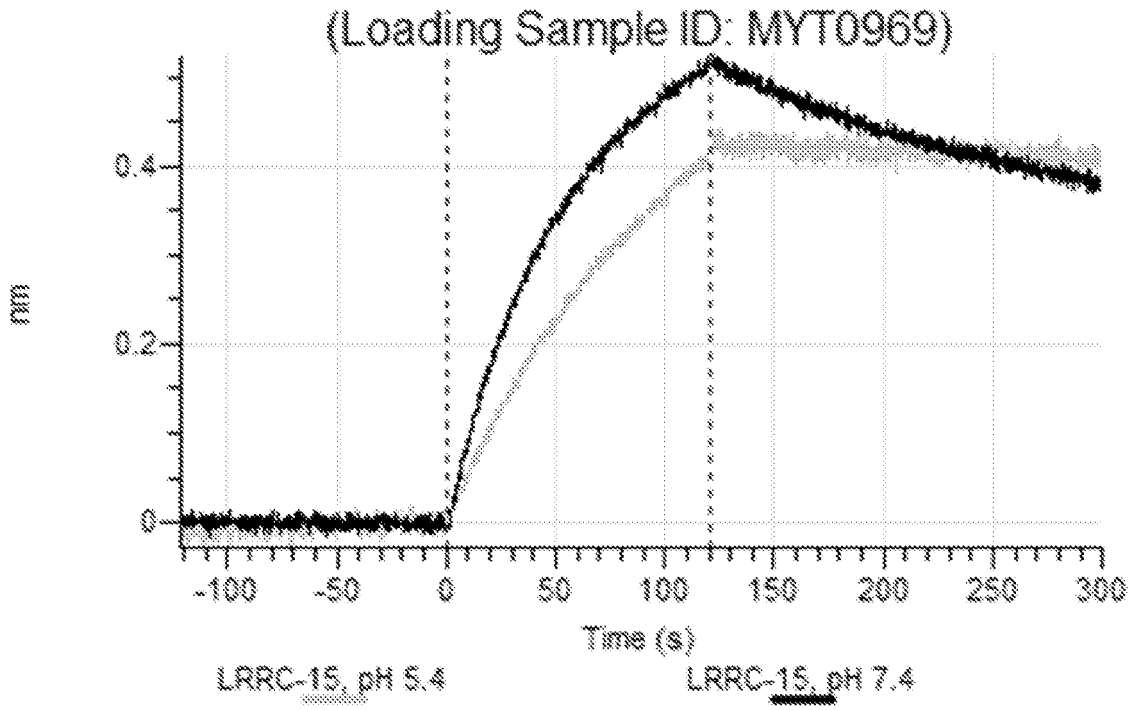

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Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2G

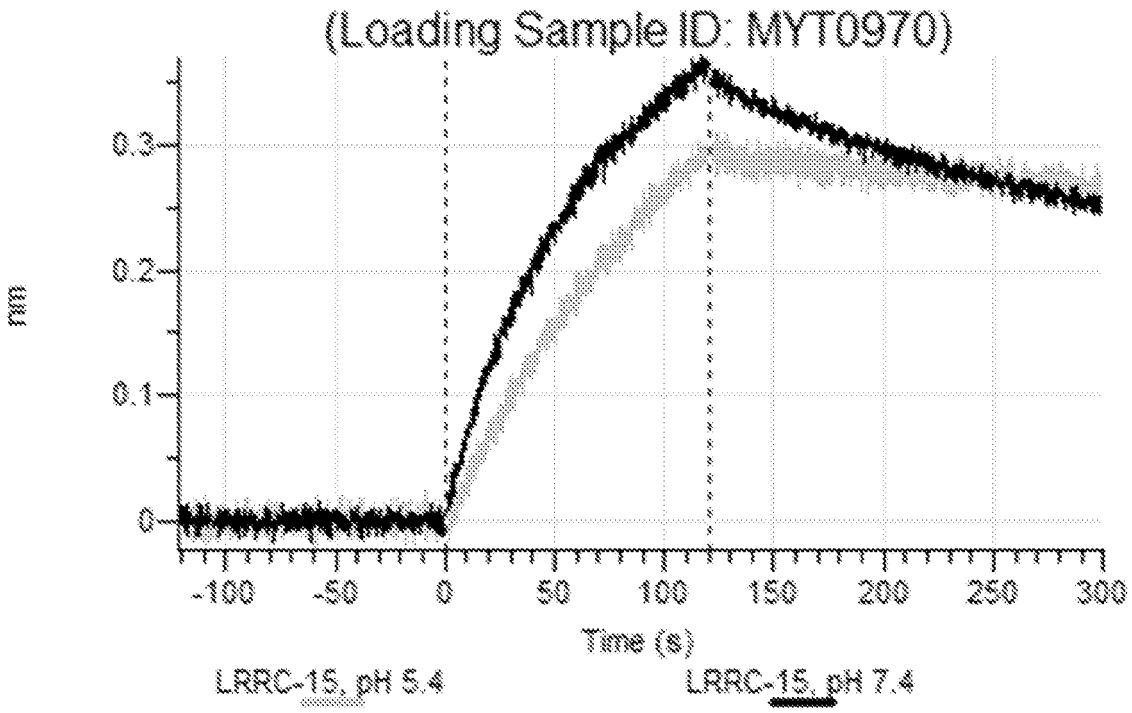

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100
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300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2H

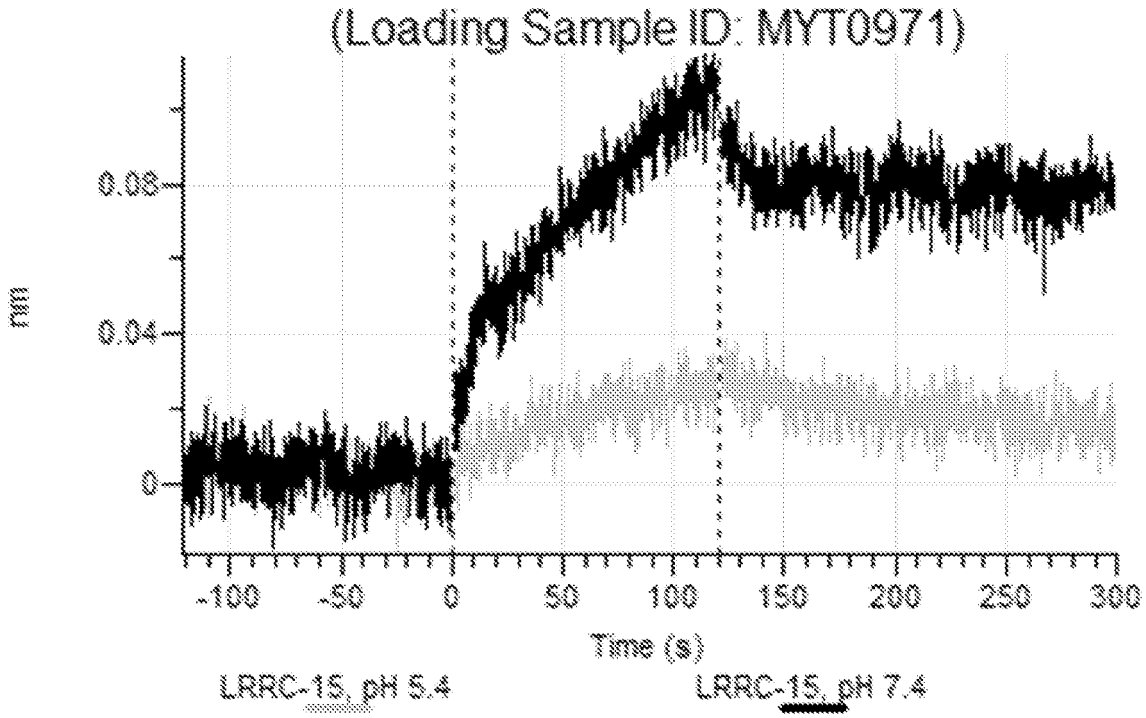

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nm
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0.04
0
-100
-50
0
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100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2I

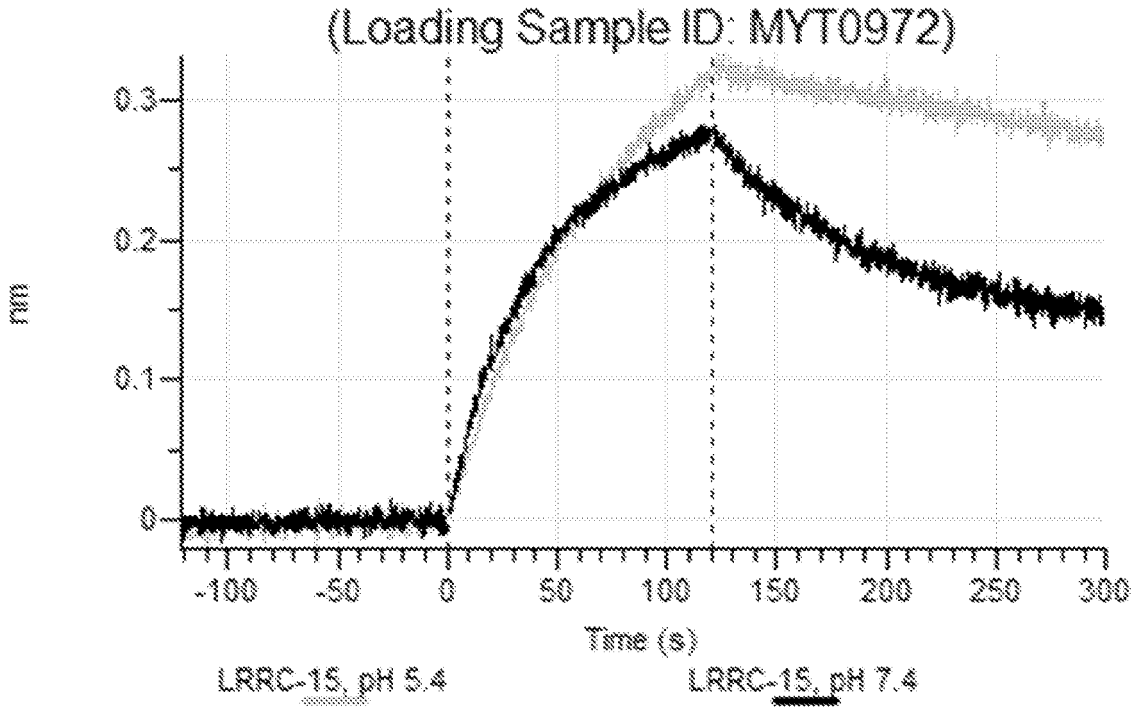

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nm
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0.1
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-100
-50
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250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2J

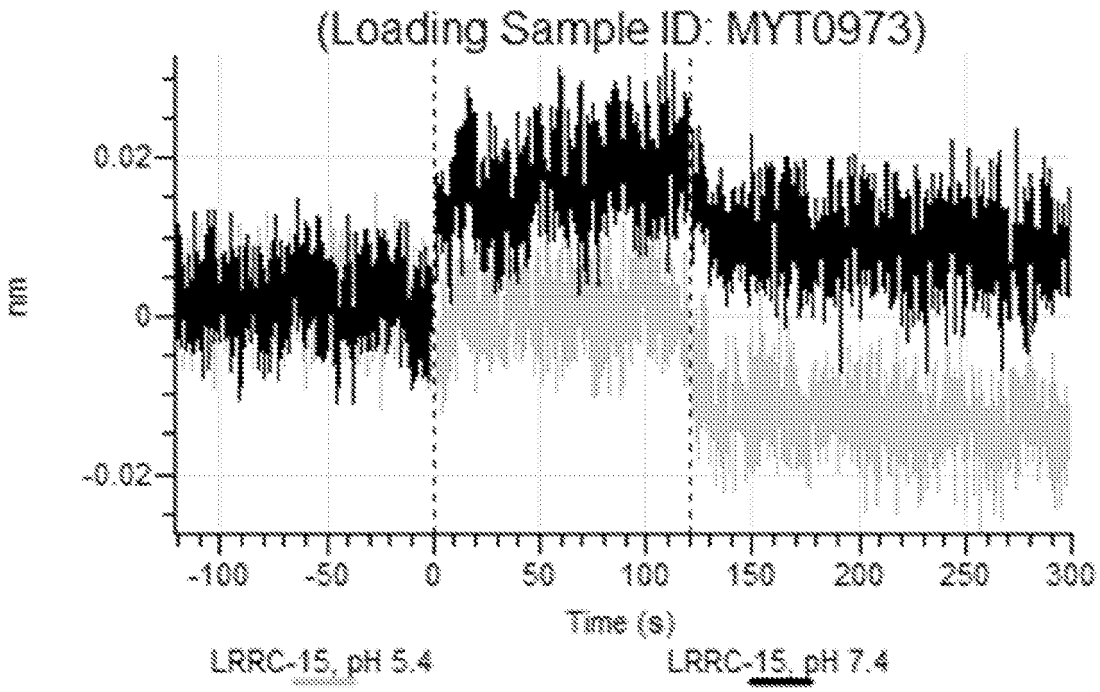

(Loading Sample ID: MYT0973)
nm
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-0.02
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2K

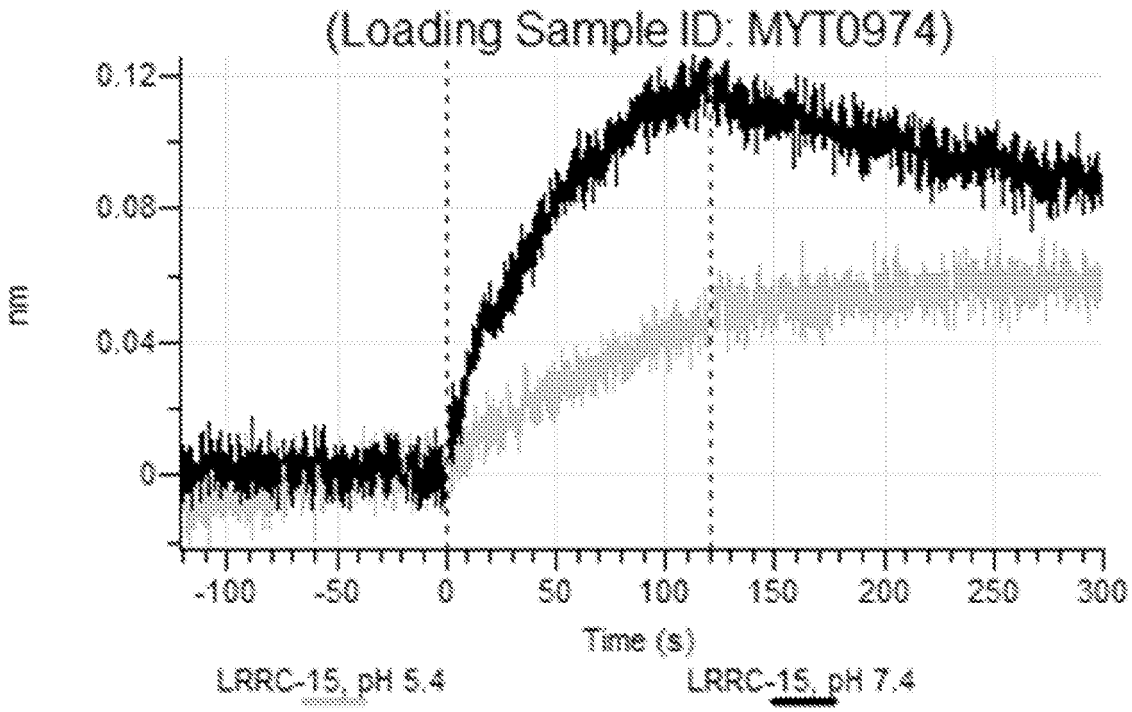

(Loading Sample ID: MYT0974)
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0.04
0
nm
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2L

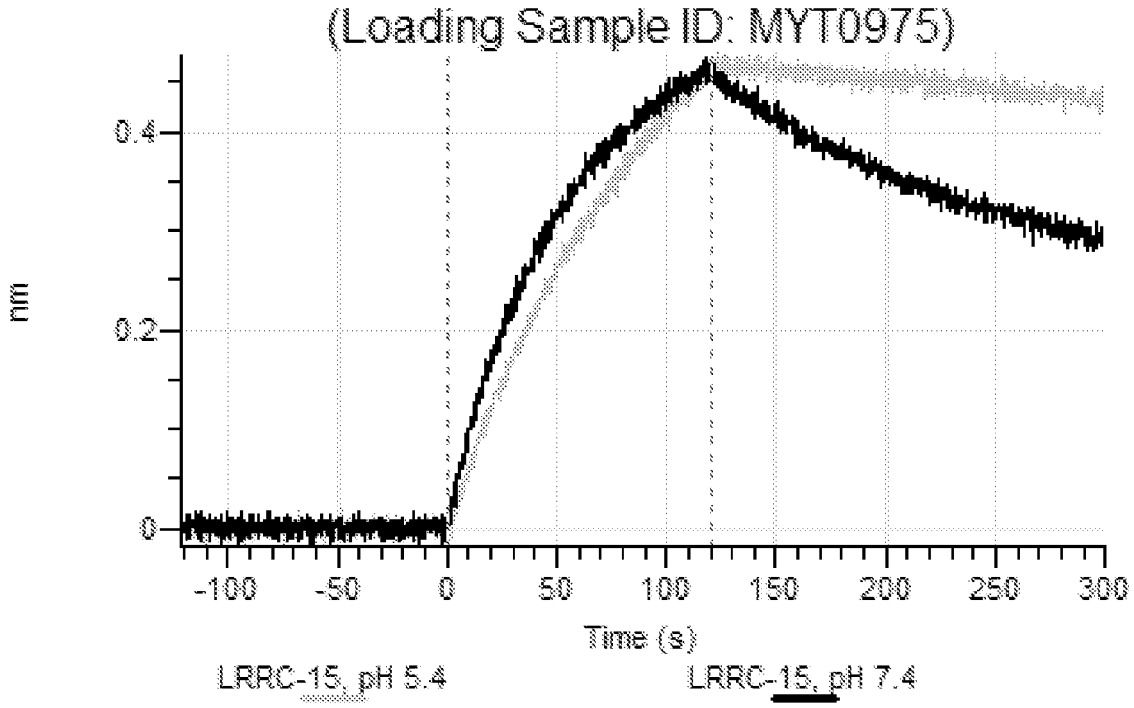

(Loading Sample ID: MYT0975)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2M

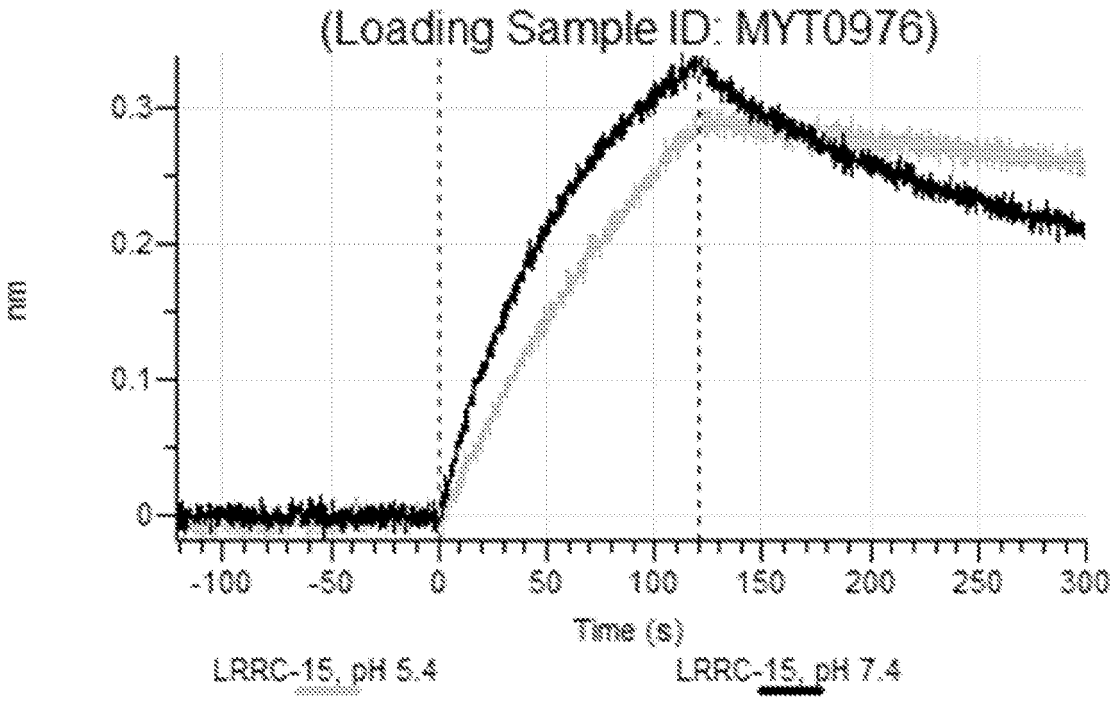

(Loading Sample ID: MYT0976)
nm
0.3
0.2
0.1
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2N

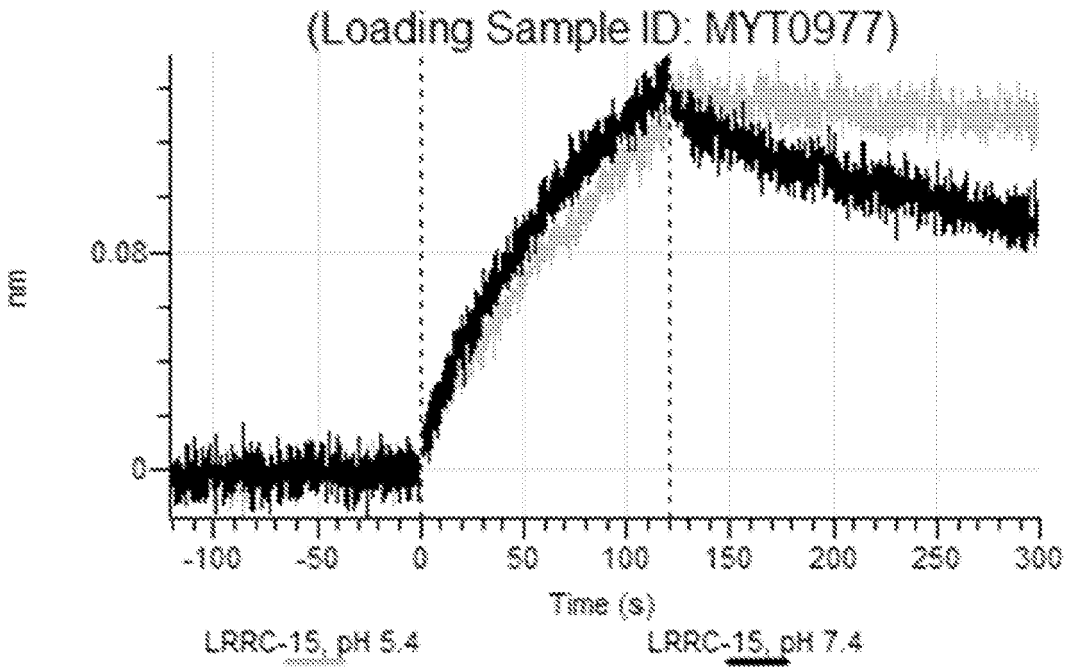

(Loading Sample ID: MYT0977)
nm
0.08
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2O

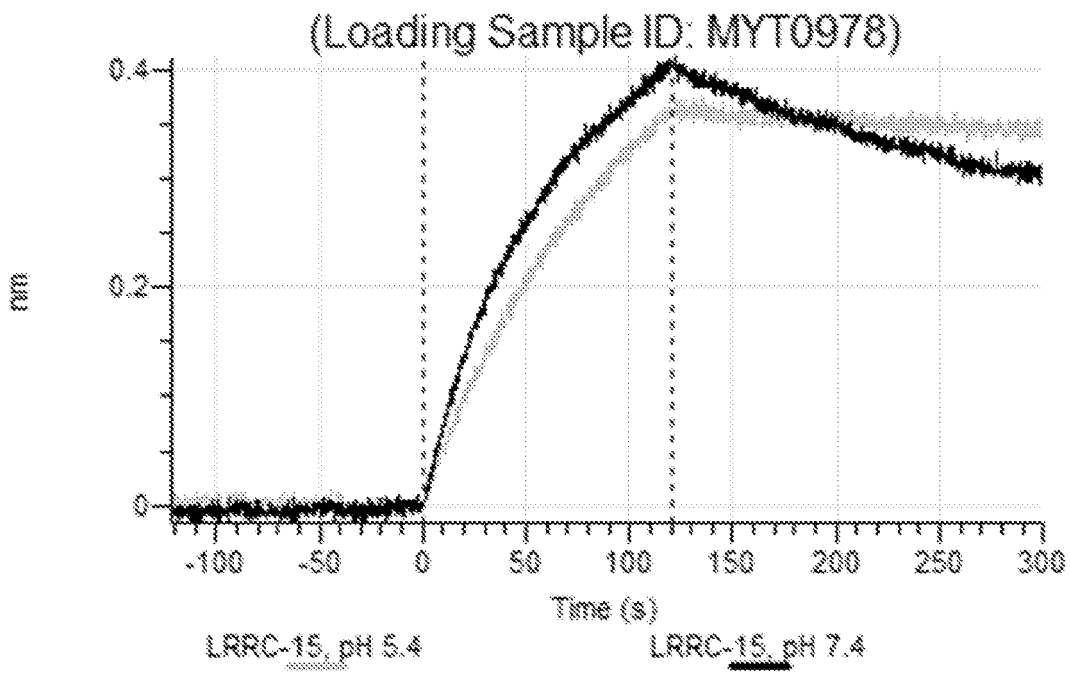

(Loading Sample ID: MYT0978)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2P

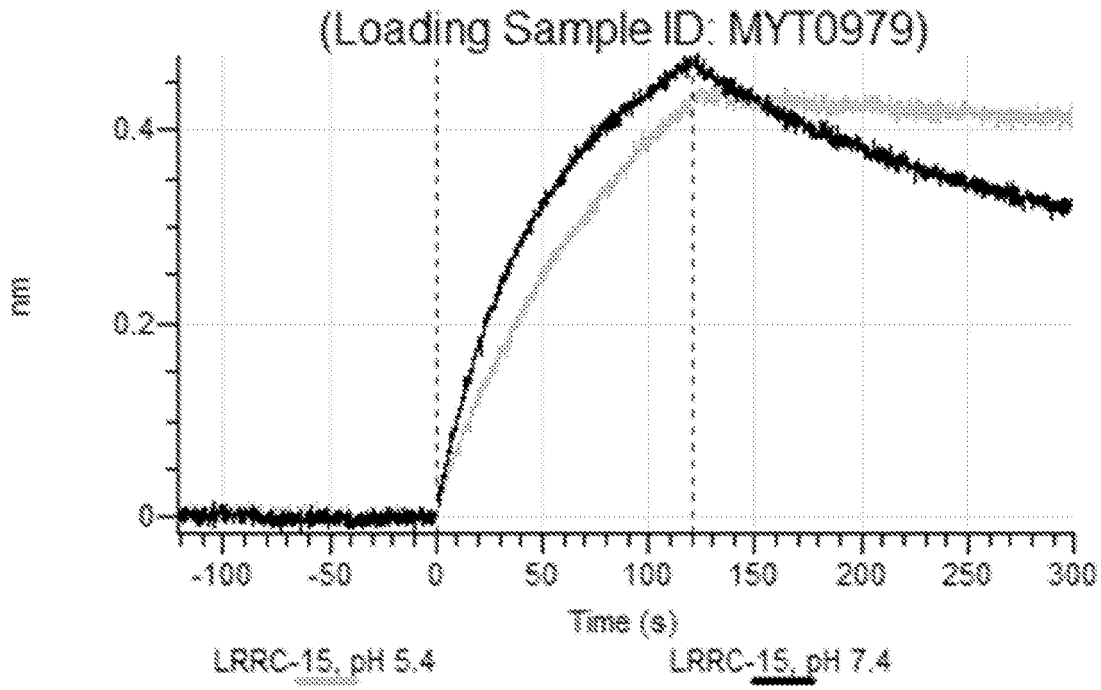

(Loading Sample ID: MYT0979)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2Q

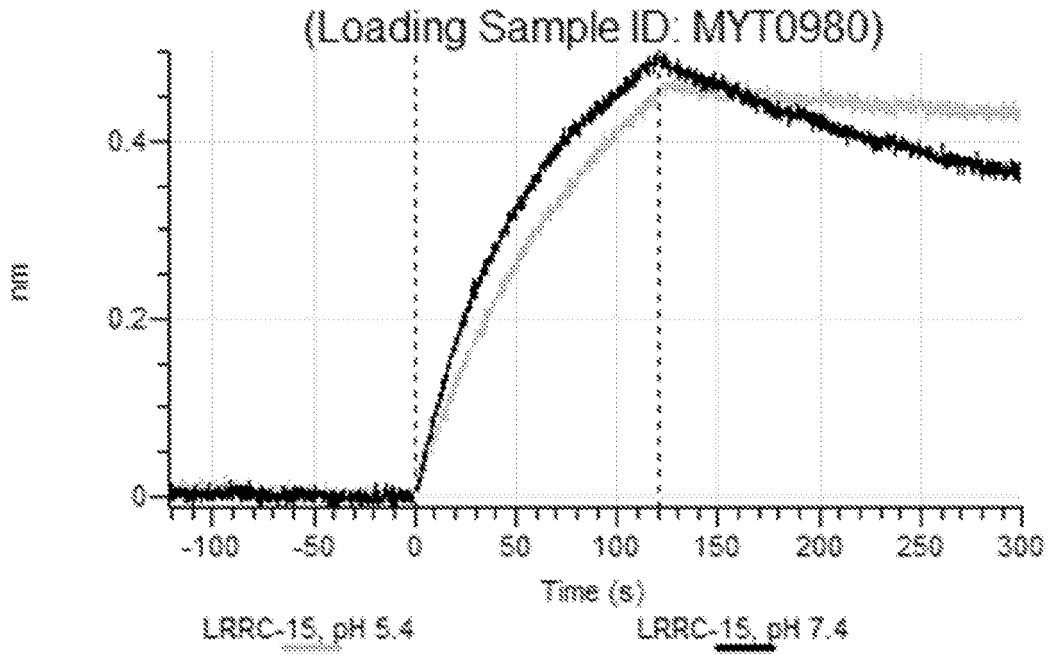

(Loading Sample ID: MYT0980)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2R

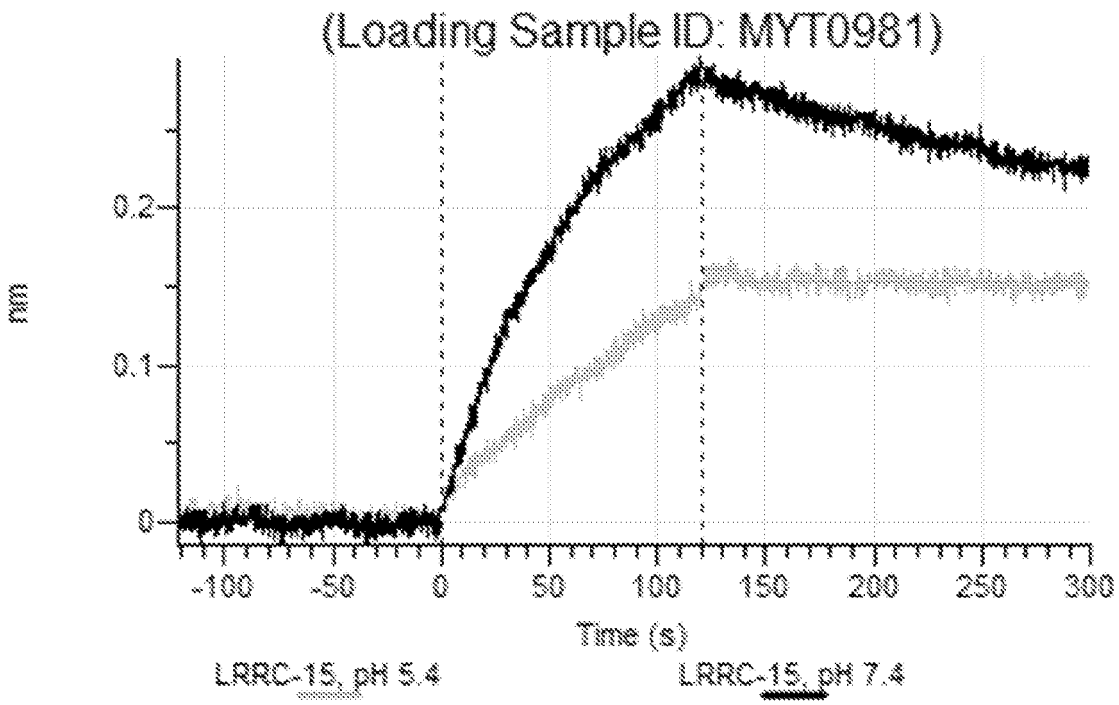

(Loading Sample ID: MYT0981)
nm
0.2
0.1
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2S

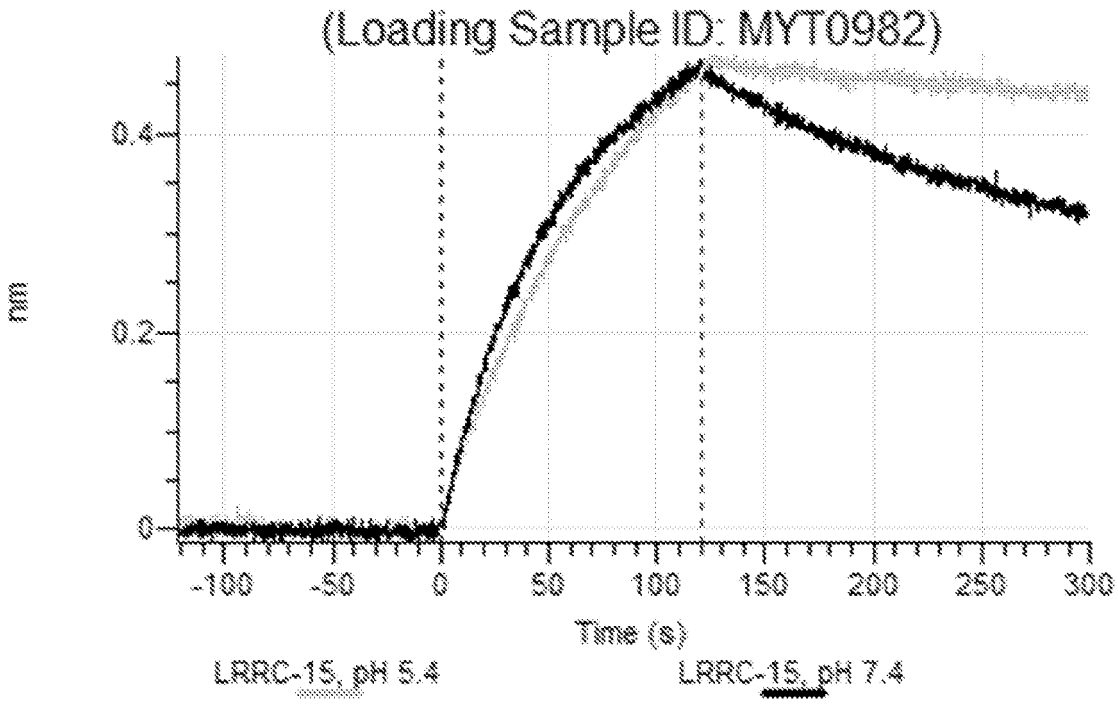

(Loading Sample ID: MYT0982)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2T

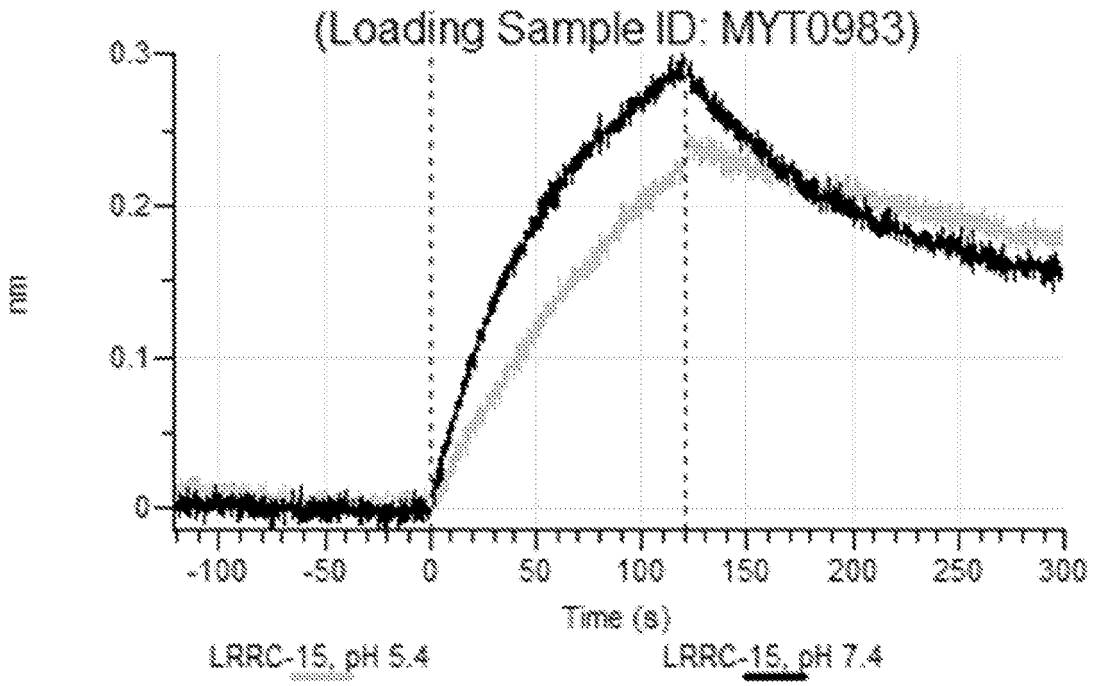

(Loading Sample ID: MYT0983)
nm
0.3
0.2
0.1
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2U

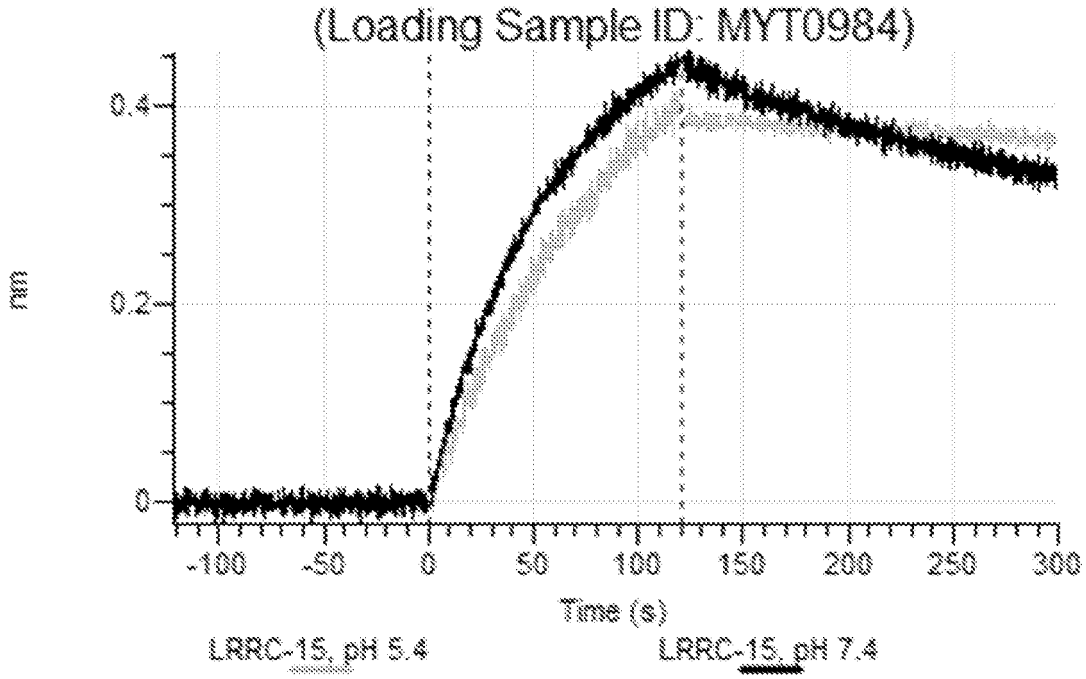

(Loading Sample ID: MYT0984)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2V

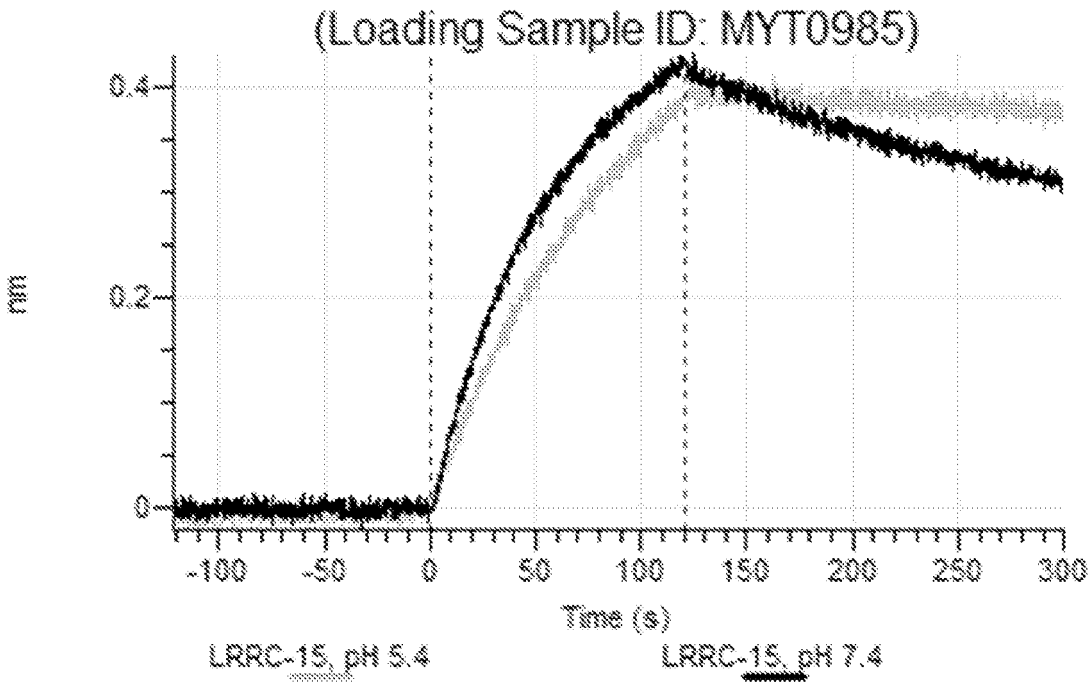

(Loading Sample ID: MYT0985)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2W

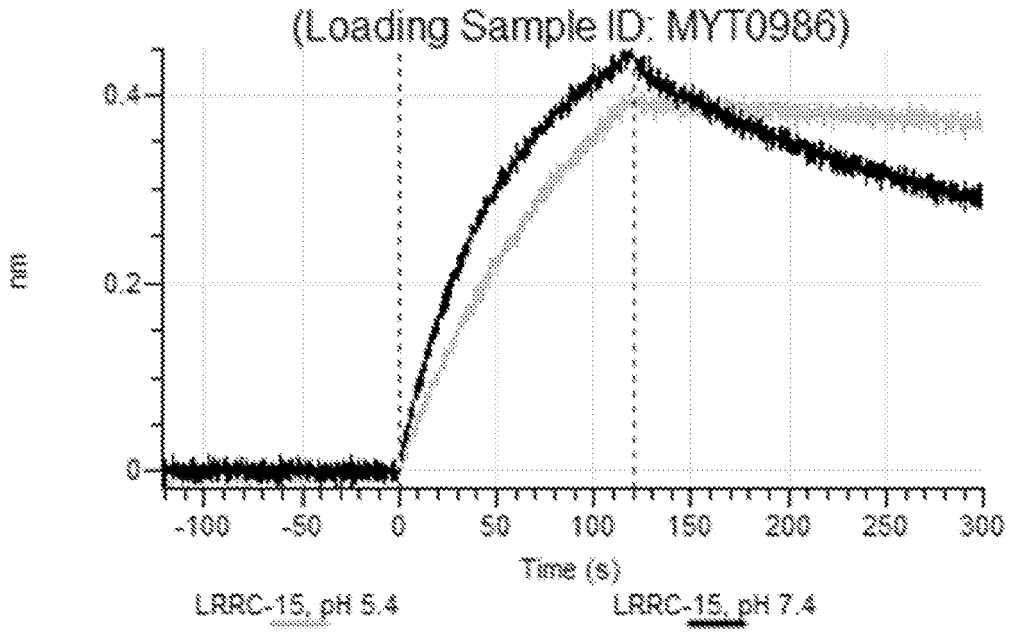

(Loading Sample ID: MYT0986)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2X

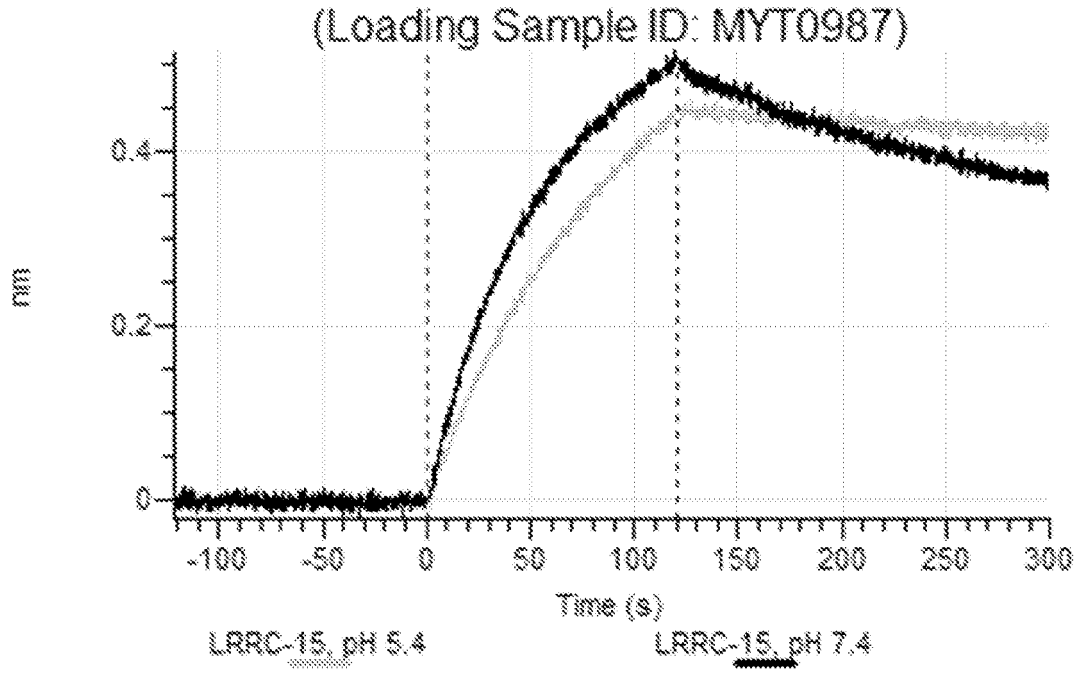

(Loading Sample ID: MYT0987)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2Y

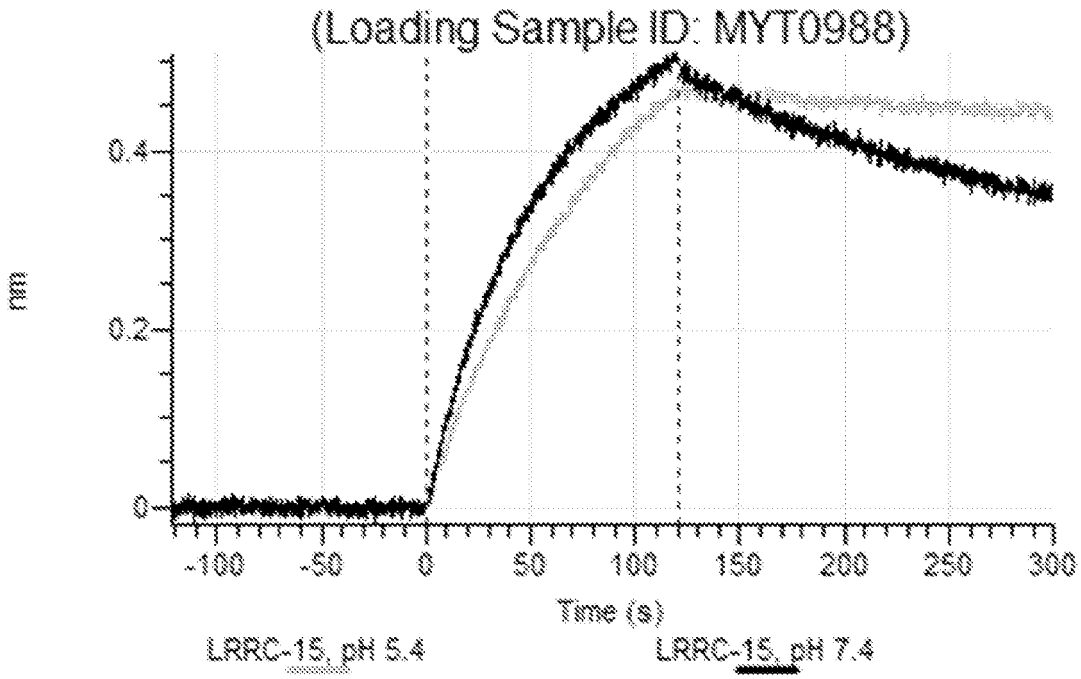

(Loading Sample ID: MYT0988)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15_pH 5.4
LRRC-15_pH 7.4

FIG. 2Z

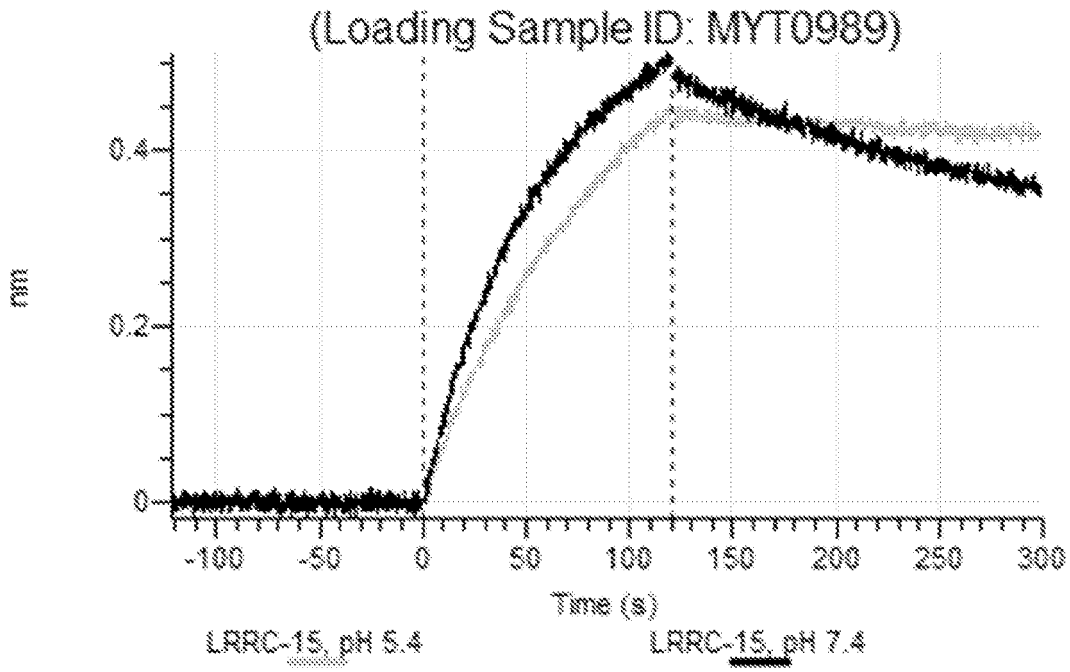

(Loading Sample ID: MYT0989)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AA

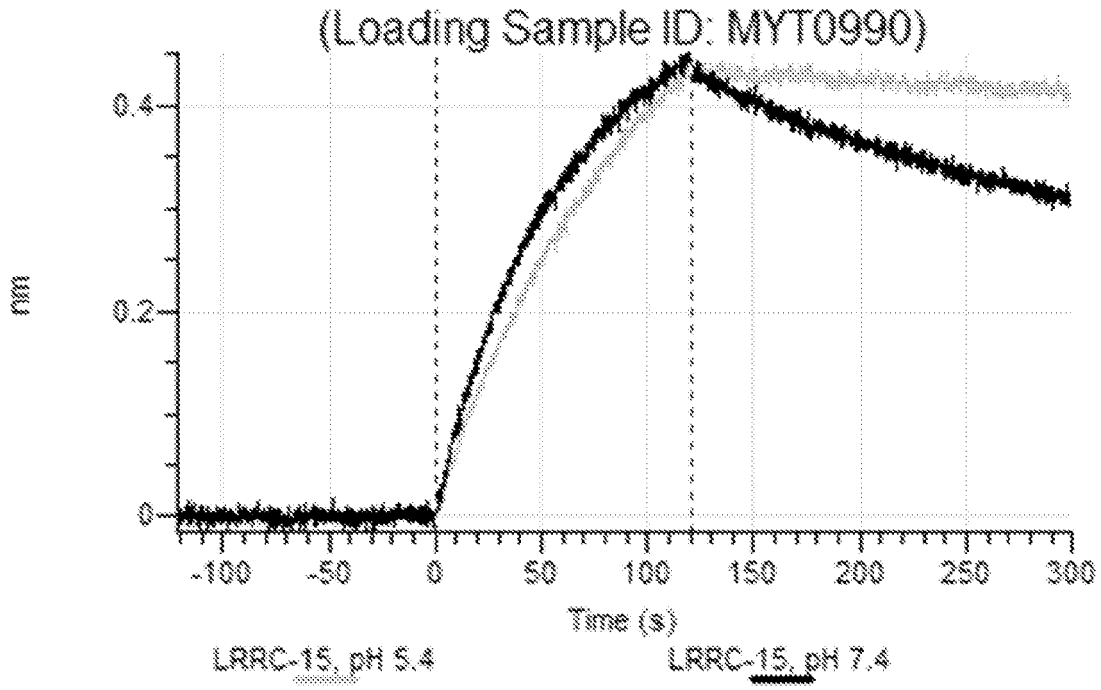

(Loading Sample ID: MYT0990)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AB

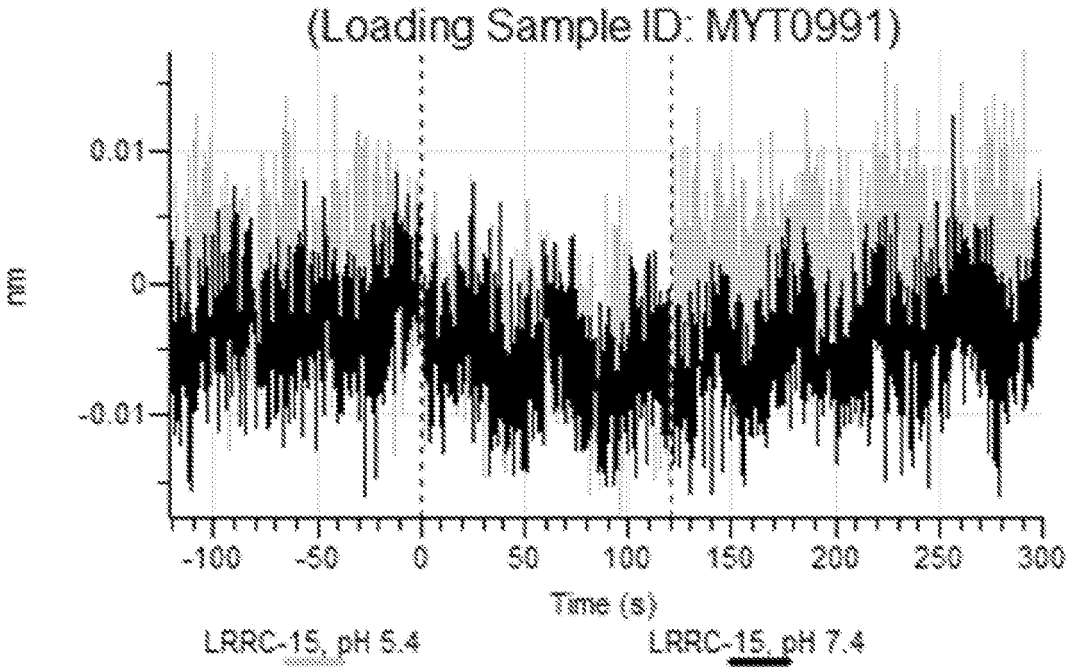

(Loading Sample ID: MYT0991)
nm
0.01
0
-0.01
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AC

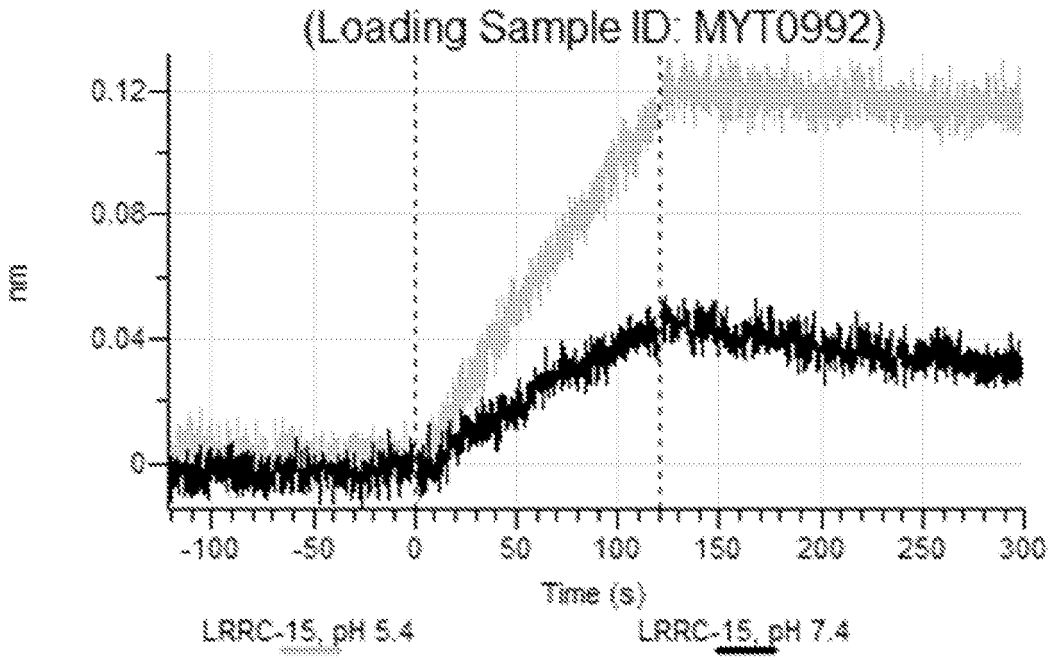

(Loading Sample ID: MYT0992)
nm
0.12
0.08
0.04
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AD

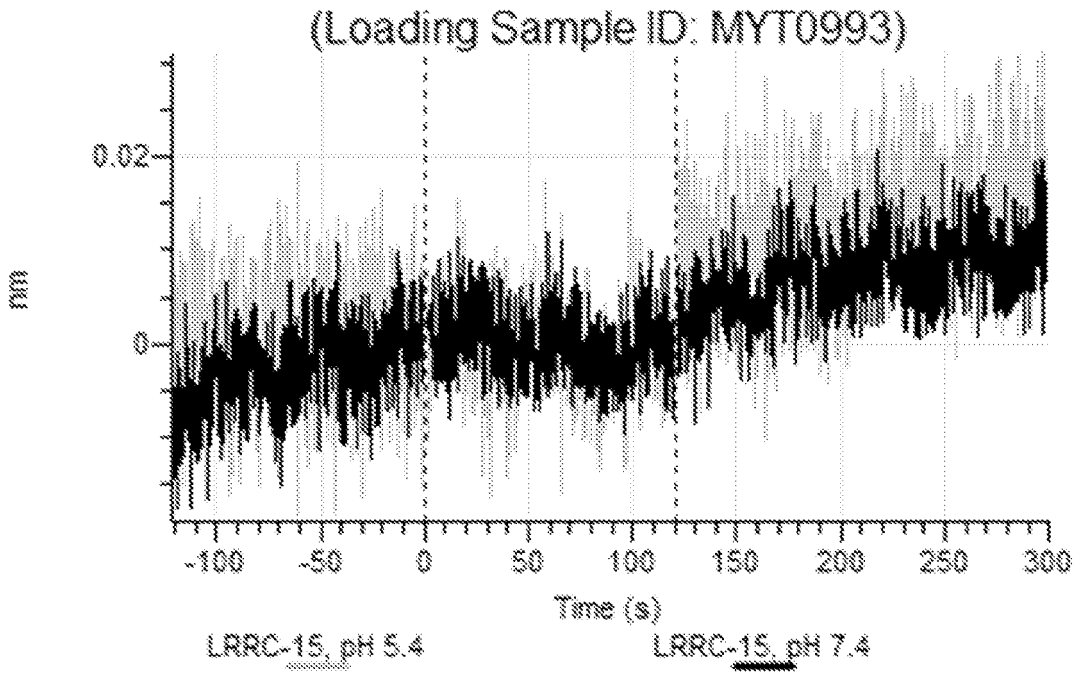

(Loading Sample ID: MYT0993)
nm
0.02
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AE

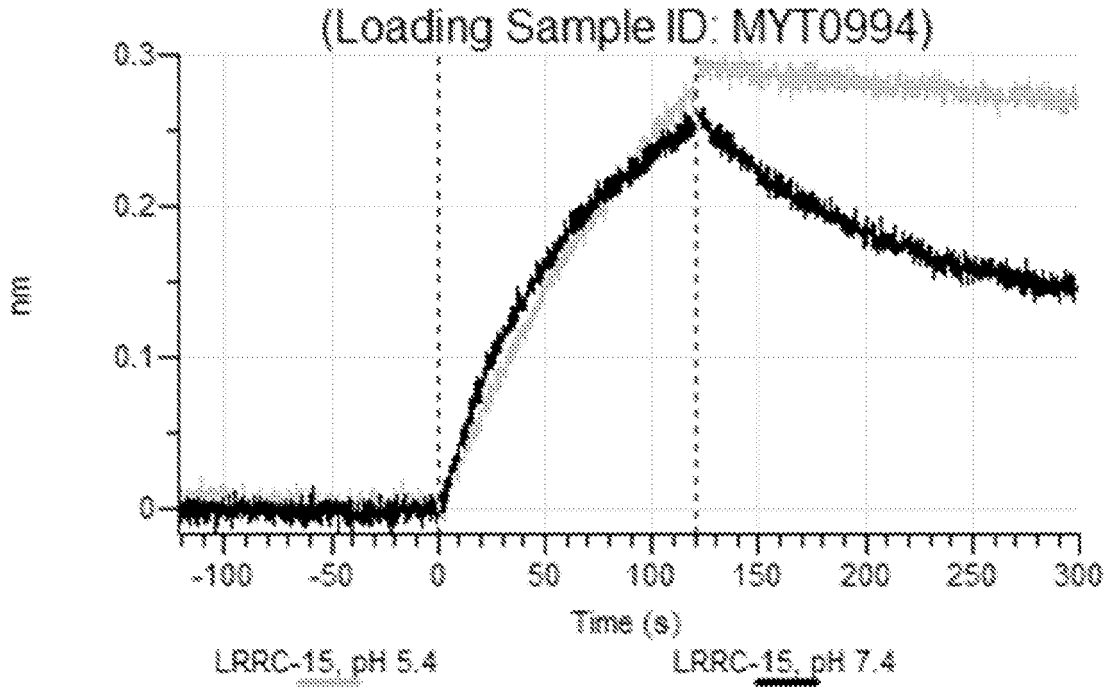

(Loading Sample ID: MYT0994)
nm
0.3
0.2
0.1
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AF

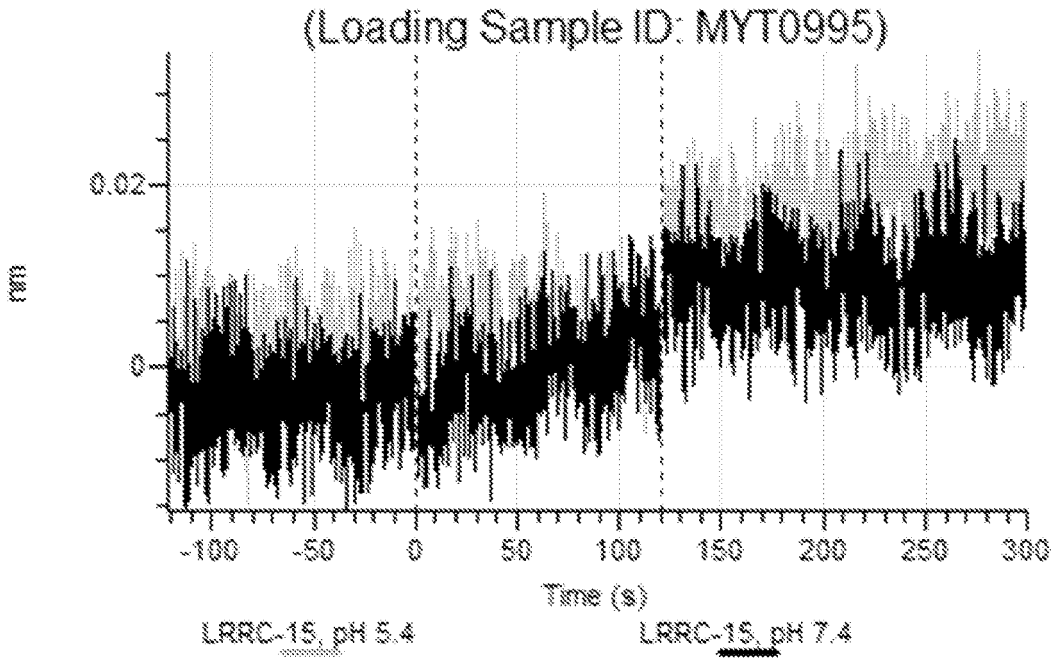

(Loading Sample ID: MYT0995)
nm
0.02
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AG

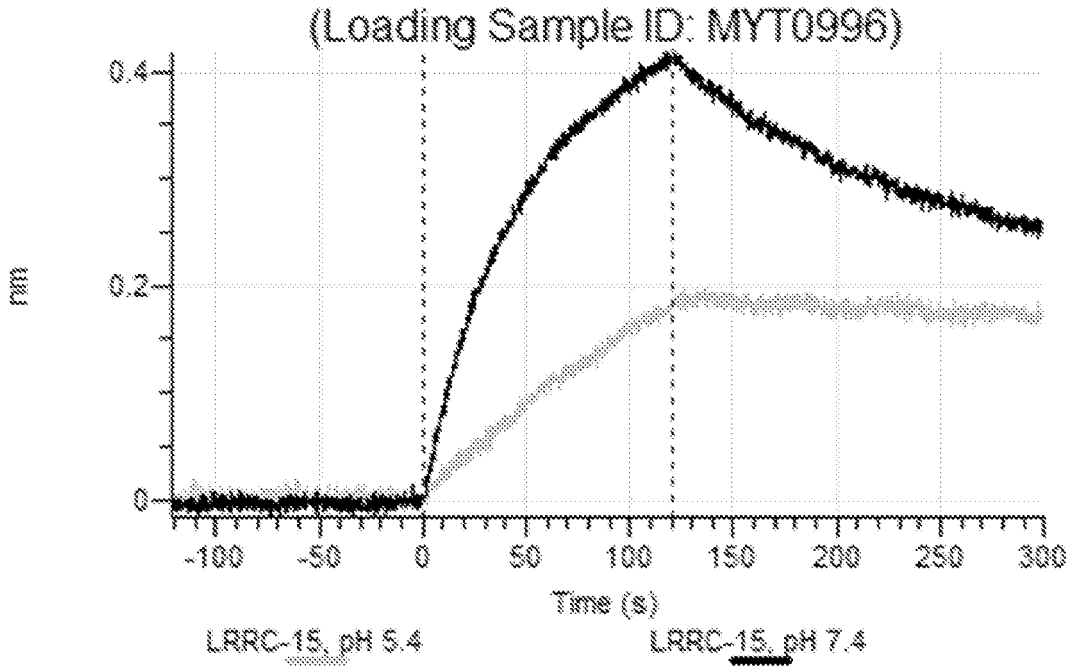

(Loading Sample ID: MYT0996)
nm
0.4
0.2
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AH

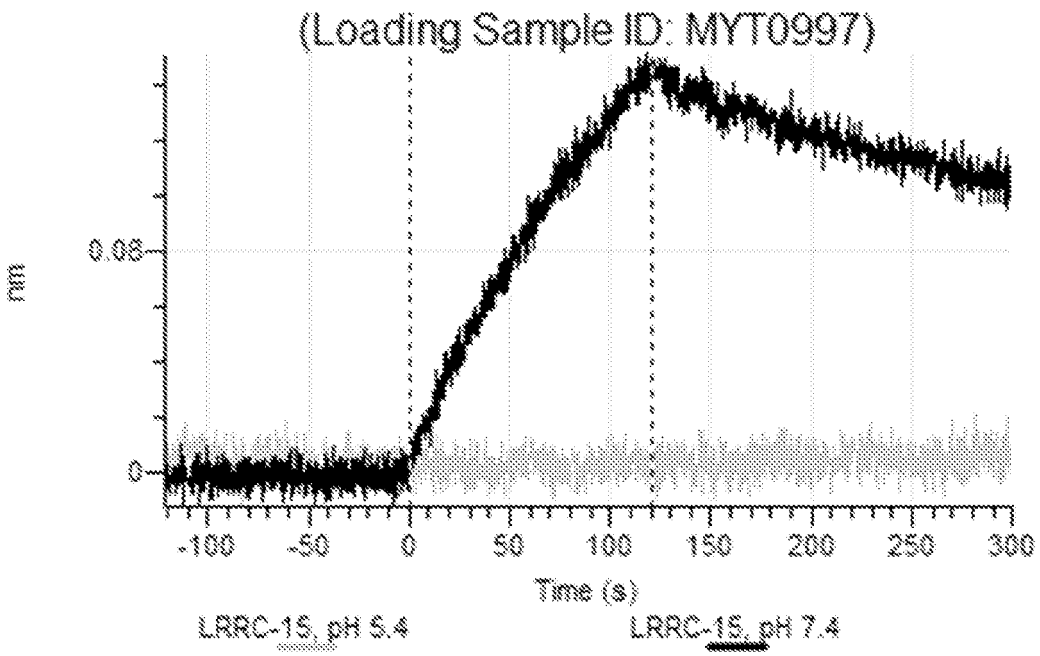

(Loading Sample ID: MYT0997)
nm
0.08
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AI

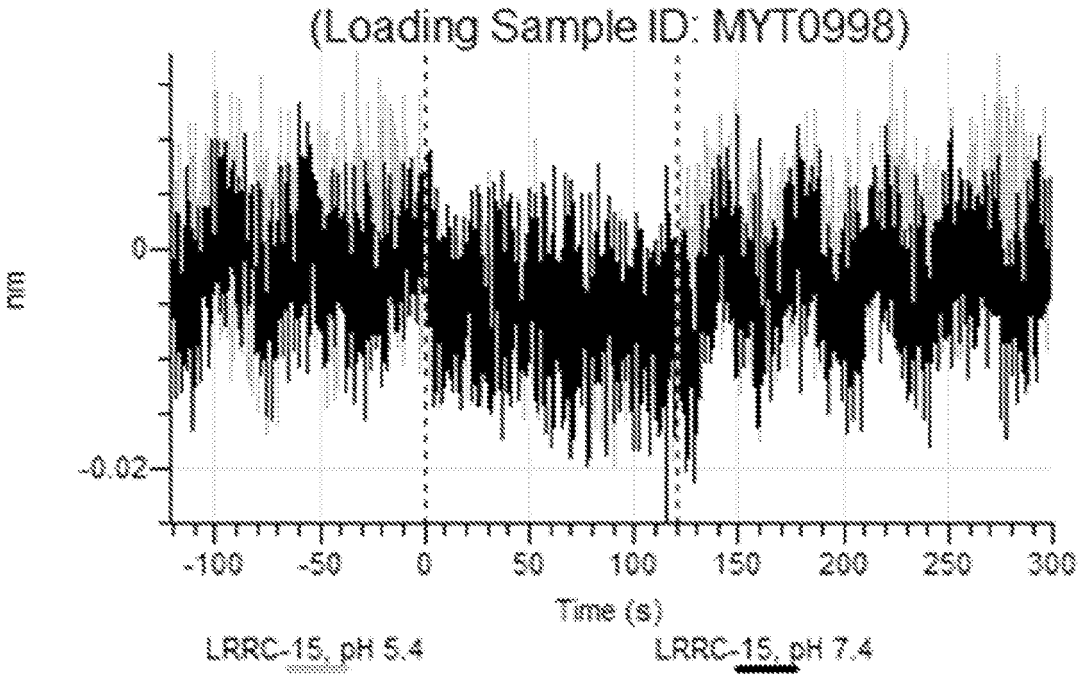

(Loading Sample ID: MYT0998)
nm
0
-0.02
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AJ

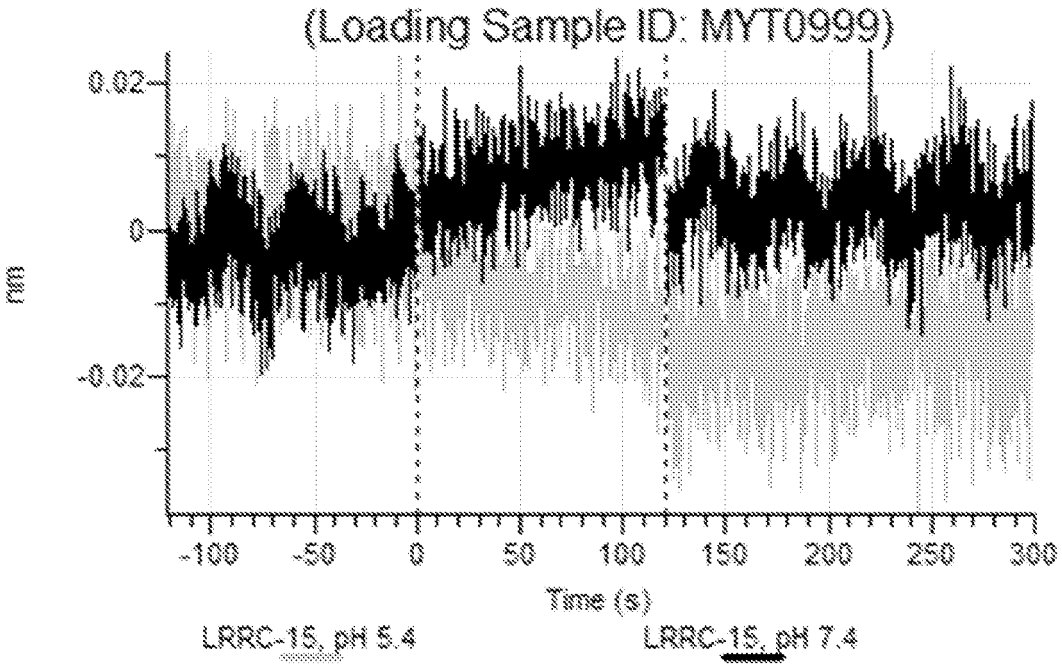

(Loading Sample ID: MYT0999)
0.02
0
-0.02
nm
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AK

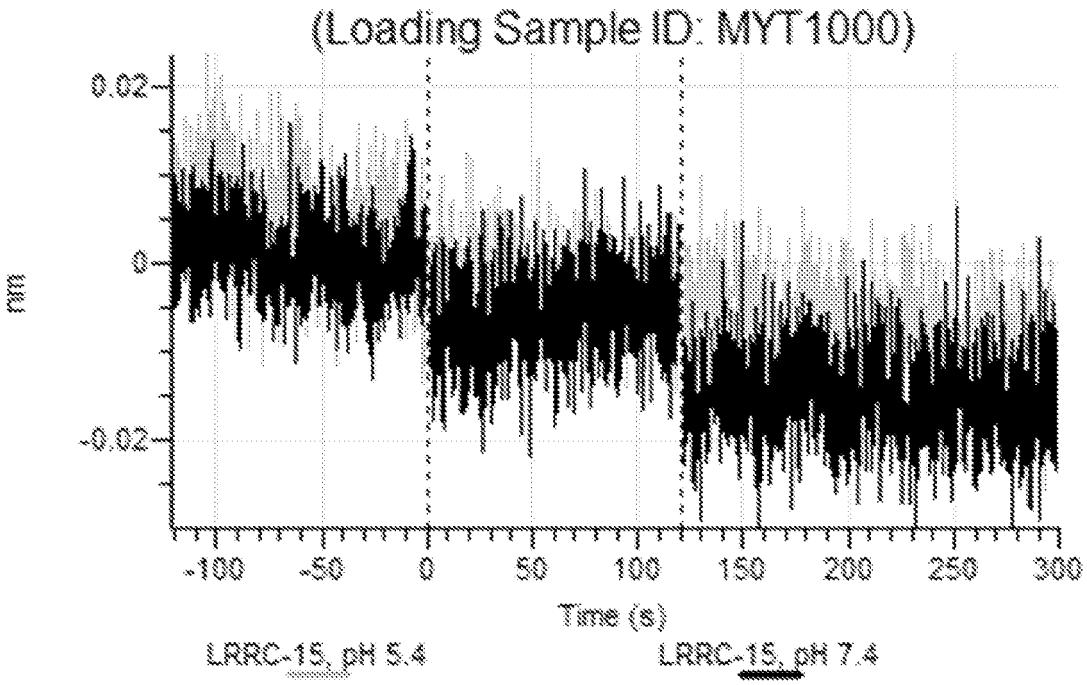

(Loading Sample ID: MYT1000)
0.02
0
-0.02
nm
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AL

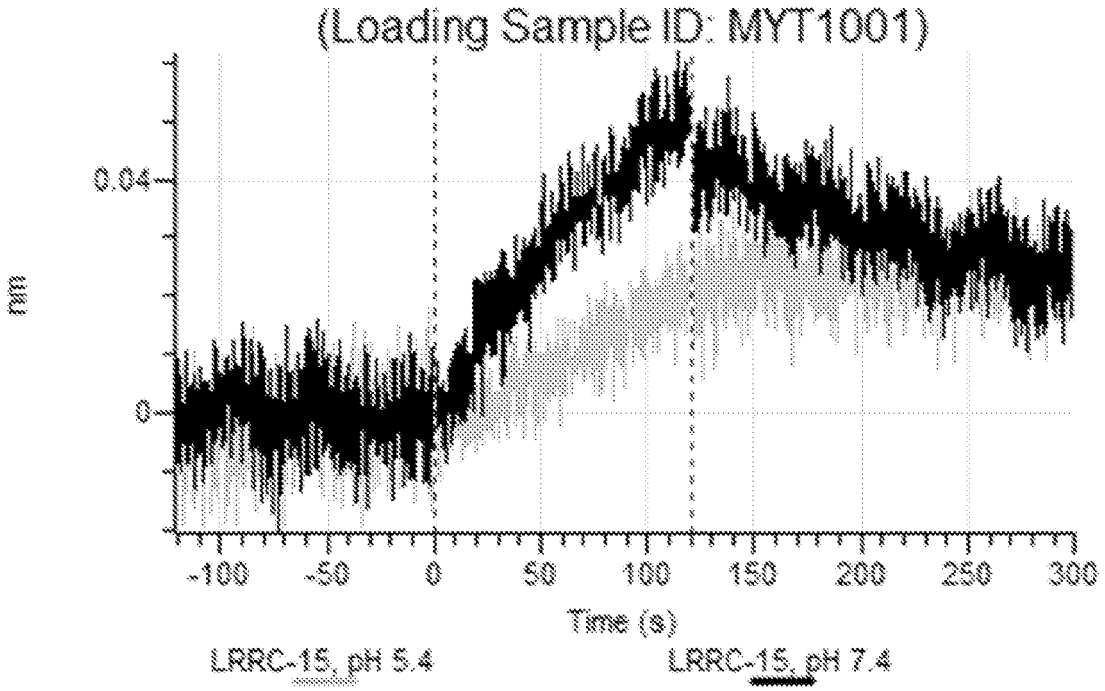

(Loading Sample ID: MYT1001)
0.04
0
nm
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AM

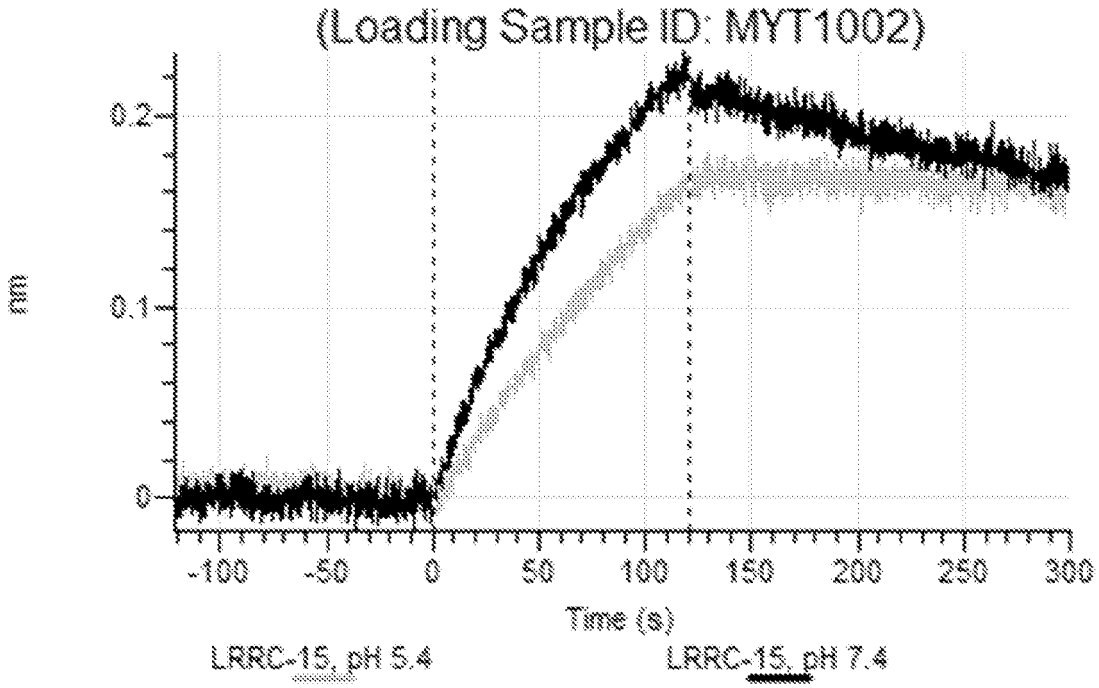

(Loading Sample ID: MYT1002)
nm
0.2
0.1
0
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AN

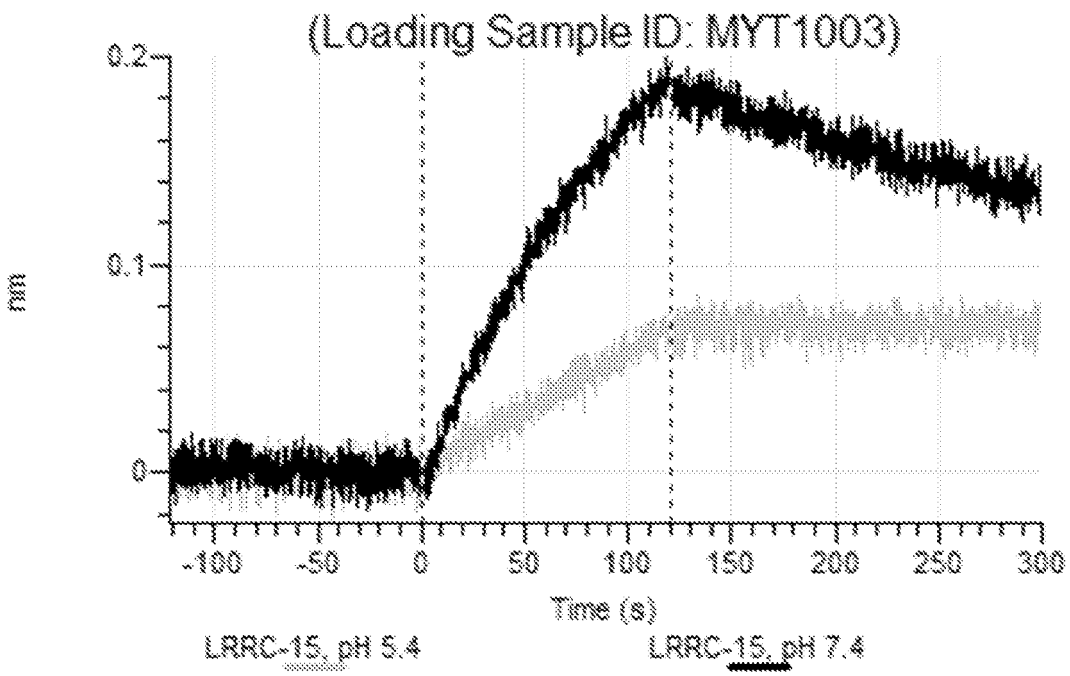

(Loading Sample ID: MYT1003)
0.2
0.1
0
nm
-100
-50
0
50
100
150
200
250
300
Time (s)
LRRC-15, pH 5.4
LRRC-15, pH 7.4

FIG. 2AO

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
MYT0963 (samrotamab)	1	2	3	4	5	6	7	8
MYT0964	13	2						
MYT0965	14	2						
MYT0966	15	2						
MYT0967	16	2						
MYT0968	17	2						
MYT0969	18	2						
MYT0970	19	2						
MYT0971	20	2						
MYT0972	21	2						
MYT0973	22	2						
MYT0974	23	2						
MYT0975	24	2						
MYT0976	25	2						
MYT0977	26	2						
MYT0978	27	2						
MYT0979	28	2						
MYT0980	29	2						
MYT0981	30	2						
MYT0982	31	2						
MYT0983	32	2						
MYT0984	33	2						
MYT0985	34	2						
MYT0986	35	2						
MYT0987	36	2						
MYT0988	37	2						
MYT0989	38	2						
MYT0990	39	2						
MYT0991	40	2						
MYT0992	41	2						
MYT0993	42	2						
MYT0994	43	2						
MYT0995	44	2						
MYT0996	45	2						
MYT0997	46	2						
MYT0998	47	2						
MYT0999	48	2						
MYT1000	49	2						
MYT1001	50	2						
MYT1002	51	2						
MYT1003	52	2						

FIG. 3

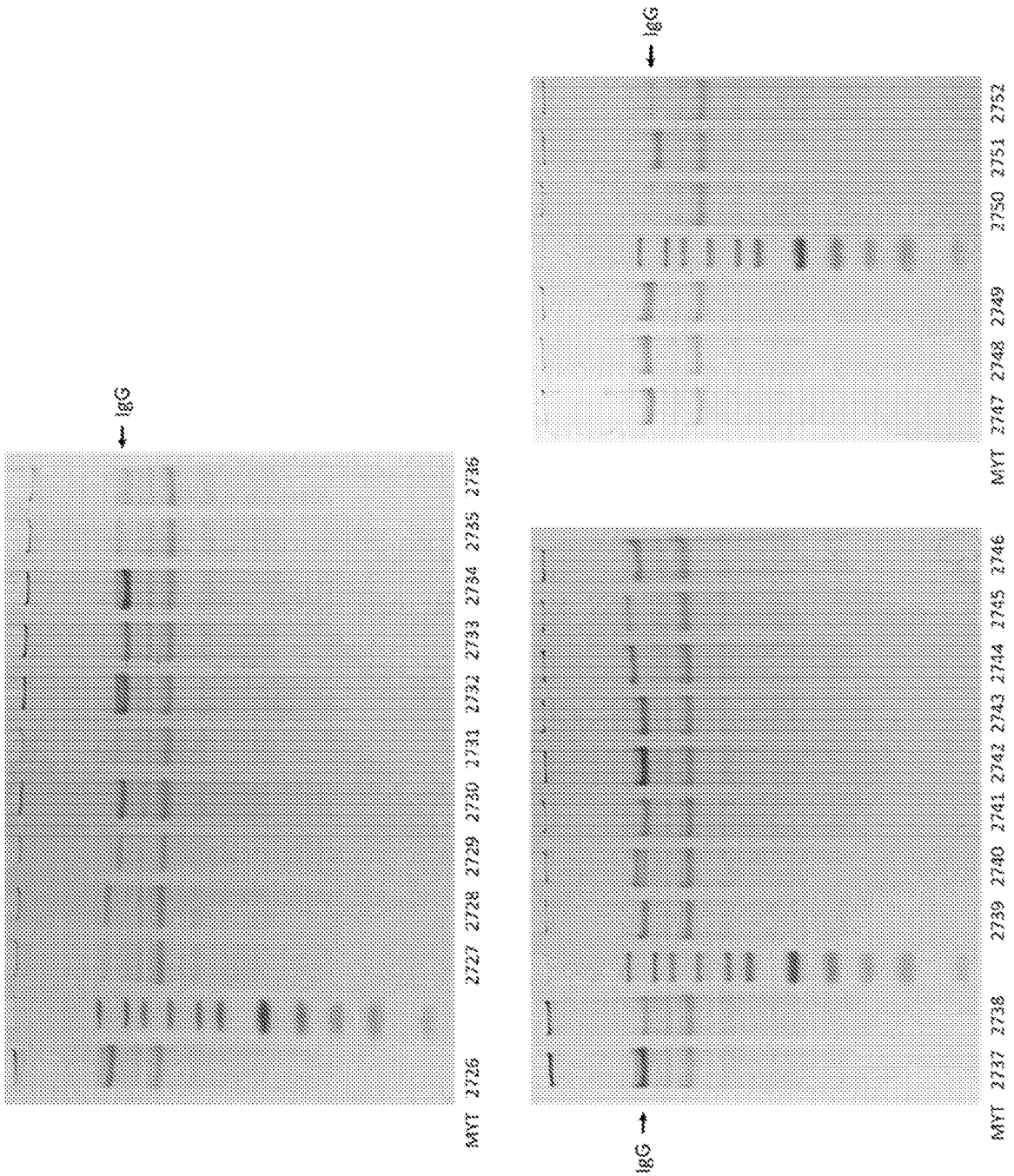

IgG
MYT 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736
IgG
MYT 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746
IgG
MYT 2747 2748 2749 2750 2751 2752

FIG. 4

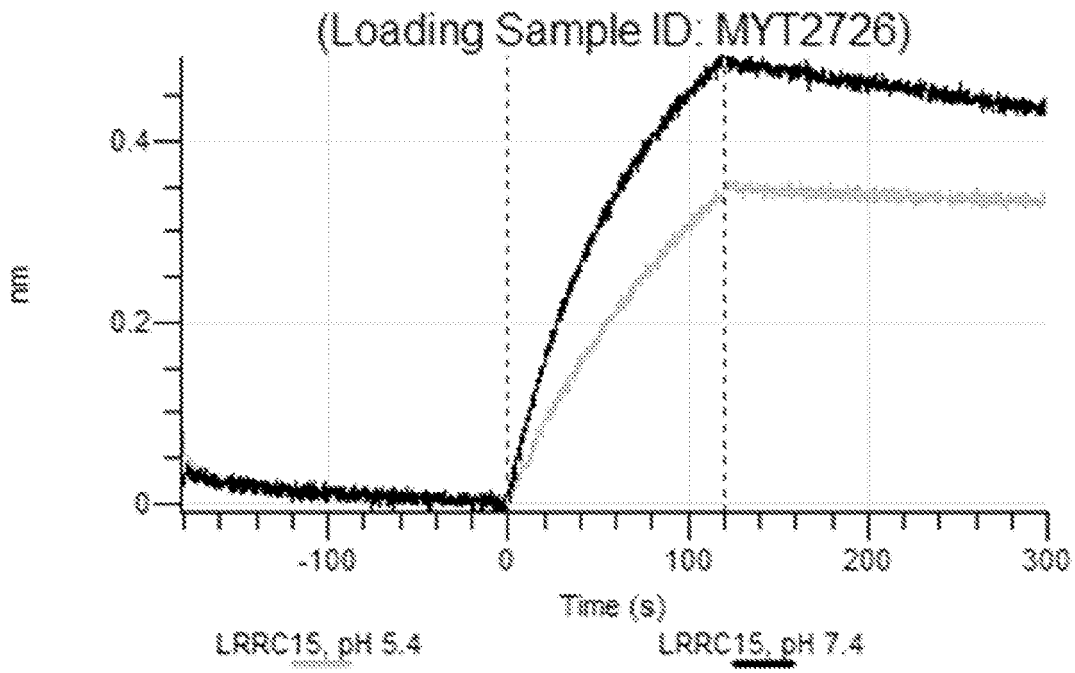

(Loading Sample ID: MYT2726)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5A

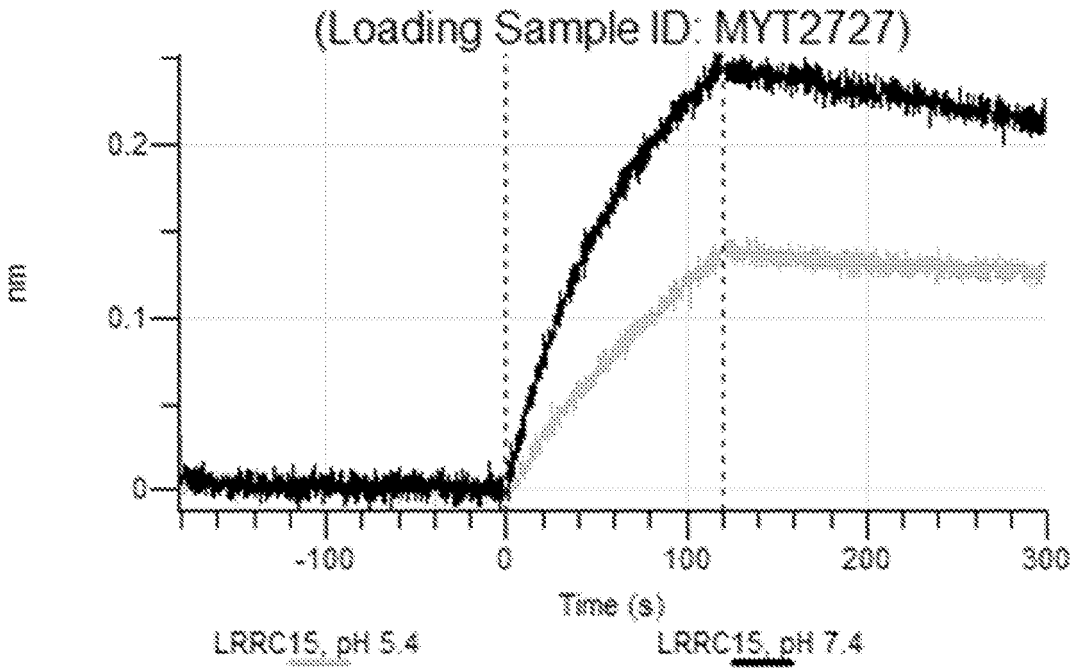

(Loading Sample ID: MYT2727)
nm
0.2
0.1
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5B

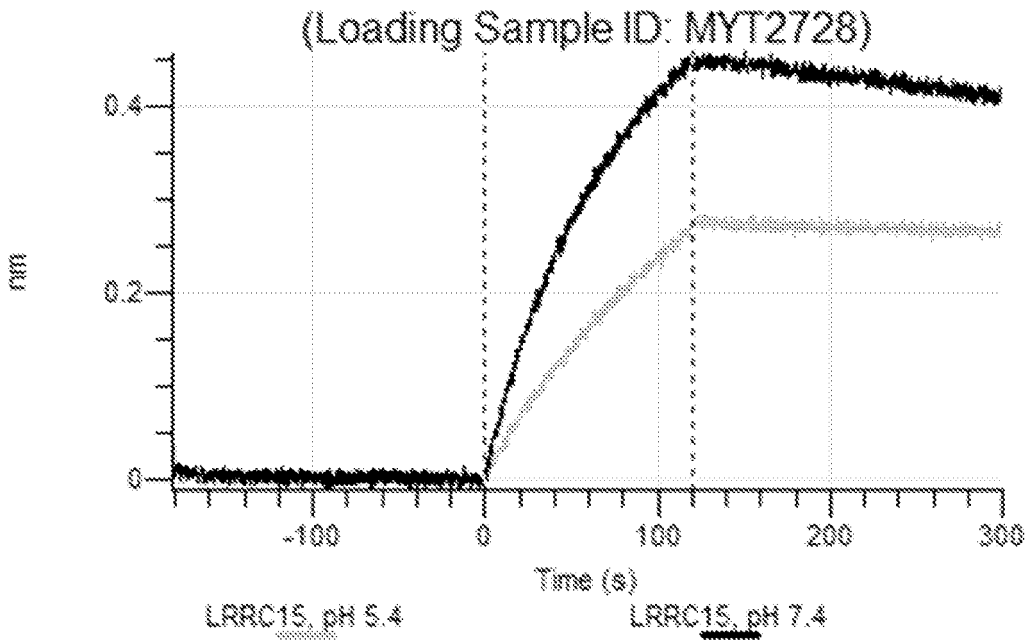

(Loading Sample ID: MYT2728)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15_pH 5.4
LRRC15_pH 7.4

FIG. 5C

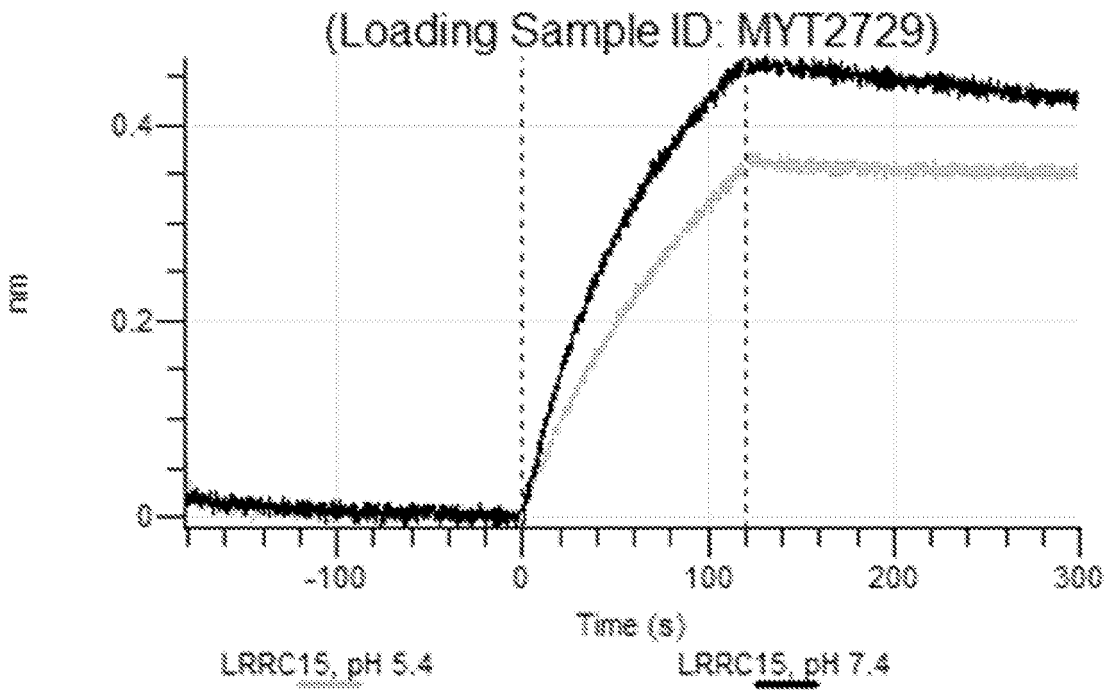

(Loading Sample ID: MYT2729)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5D

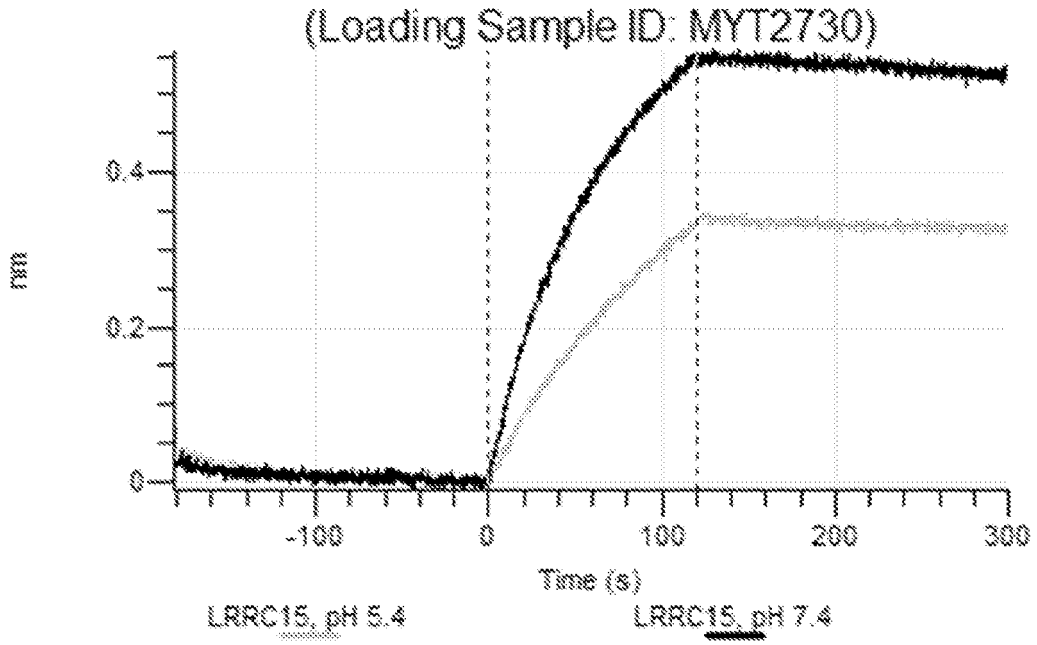

(Loading Sample ID: MYT2730)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5E

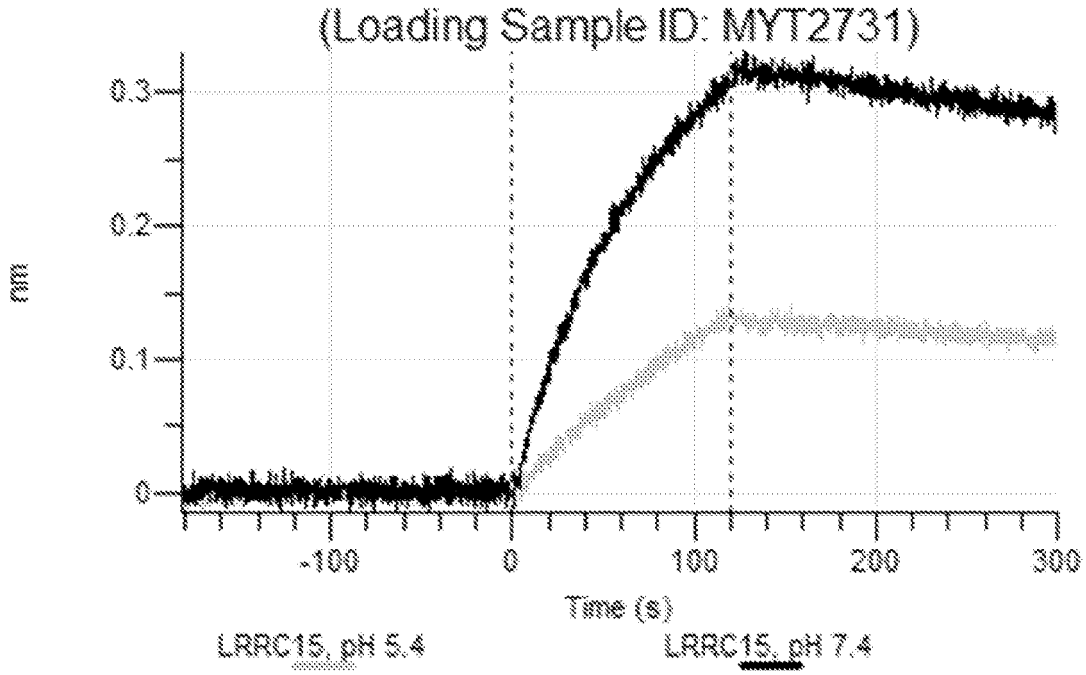

(Loading Sample ID: MYT2731)
0.3
0.2
0.1
0
nm
-100
0
100
200
300
Time (s)
LRRC15_pH 5.4
LRRC15_pH 7.4

FIG. 5F

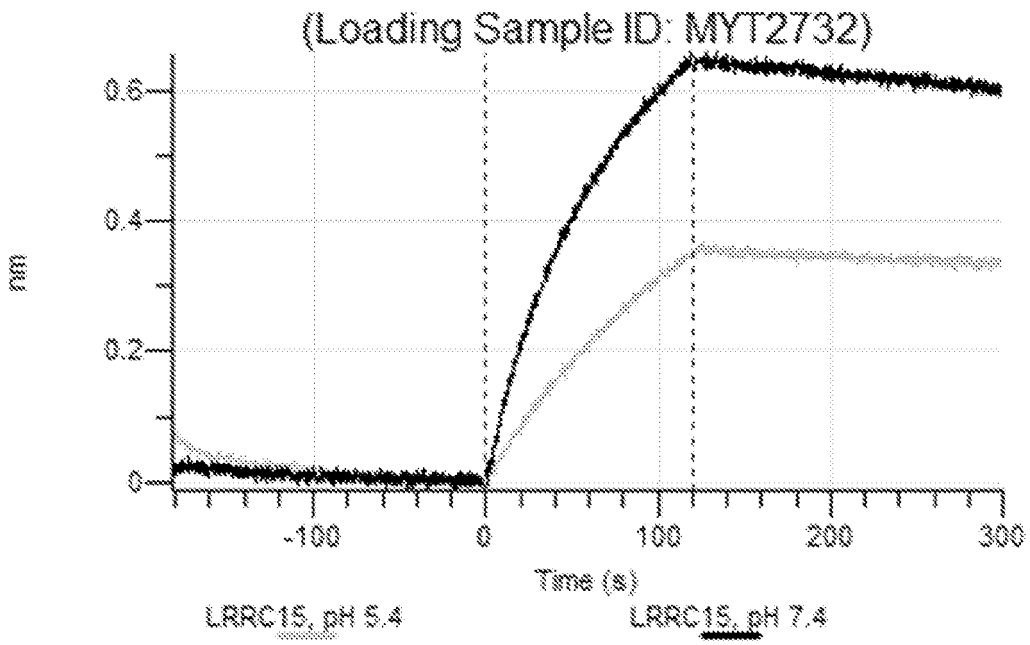

(Loading Sample ID: MYT2732)
0.6
0.4
0.2
0
nm
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5G

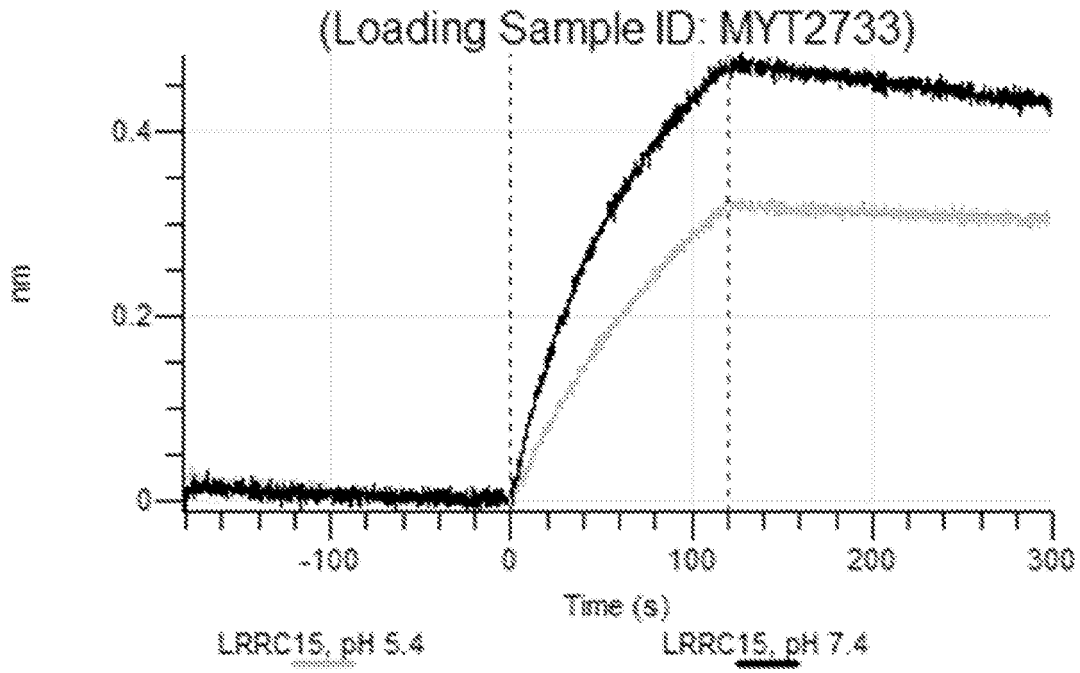

(Loading Sample ID: MYT2733)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5H

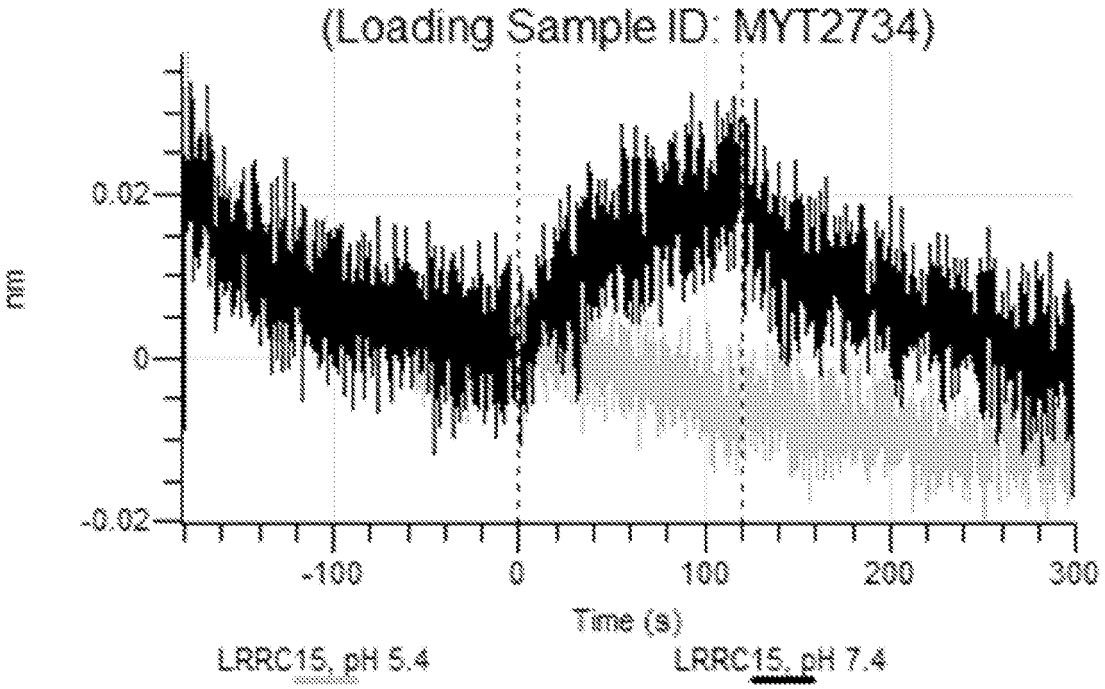

(Loading Sample ID: MYT2734)
nm
0.02
0
-0.02
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5I

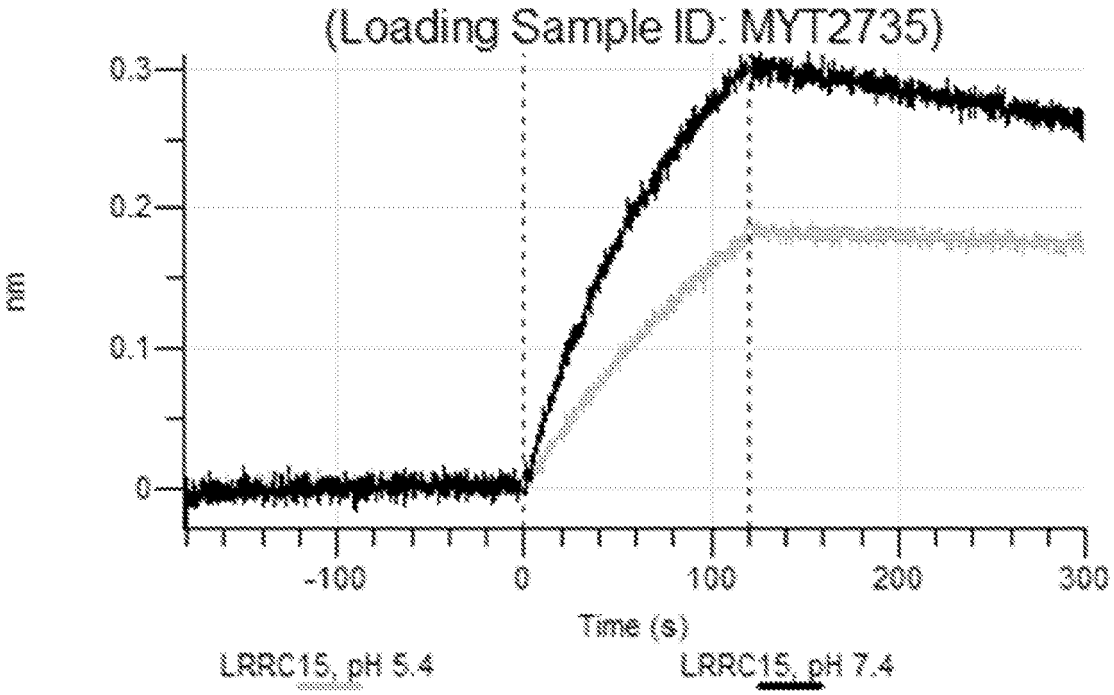

(Loading Sample ID: MYT2735)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5J

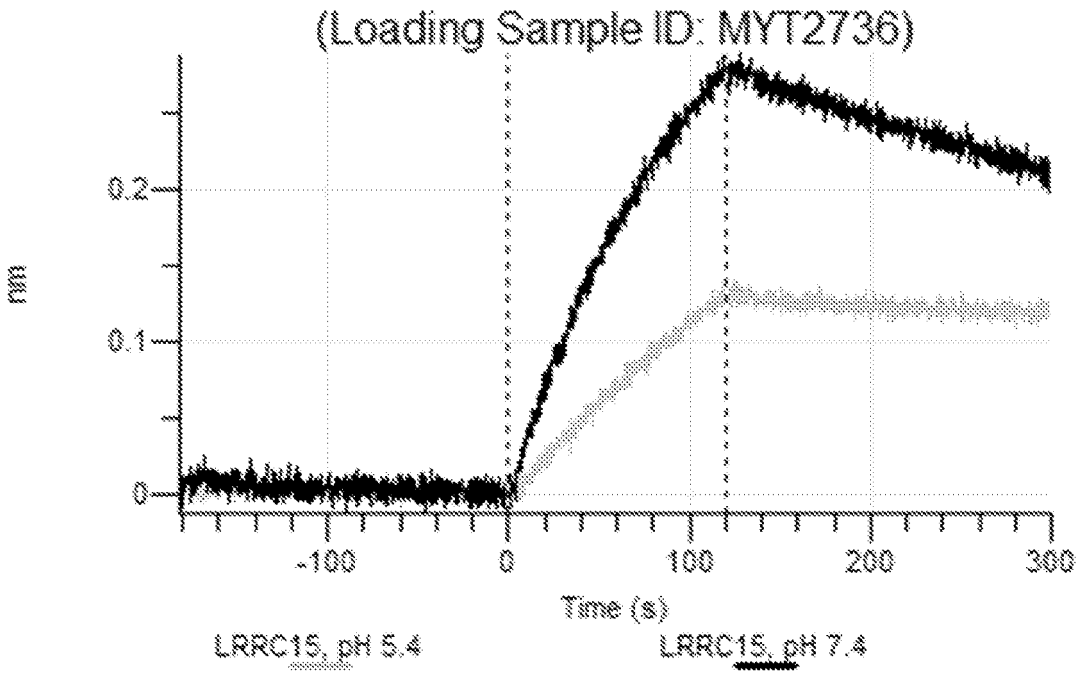

(Loading Sample ID: MYT2736)
nm
0.2
0.1
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5K

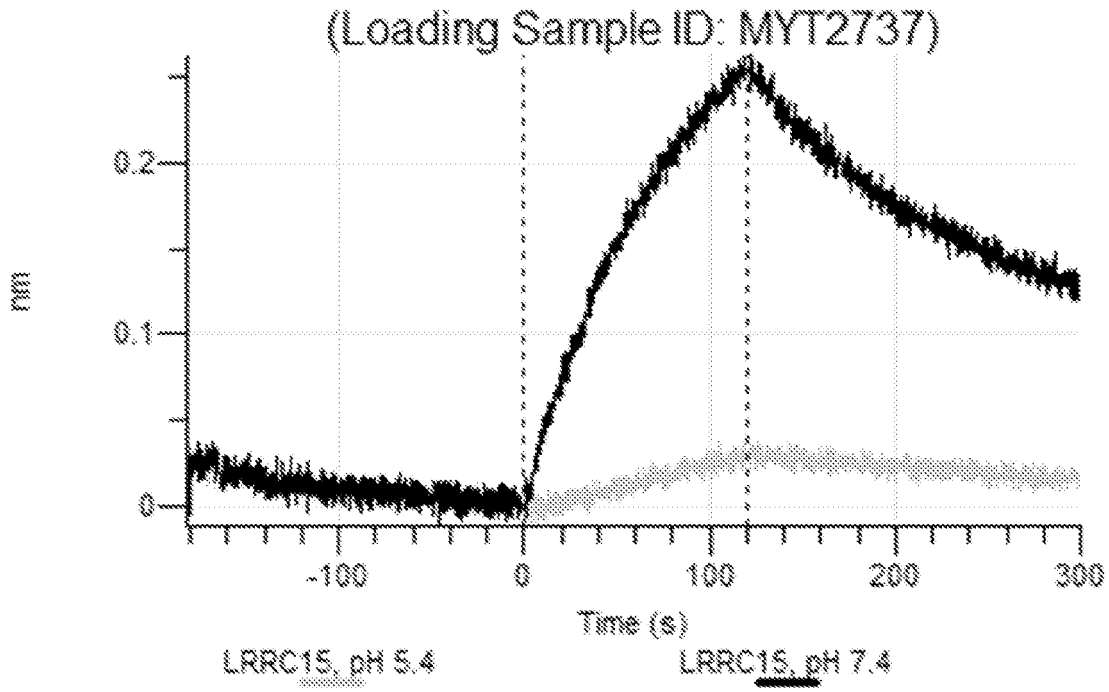

(Loading Sample ID: MYT2737)
nm
0.2
0.1
0
-100
0
100
200
300
Time (s)
LRRC15_pH 5.4
LRRC15_pH 7.4

FIG. 5L

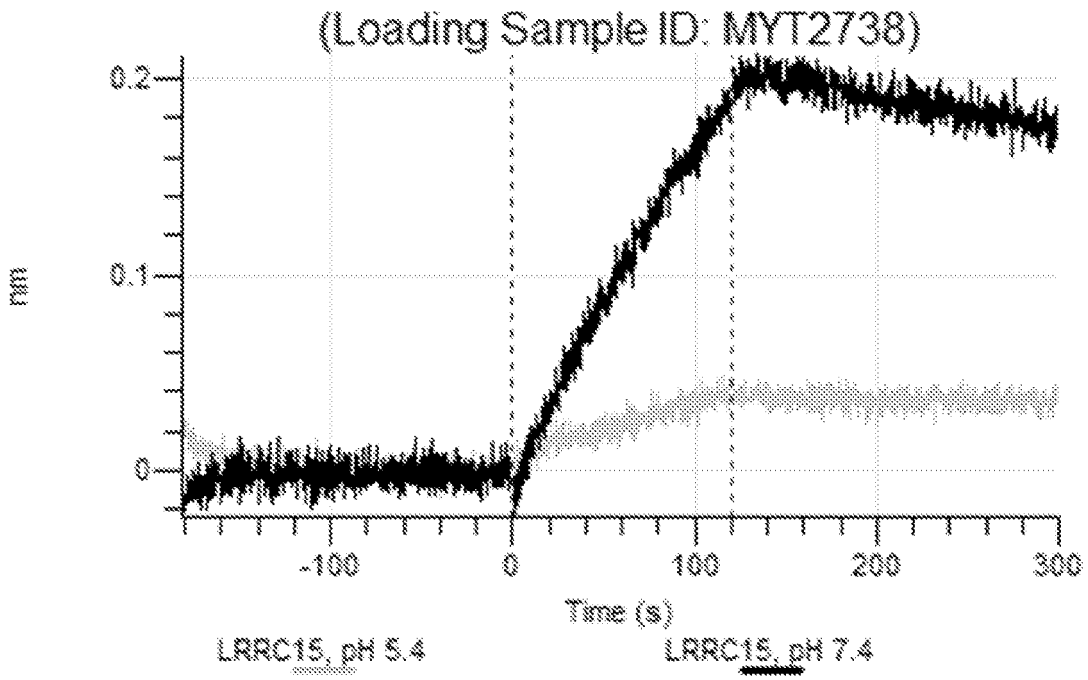

(Loading Sample ID: MYT2738)
nm
0.2
0.1
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5M

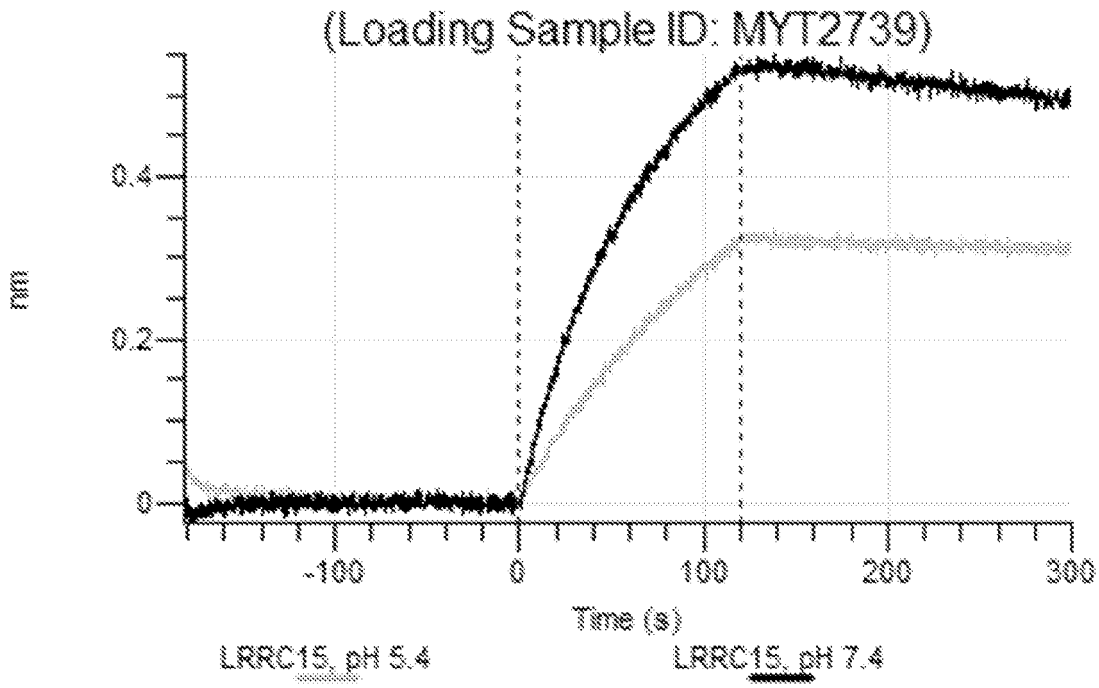

(Loading Sample ID: MYT2739)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15_pH 5.4
LRRC15_pH 7.4

FIG. 5N

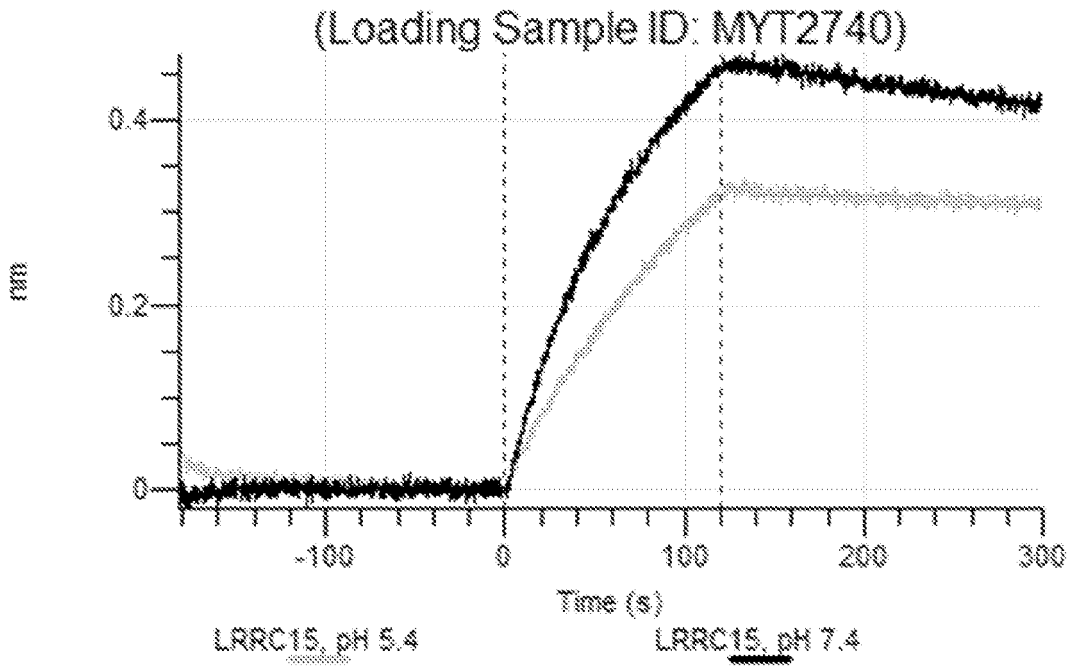

(Loading Sample ID: MYT2740)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5O

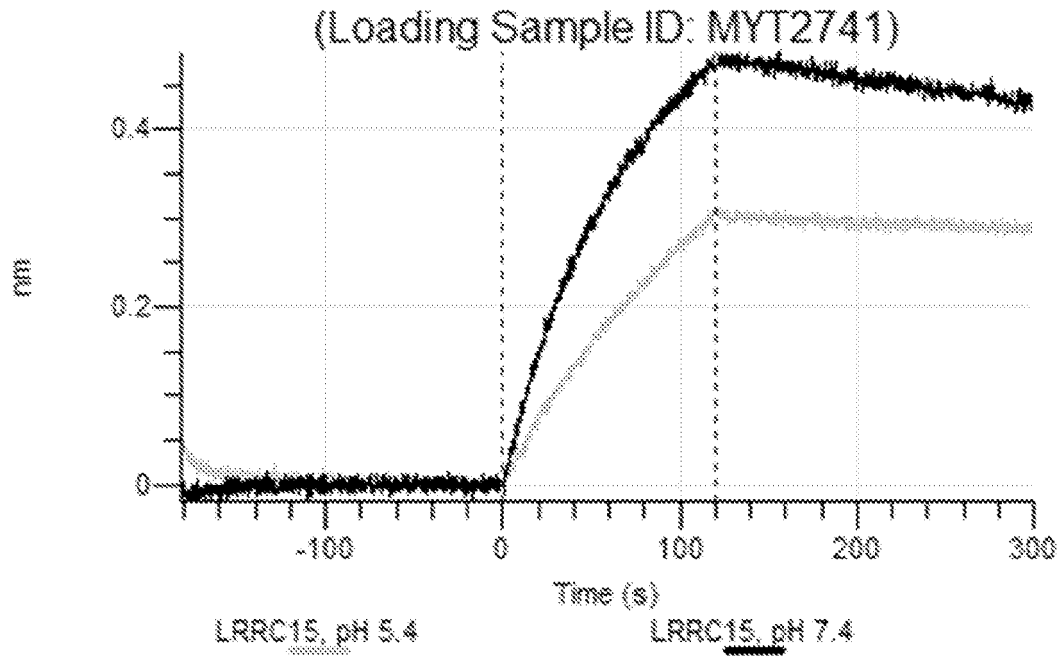

(Loading Sample ID: MYT2741)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5P

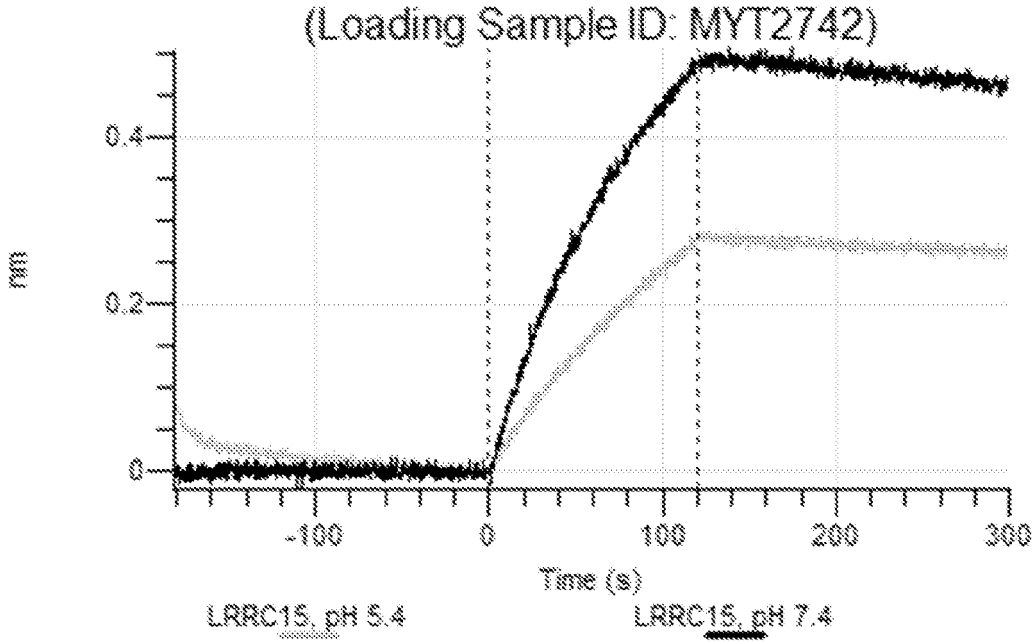

(Loading Sample ID: MYT2742)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5Q

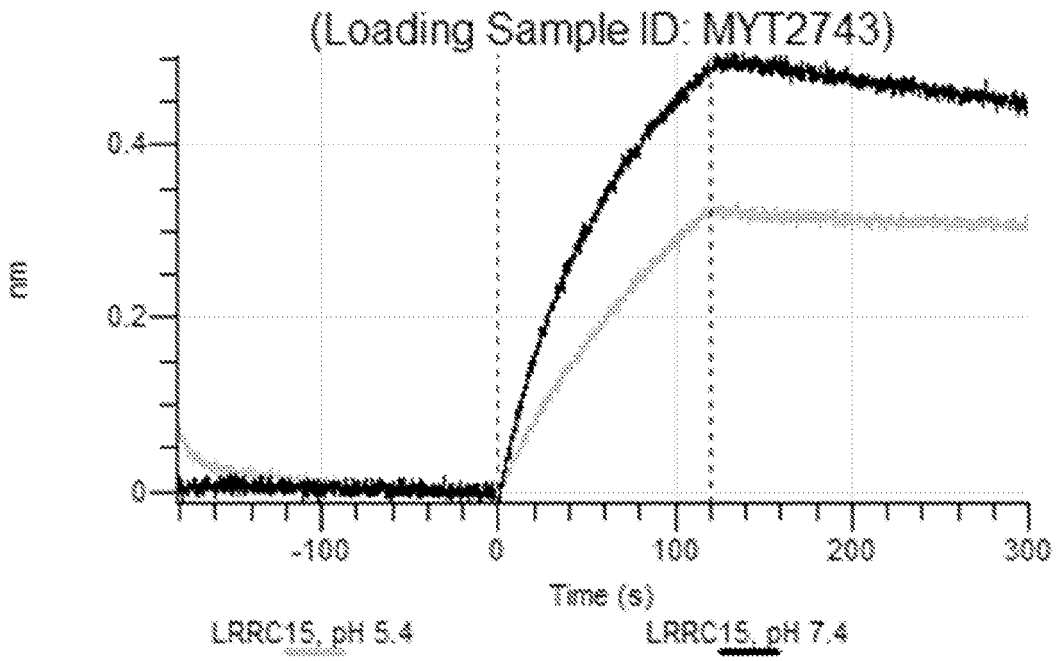

(Loading Sample ID: MYT2743)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15_pH 5.4
LRRC15_pH 7.4

FIG. 5R

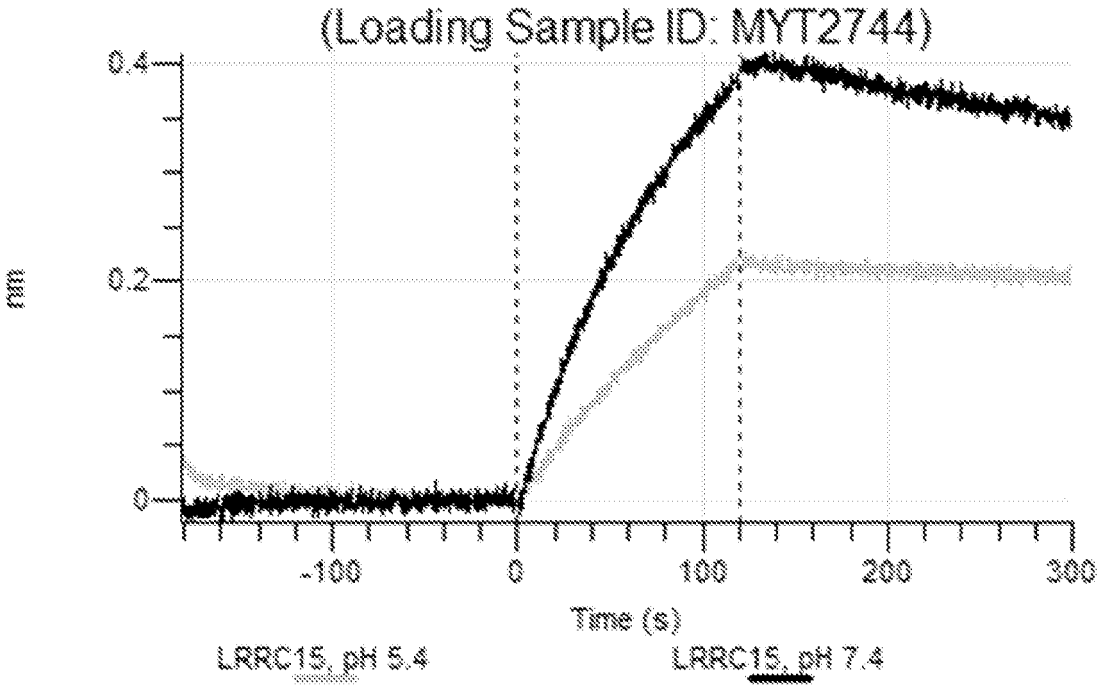

(Loading Sample ID: MYT2744)
0.4
0.2
0
nm
-100
0
100
200
300
Time (s)
LRRC15_pH 5.4
LRRC15_pH 7.4

FIG. 5S

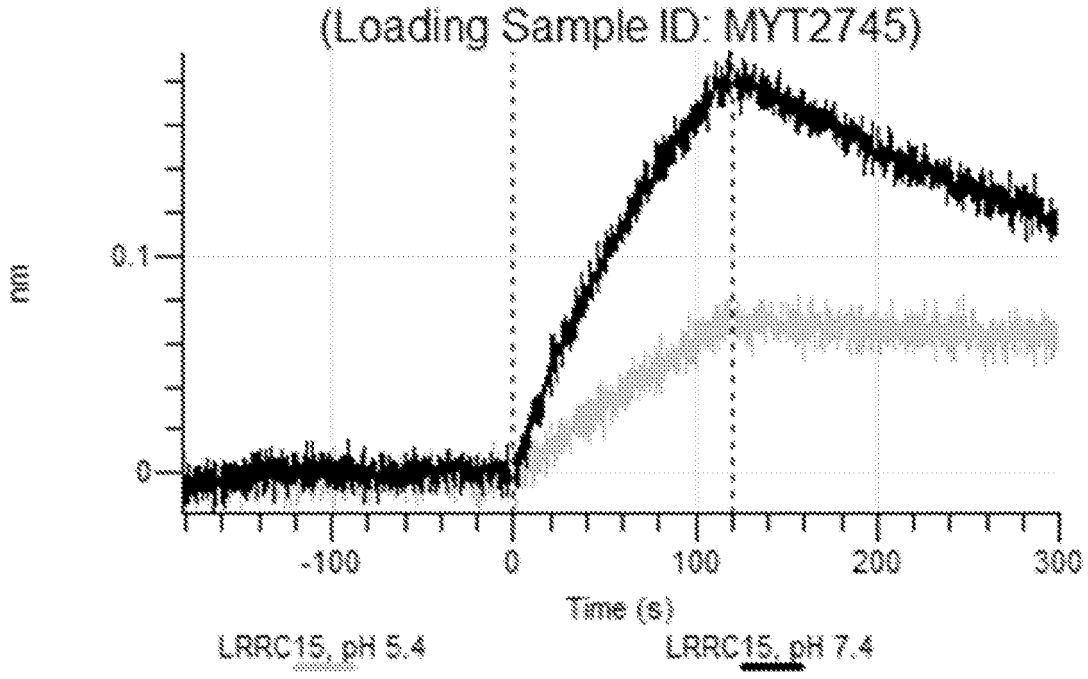

(Loading Sample ID: MYT2745)
nm
0.1
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5T

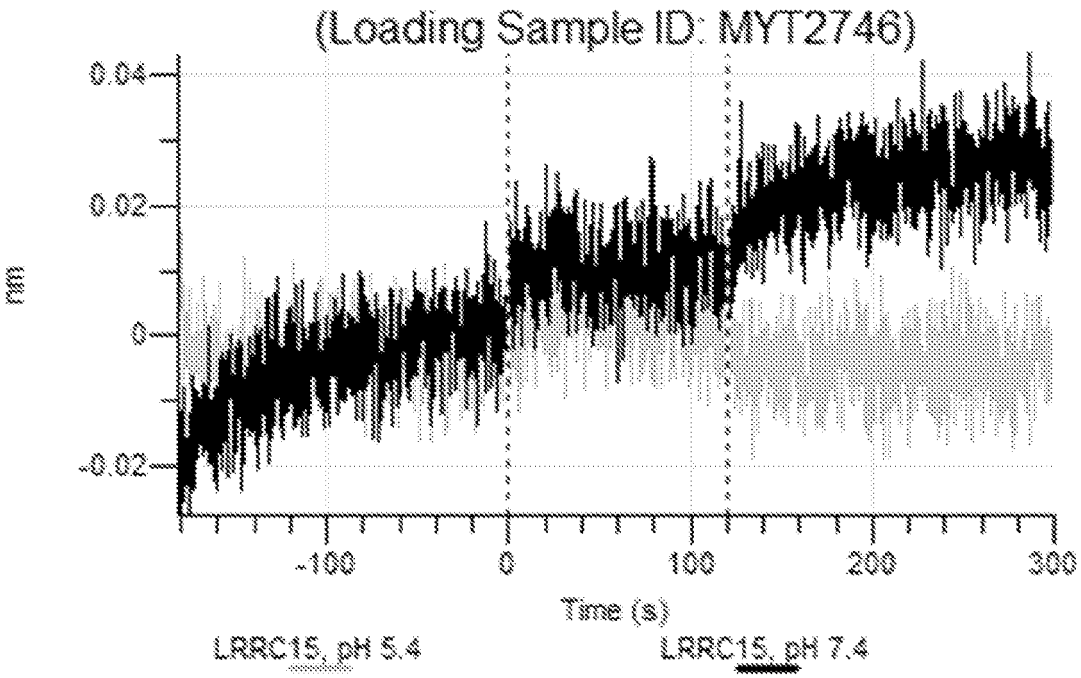

(Loading Sample ID: MYT2746)
0.04
0.02
0
-0.02
nm
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5U

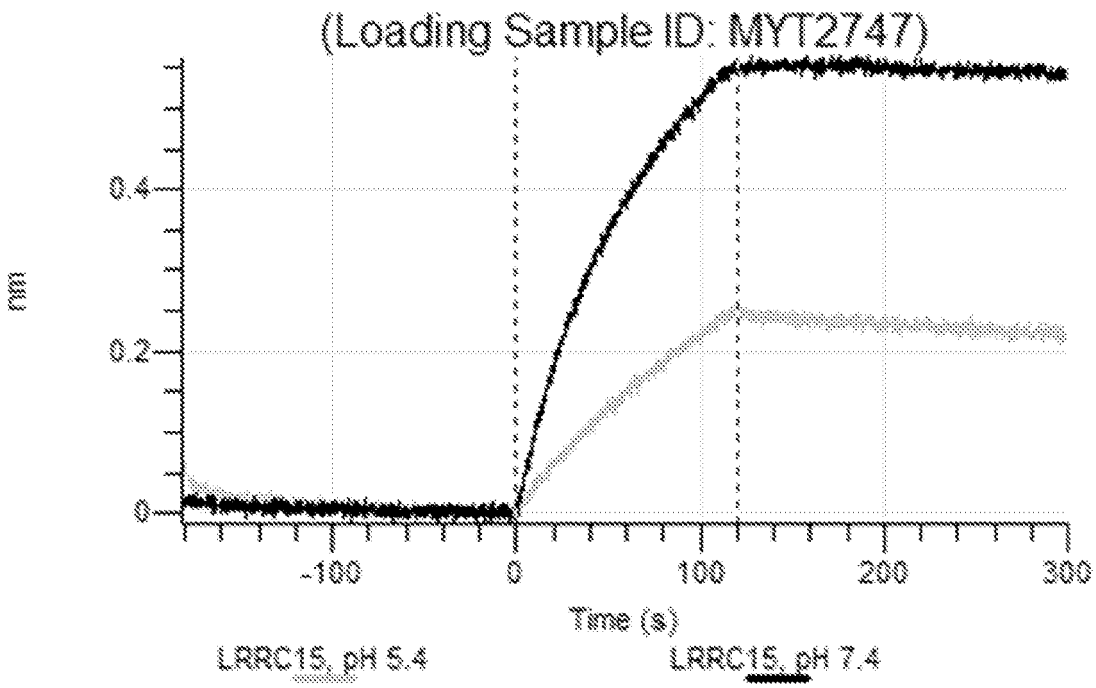

(Loading Sample ID: MYT2747)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5V

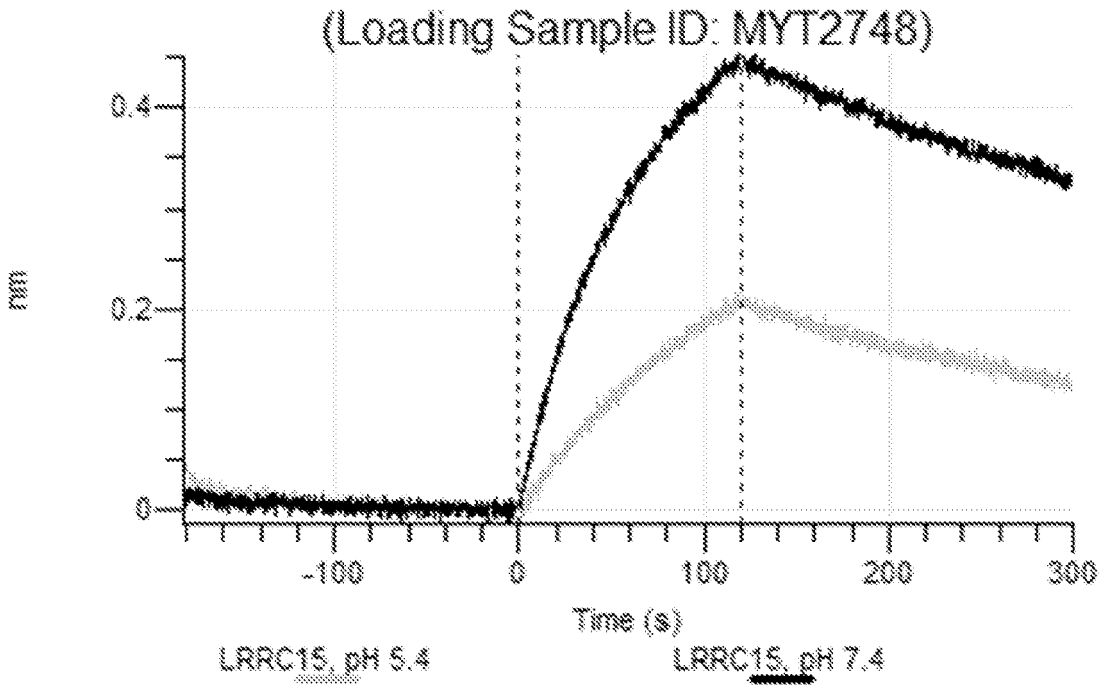

(Loading Sample ID: MYT2748)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15_pH 5.4
LRRC15_pH 7.4

FIG. 5W

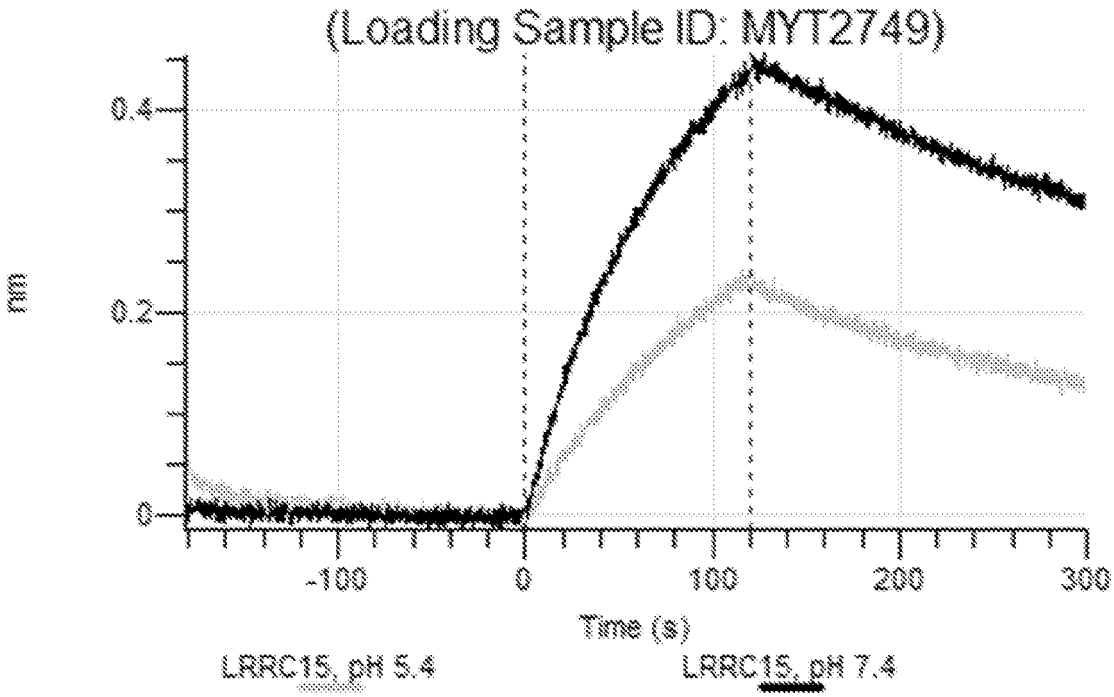

(Loading Sample ID: MYT2749)
nm
0.4
0.2
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 5X

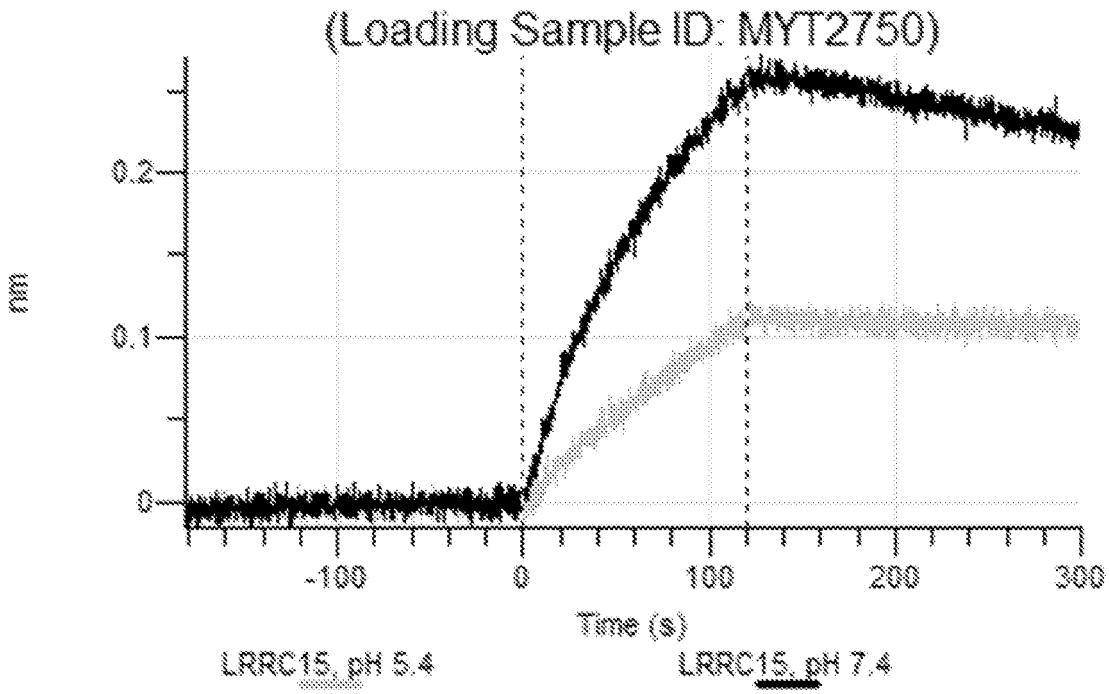

(Loading Sample ID: MYT2750)
nm
0.2
0.1
0
-100
0
100
200
300
Time (s)
LRRC15_pH 5.4
LRRC15_pH 7.4

FIG. 5Y

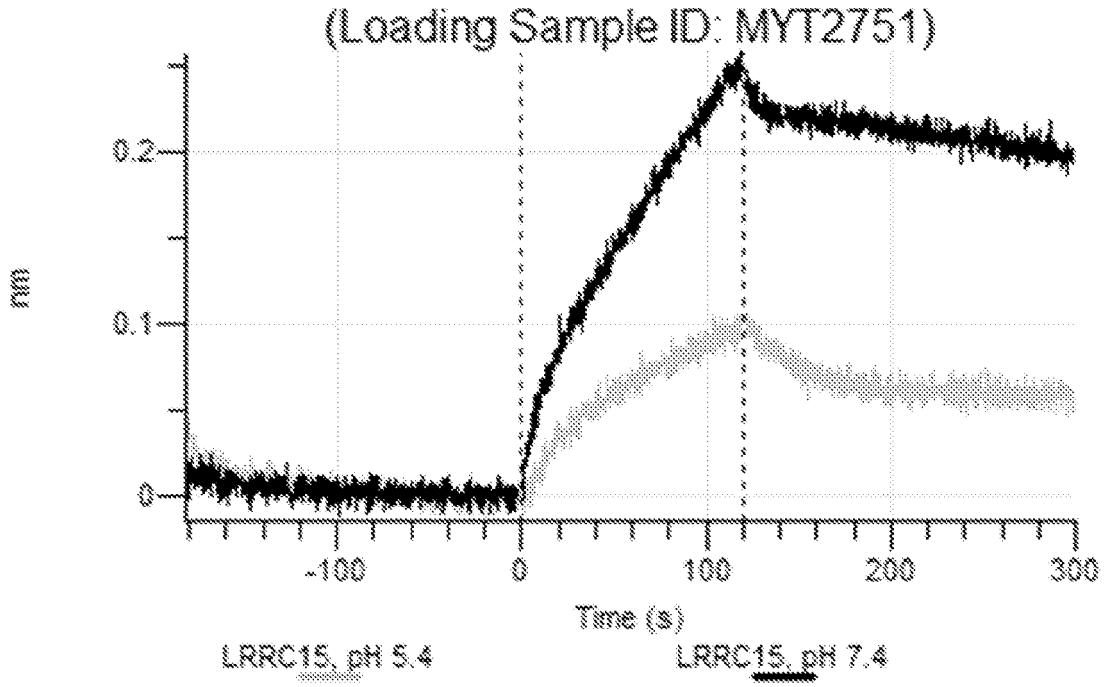

(Loading Sample ID: MYT2751)
nm
0.2
0.1
0
-100
0
100
200
300
Time (s)
LRRC15_pH 5.4
LRRC15_pH 7.4

FIG. 5Z

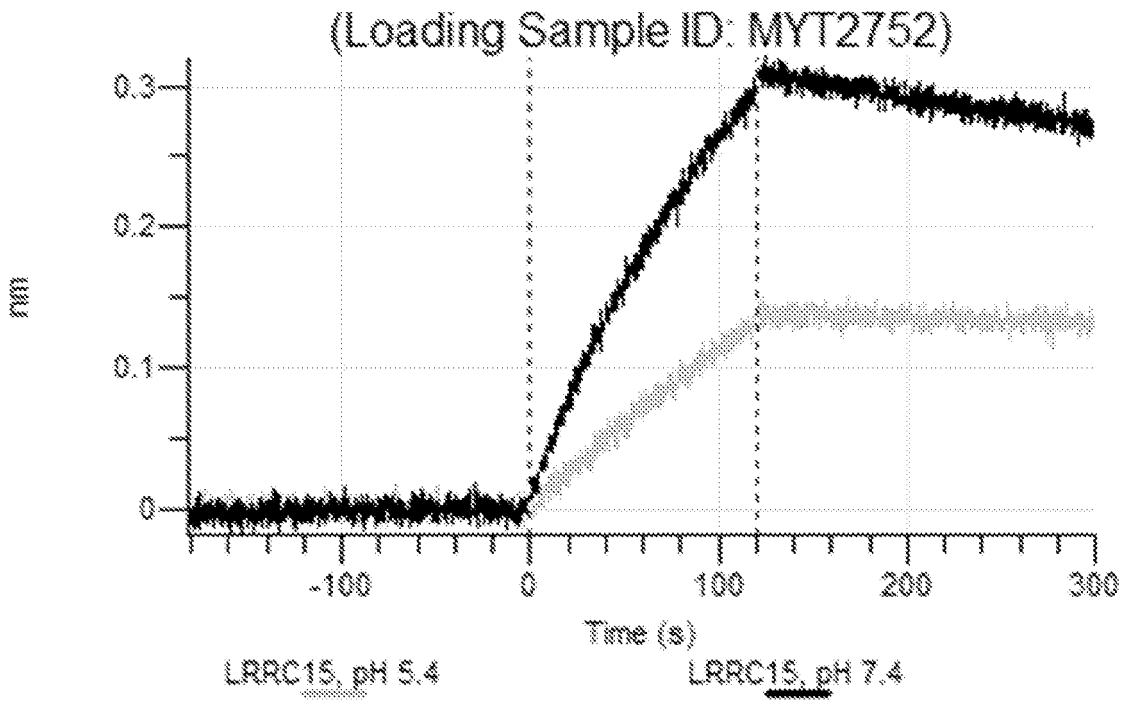

(Loading Sample ID: MYT2752)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
Time (s)
LRRC15_pH 5.4
LRRC15_pH 7.4

FIG. 5AA

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
MYT0963 (samrotamab)	1	2	3	4	5	6	7	8
MYT2726	1	53						
MYT2727	1	54						
MYT2728	1	55						
MYT2729	1	56						
MYT2730	1	57						
MYT2731	1	58						
MYT2732	1	59						
MYT2733	1	60						
MYT2734	1	61						
MYT2735	1	62						
MYT2736	1	63						
MYT2737	1	64						
MYT2738	1	65						
MYT2739	1	66						
MYT2740	1	67						
MYT2741	1	68						
MYT2742	1	69						
MYT2743	1	70						
MYT2744	1	71						
MYT2745	1	72						
MYT2746	1	73						
MYT2747	1	74						
MYT2748	1	75						
MYT2749	1	76						
MYT2750	1	77						
MYT2751	1	78						
MYT2752	1	79						

FIG. 6

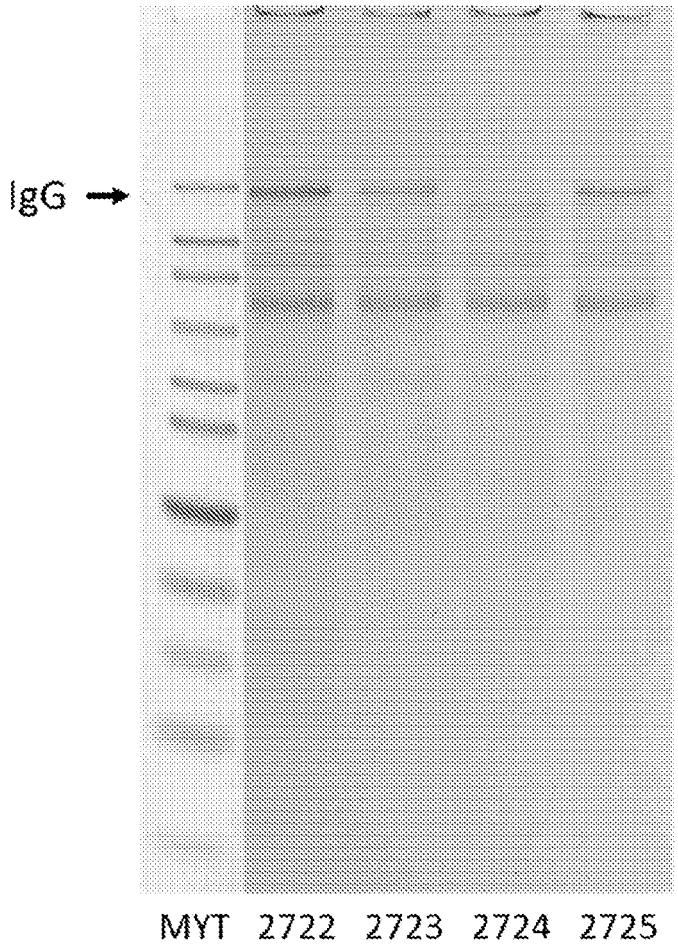


FIG. 7

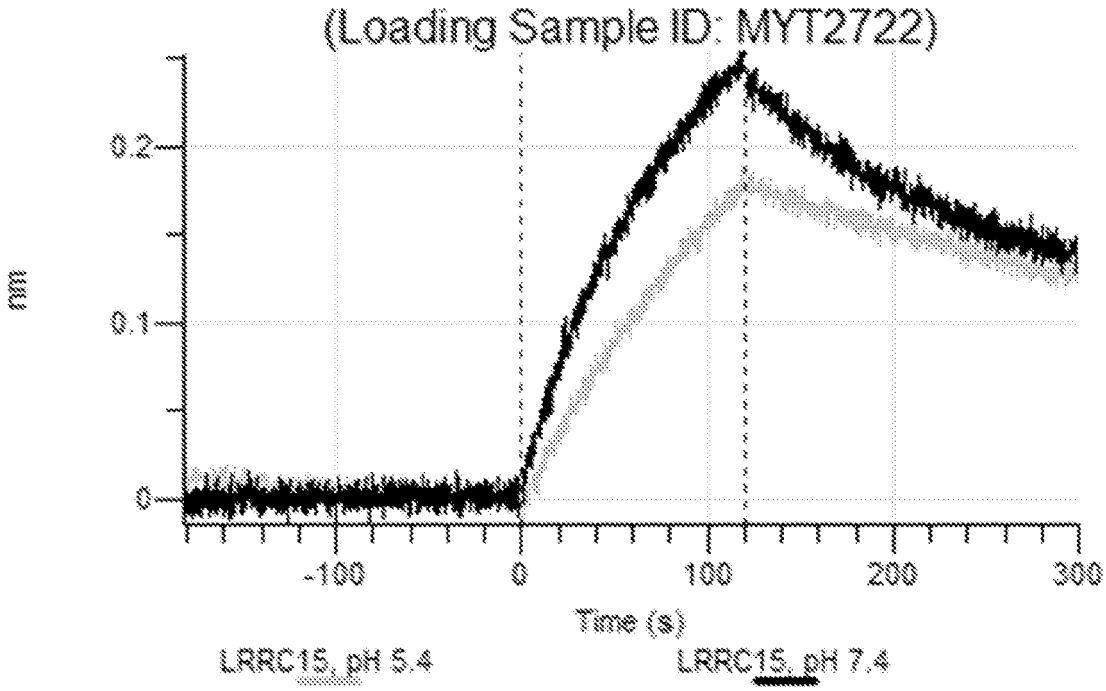

(Loading Sample ID: MYT2722)
nm
0.2
0.1
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 8A

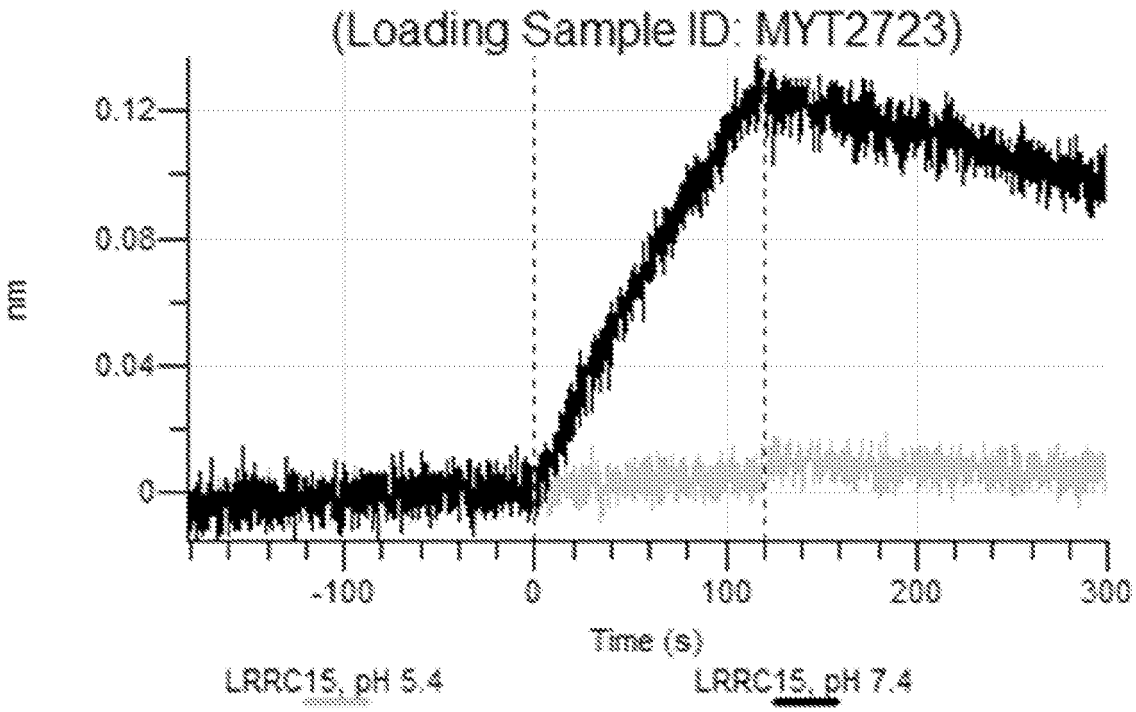

(Loading Sample ID: MYT2723)
0.12
0.08
0.04
0
nm
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 8B

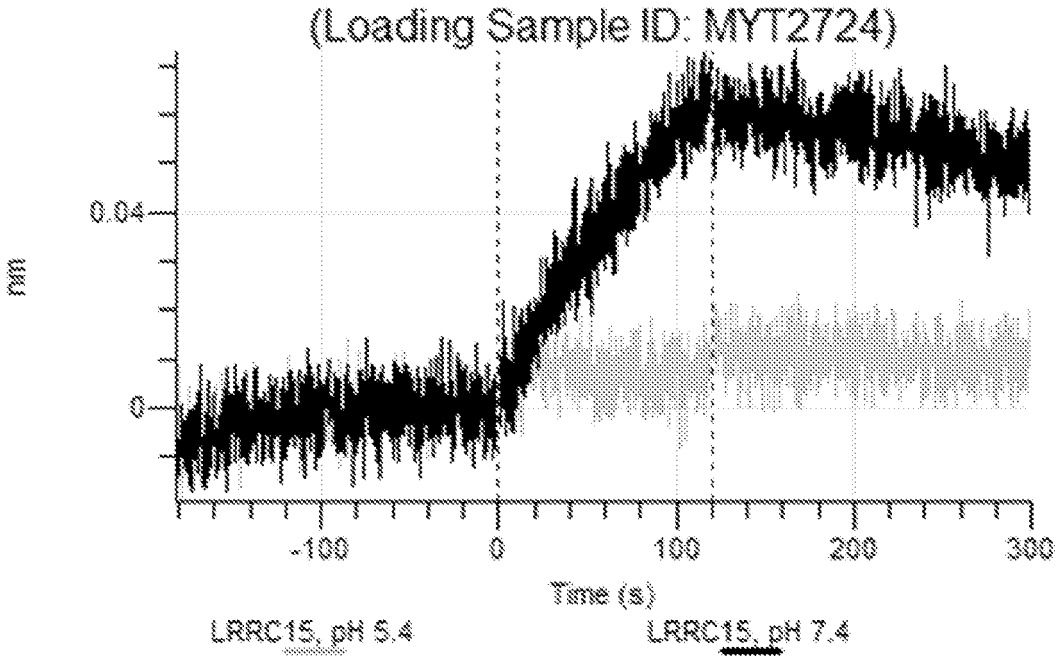

(Loading Sample ID: MYT2724)
nm
0.04
0
-100
0
100
200
300
Time (s)
LRRC15, pH 5.4
LRRC15, pH 7.4

FIG. 8C

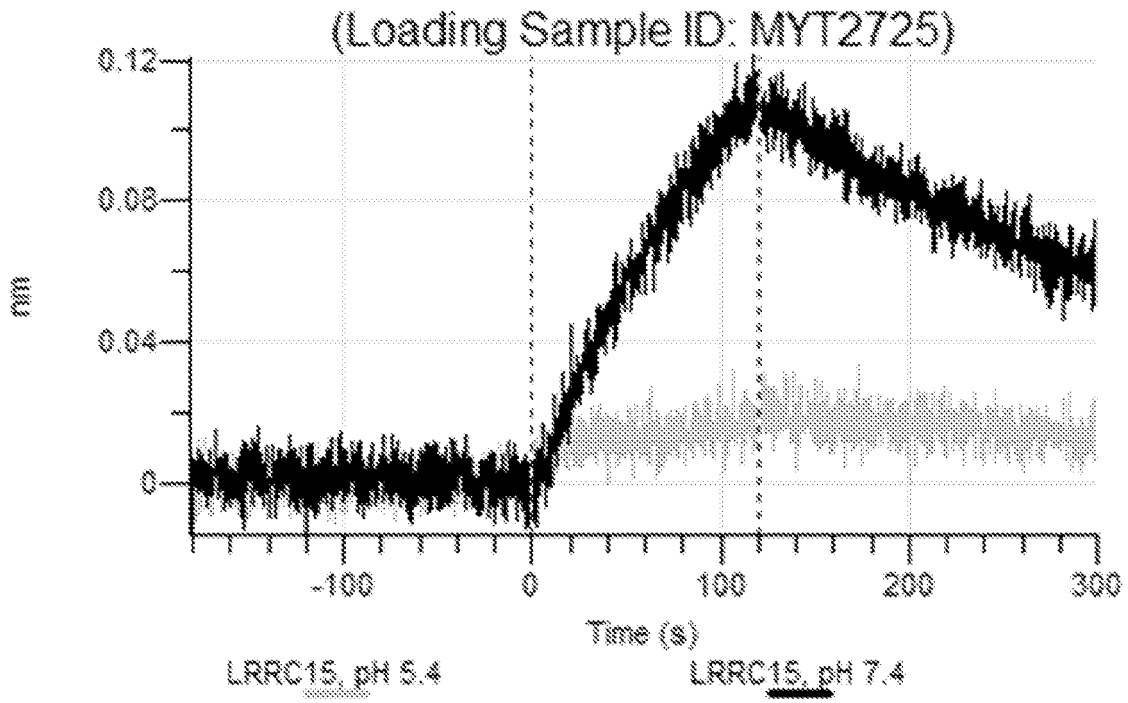

(Loading Sample ID: MYT2725)
0.12
0.08
0.04
0
nm
-100
0
100
200
300
Time (s)
LRRC15_pH 5.4
LRRC15_pH 7.4

FIG. 8D

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
MYT0963 (samrotamab)	1	2	3	4	5	6	7	8
MYT2722	80	2						
MYT2723	81	2						
MYT2724	82	2						
MYT2725	83	2						

FIG. 9

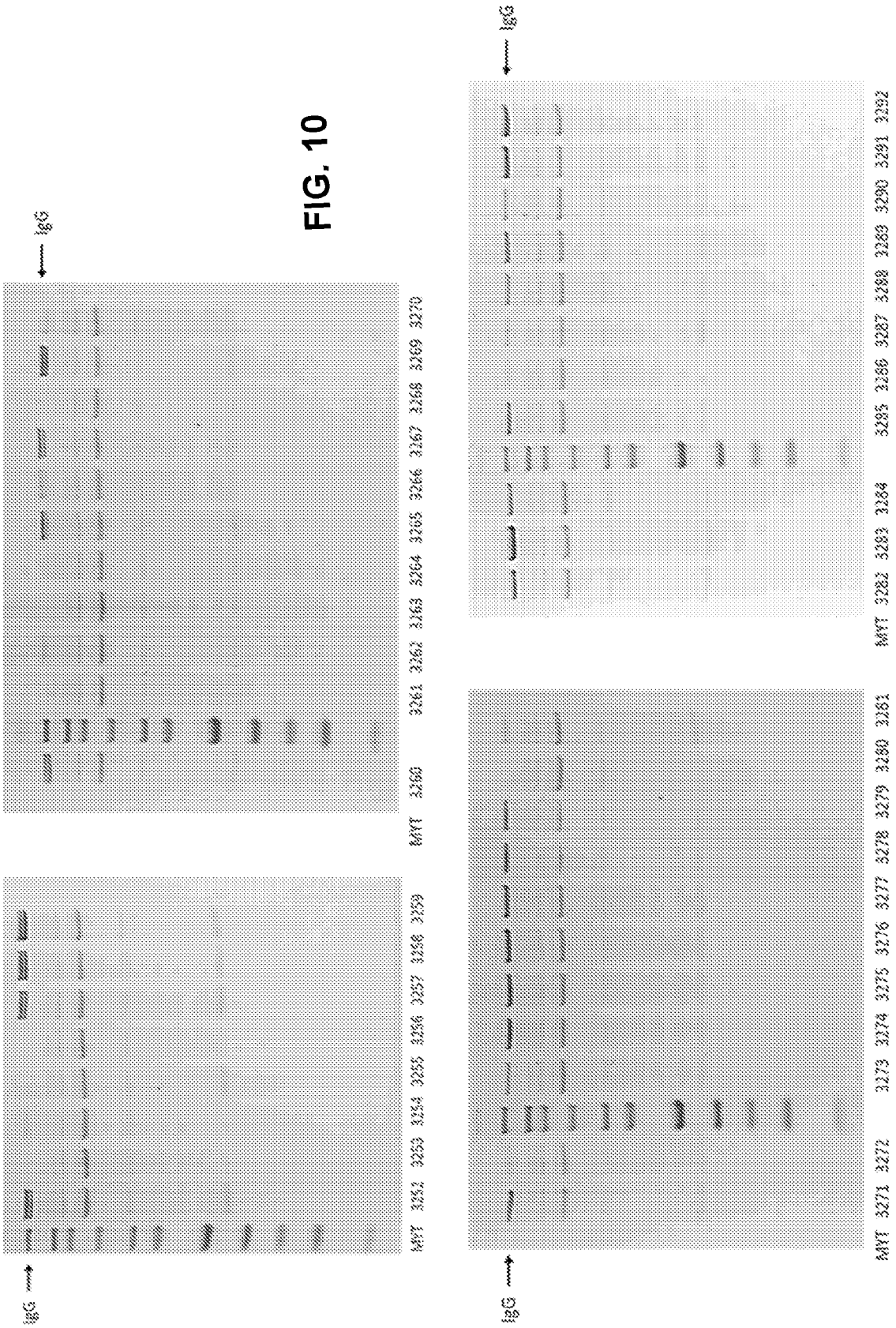

IgG
IgG
IgG
IgG
MWT 3252 3253 3254 3255 3256 3257 3258 3259
MWT 3260 3261 3262 3263 3264 3265 3266 3267 3268 3269 3270
MWT 3271 3272 3273 3274 3275 3276 3277 3278 3279 3280 3281
MWT 3282 3283 3284 3285 3286 3287 3288 3289 3290 3291 3292

FIG. 10

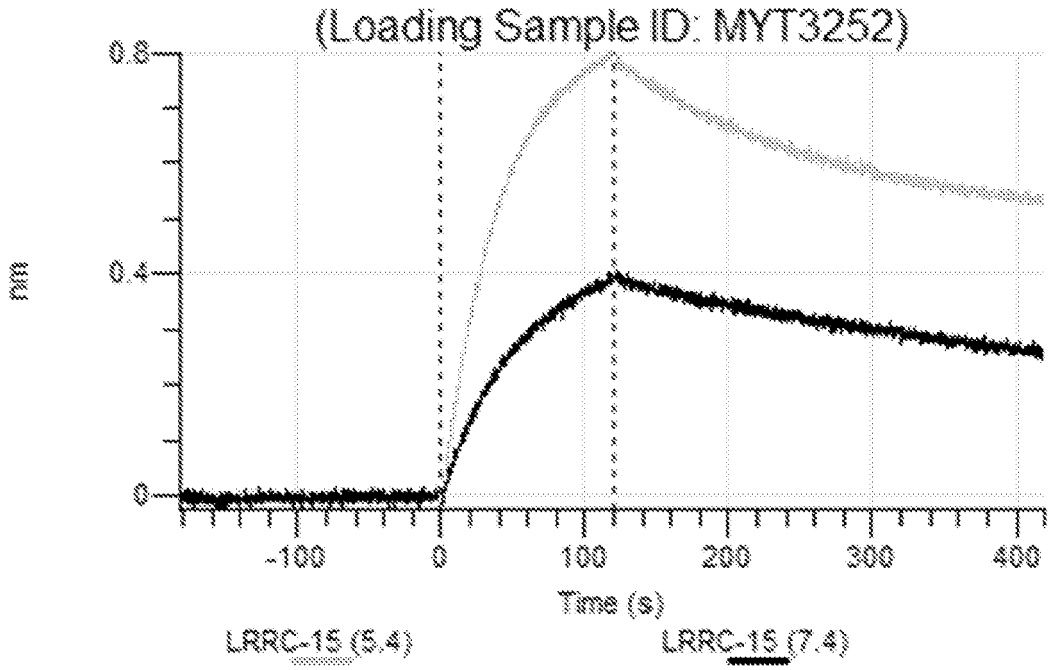

(Loading Sample ID: MYT3252)
0.8
0.4
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11A

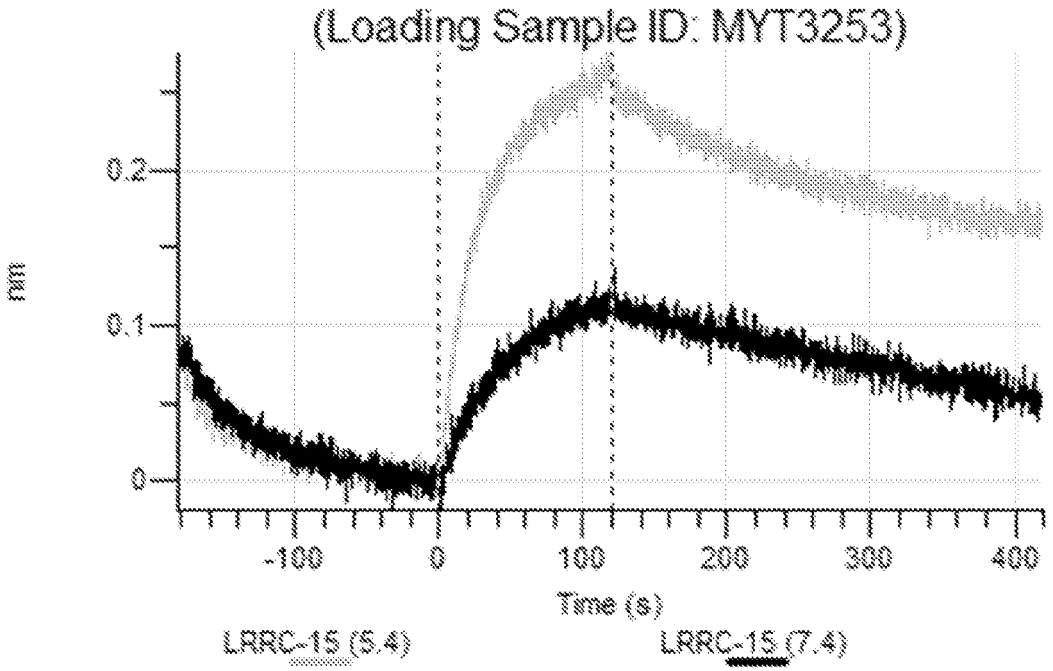

(Loading Sample ID: MYT3253)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11B

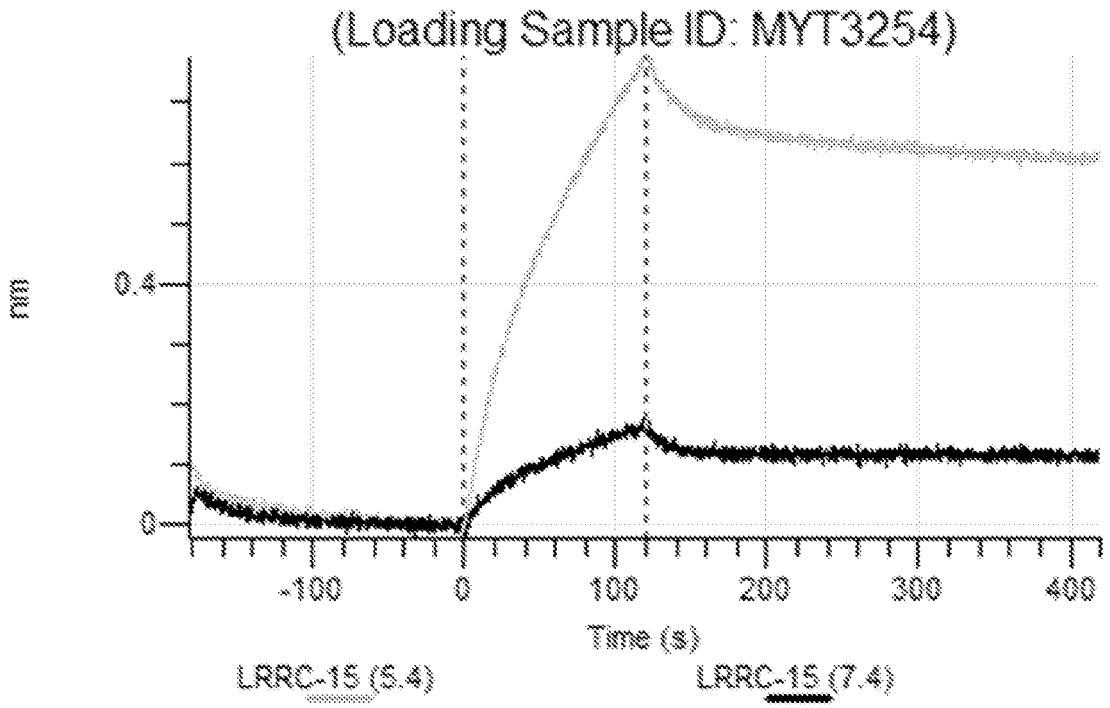

(Loading Sample ID: MYT3254)
nm
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11C

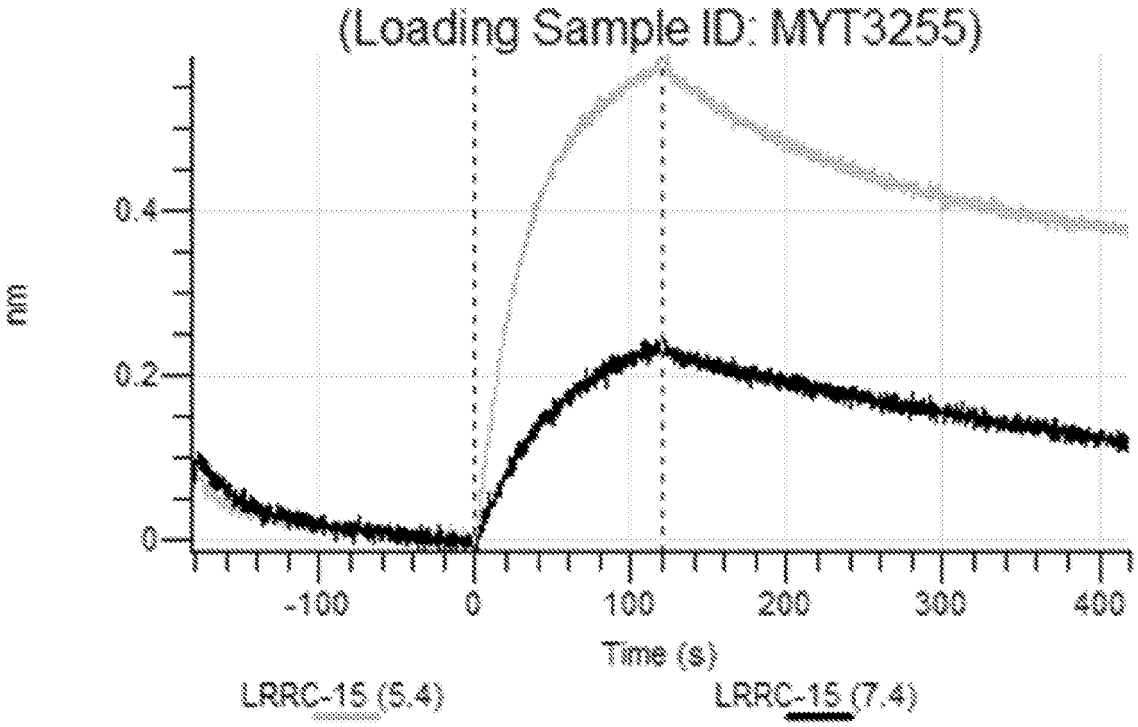

(Loading Sample ID: MYT3255)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11D

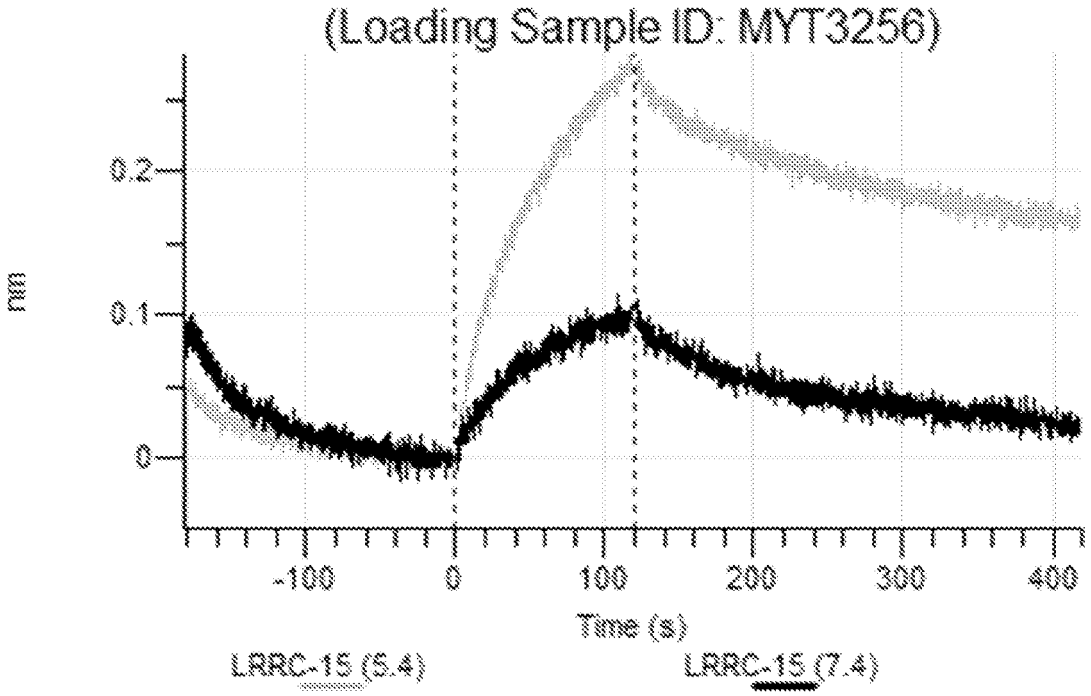

(Loading Sample ID: MYT3256)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11E

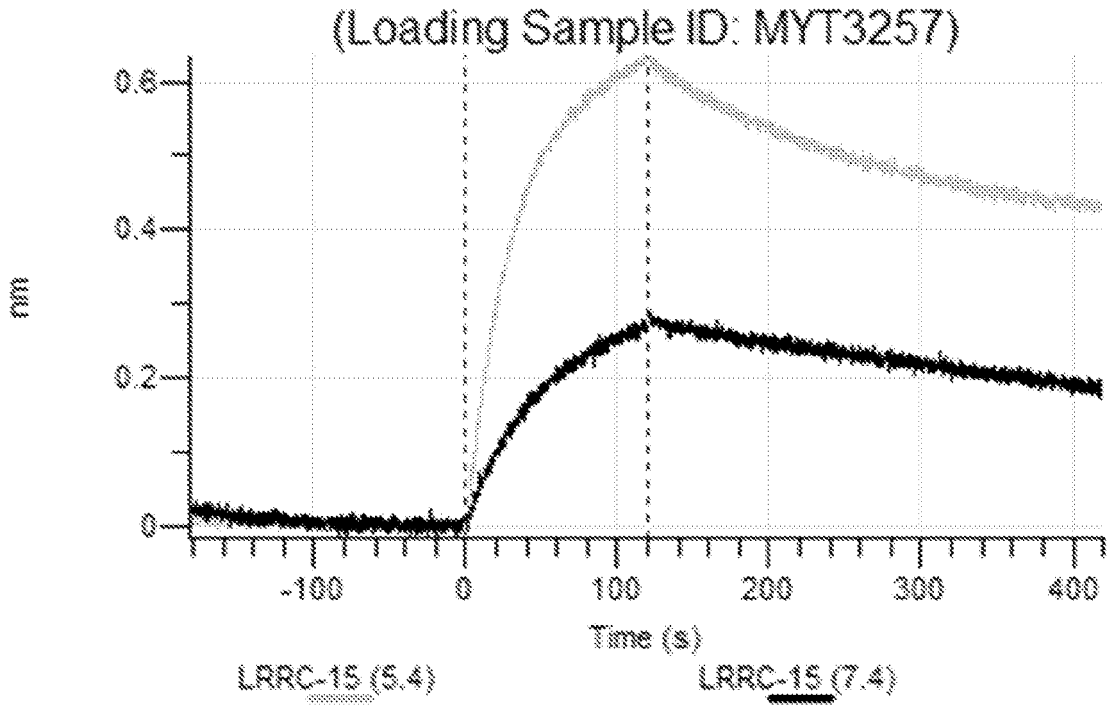

(Loading Sample ID: MYT3257)
nm
0.6
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11F

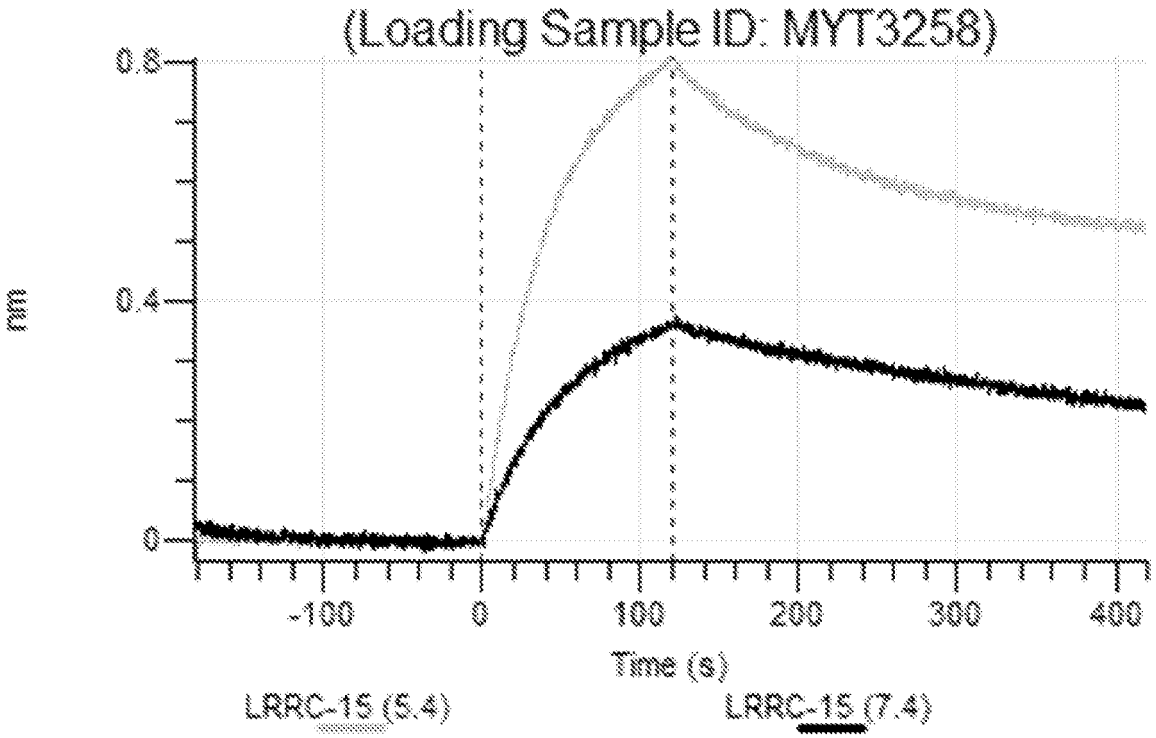

(Loading Sample ID: MYT3258)
0.8
0.4
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11G

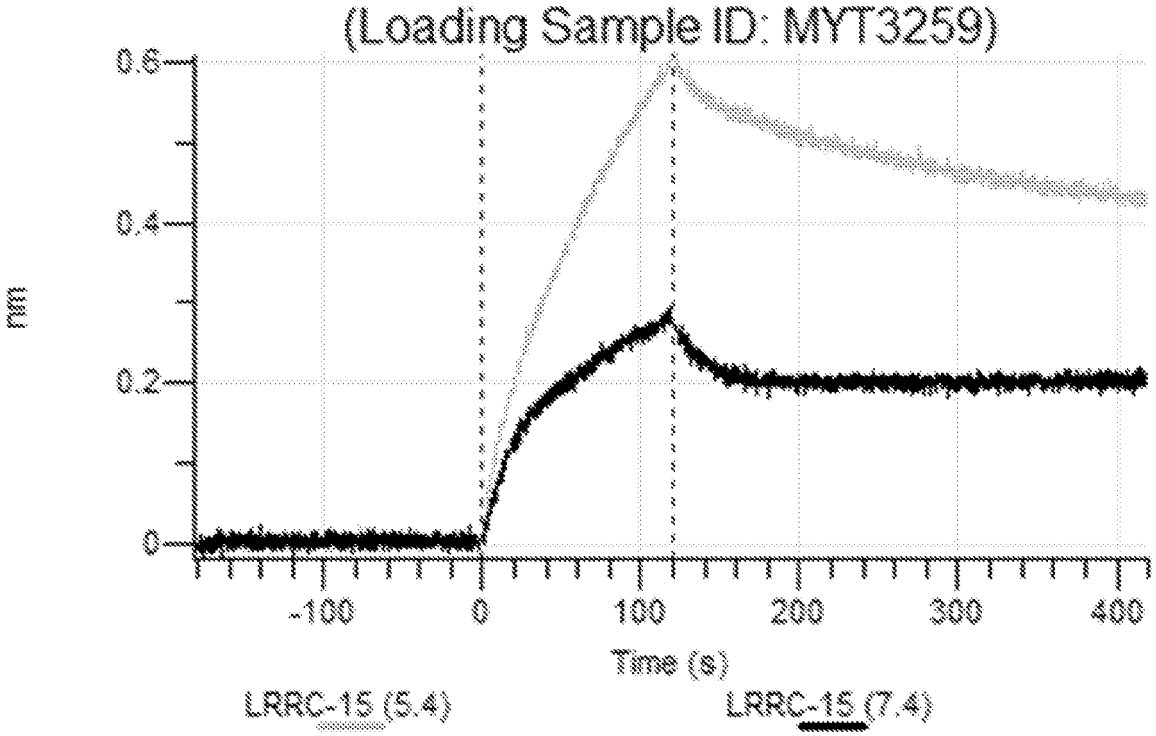

(Loading Sample ID: MYT3259)
nm
0.6
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11H

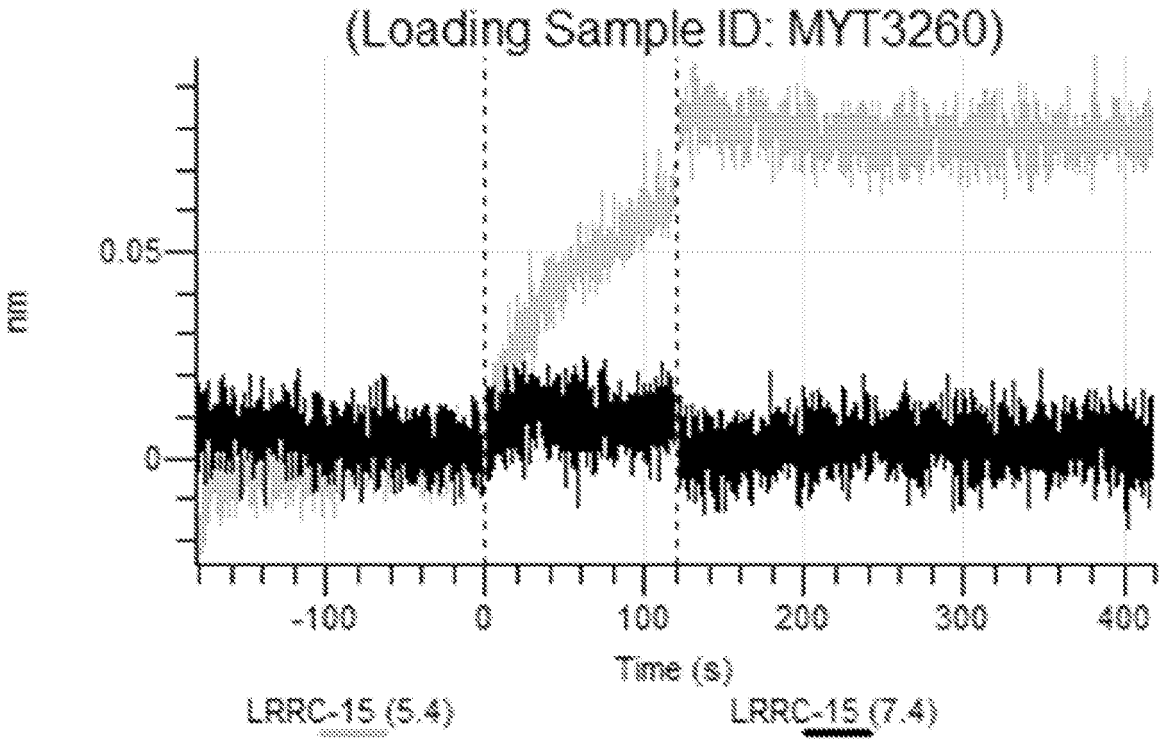

(Loading Sample ID: MYT3260)
nm
0.05
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11I

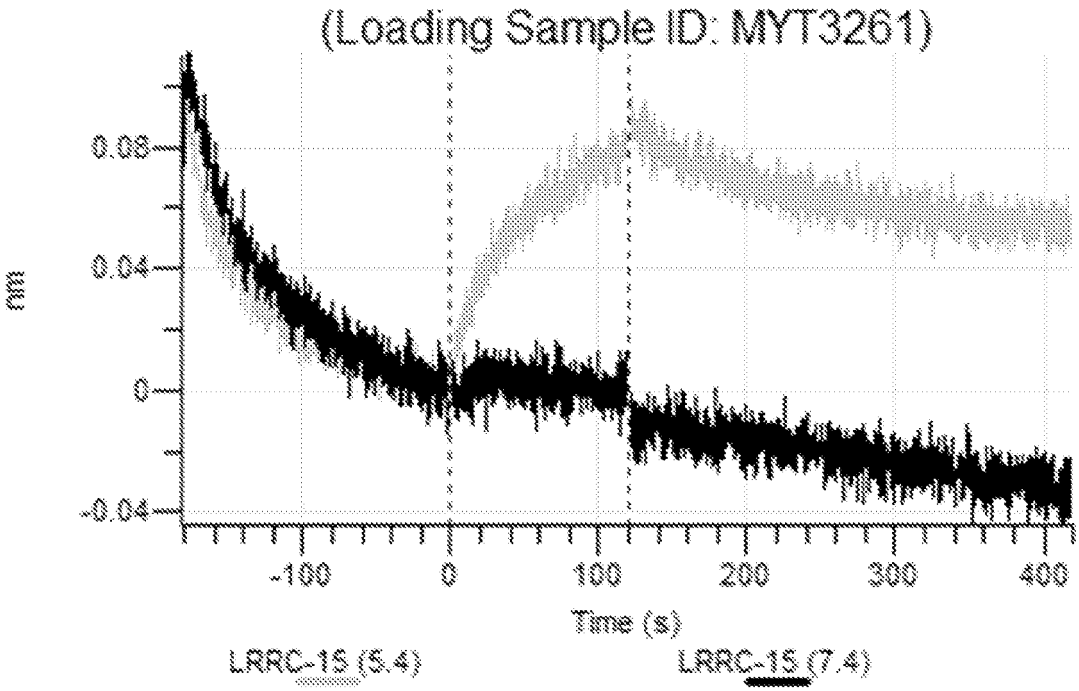

(Loading Sample ID: MYT3261)
nm
0.08
0.04
0
-0.04
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11J

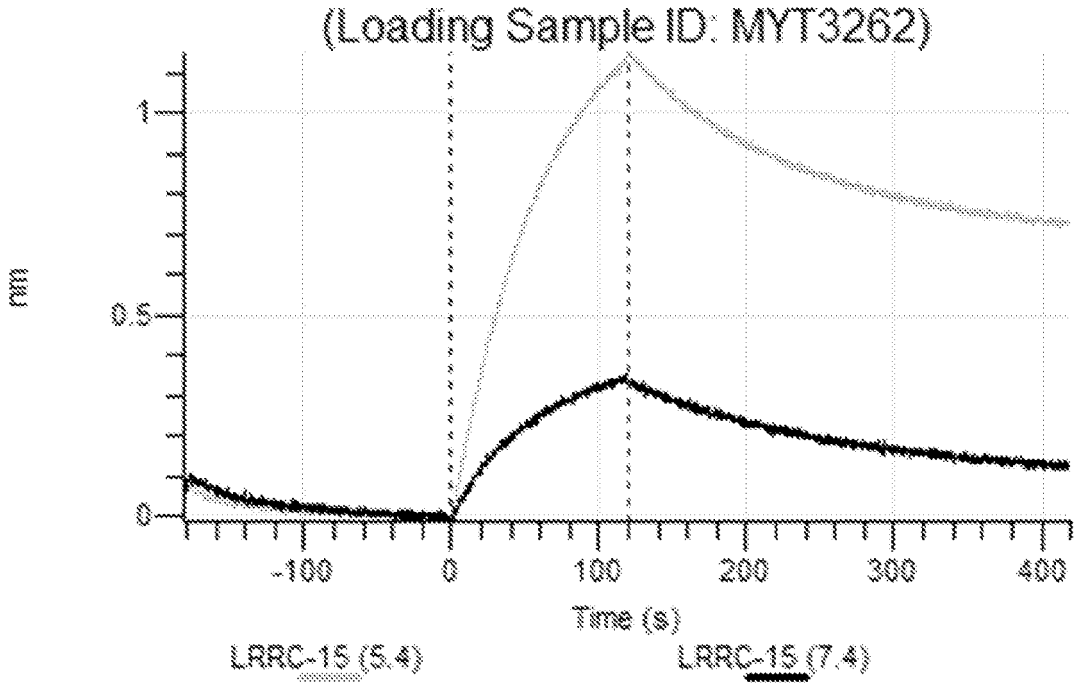

(Loading Sample ID: MYT3262)
nm
1
0.5
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11K

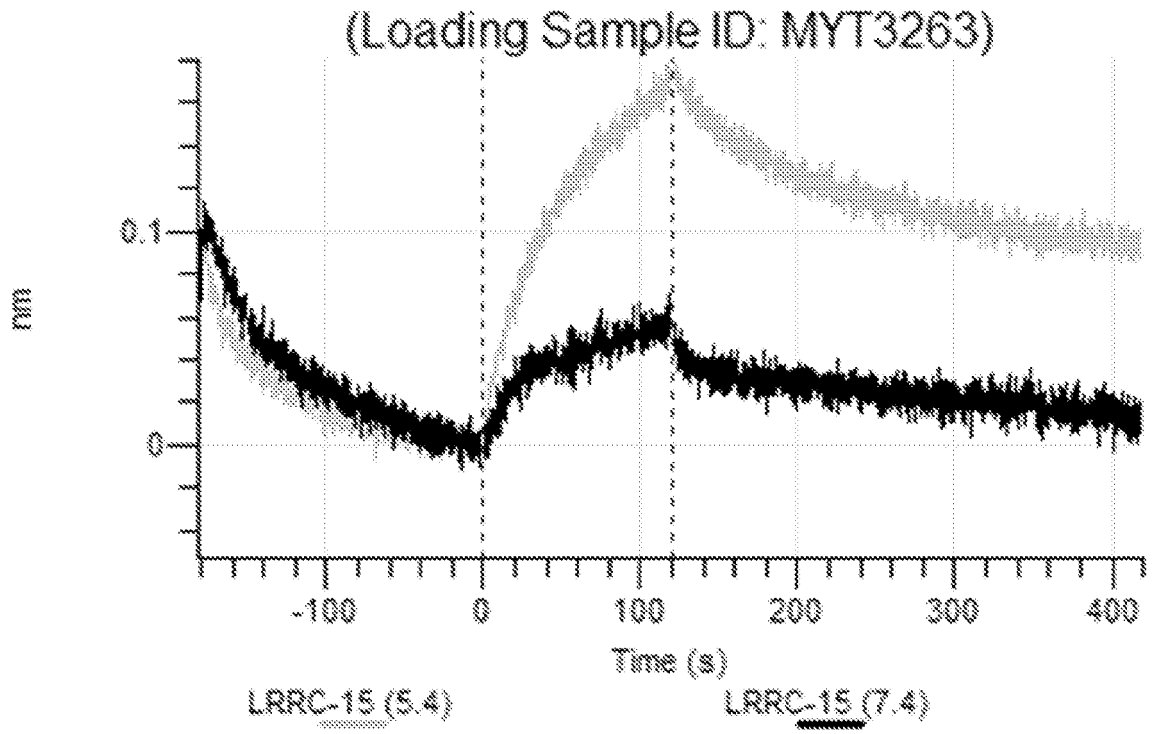

(Loading Sample ID: MYT3263)
nm
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11L

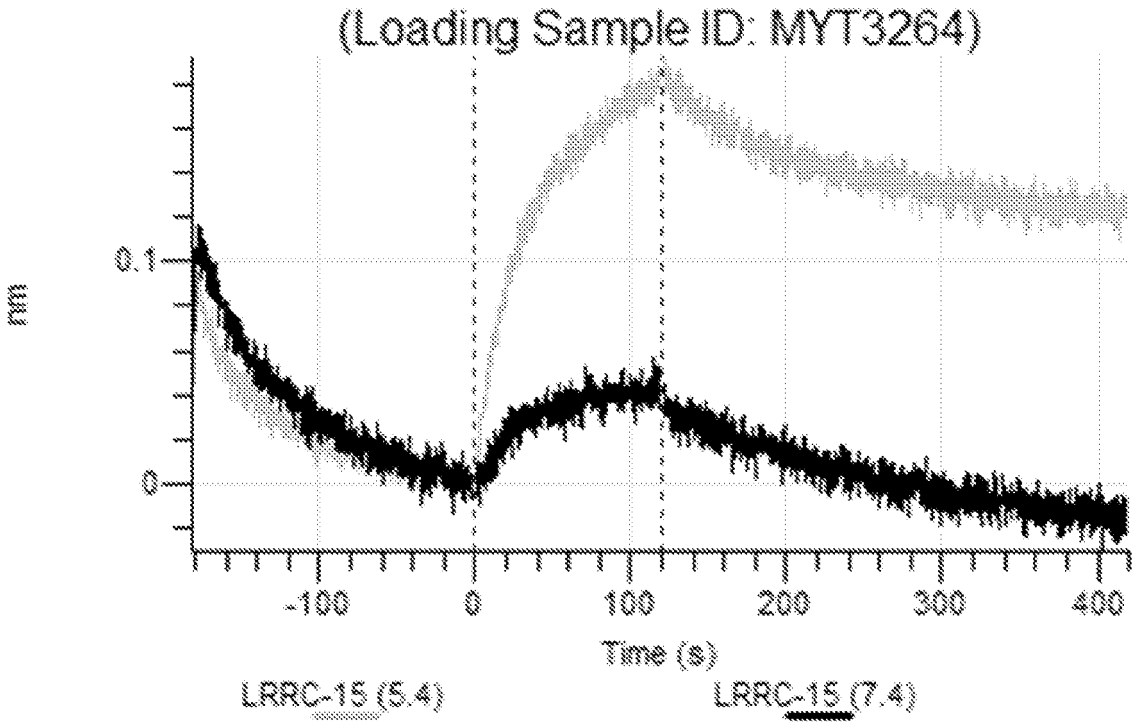

(Loading Sample ID: MYT3264)
nm
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11M

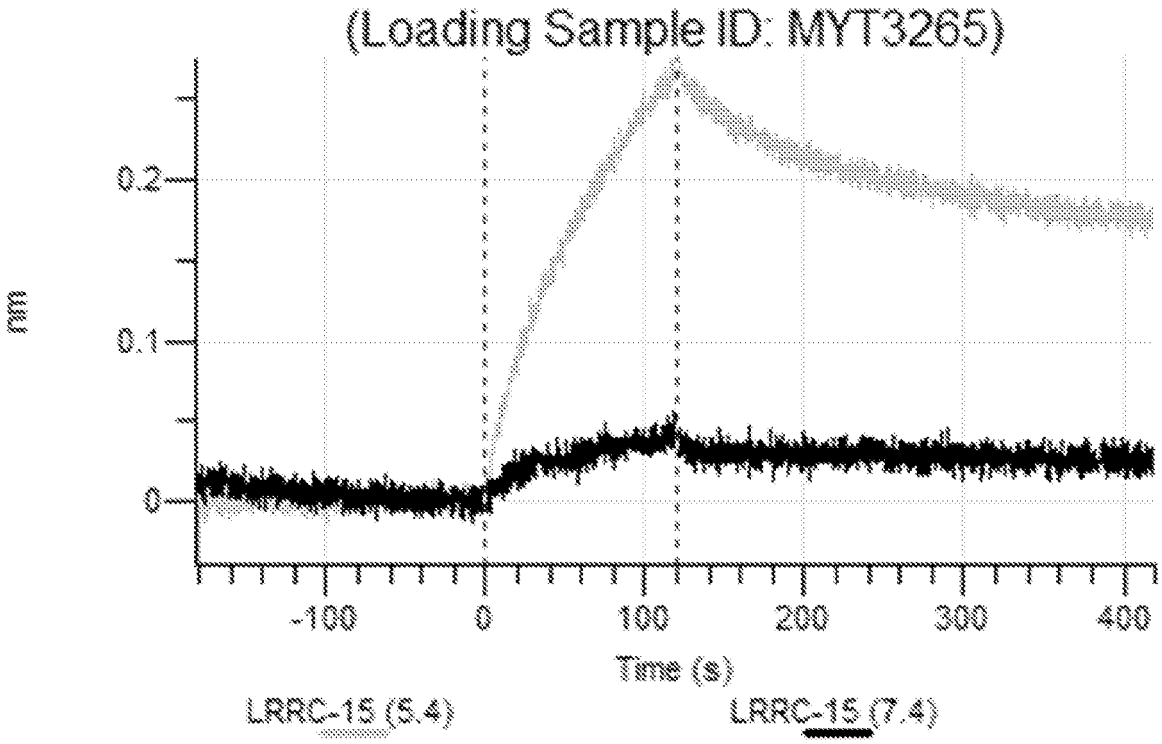

(Loading Sample ID: MYT3265)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11N

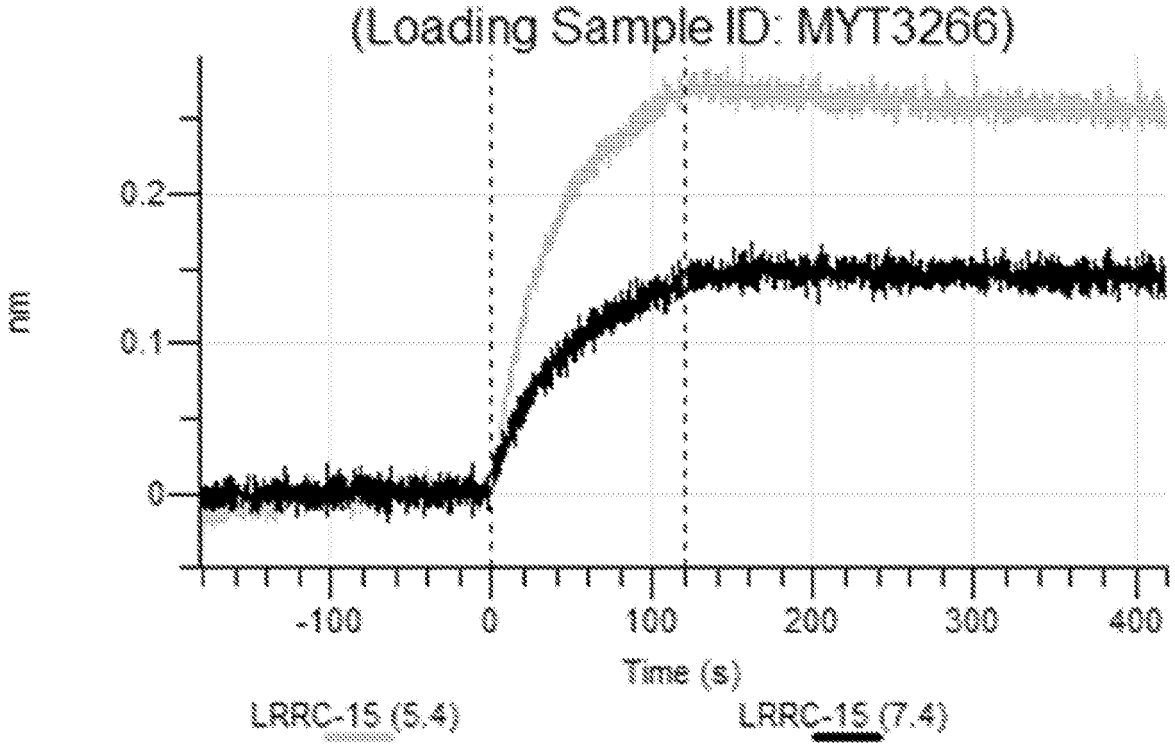

(Loading Sample ID: MYT3266)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11O

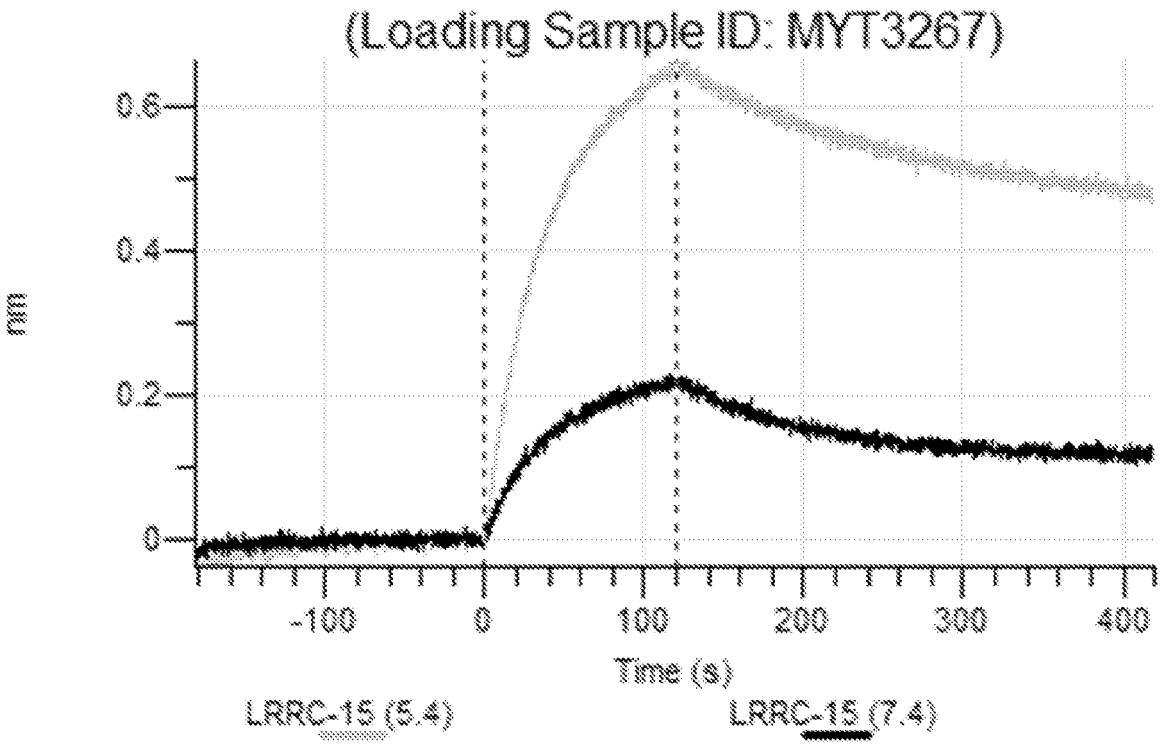

(Loading Sample ID: MYT3267)
nm
0.6
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11P

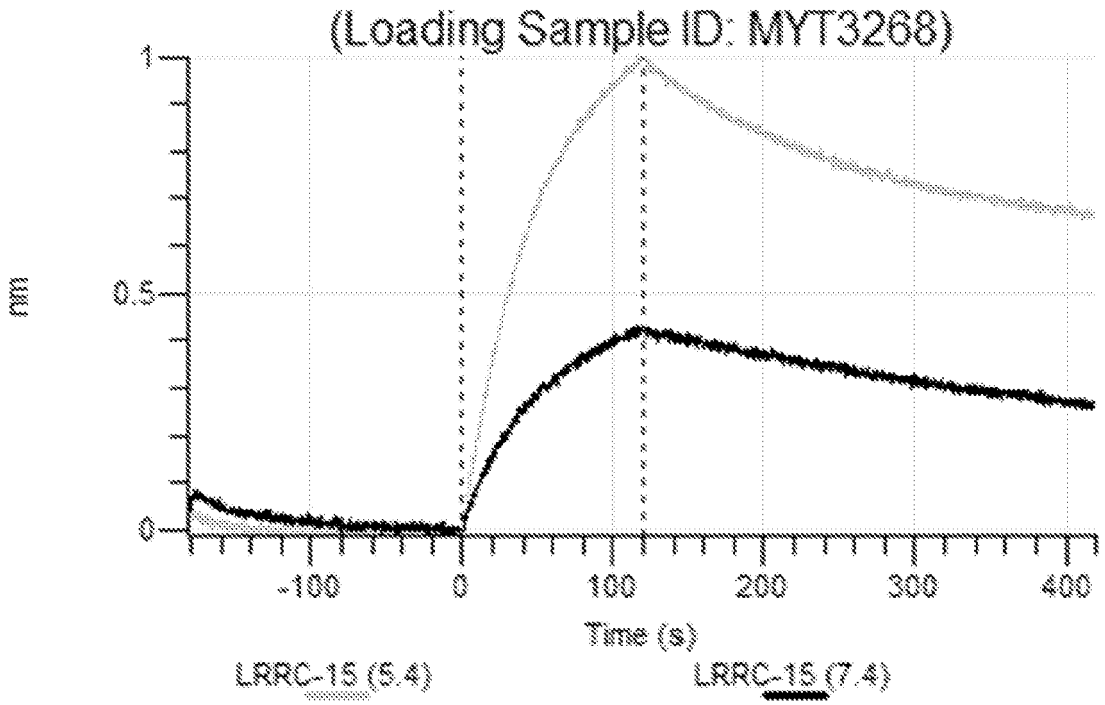

(Loading Sample ID: MYT3268)
nm
1
0.5
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11Q

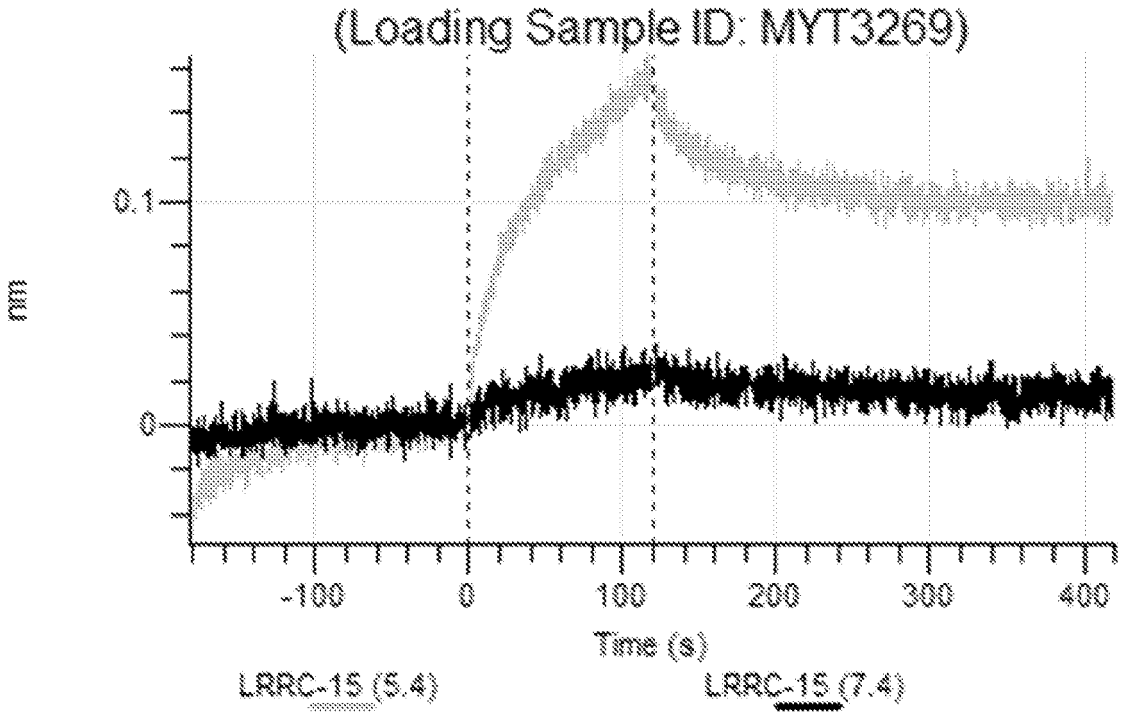

(Loading Sample ID: MYT3269)
nm
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11R

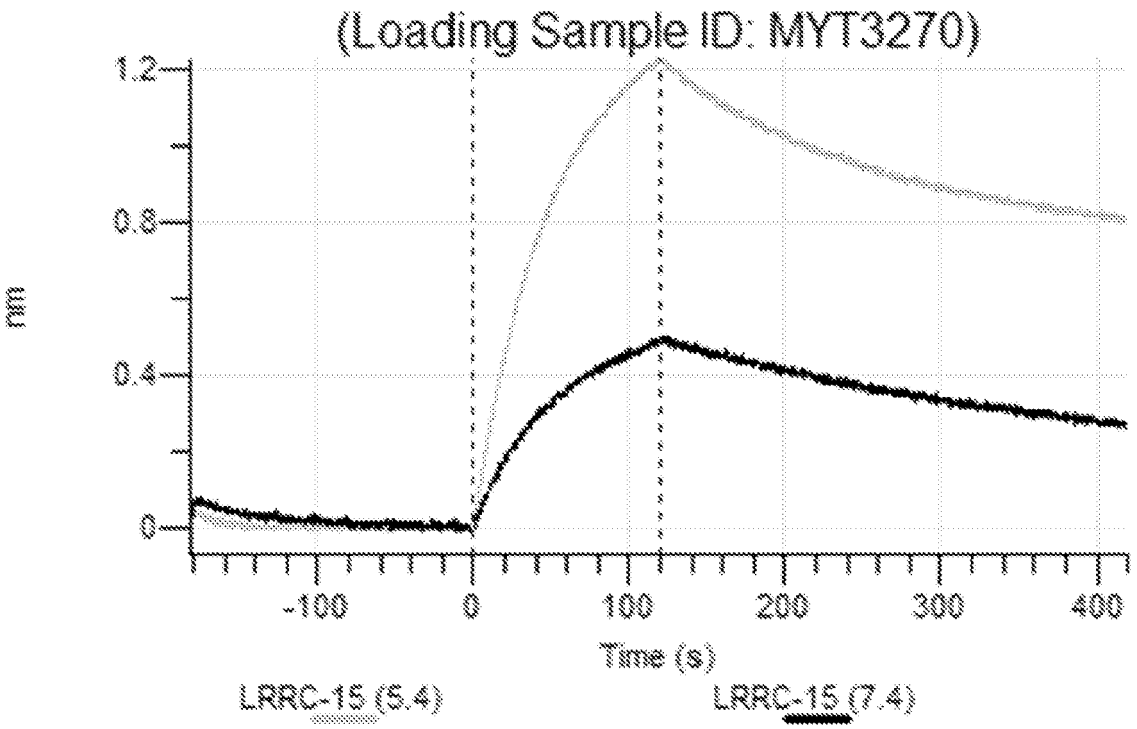

(Loading Sample ID: MYT3270)
1.2
0.8
0.4
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11S

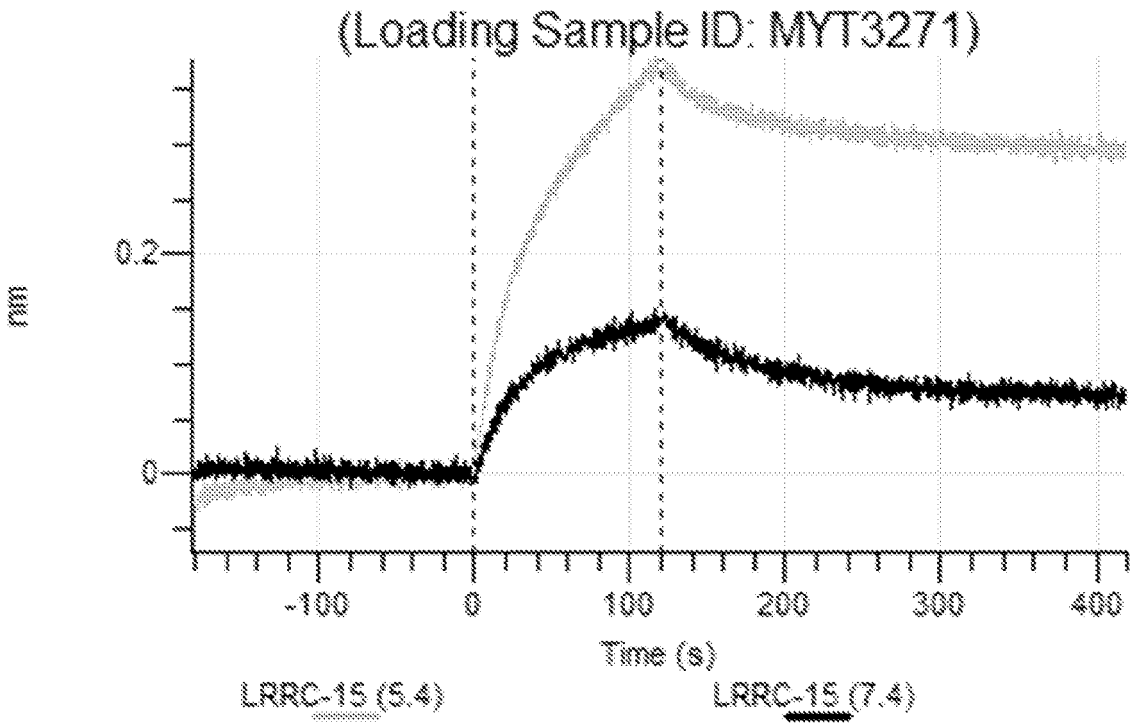

(Loading Sample ID: MYT3271)
nm
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11T

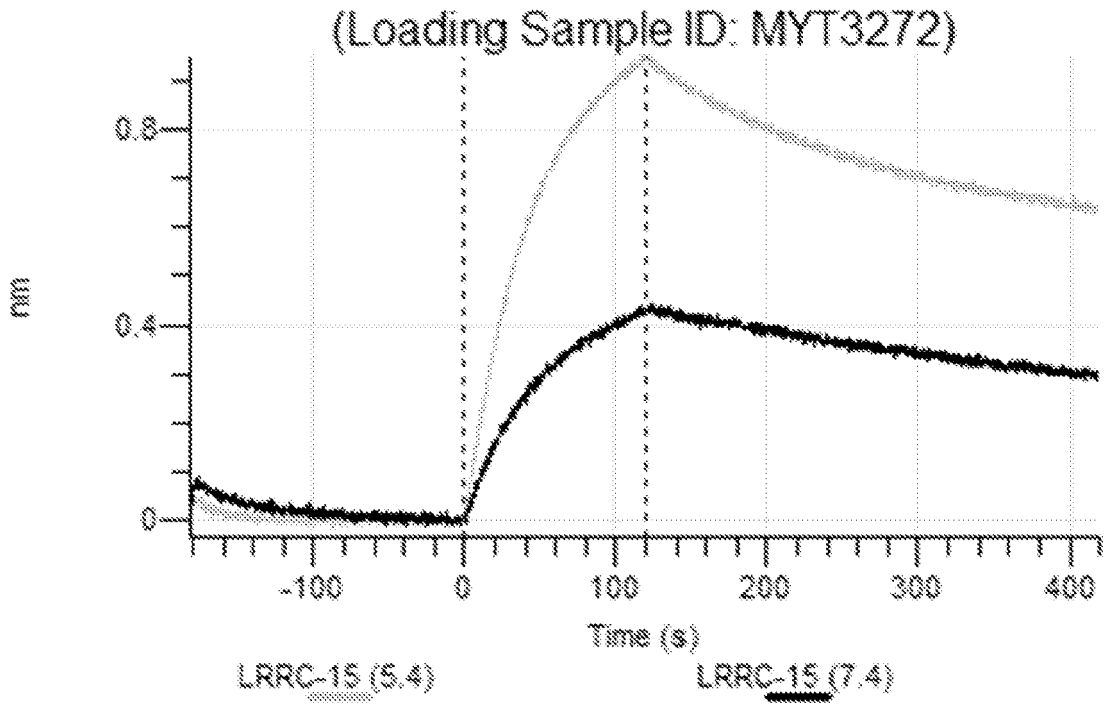

(Loading Sample ID: MYT3272)
nm
0.8
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11U

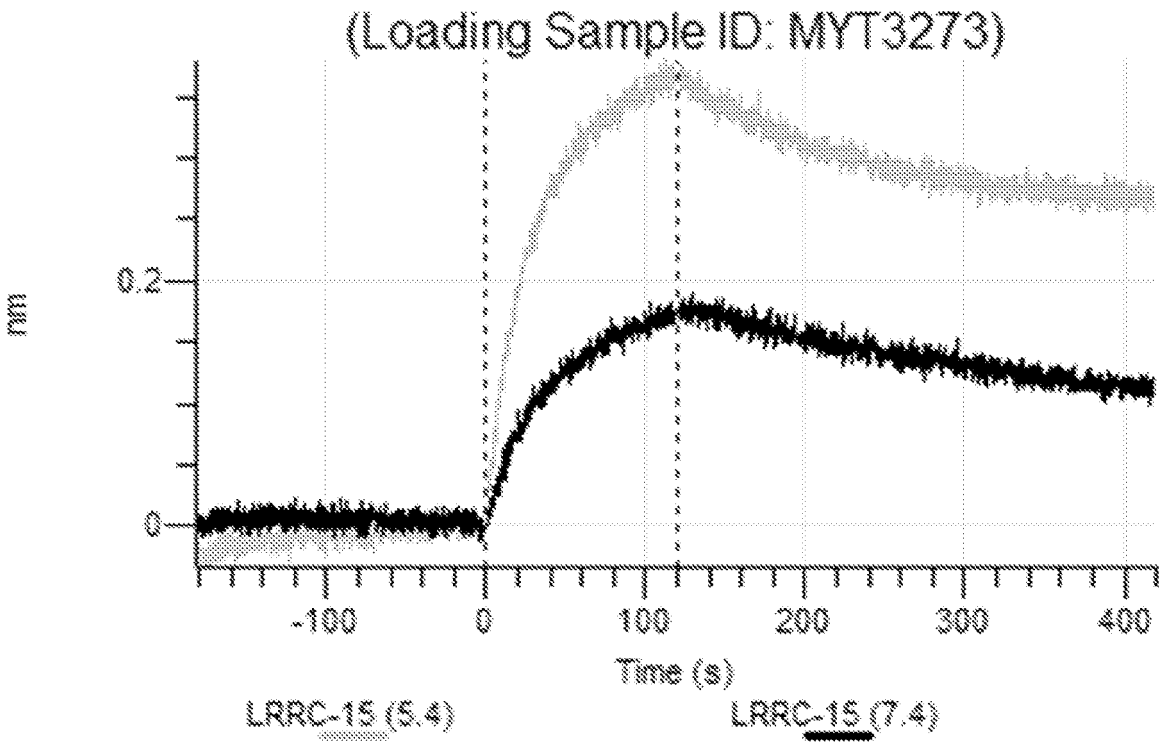

(Loading Sample ID: MYT3273)
nm
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11V

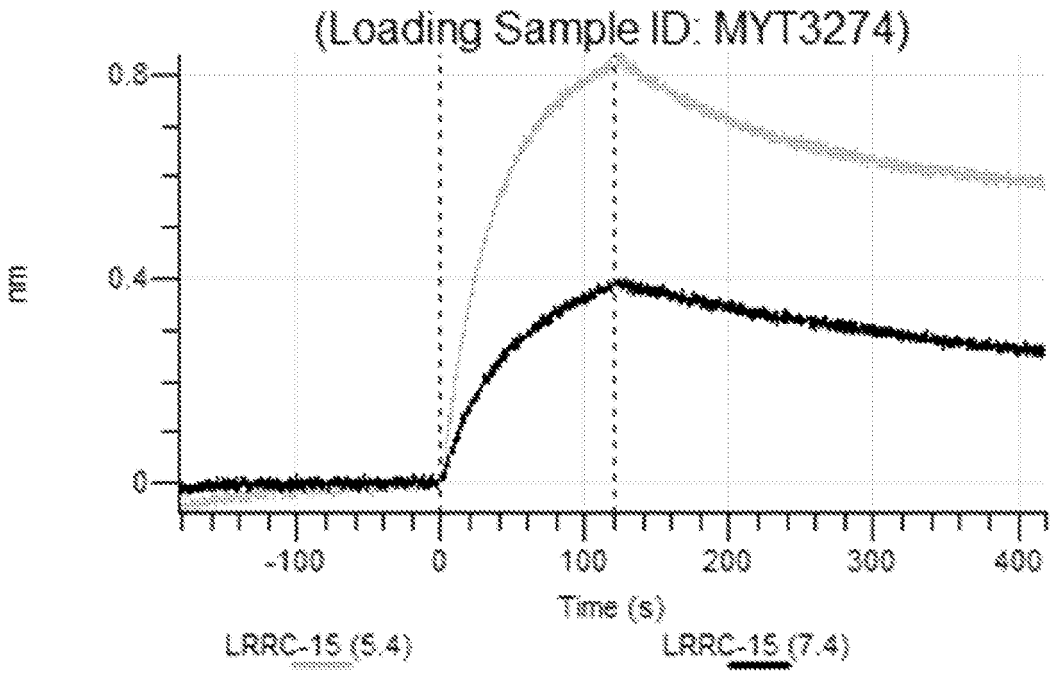

(Loading Sample ID: MYT3274)
0.8
0.4
0
(nm)
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11W

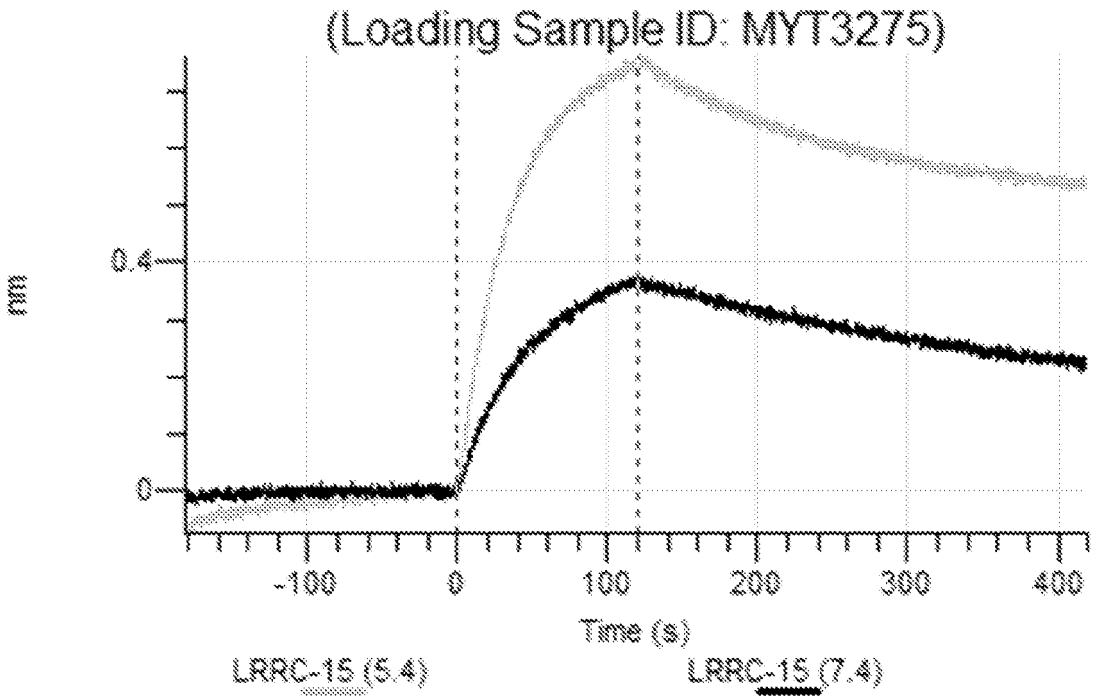

(Loading Sample ID: MYT3275)
nm
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11X

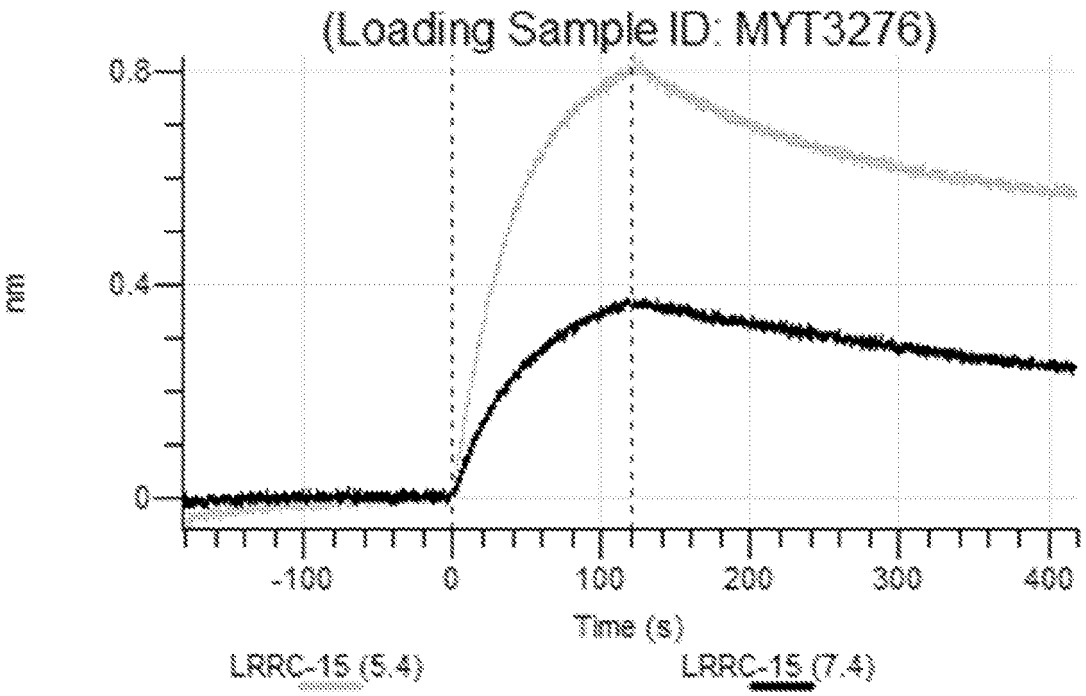

(Loading Sample ID: MYT3276)
nm
0.8
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11Y

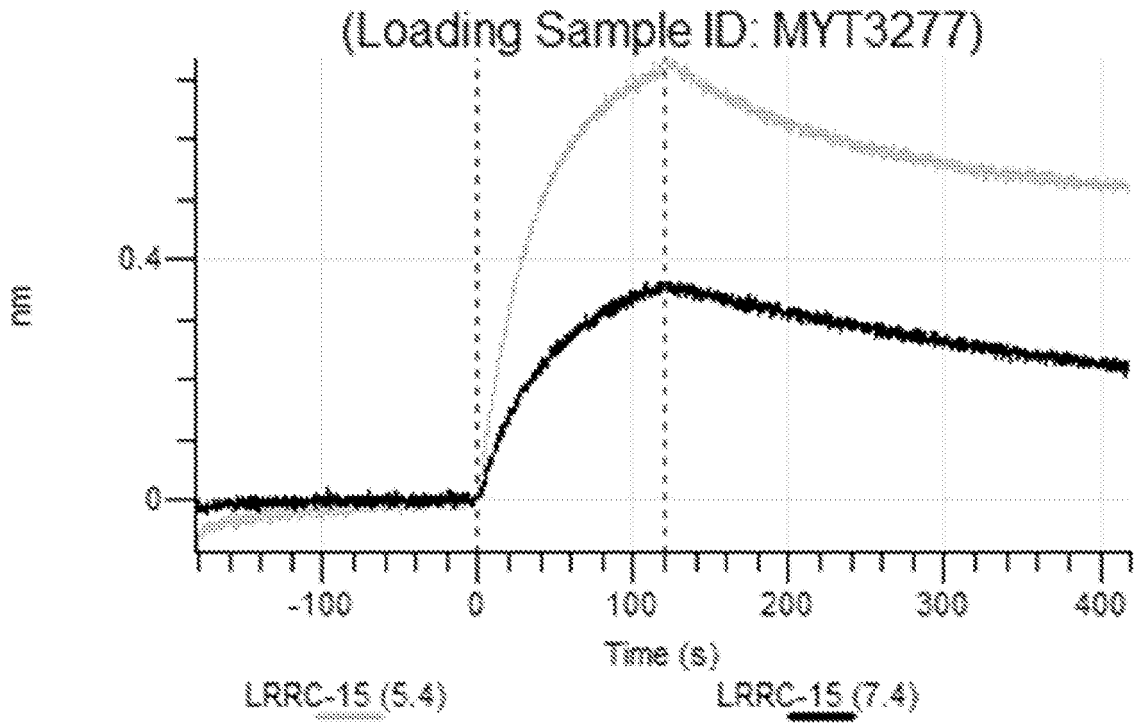

(Loading Sample ID: MYT3277)
nm
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11Z

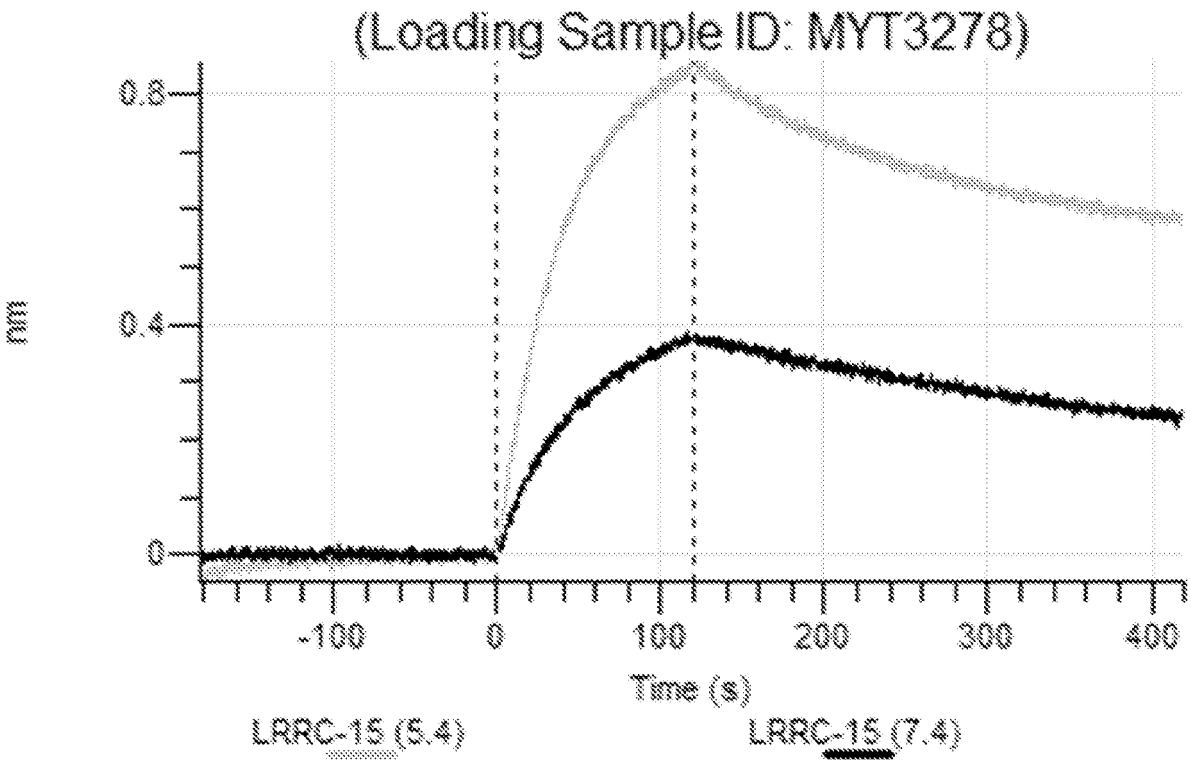

(Loading Sample ID: MYT3278)
nm
0.8
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AA

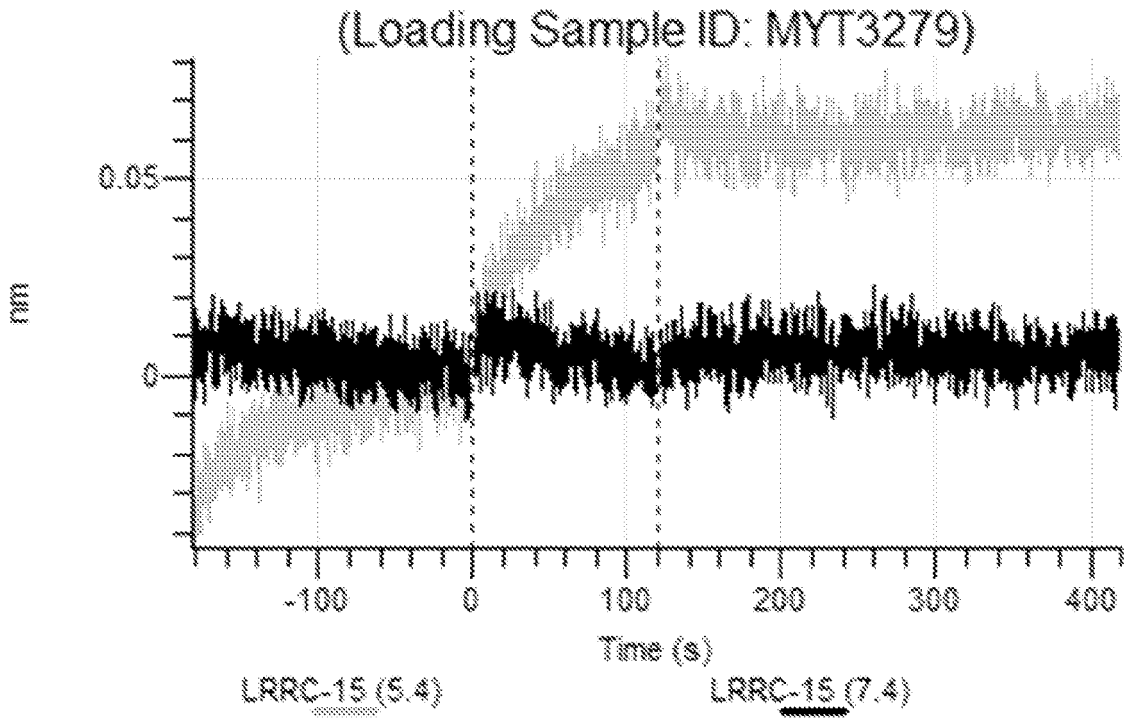

(Loading Sample ID: MYT3279)
nm
0.05
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AB

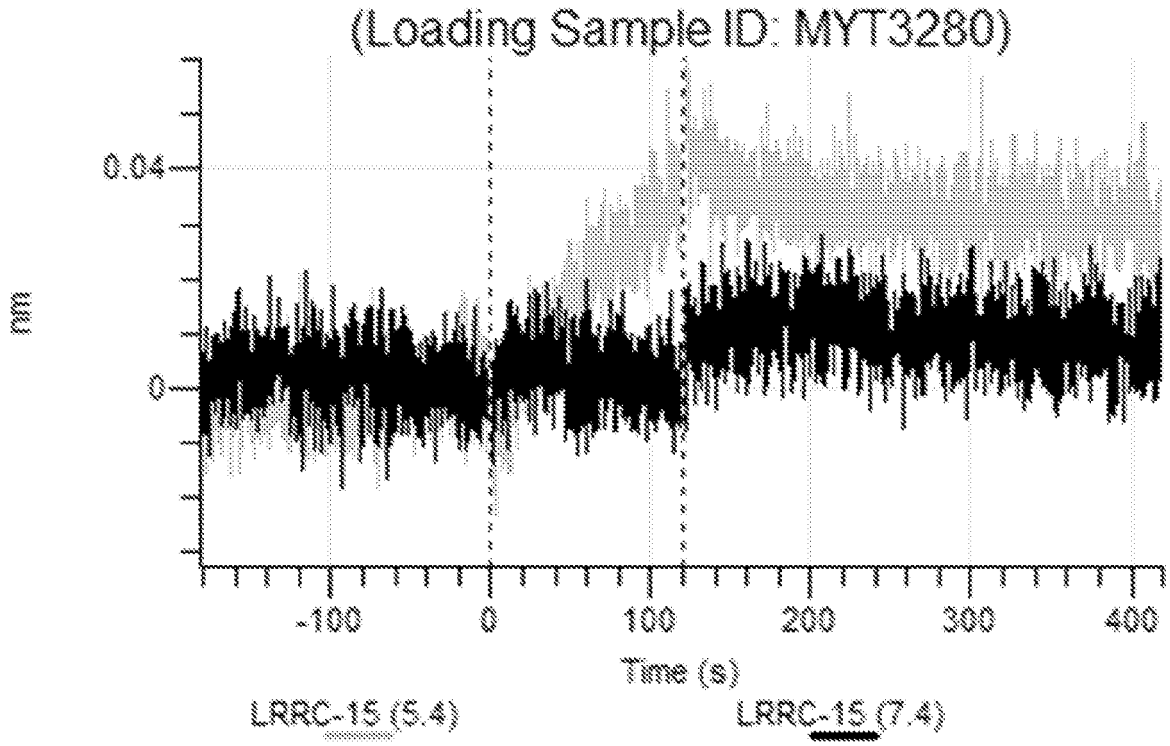

(Loading Sample ID: MYT3280)
0.04
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AC

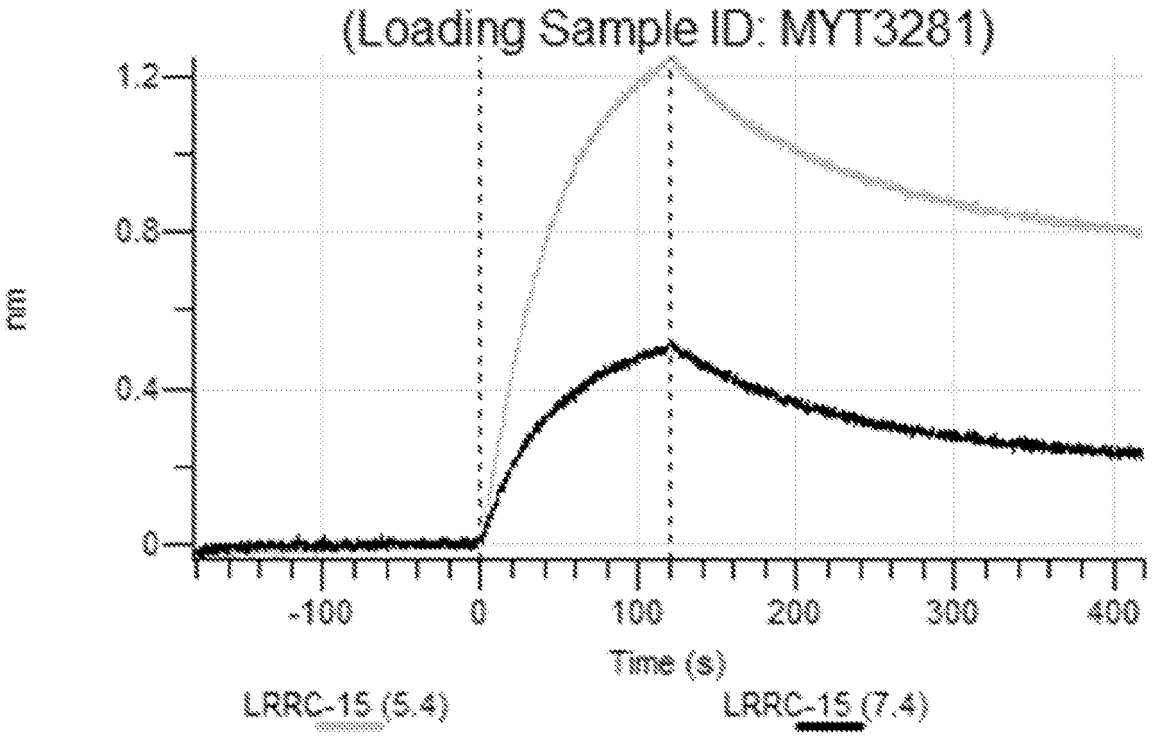

(Loading Sample ID: MYT3281)
1.2
0.8
0.4
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AD

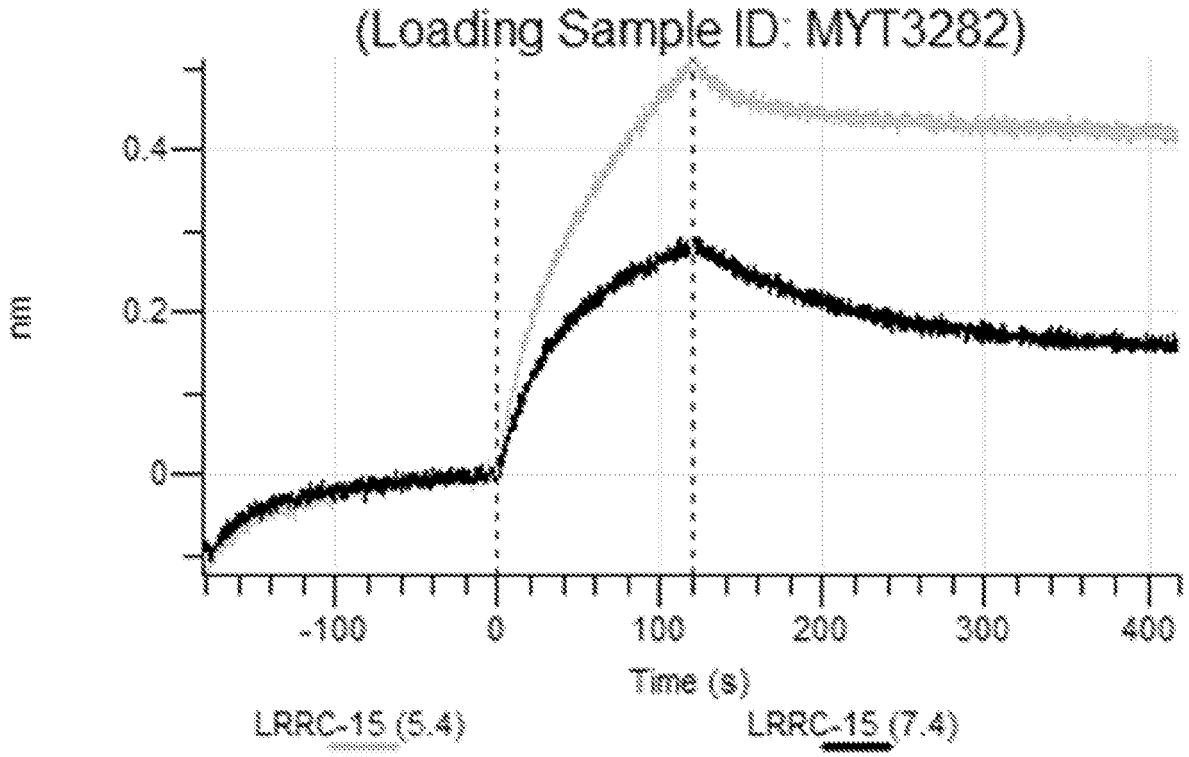

(Loading Sample ID: MYT3282)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AE

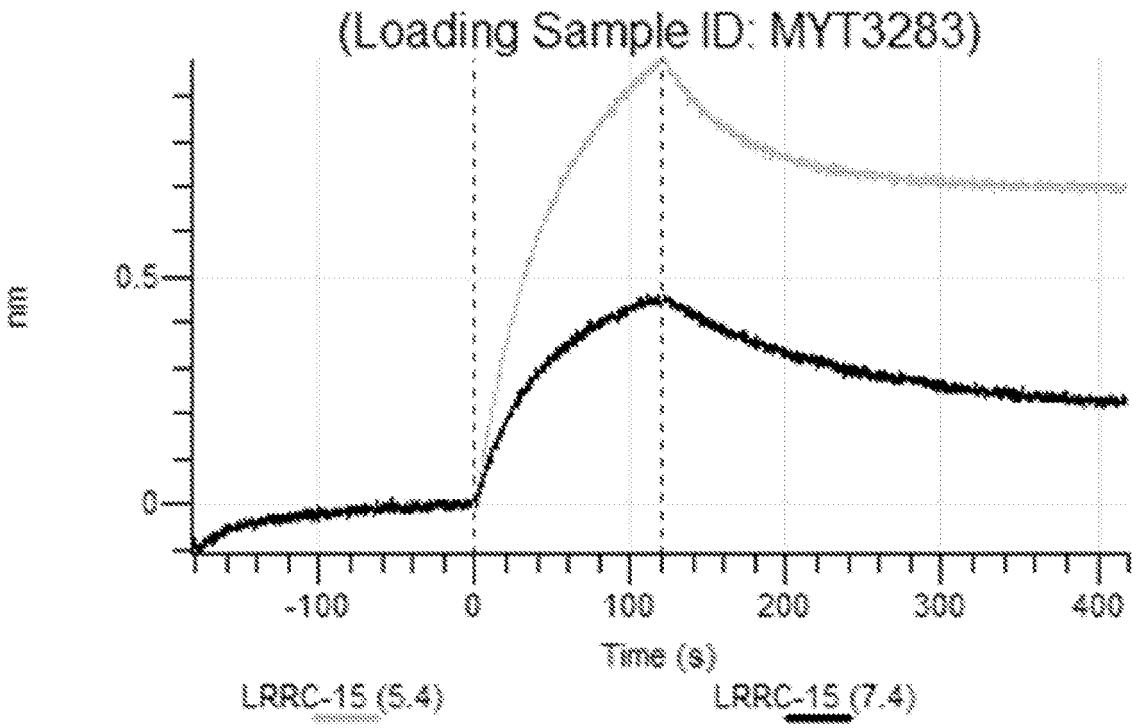

(Loading Sample ID: MYT3283)
nm
0.5
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AF

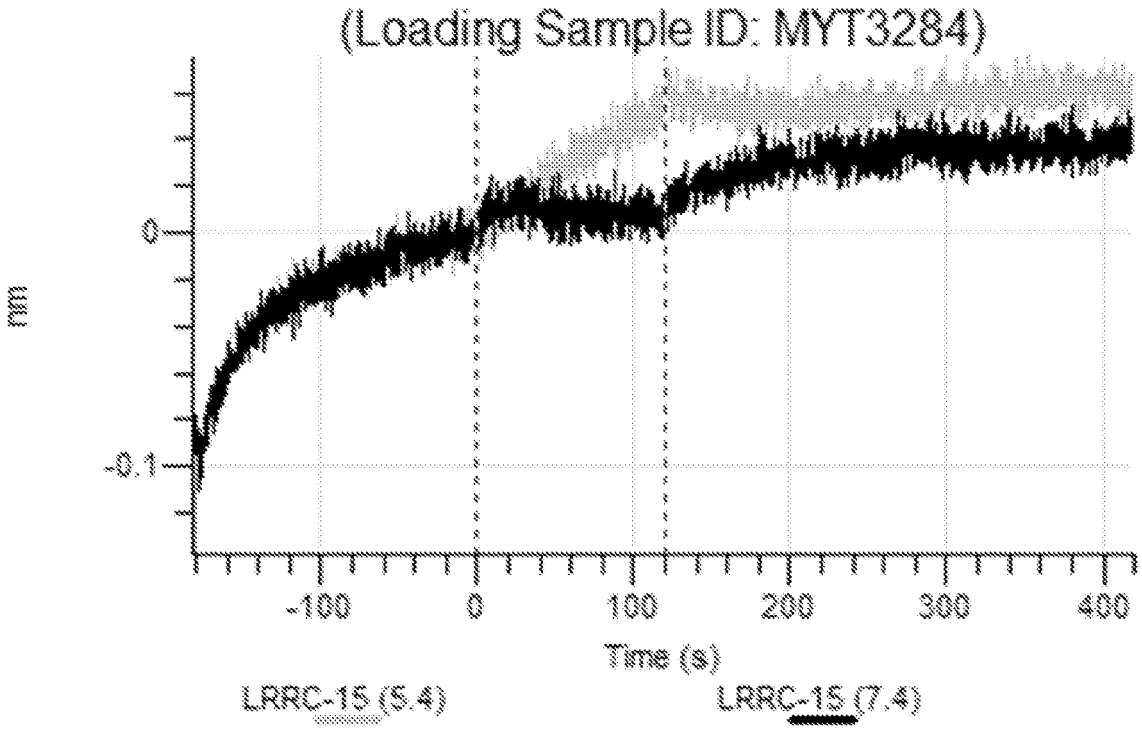

(Loading Sample ID: MYT3284)
nm
0
-0.1
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AG

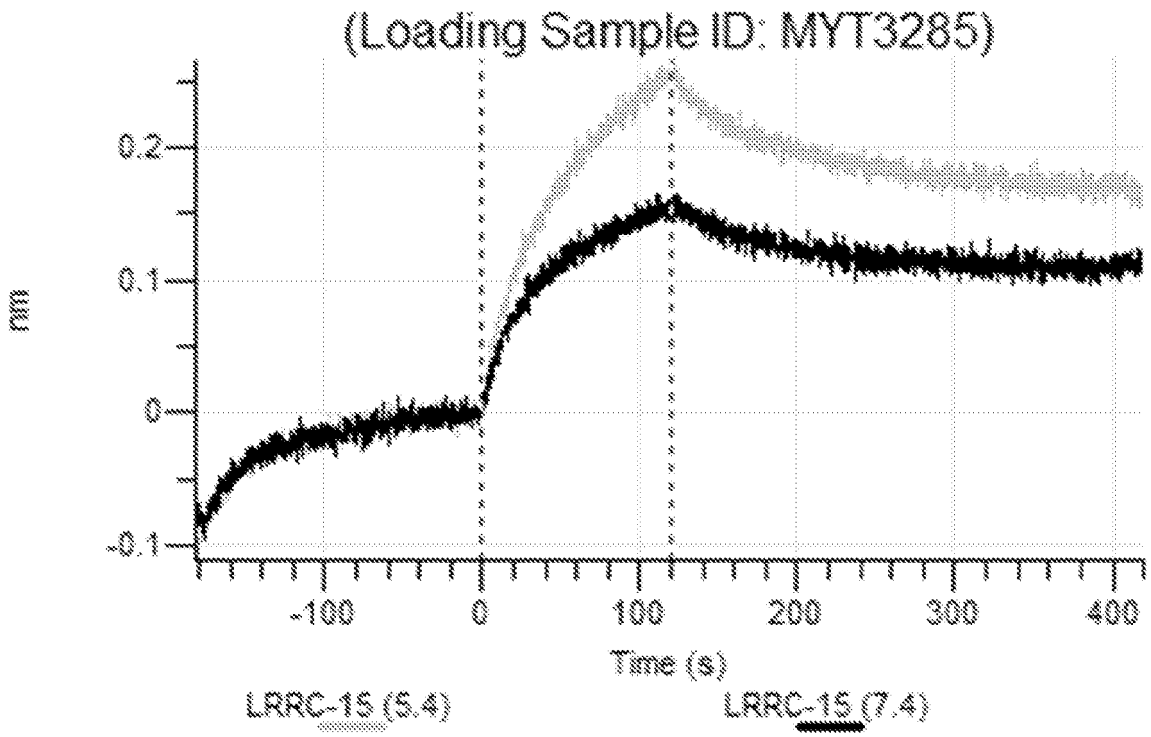

(Loading Sample ID: MYT3285)
nm
0.2
0.1
0
-0.1
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AH

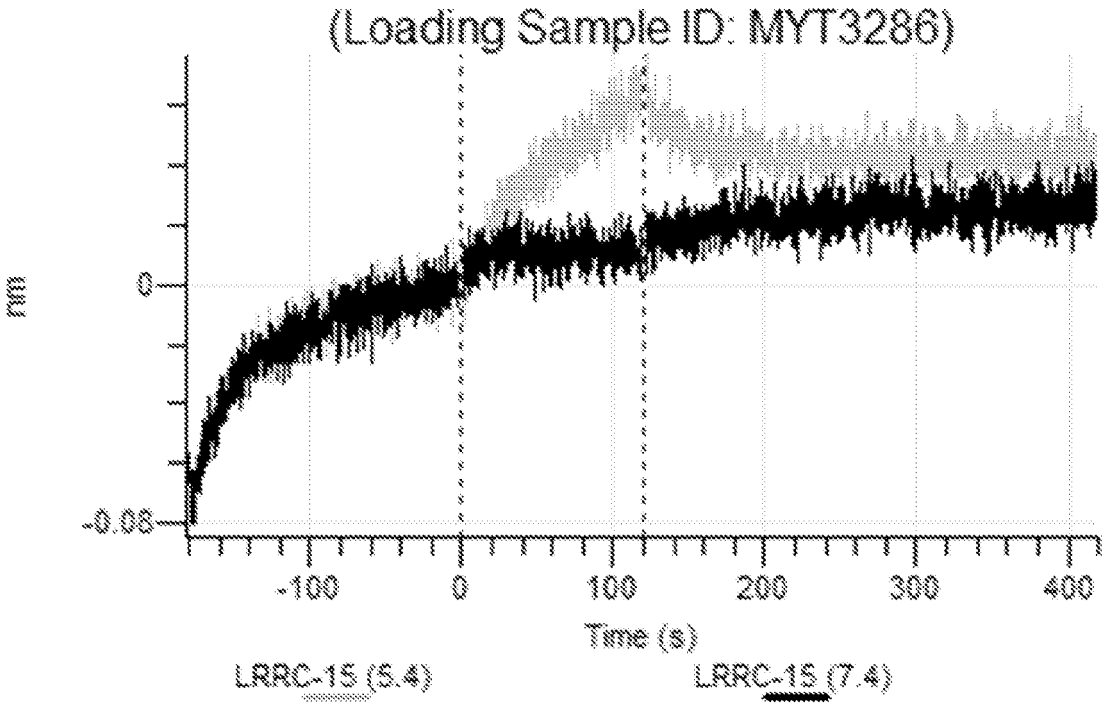

(Loading Sample ID: MYT3286)
nm
0
-0.08
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AI

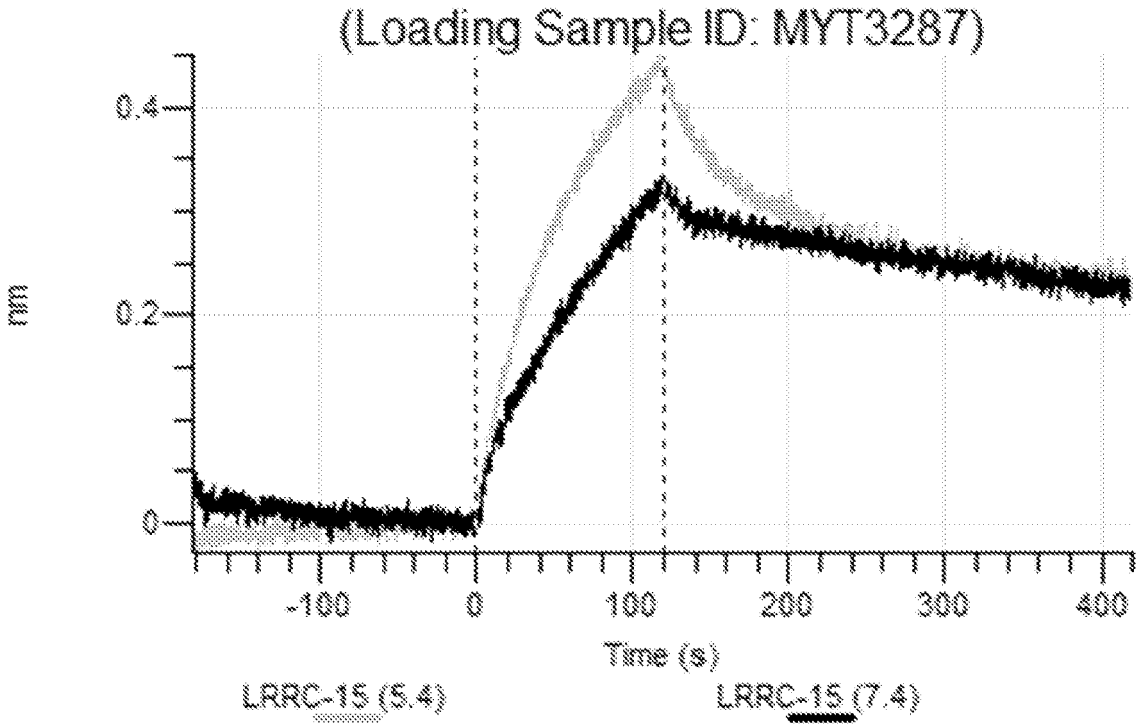

(Loading Sample ID: MYT3287)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AJ

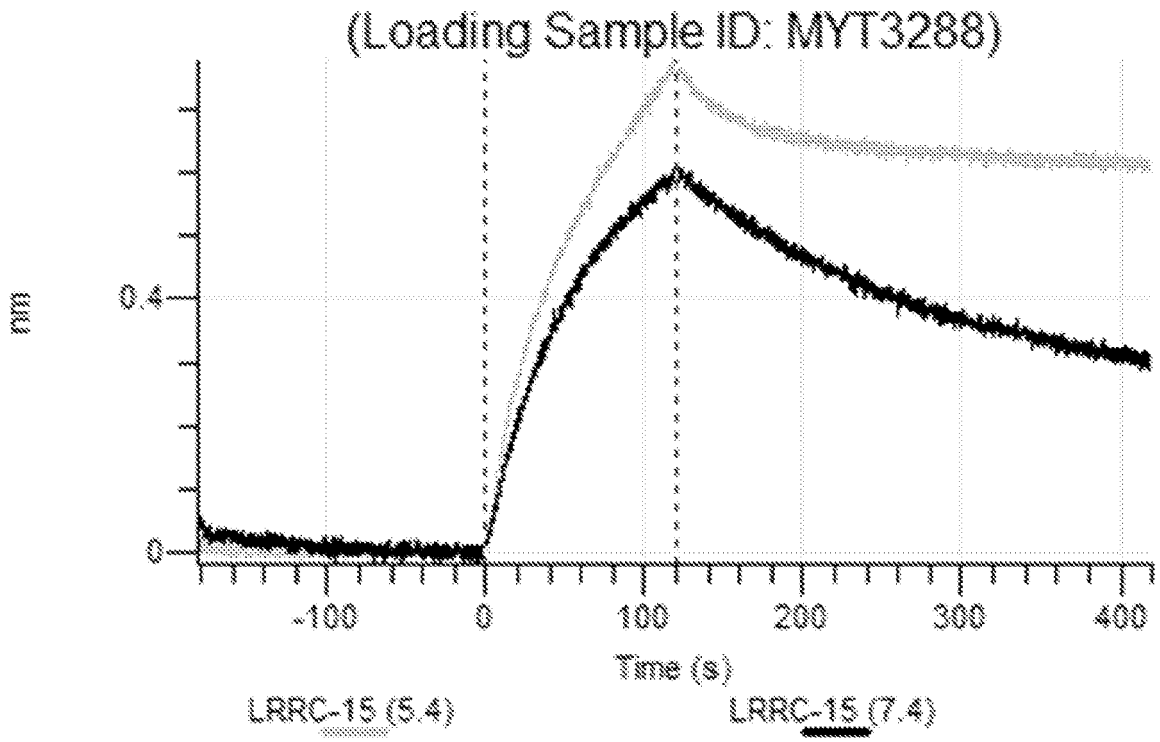

(Loading Sample ID: MYT3288)
nm
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG 11AK

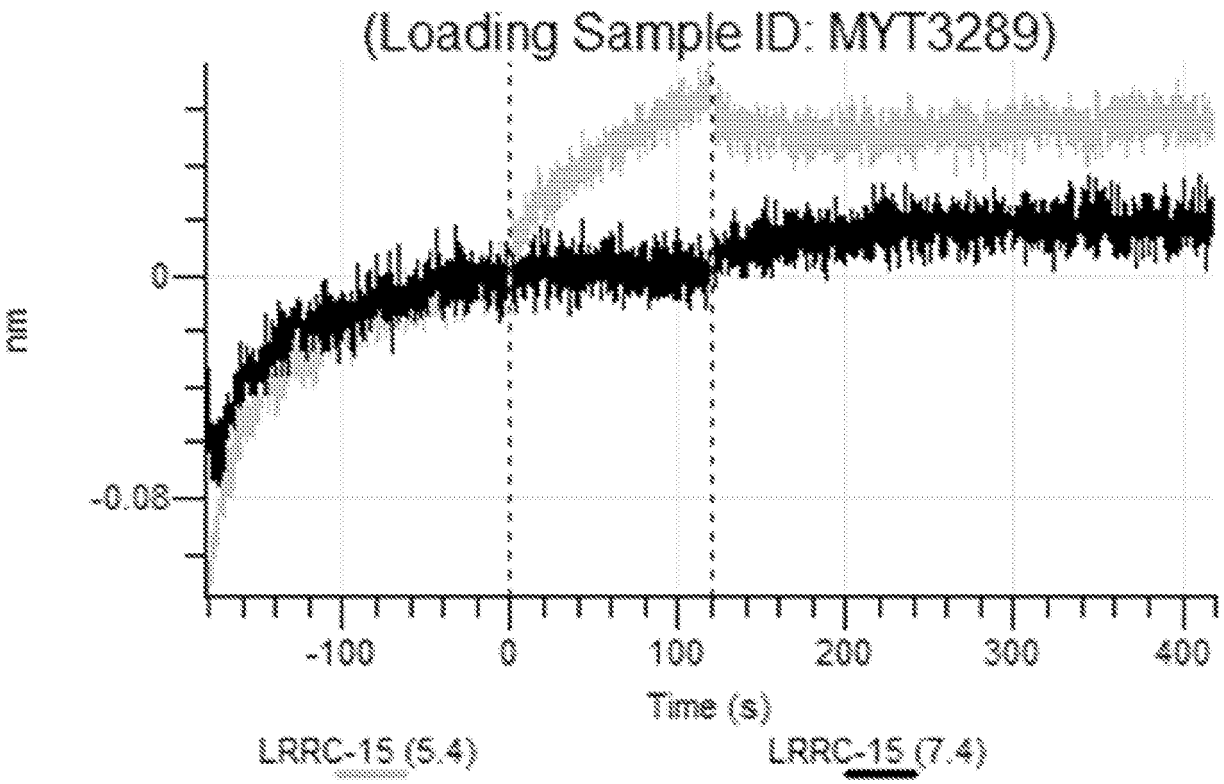

(Loading Sample ID: MYT3289)
nm
0
-0.08
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AL

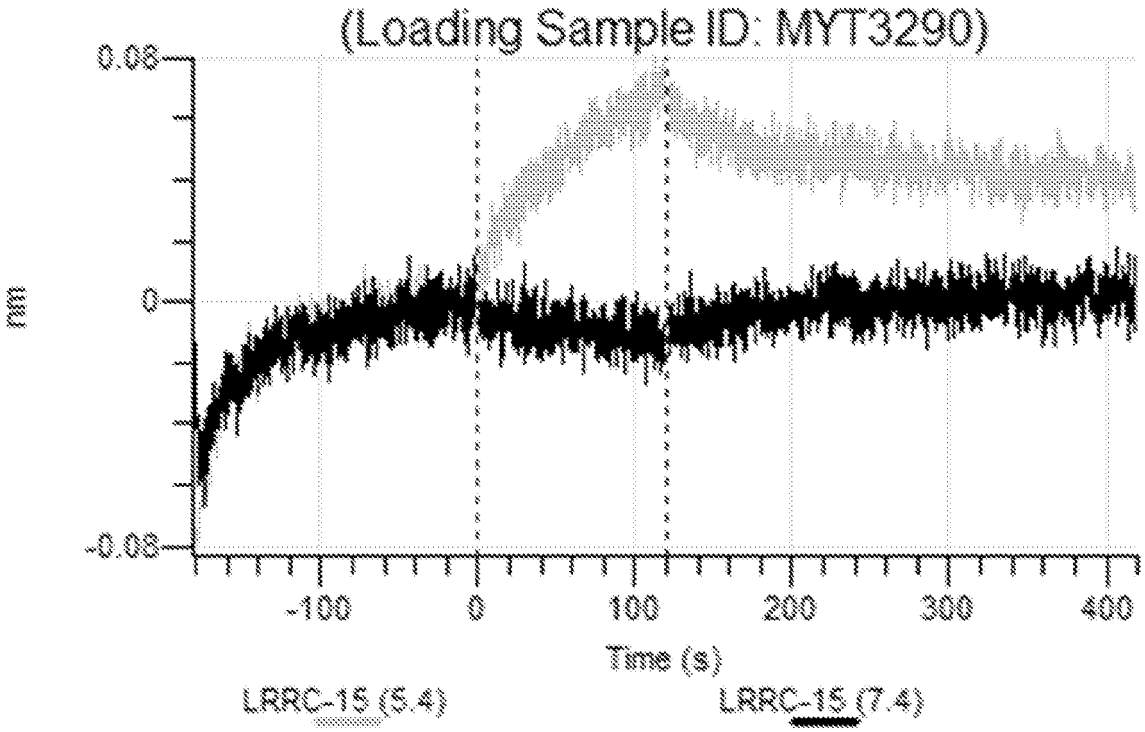

(Loading Sample ID: MYT3290)
0.08
0
-0.08
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AM

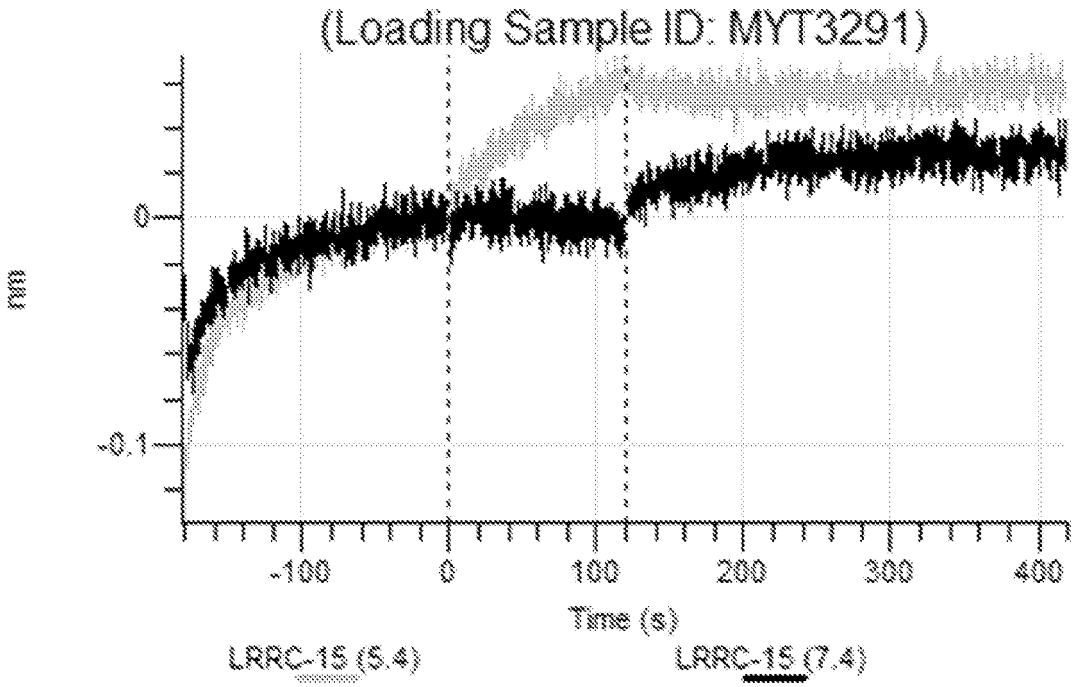

(Loading Sample ID: MYT3291)
nm
0
-0.1
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AN

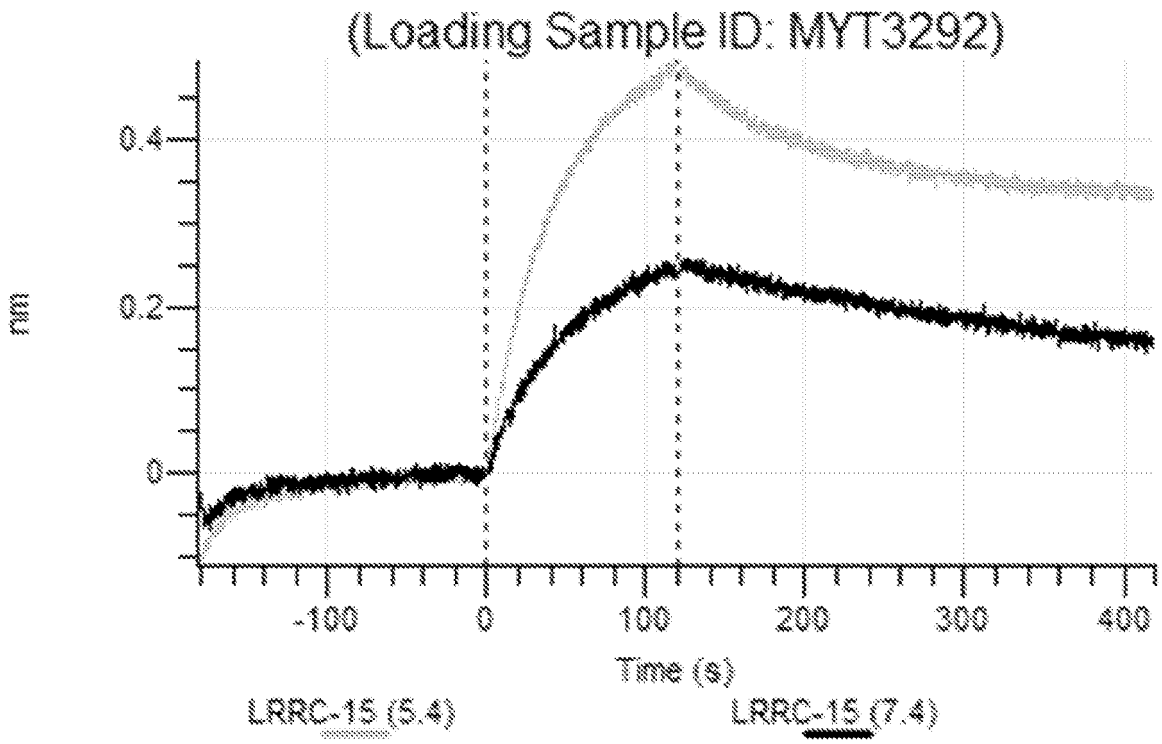

(Loading Sample ID: MYT3292)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 11AO

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
MYT3252 (hu139.10)	84	85	86	87	88	89	90	91
MYT3253	92	85						
MYT3254	93	85						
MYT3255	94	85						
MYT3256	95	85						
MYT3257	96	85						
MYT3258	97	85						
MYT3259	98	85						
MYT3260	99	85						
MYT3261	100	85						
MYT3262	101	85						
MYT3263	102	85						
MYT3264	103	85						
MYT3265	104	85						
MYT3266	105	85						
MYT3267	106	85						
MYT3268	107	85						
MYT3269	108	85						
MYT3270	109	85						
MYT3271	110	85						
MYT3272	111	85						
MYT3273	112	85						
MYT3274	113	85						
MYT3275	114	85						
MYT3276	115	85						
MYT3277	116	85						
MYT3278	117	85						
MYT3279	118	85						
MYT3280	119	85						
MYT3281	120	85						
MYT3282	121	85						
MYT3283	122	85						
MYT3284	123	85						
MYT3285	124	85						
MYT3286	125	85						
MYT3287	126	85						
MYT3288	127	85						
MYT3289	128	85						
MYT3290	129	85						
MYT3291	130	85						
MYT3292	131	85						

FIG. 12

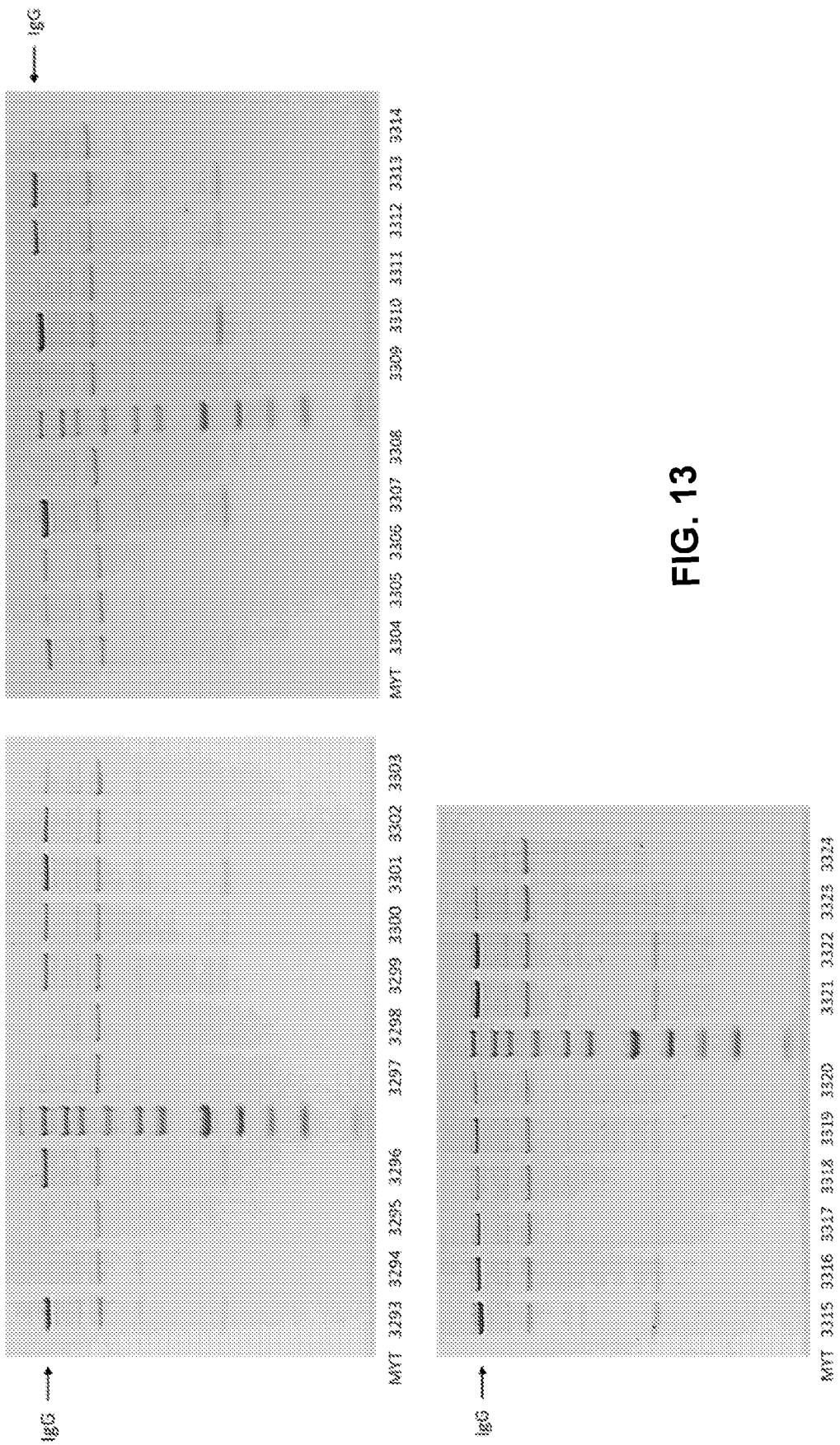

IgG
MYT 3293 3294 3295 3296 3297 3298 3299 3300 3301 3302 3303
IgG
MYT 3304 3305 3306 3307 3308 3309 3310 3311 3312 3313 3314
IgG
MYT 3315 3316 3317 3318 3319 3320 3321 3322 3323 3324

FIG. 13

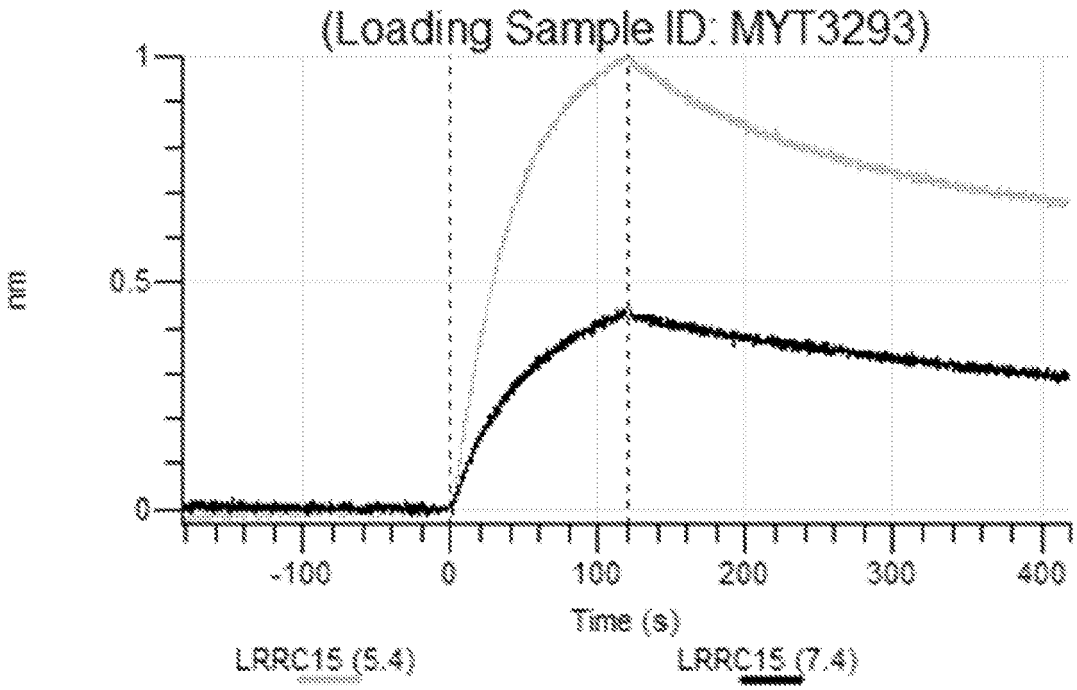

(Loading Sample ID: MYT3293)
nm
1
0.5
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14A

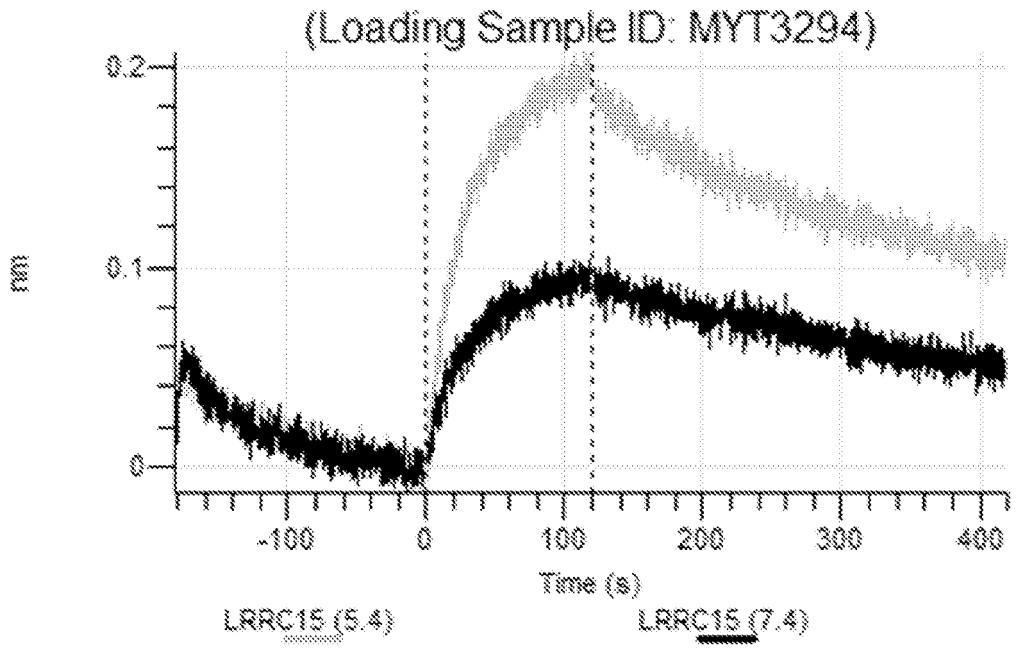

(Loading Sample ID: MYT3294)
0.2
0.1
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14B

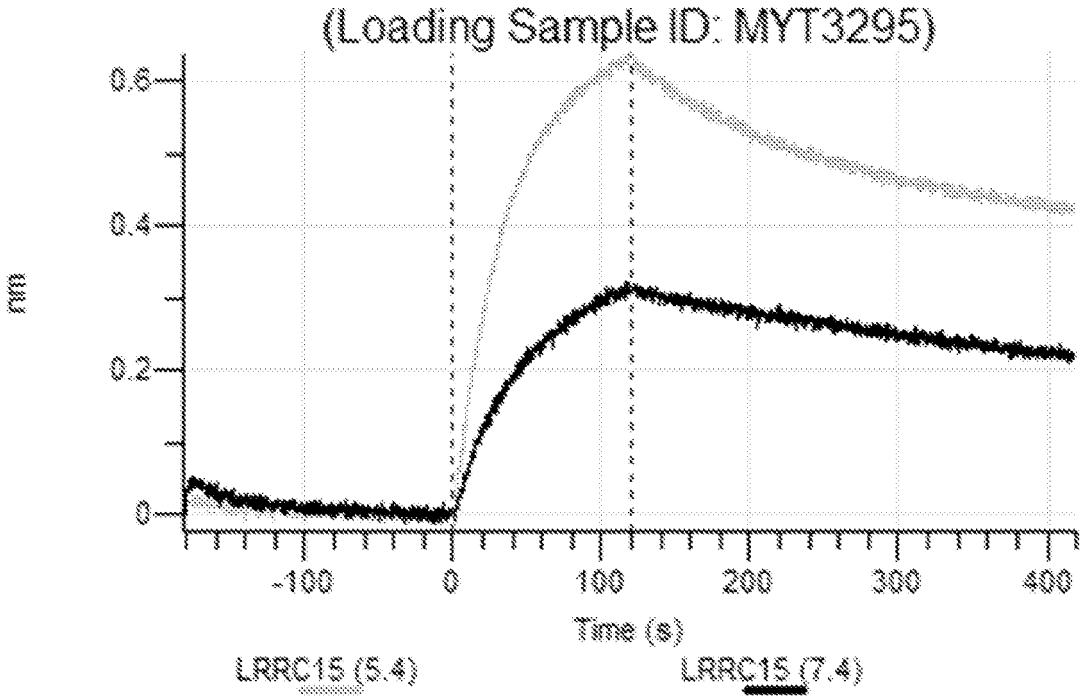

(Loading Sample ID: MYT3295)
nm
0.6
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14C

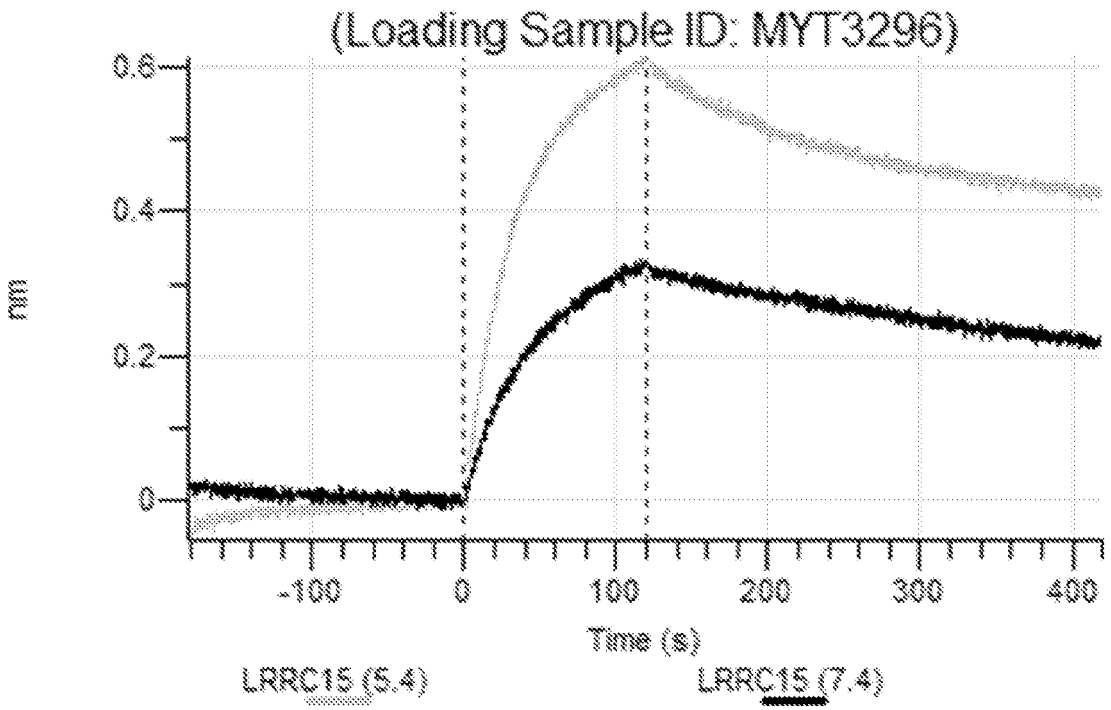

(Loading Sample ID: MYT3296)
nm
0.6
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14D

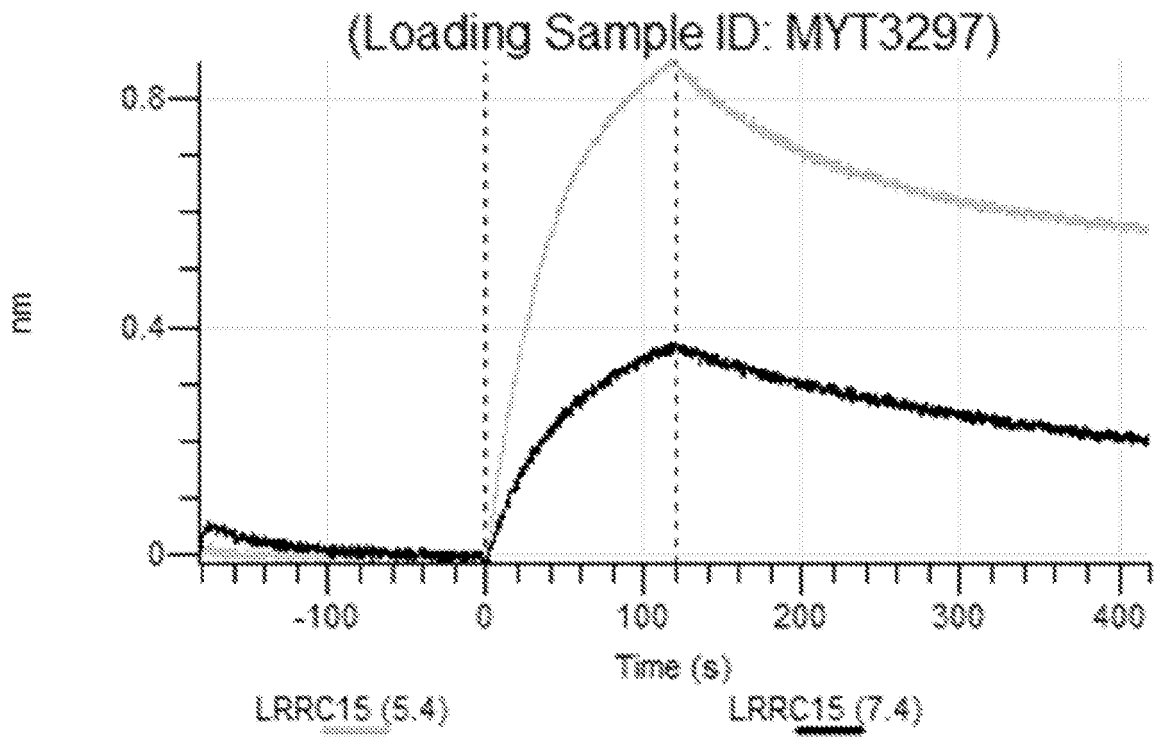

(Loading Sample ID: MYT3297)
nm
0.8
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14E

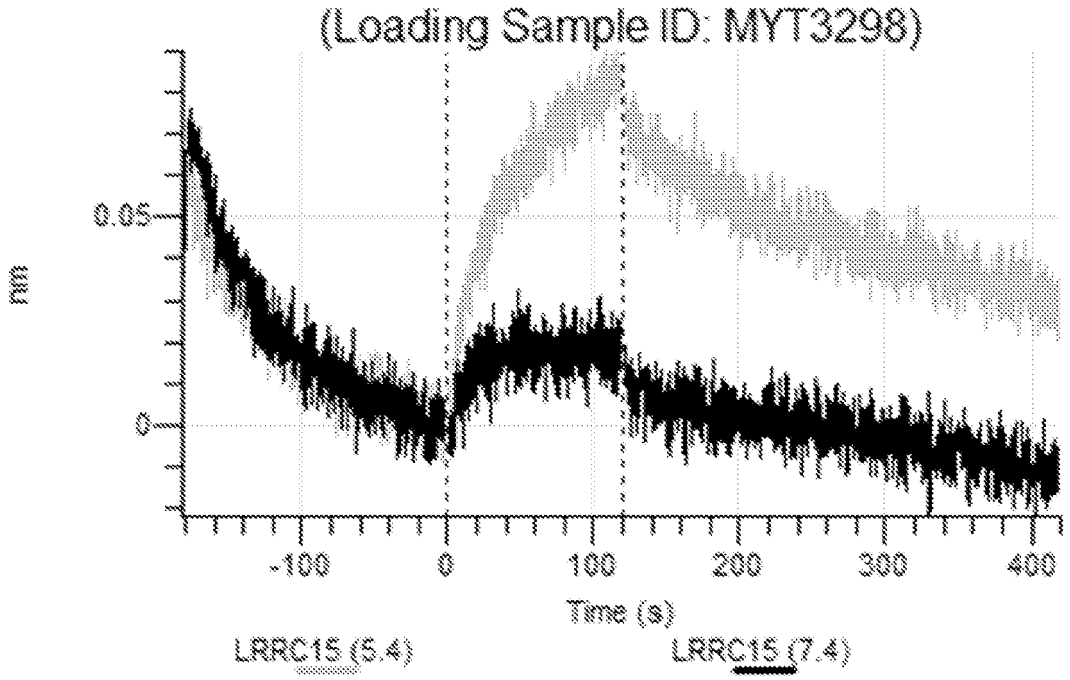

(Loading Sample ID: MYT3298)
nm
0.05
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14F

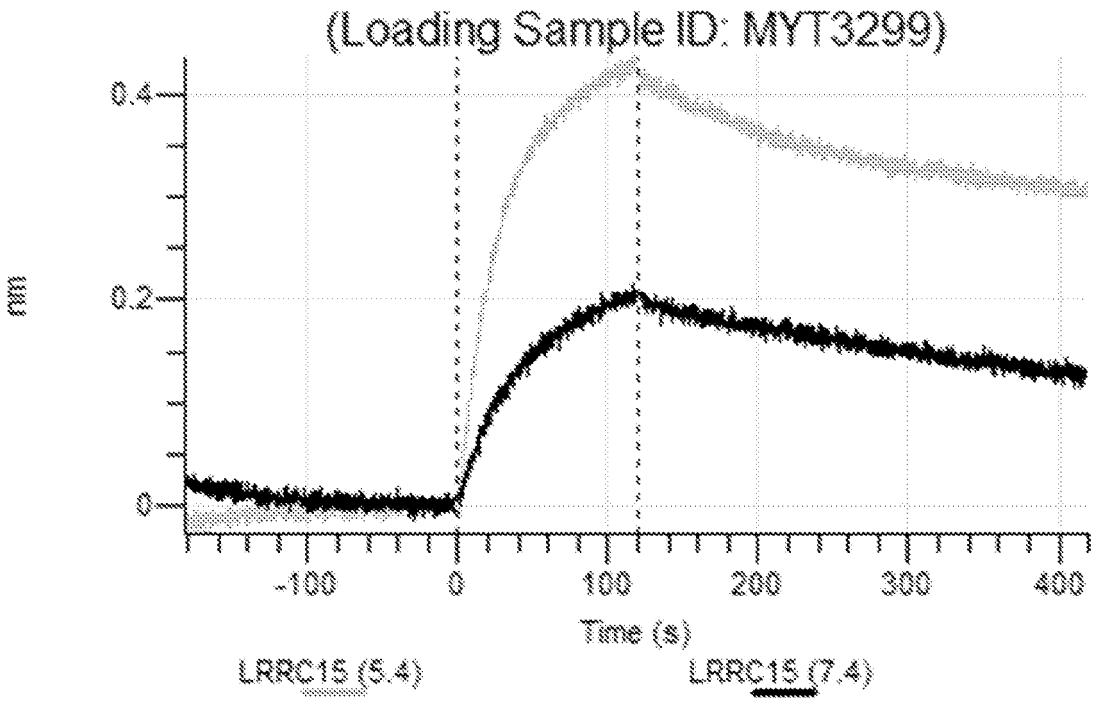

(Loading Sample ID: MYT3299)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14G

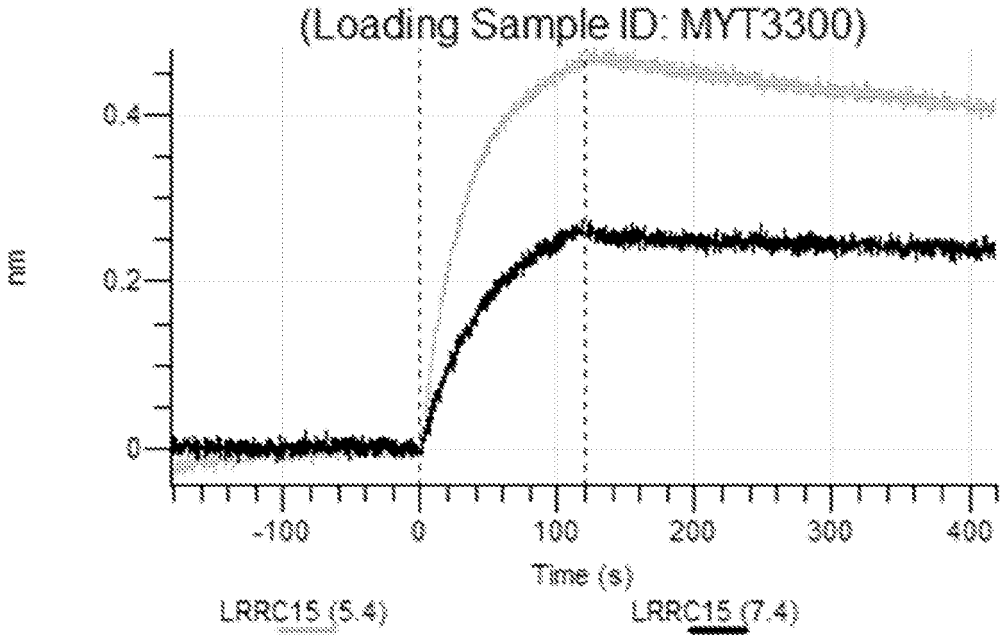

(Loading Sample ID: MYT3300)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14H

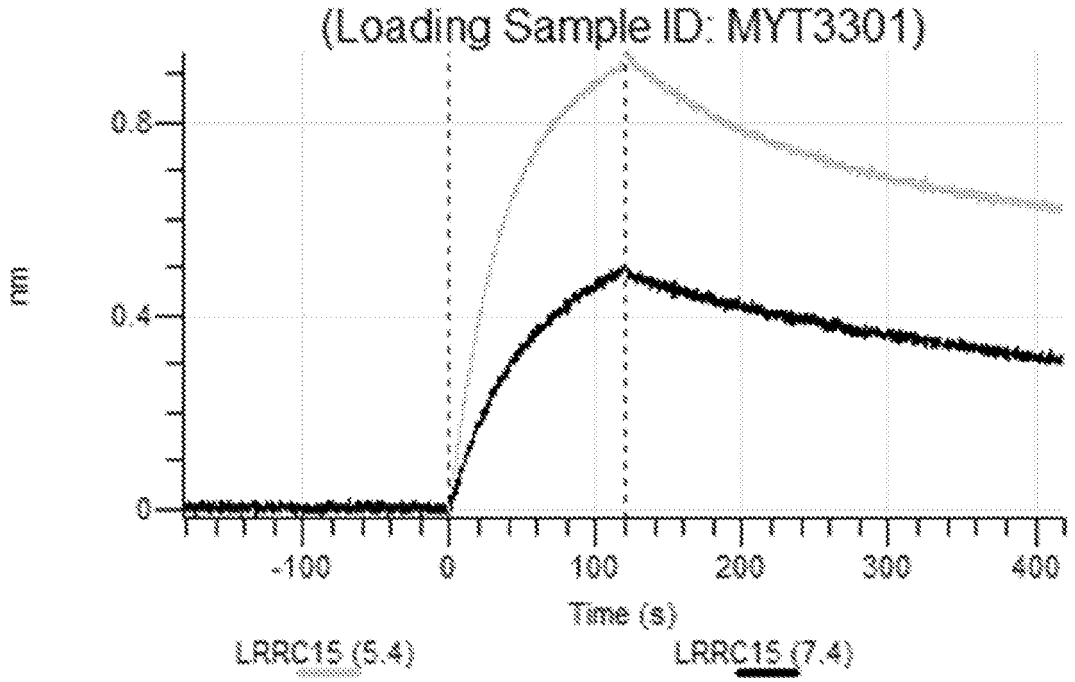

(Loading Sample ID: MYT3301)
0.8
0.4
0
(nm)
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14I

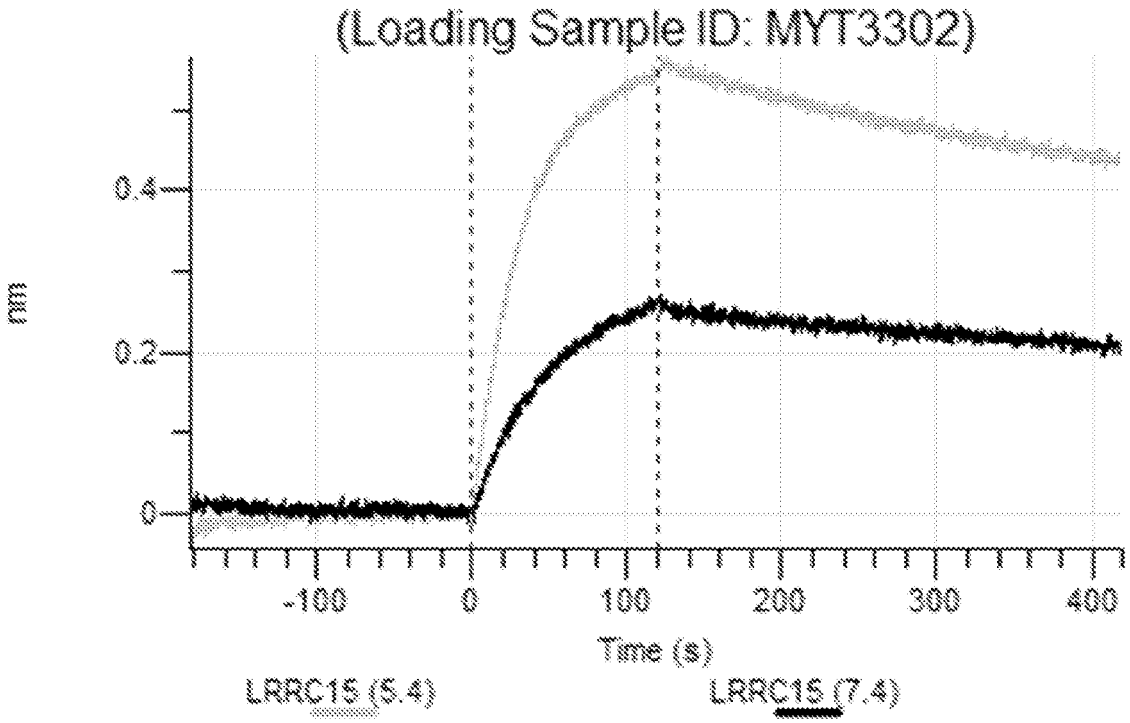

(Loading Sample ID: MYT3302)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14J

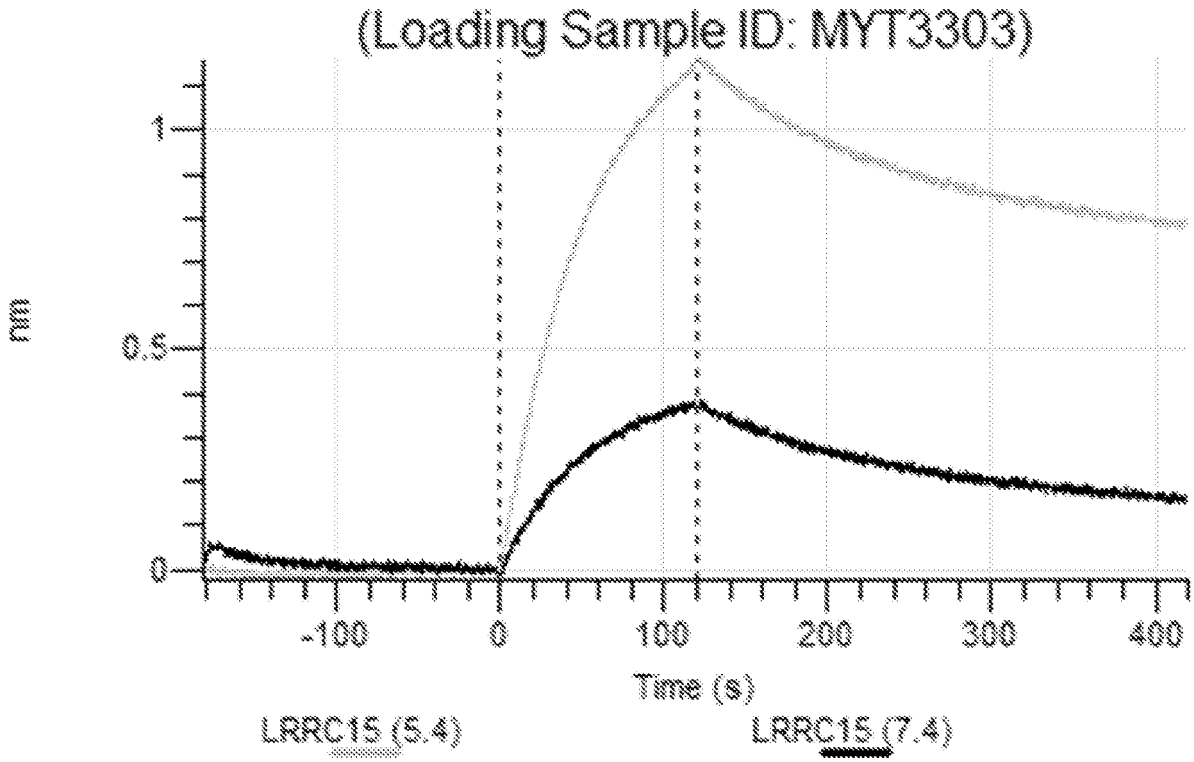

(Loading Sample ID: MYT3303)
nm
1
0.5
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14K

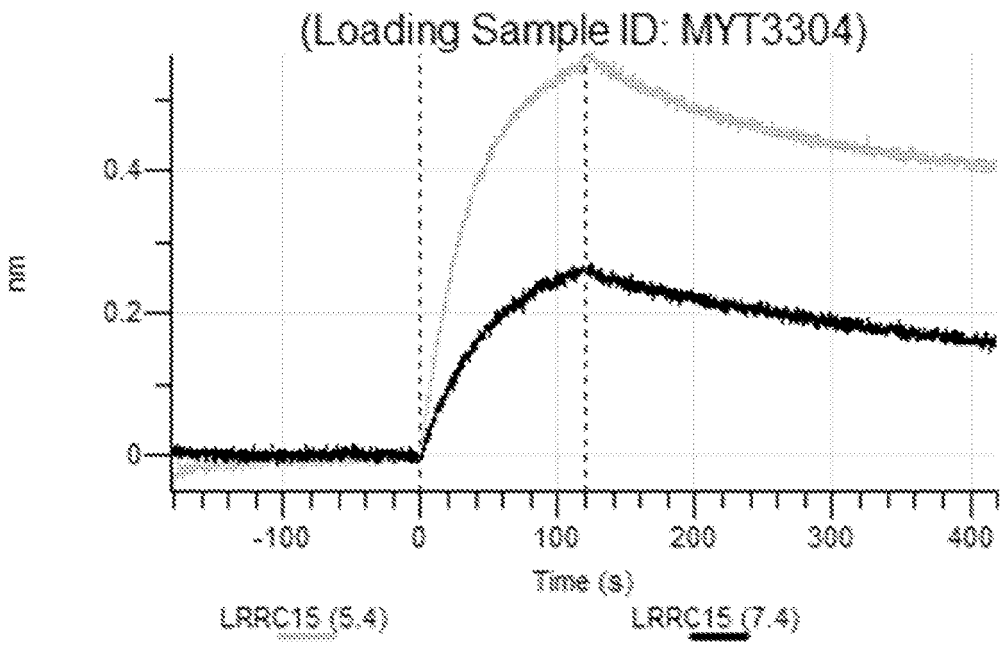

(Loading Sample ID: MYT3304)
RFU
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14L

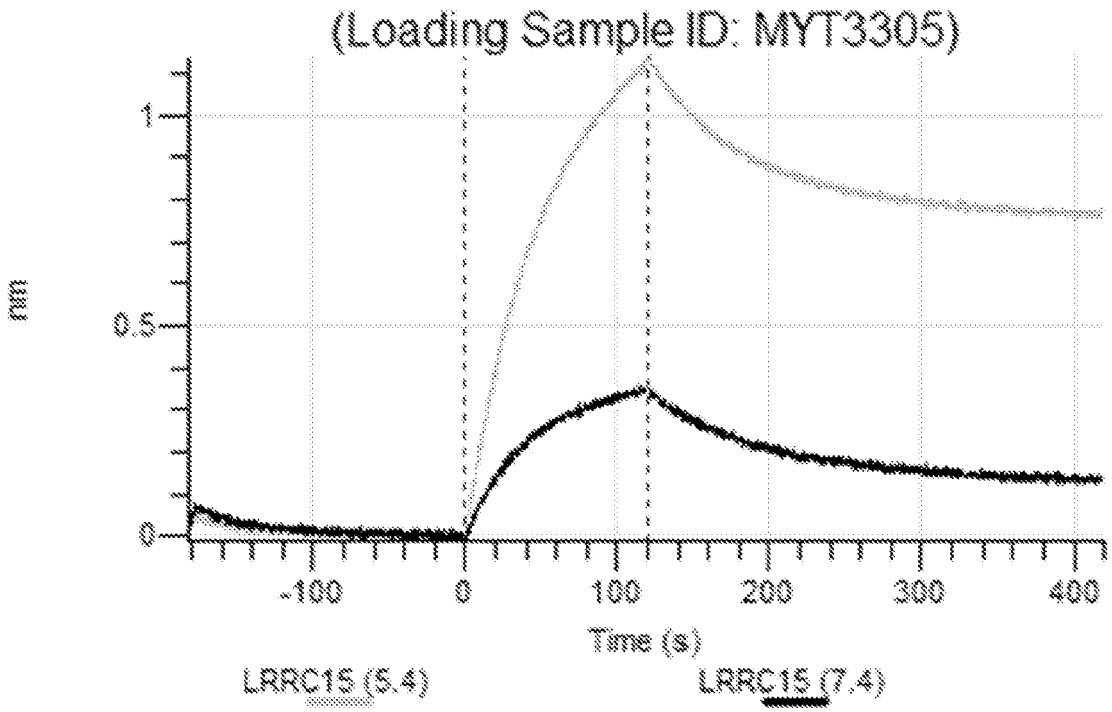

(Loading Sample ID: MYT3305)
nm
1
0.5
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14M

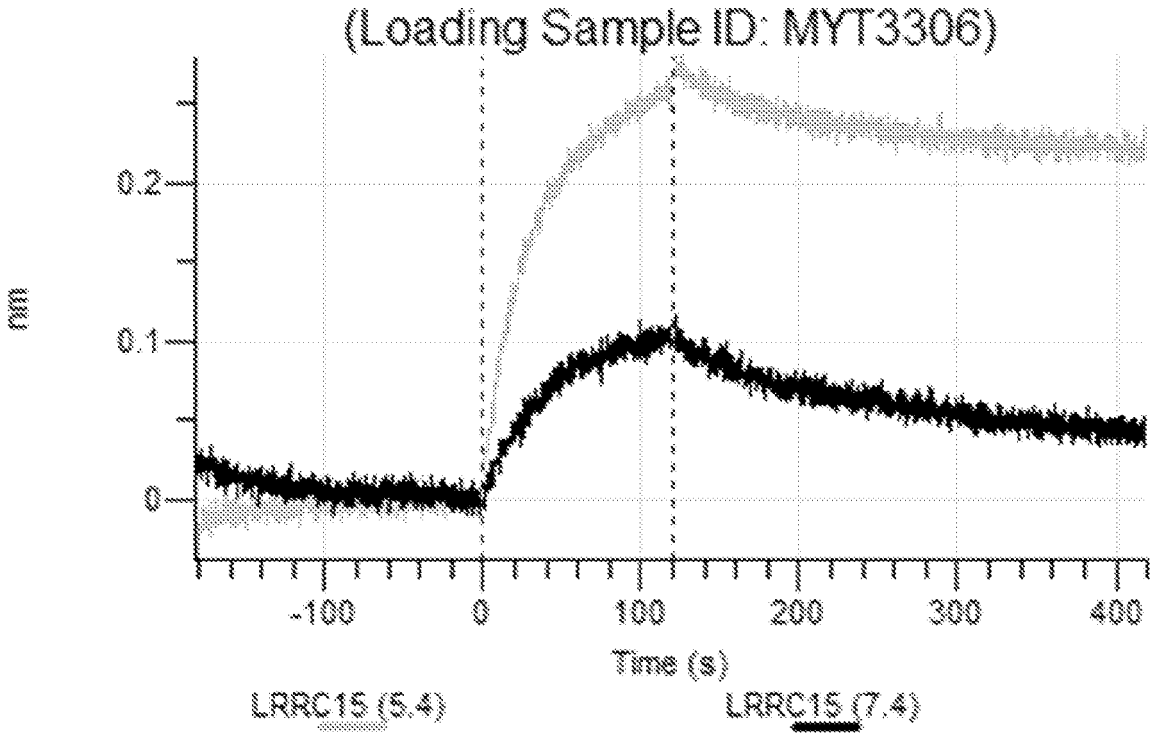

(Loading Sample ID: MYT3306)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14N

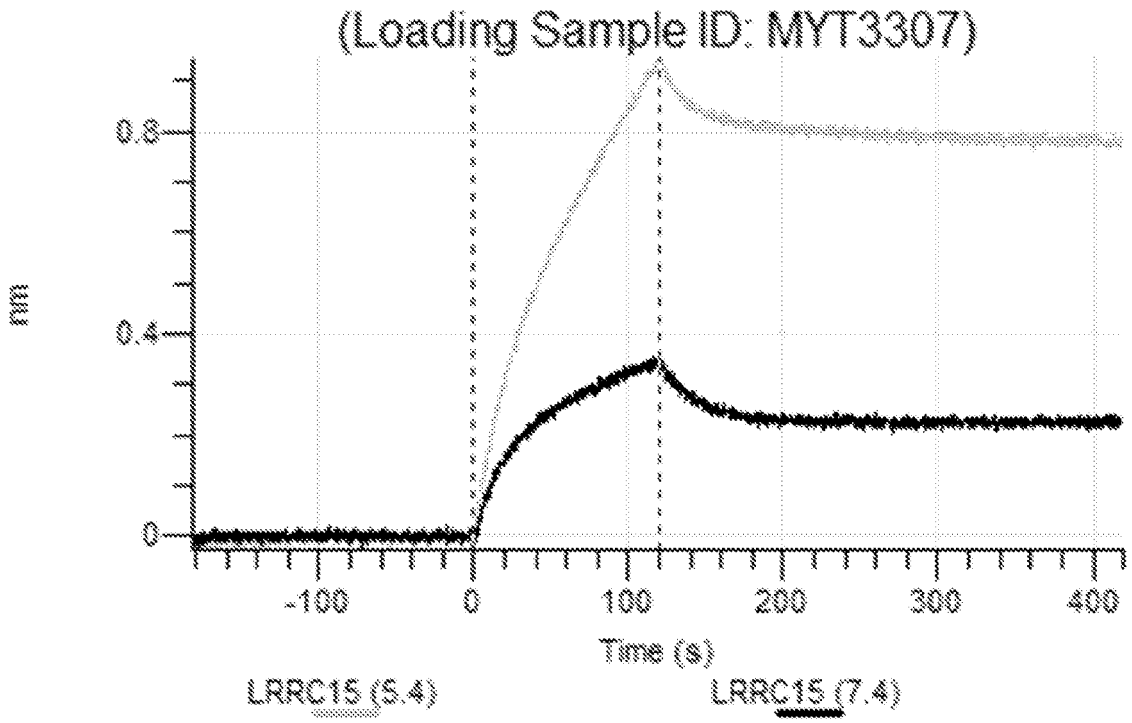

(Loading Sample ID: MYT3307)
nm
0.8
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14O

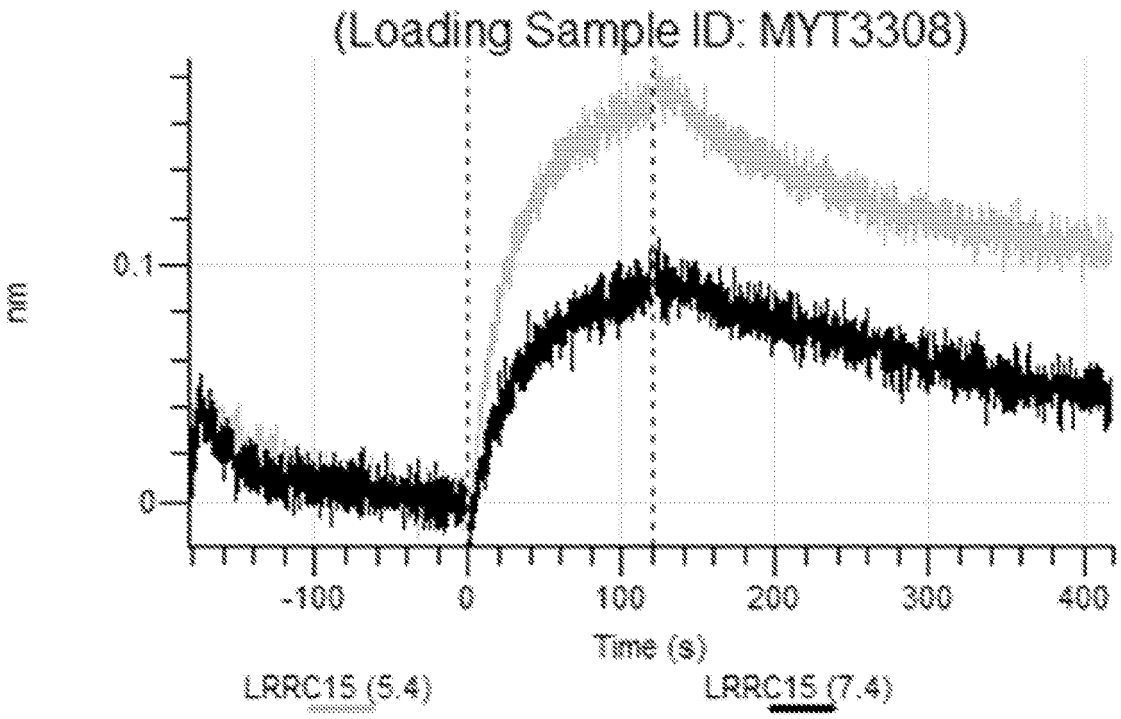

(Loading Sample ID: MYT3308)
nm
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14P

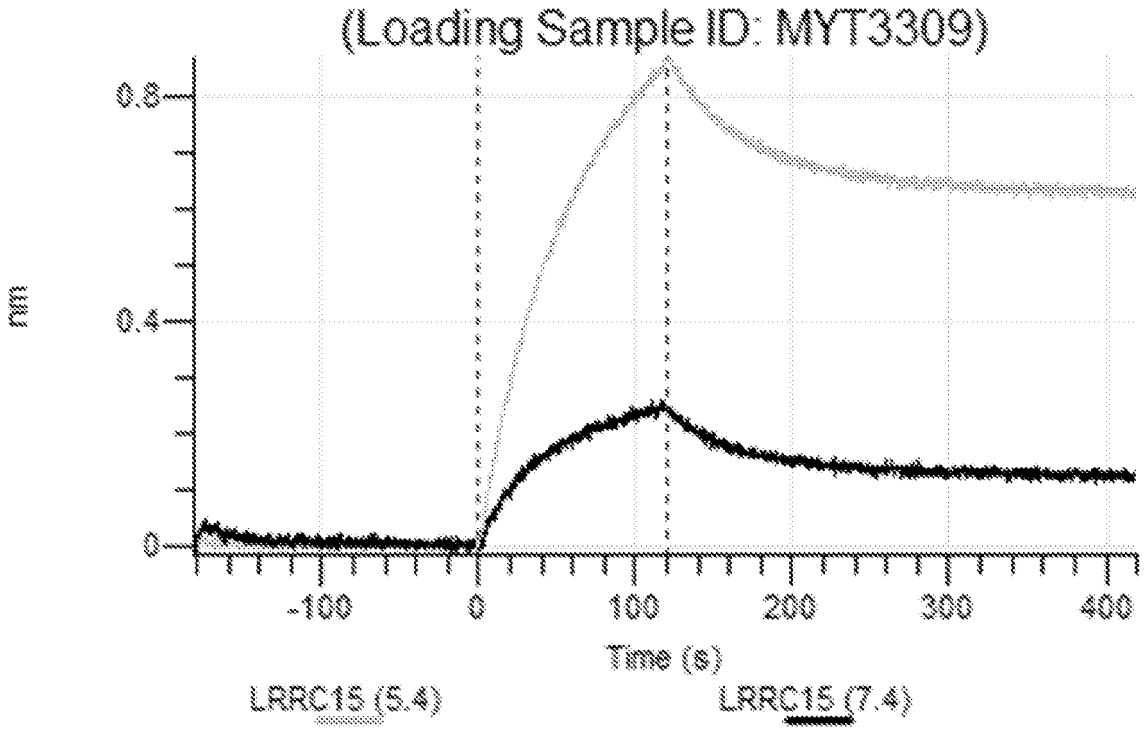

(Loading Sample ID: MYT3309)
0.8
0.4
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14Q

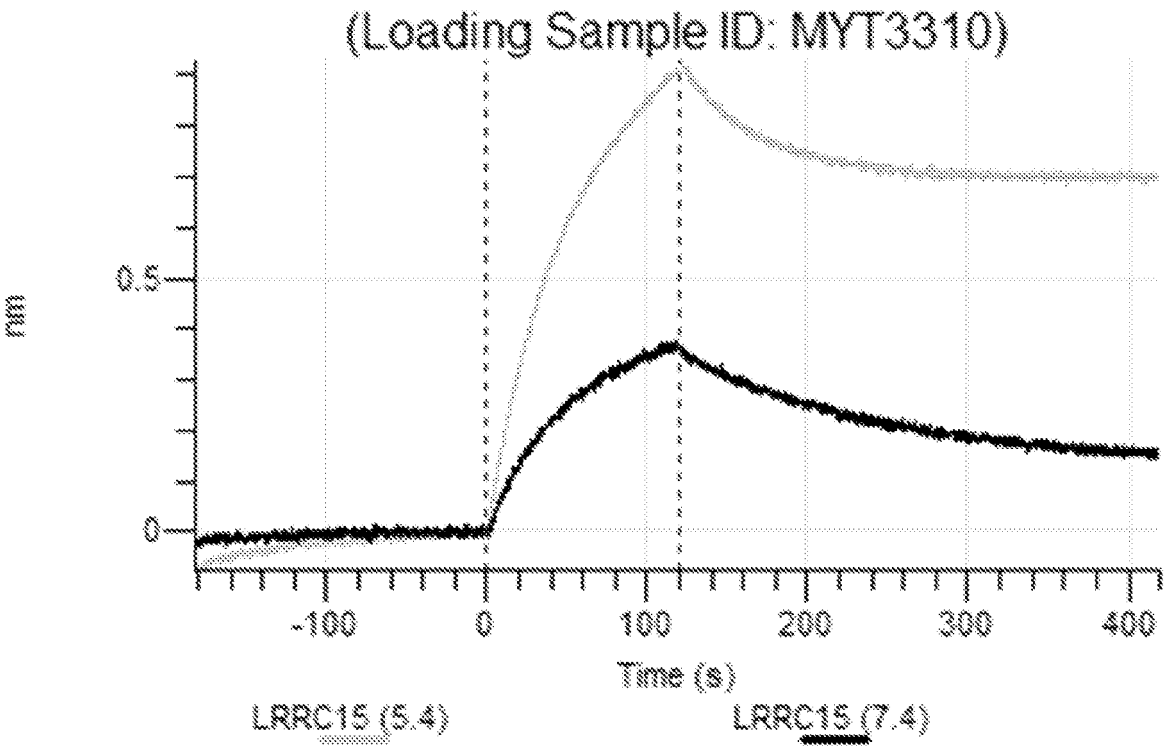

(Loading Sample ID: MYT3310)
nm
0.5
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14R

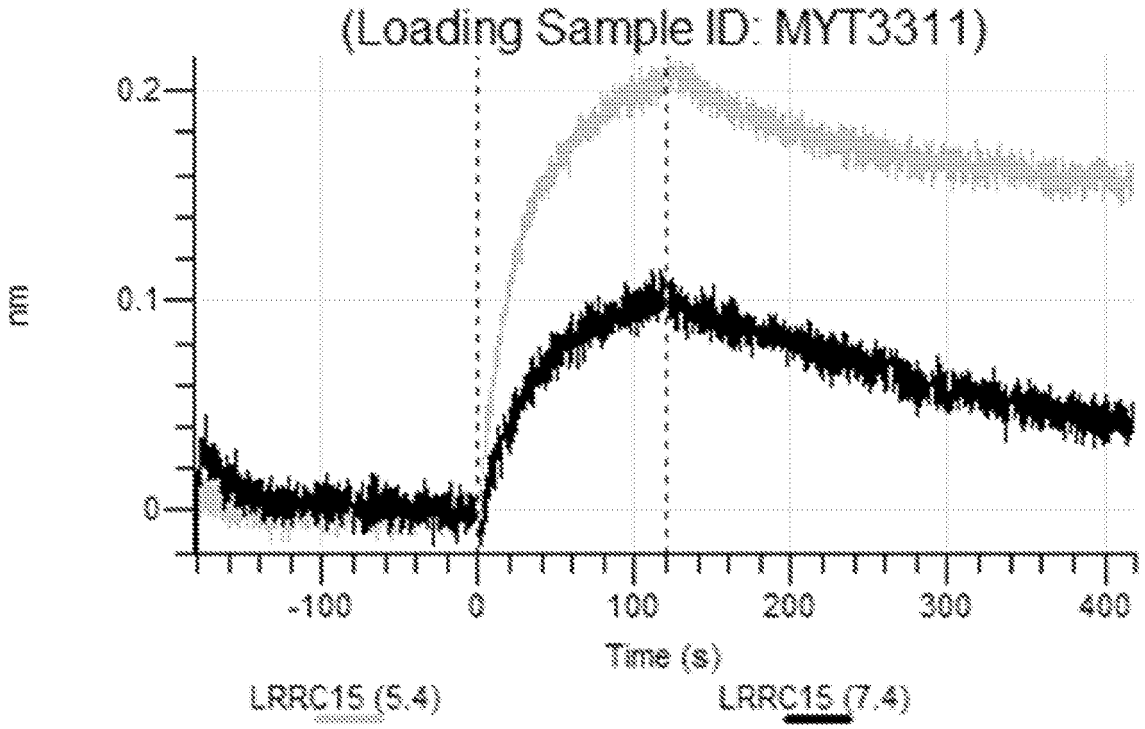

(Loading Sample ID: MYT3311)
0.2
0.1
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14S

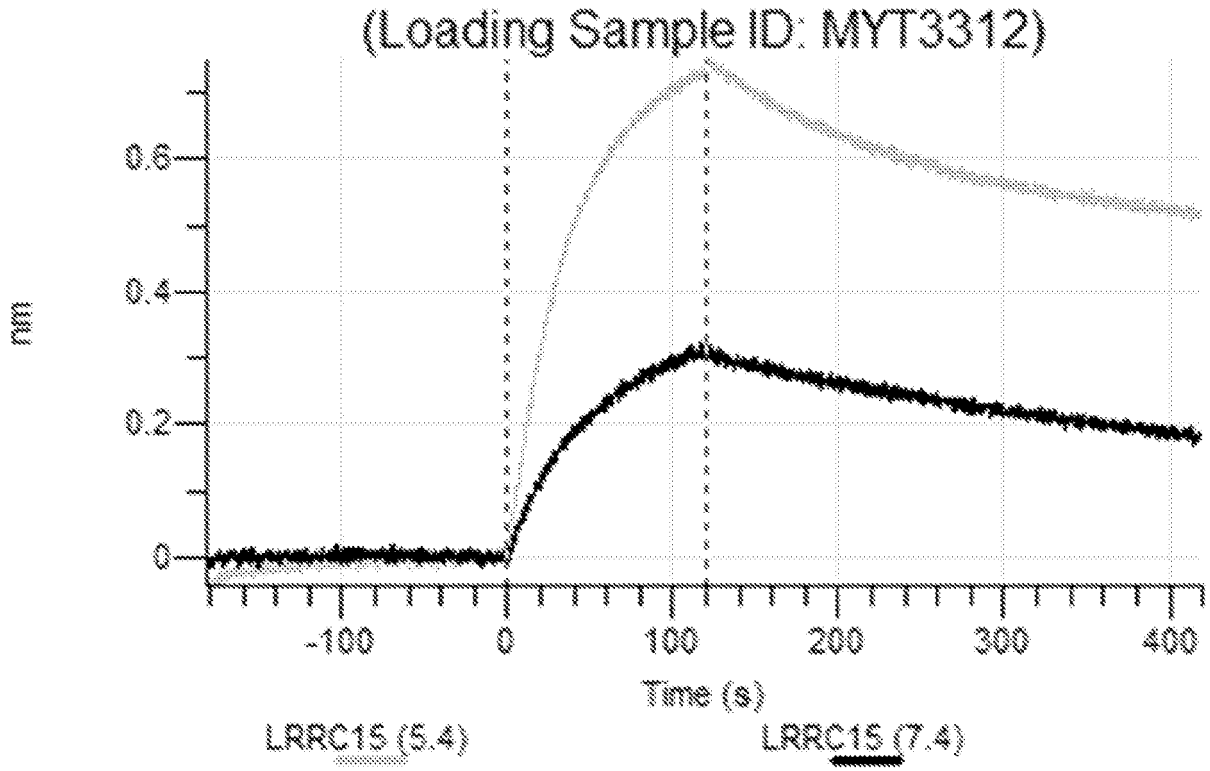

(Loading Sample ID: MYT3312)
nm
0.6
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14T

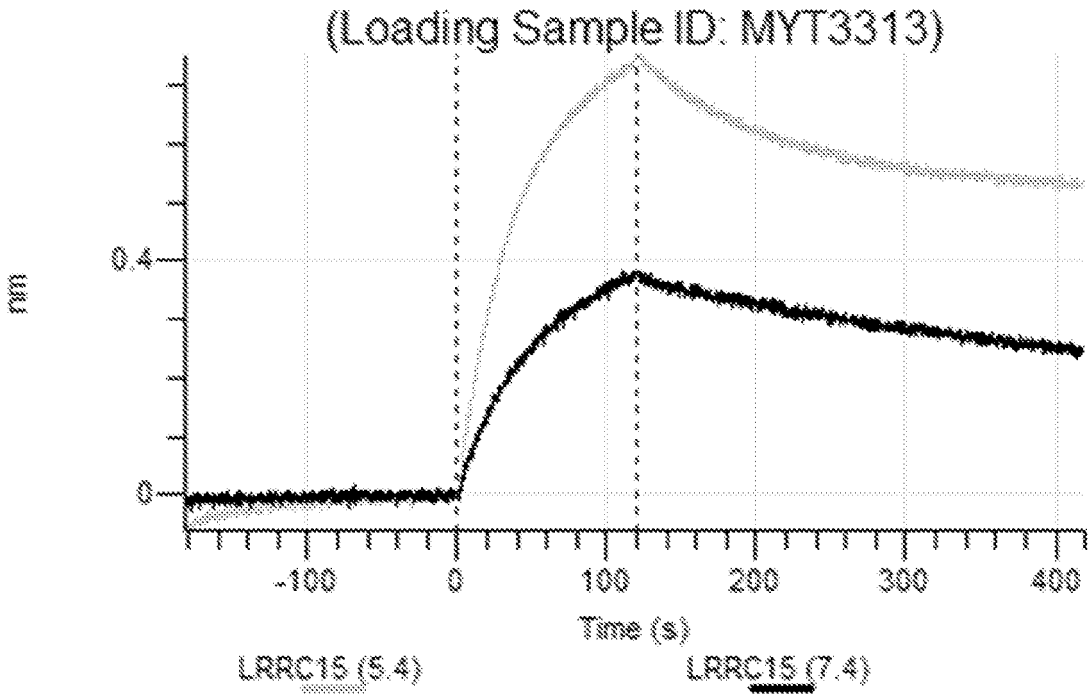

(Loading Sample ID: MYT3313)
nm
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14U

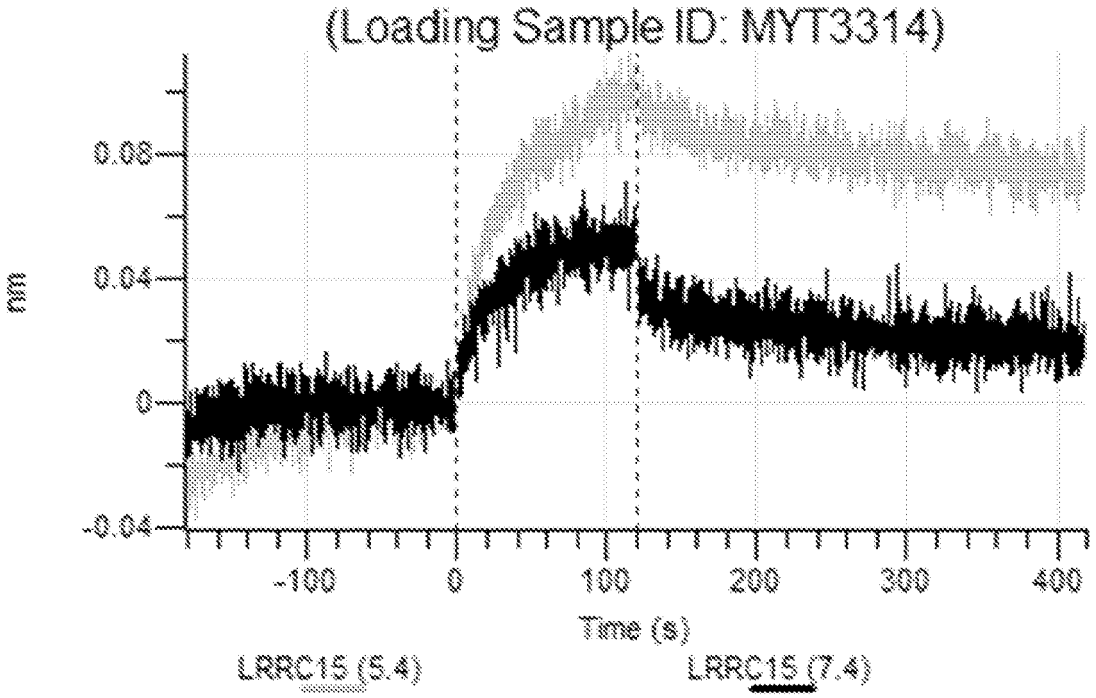

(Loading Sample ID: MYT3314)
nm
0.08
0.04
0
-0.04
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14V

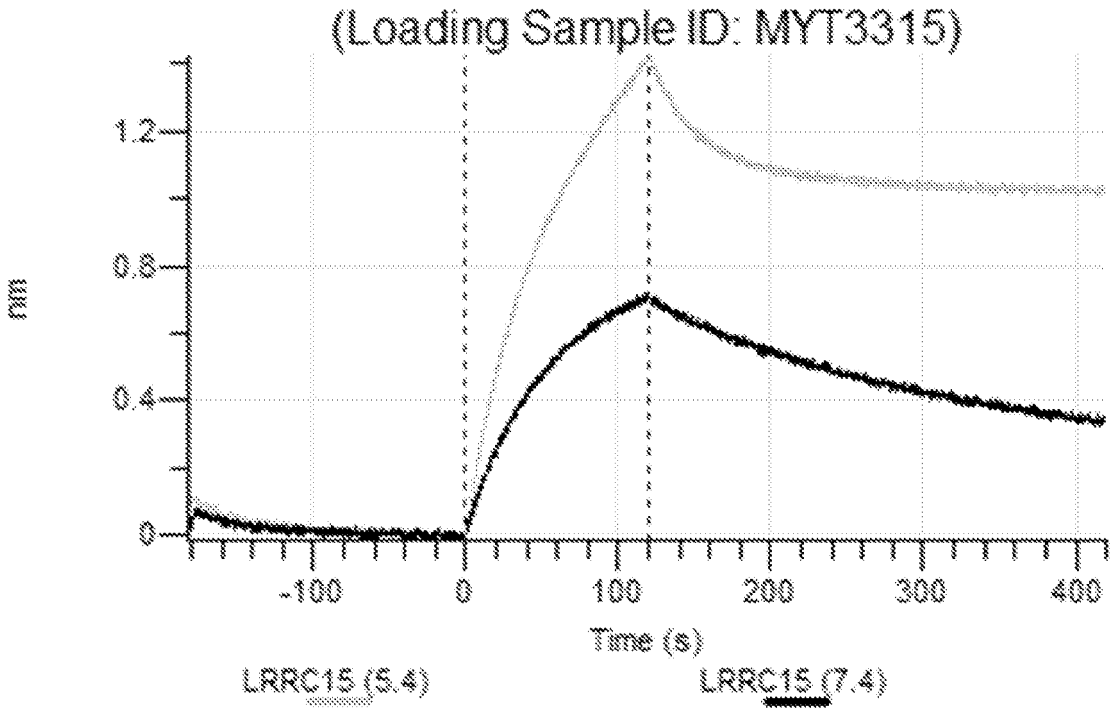

(Loading Sample ID: MYT3315)
nm
1.2
0.8
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14W

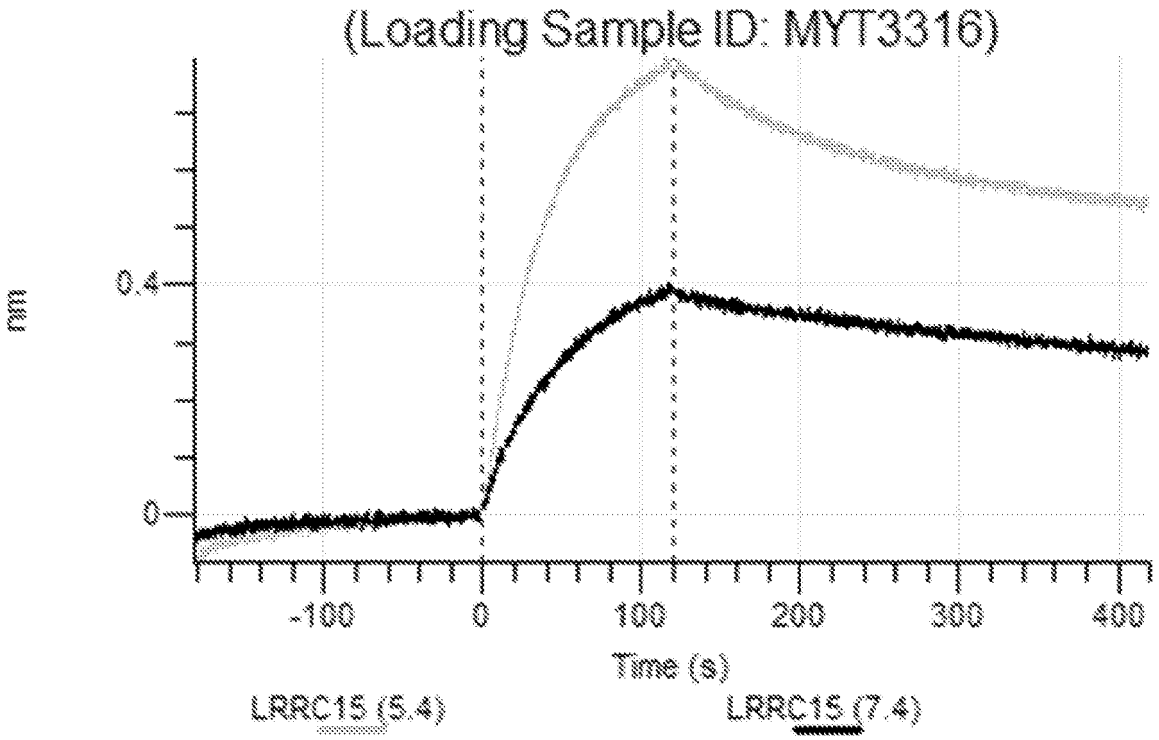

(Loading Sample ID: MYT3316)
nm
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14X

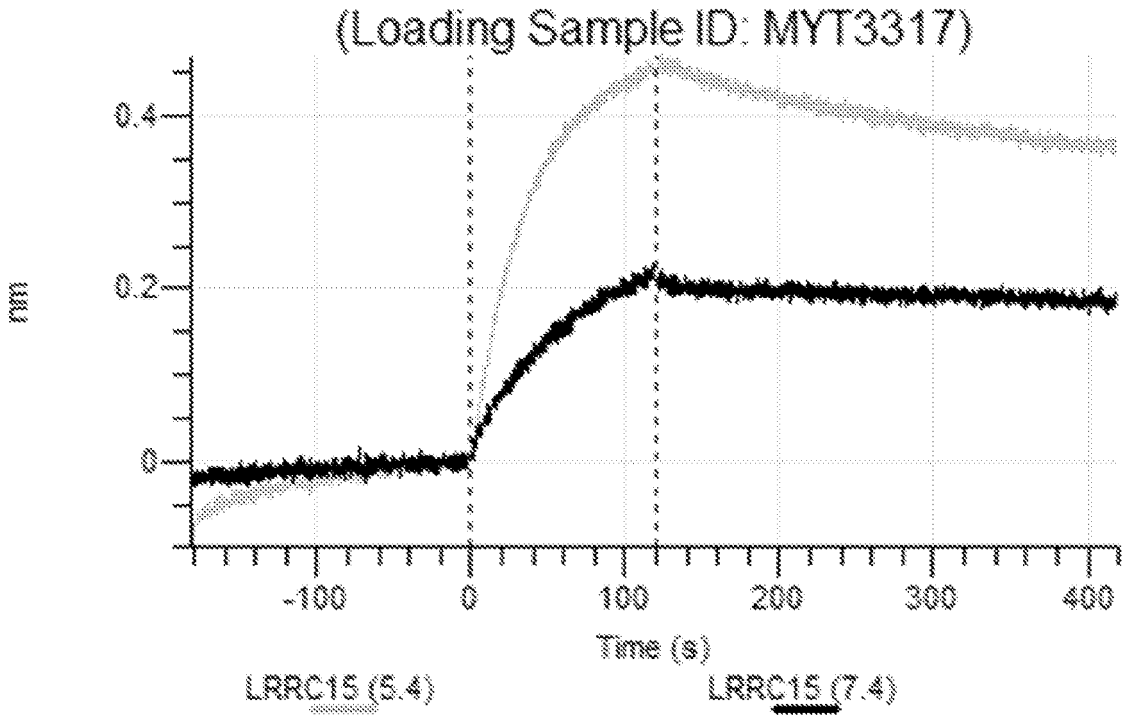

(Loading Sample ID: MYT3317)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14Y

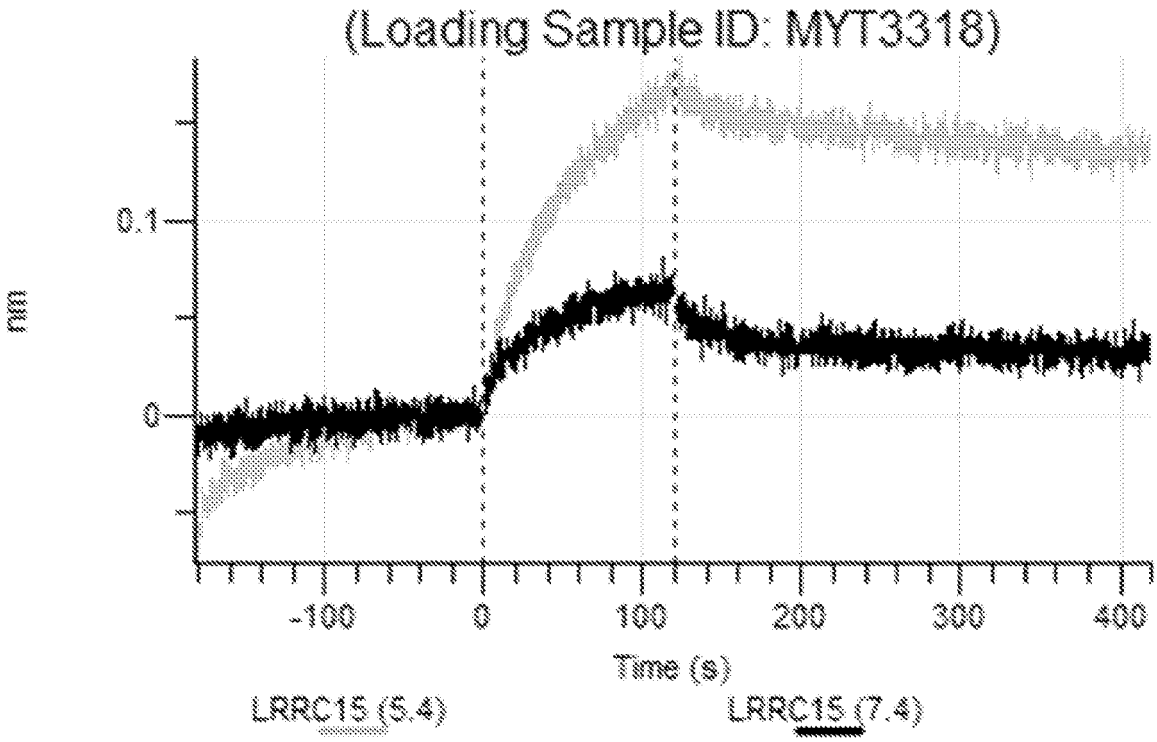

(Loading Sample ID: MYT3318)
nm
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14Z

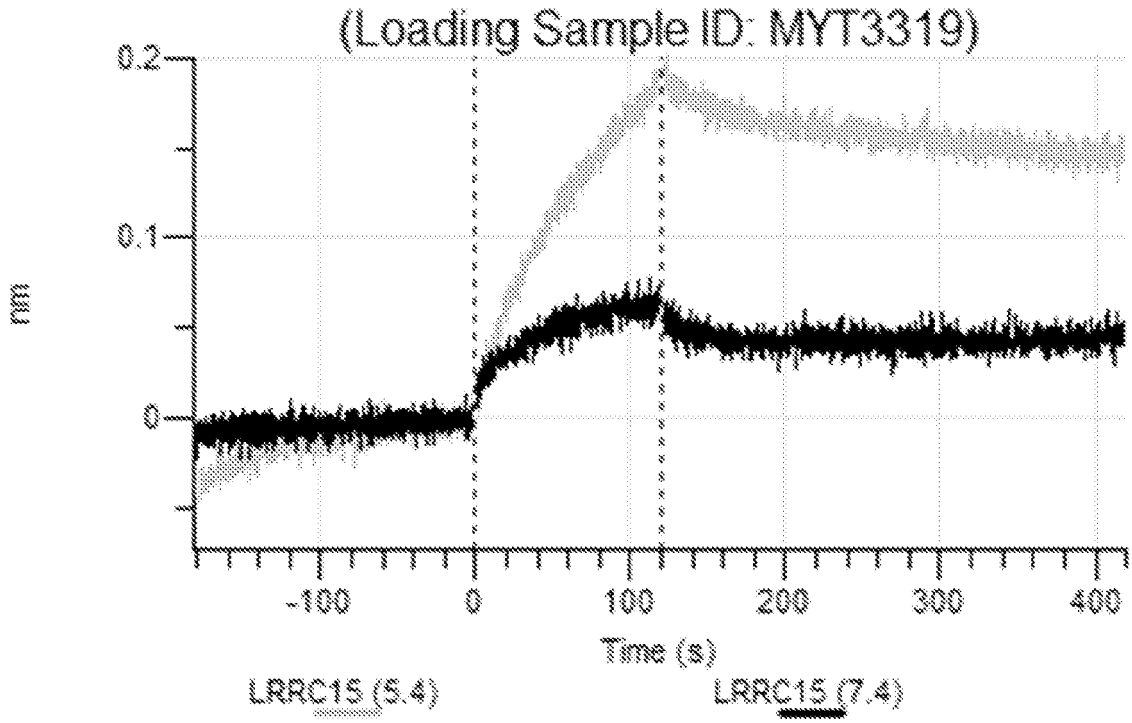

(Loading Sample ID: MYT3319)
0.2
0.1
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14AA

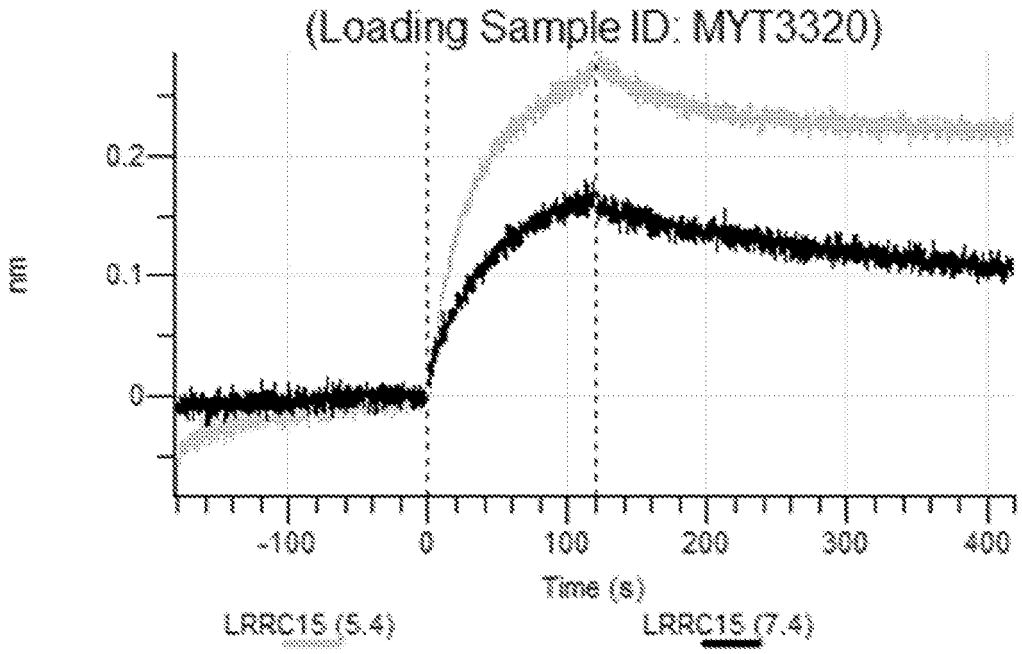

(Loading Sample ID: MYT3320)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14AB

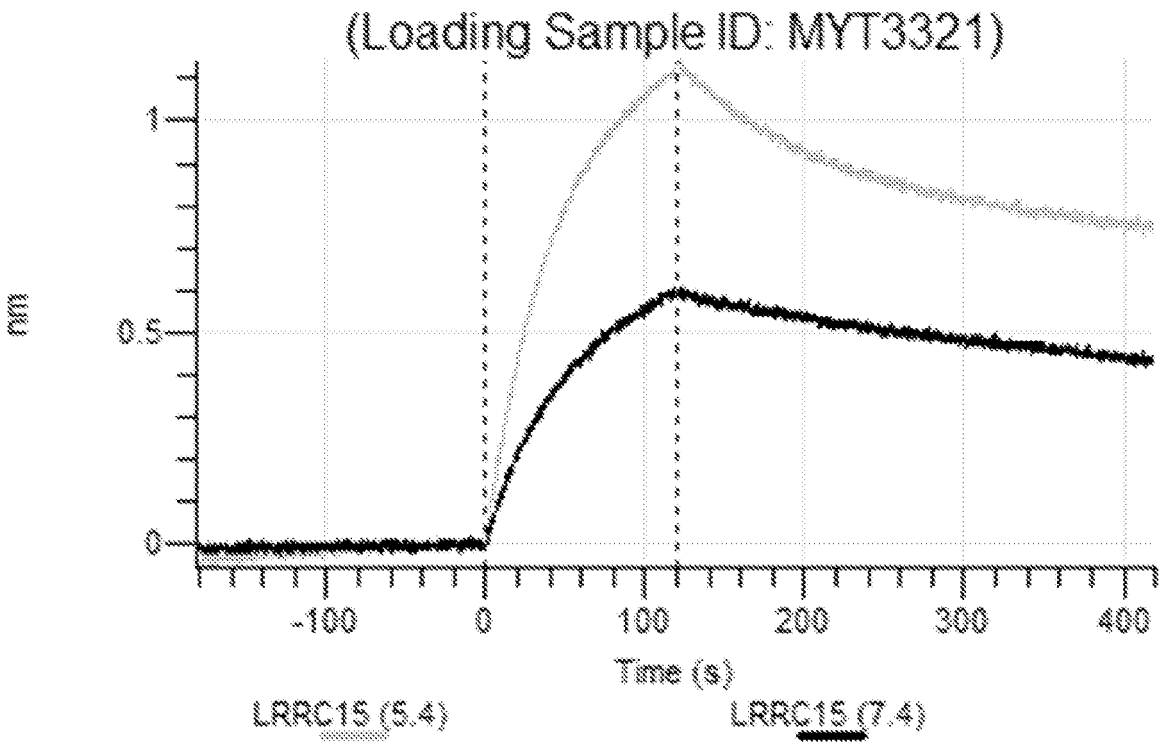

(Loading Sample ID: MYT3321)
nm
1
0.5
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14AC

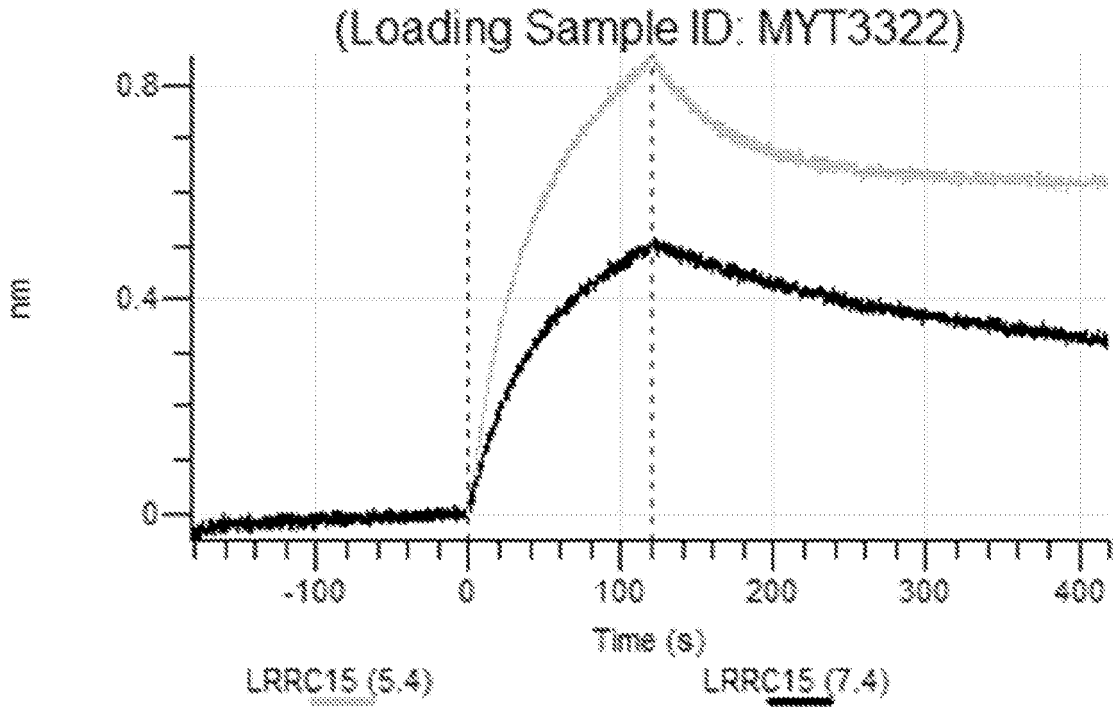

(Loading Sample ID: MYT3322)
0.8
0.4
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14AD

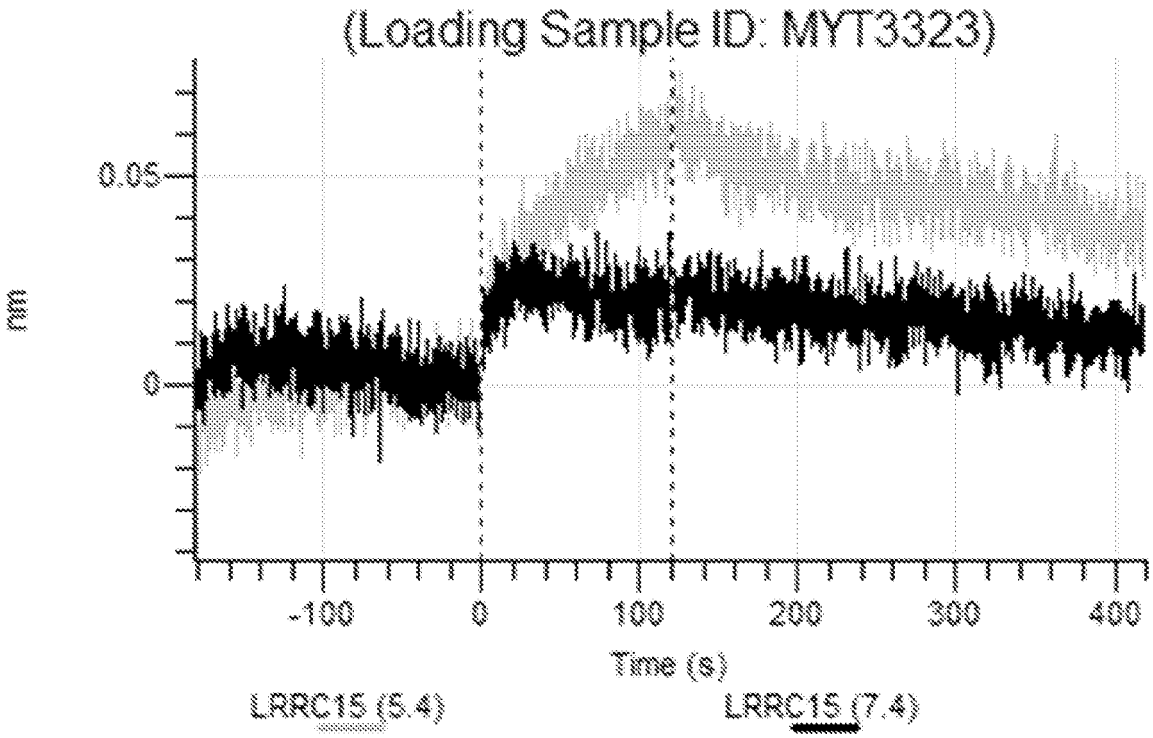

(Loading Sample ID: MYT3323)
0.05
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14AE

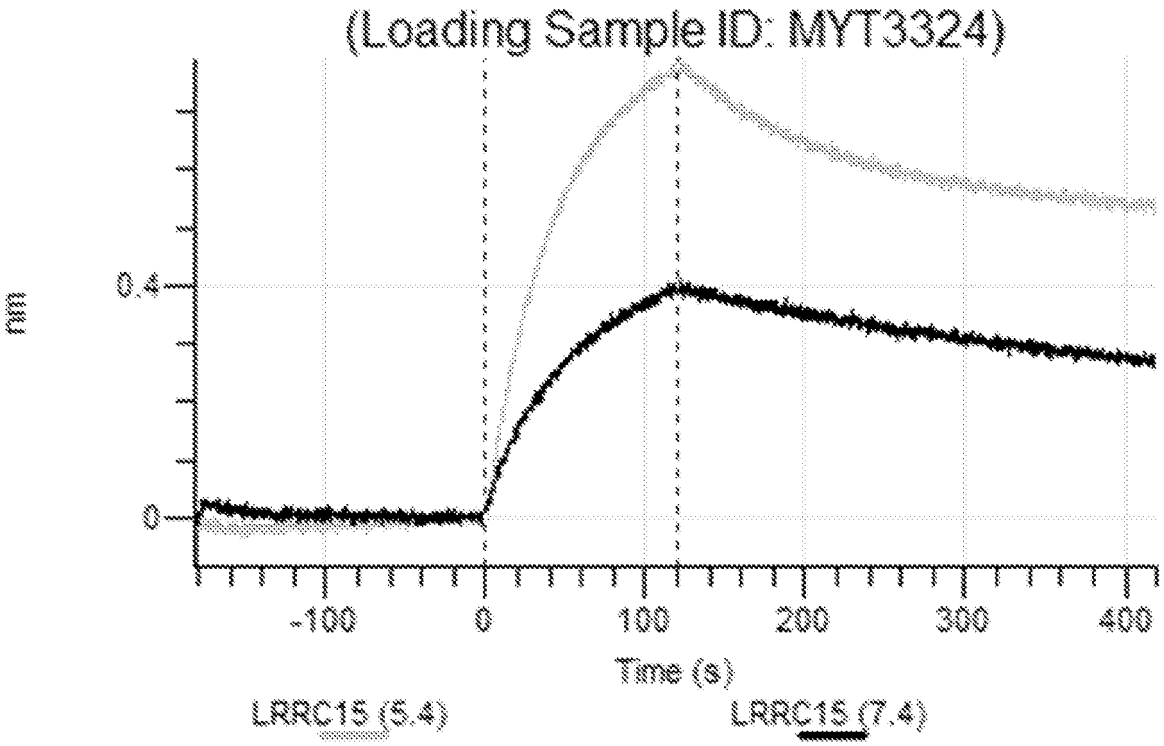

(Loading Sample ID: MYT3324)
nm
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 14AF

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
MYT3252 (hu139.10)	84	85	86	87	88	89	90	91
MYT3293	84	132						
MYT3294	84	133						
MYT3295	84	134						
MYT3296	84	135						
MYT3297	84	136						
MYT3298	84	137						
MYT3299	84	138						
MYT3300	84	139						
MYT3301	84	140						
MYT3302	84	141						
MYT3303	84	142						
MYT3304	84	143						
MYT3305	84	144						
MYT3306	84	145						
MYT3307	84	146						
MYT3308	84	147						
MYT3309	84	148						
MYT3310	84	149						
MYT3311	84	150						
MYT3312	84	151						
MYT3313	84	152						
MYT3314	84	153						
MYT3315	84	154						
MYT3316	84	155						
MYT3317	84	156						
MYT3318	84	157						
MYT3319	84	158						
MYT3320	84	159						
MYT3321	84	160						
MYT3322	84	161						
MYT3323	84	162						
MYT3324	84	163						

FIG. 15

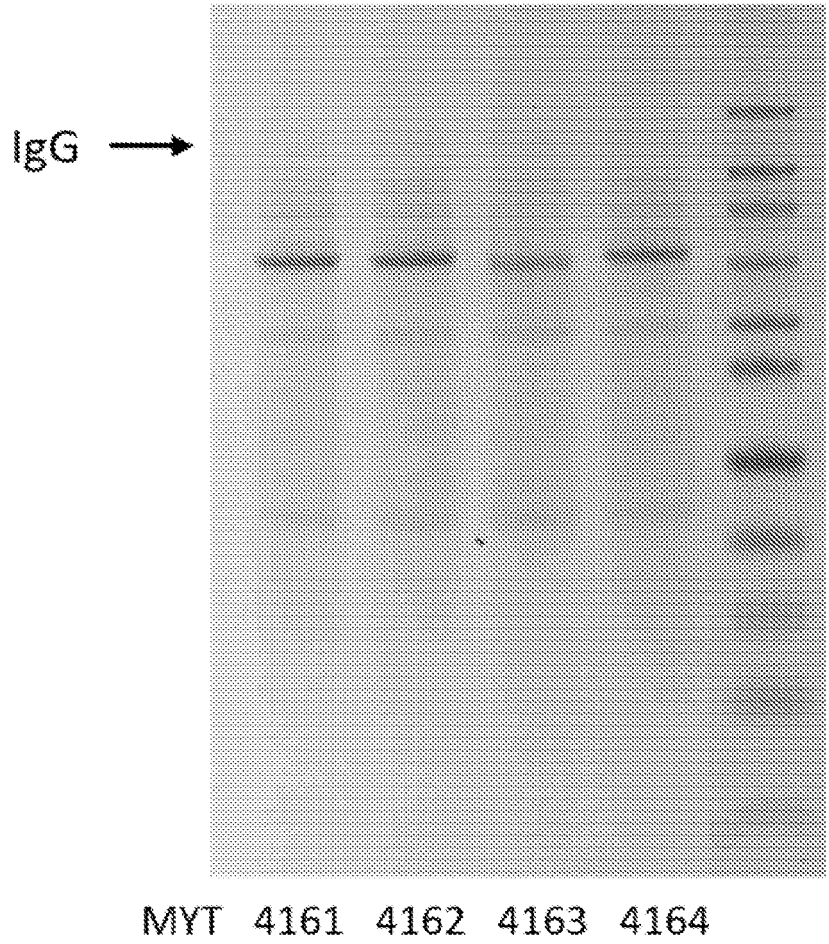


FIG. 16

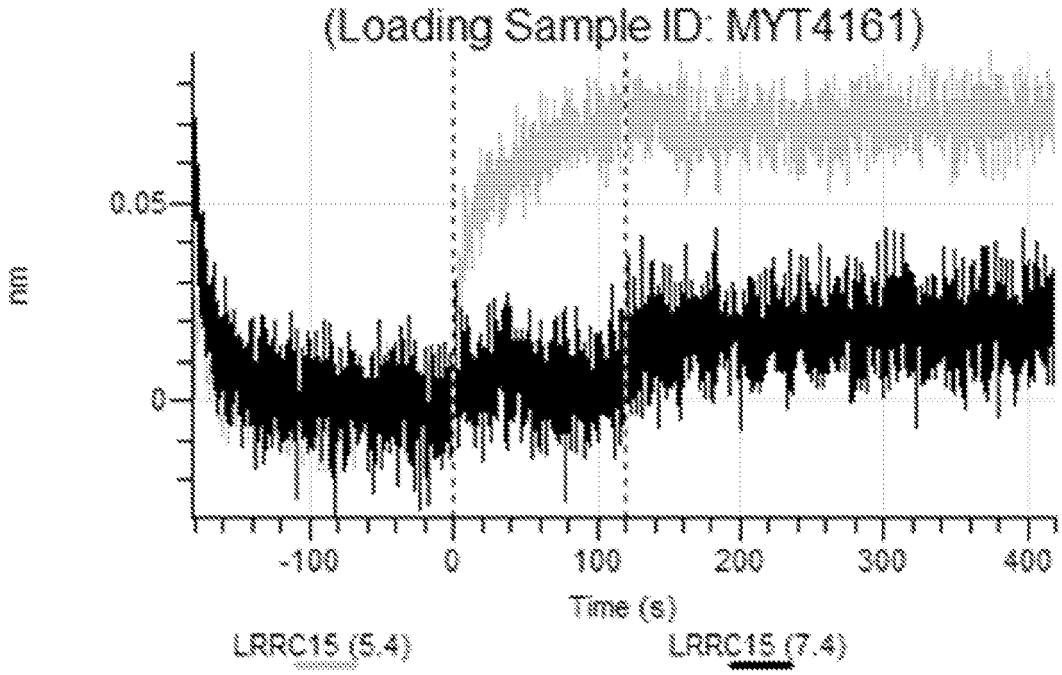

(Loading Sample ID: MYT4161)
0.05
0
(nm)
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 17A

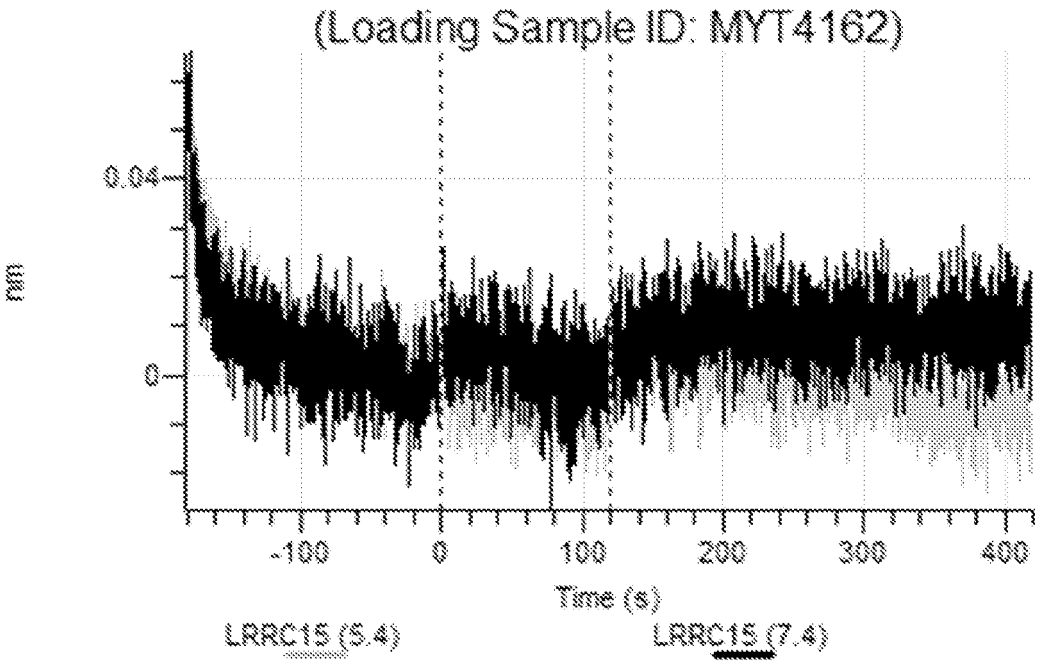

(Loading Sample ID: MYT4162)
0.04
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 17B

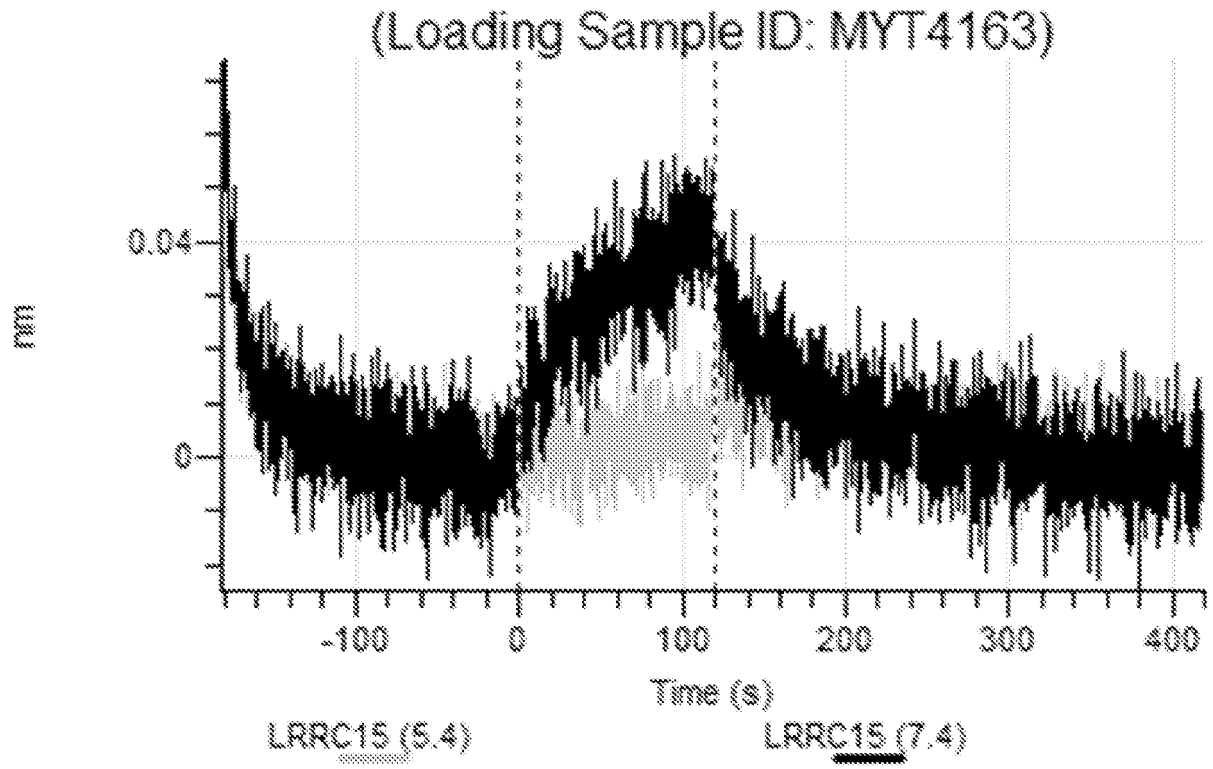

(Loading Sample ID: MYT4163)
nm
0.04
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 17C

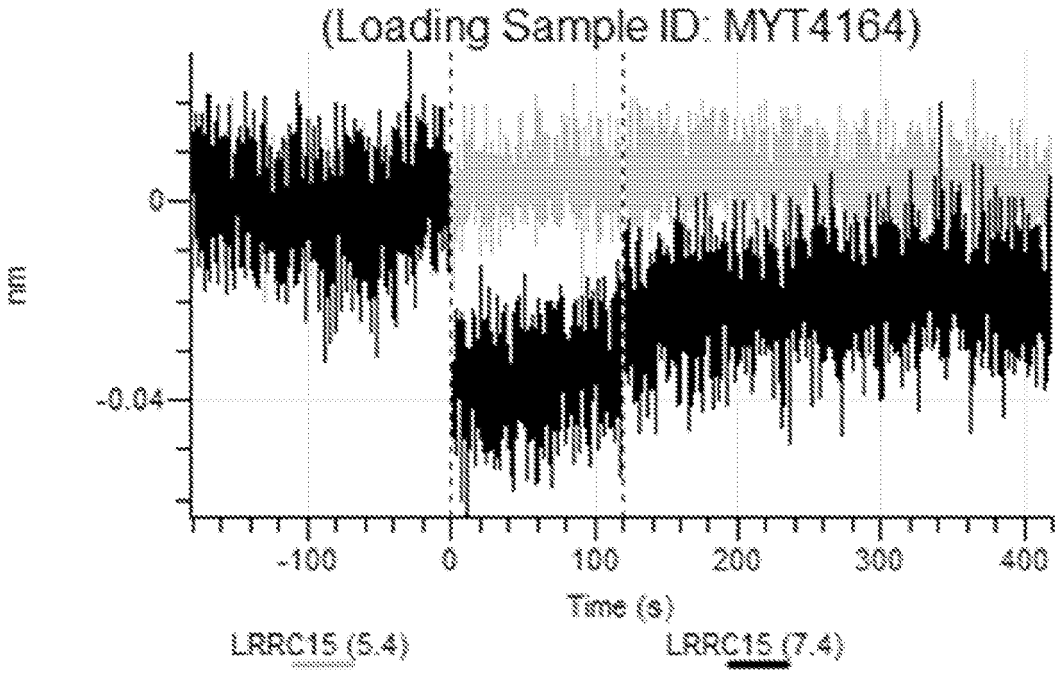

(Loading Sample ID: MYT4164)
nm
0
-0.04
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 17D

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
MYT3252 (hu139.10)	84	85	86	87	88	89	90	91
MYT4161	164	85						
MYT4162	165	85						
MYT4163	166	85						
MYT4164	167	85						

FIG. 18

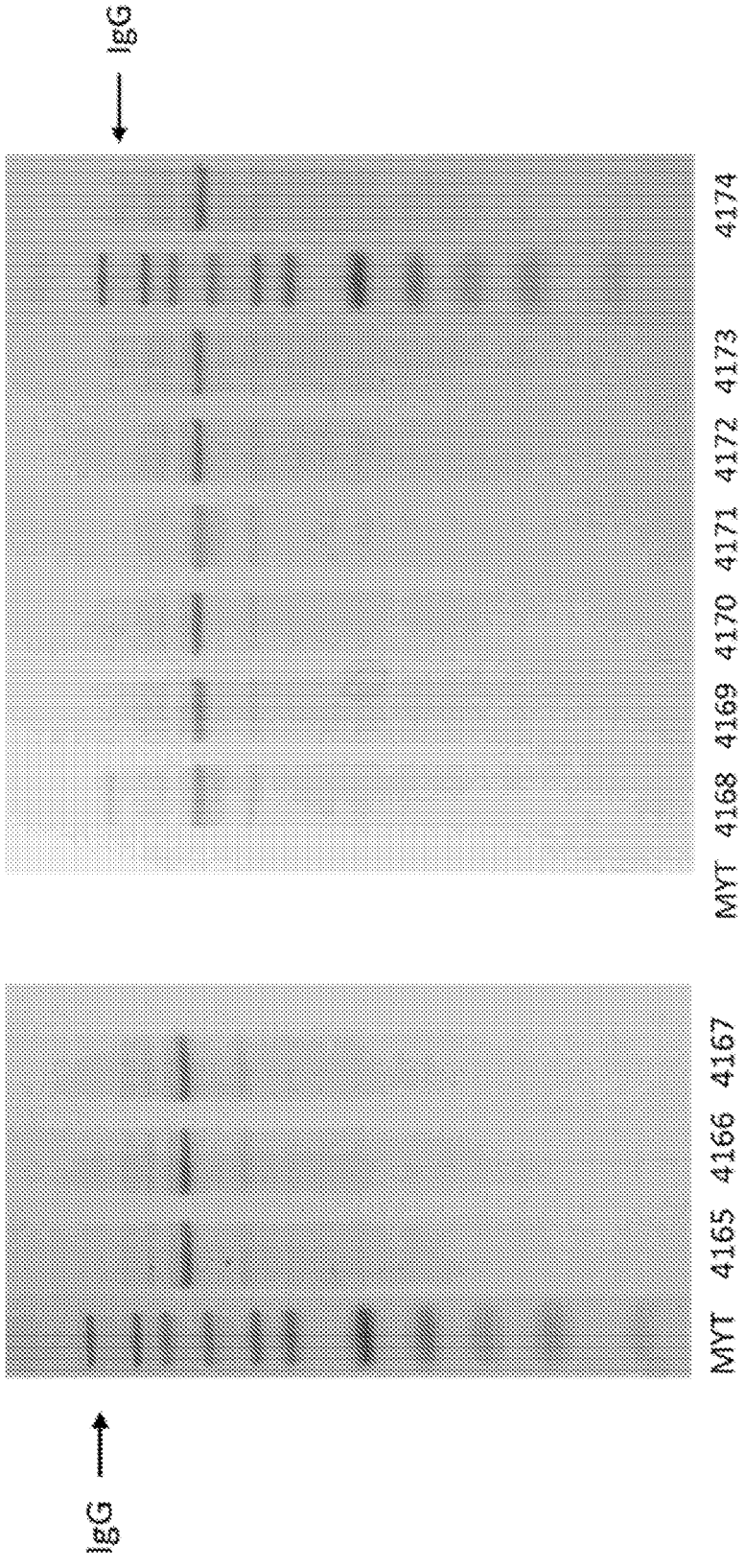

IgG
MYT 4168 4169 4170 4171 4172 4173 4174
MYT 4165 4166 4167
IgG

FIG. 19

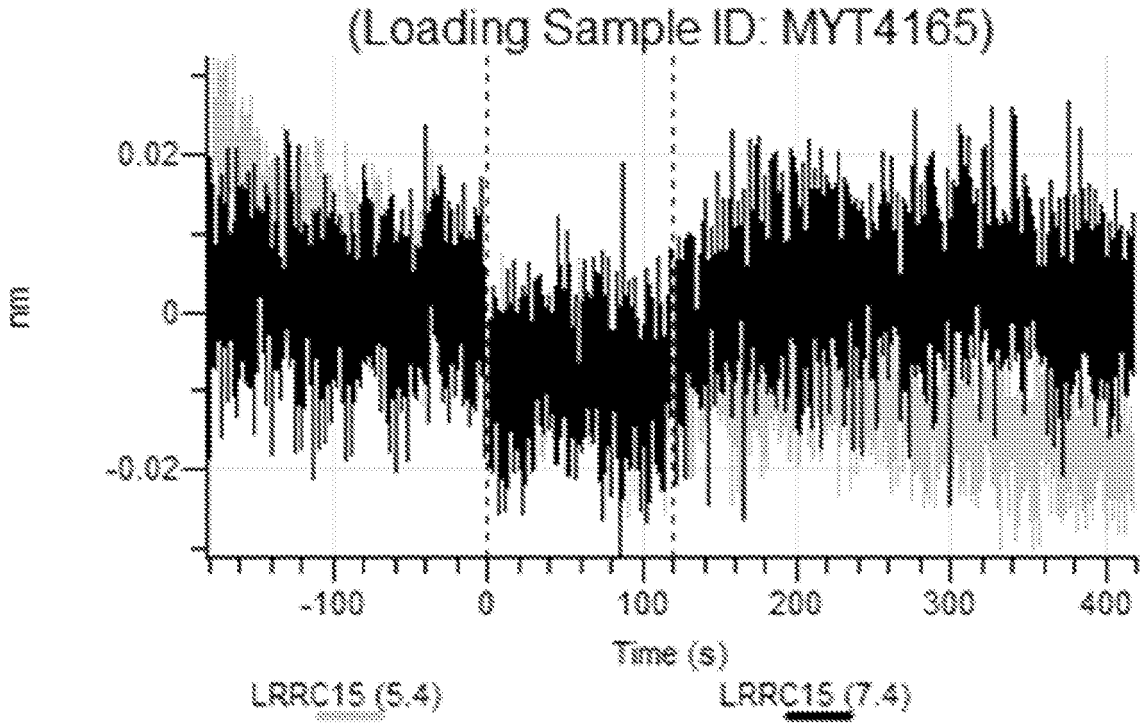

(Loading Sample ID: MYT4165)
0.02
0
-0.02
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 20A

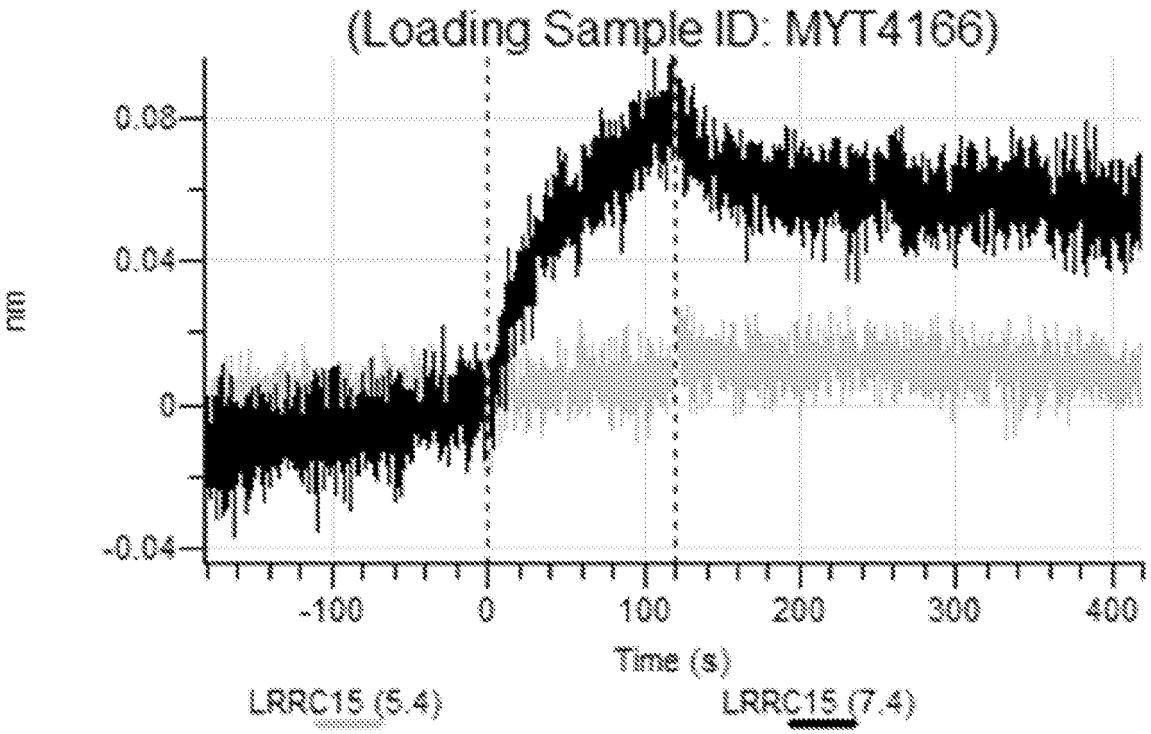

(Loading Sample ID: MYT4166)
0.08
0.04
0
-0.04
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 20B

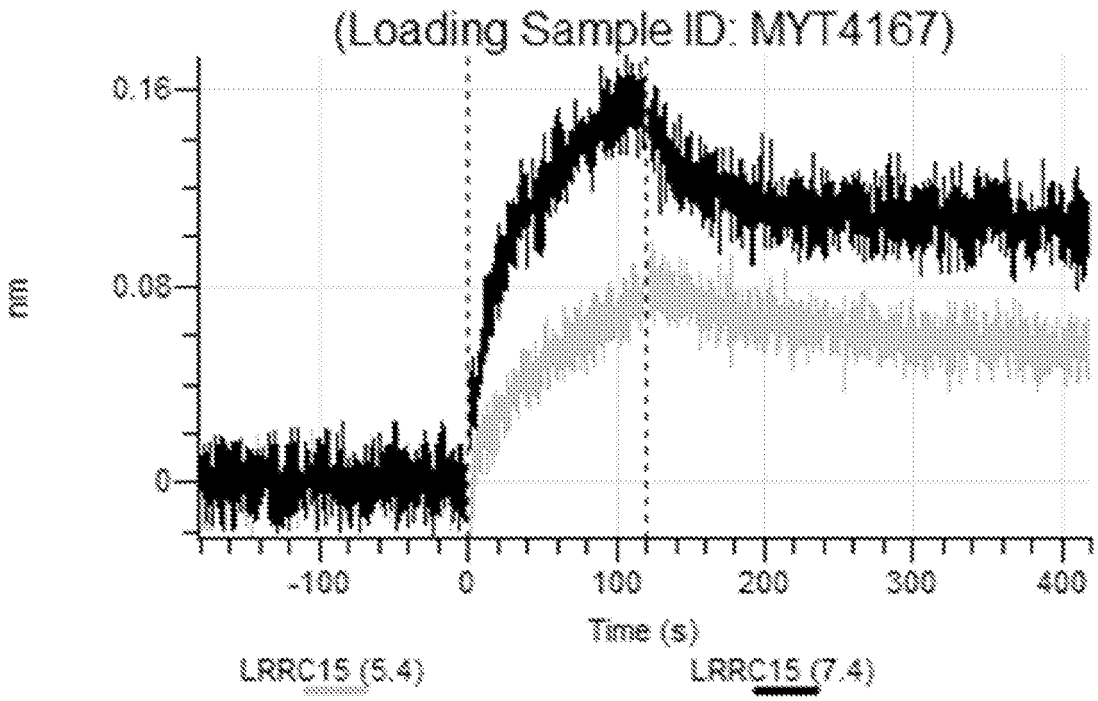

(Loading Sample ID: MYT4167)
0.16
0.08
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 20C

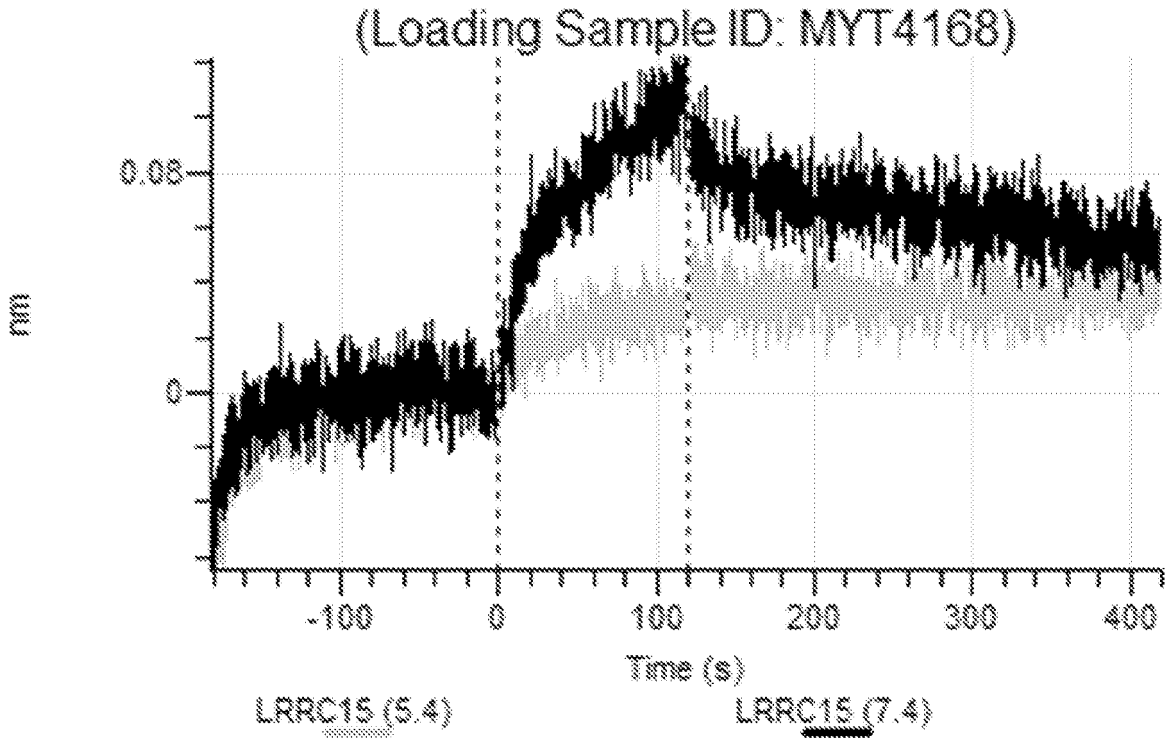

(Loading Sample ID: MYT4168)
0.08
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 20D

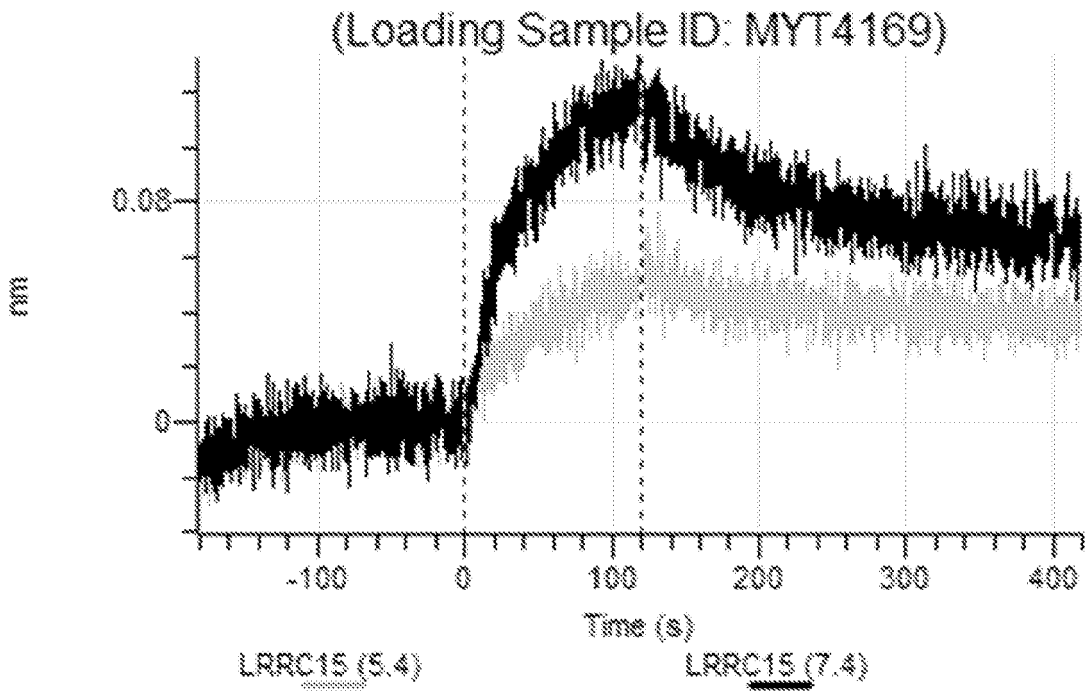

(Loading Sample ID: MYT4169)
nm
0.08
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 20E

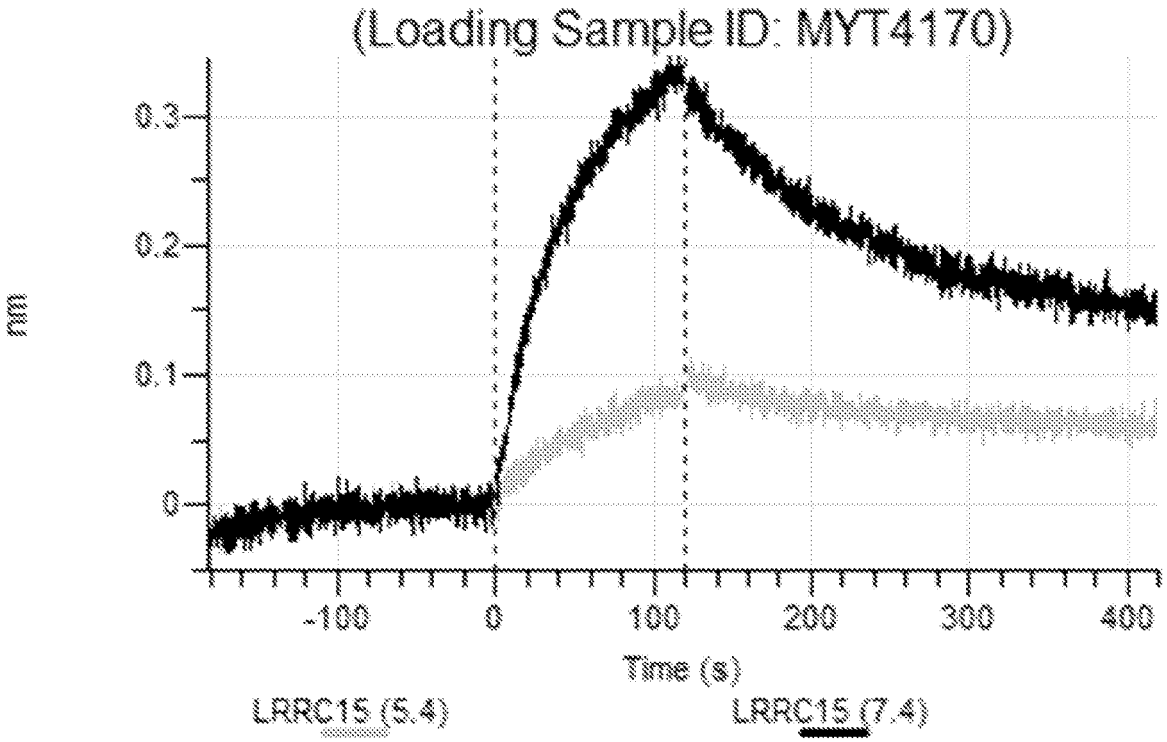

(Loading Sample ID: MYT4170)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 20F

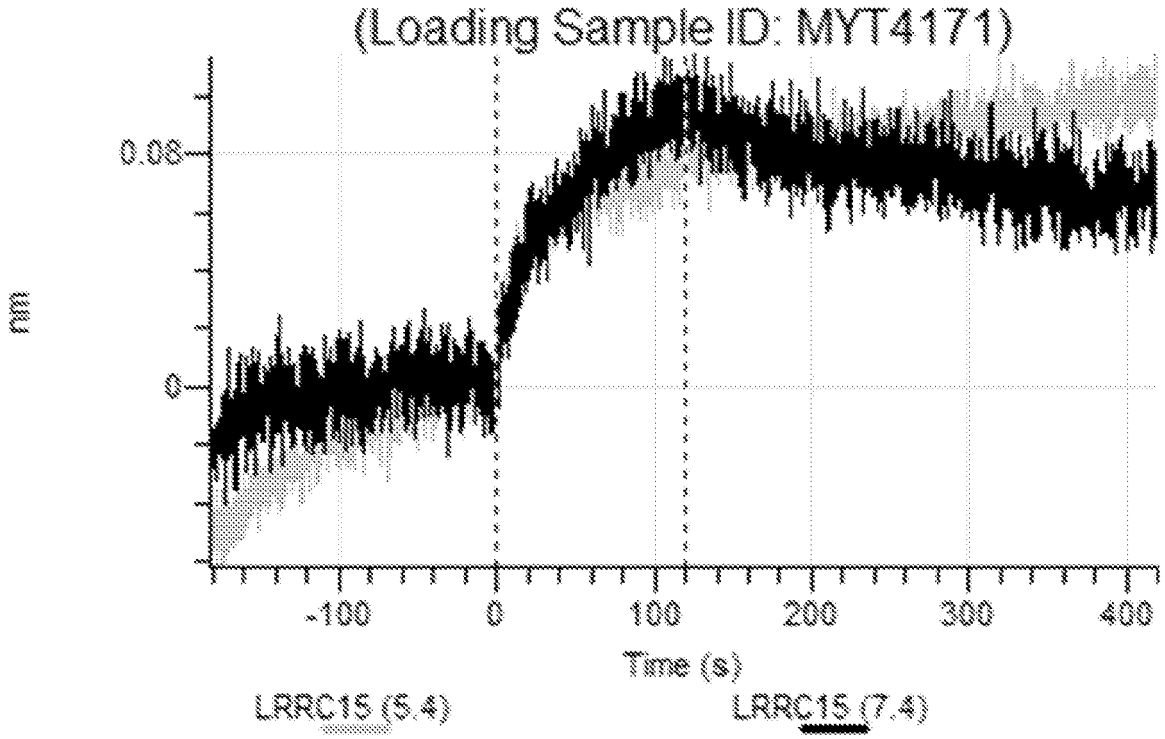

(Loading Sample ID: MYT4171)
nm
0.08
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 20G

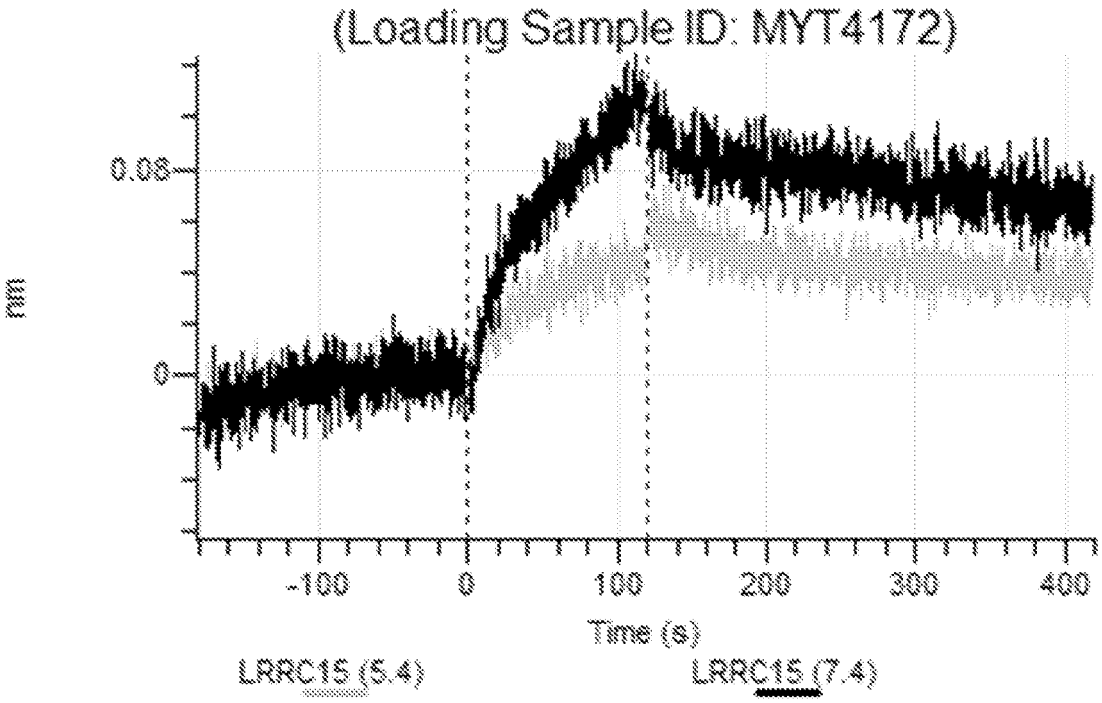

(Loading Sample ID: MYT4172)
0.08
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 20H

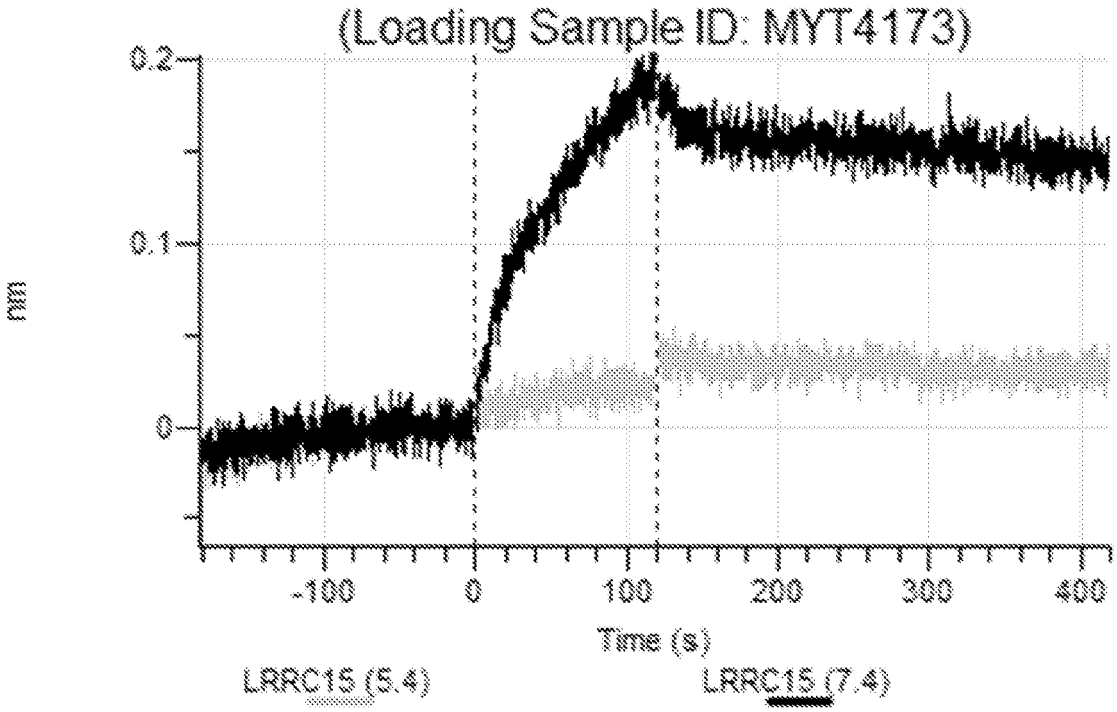

(Loading Sample ID: MYT4173)
0.2
0.1
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 20I

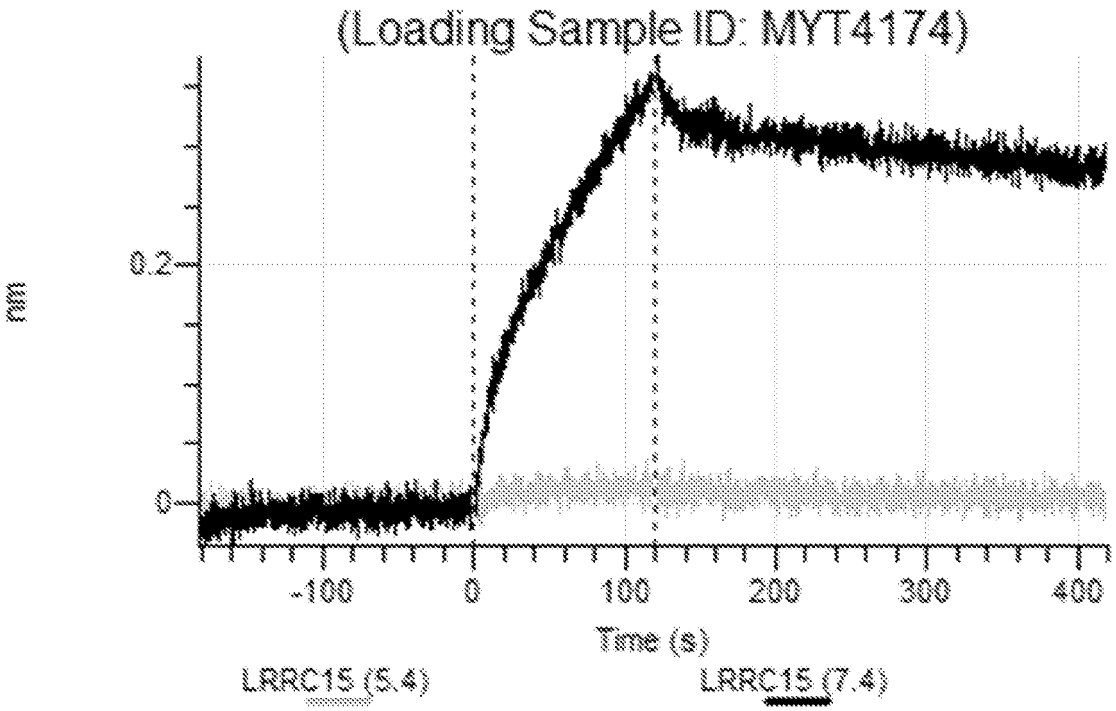

(Loading Sample ID: MYT4174)
nm
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 20J

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
MYT3252 (hu139.10)	84	85	86	87	88	89	90	91
MYT4165	84	168						
MYT4166	84	169						
MYT4167	84	170						
MYT4168	84	171						
MYT4169	84	172						
MYT4170	84	173						
MYT4171	84	174						
MYT4172	84	175						
MYT4173	84	176						
MYT4174	84	177						

FIG. 21

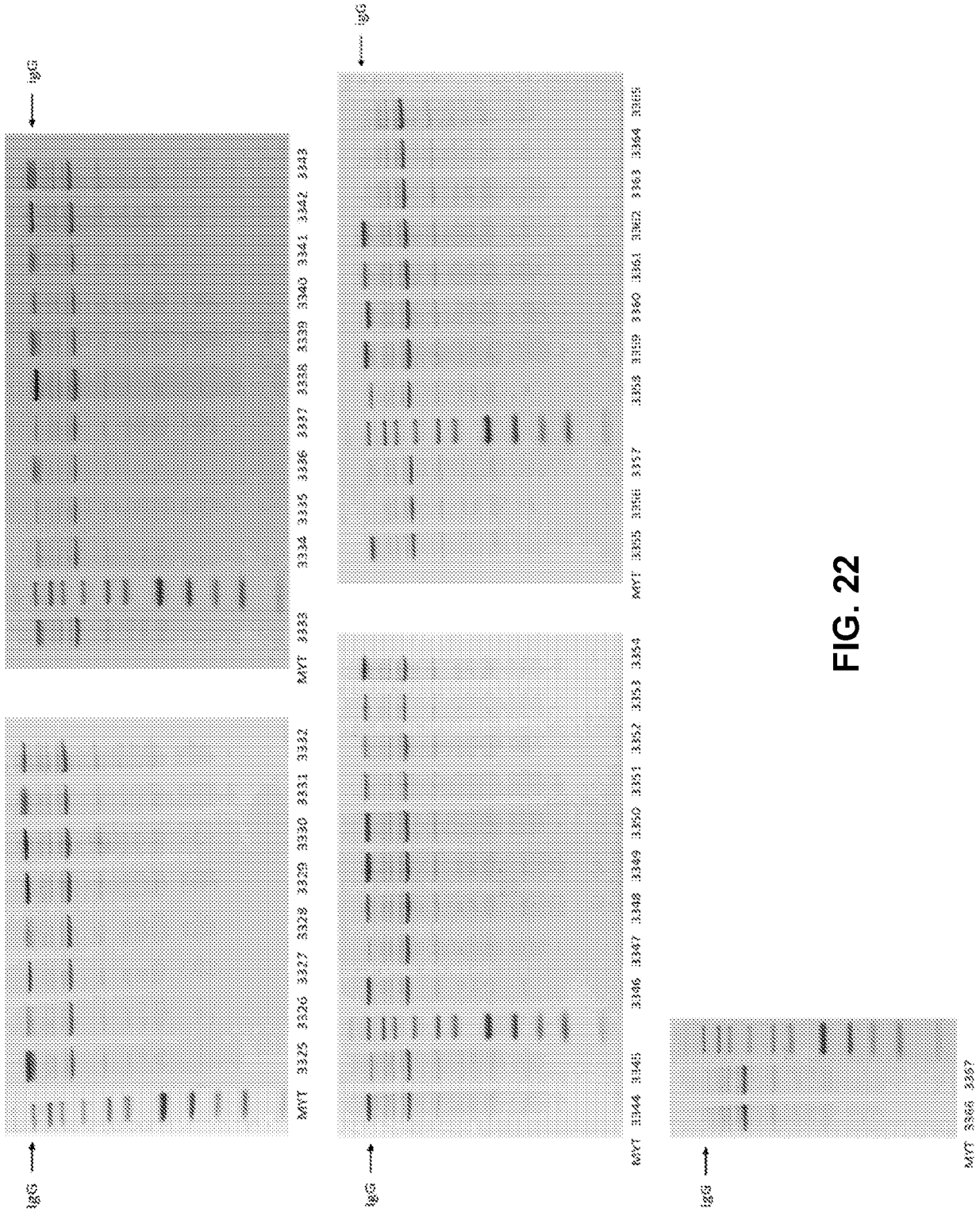

IgG
MYT 3325 3326 3327 3328 3329 3330 3331 3332
IgG
MYT 3333 3334 3335 3336 3337 3338 3339 3340 3341 3342 3343
IgG
MYT 3344 3345 3346 3347 3348 3349 3350 3351 3352 3353 3354
IgG
MYT 3355 3356 3357 3358 3359 3360 3361 3362 3363 3364 3365
IgG
MYT 3366 3367

FIG. 22

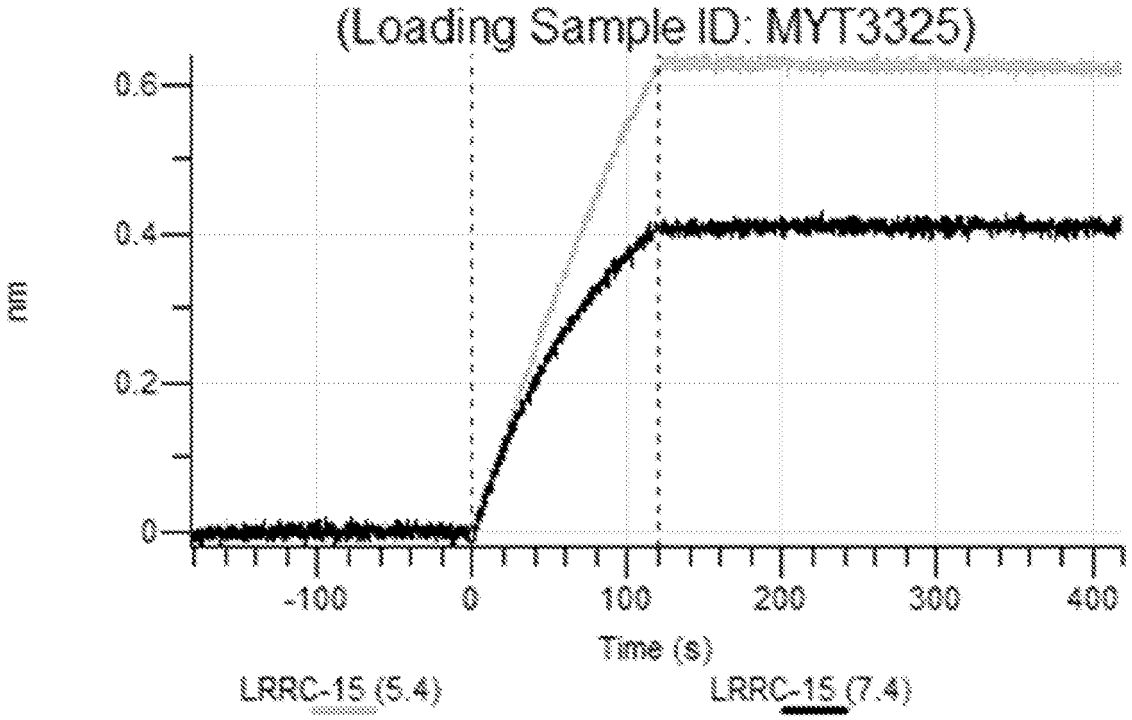

(Loading Sample ID: MYT3325)
nm
0.6
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23A

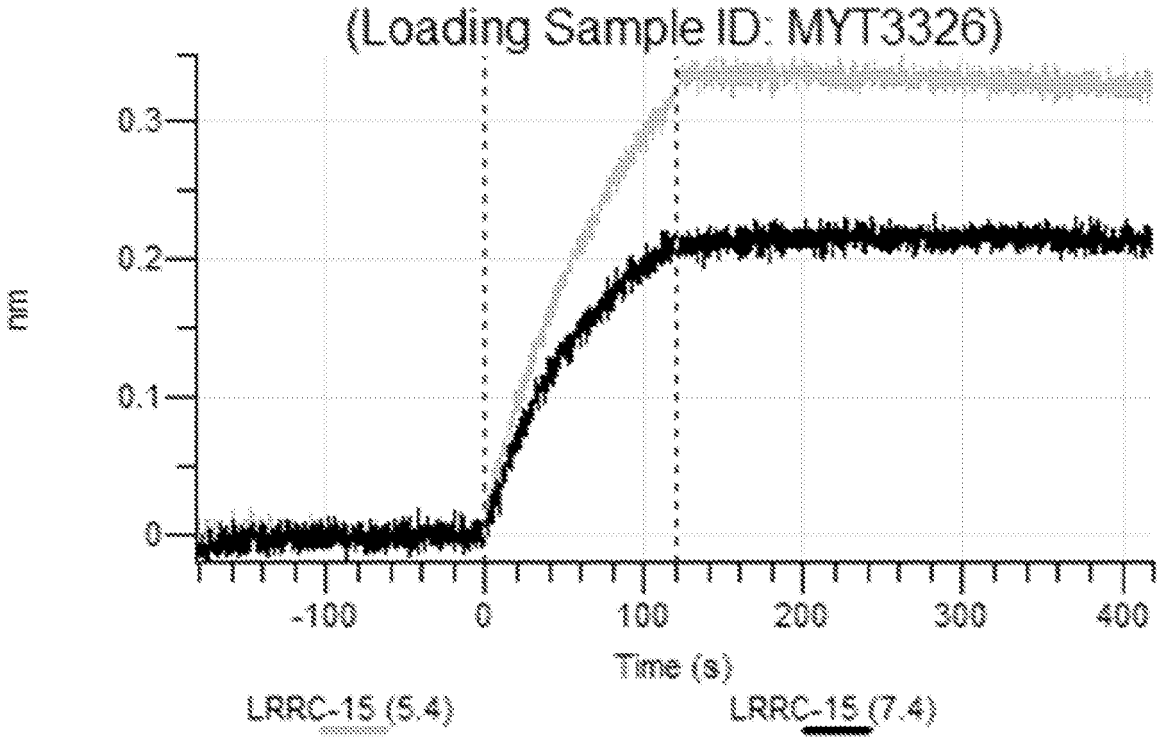

(Loading Sample ID: MYT3326)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23B

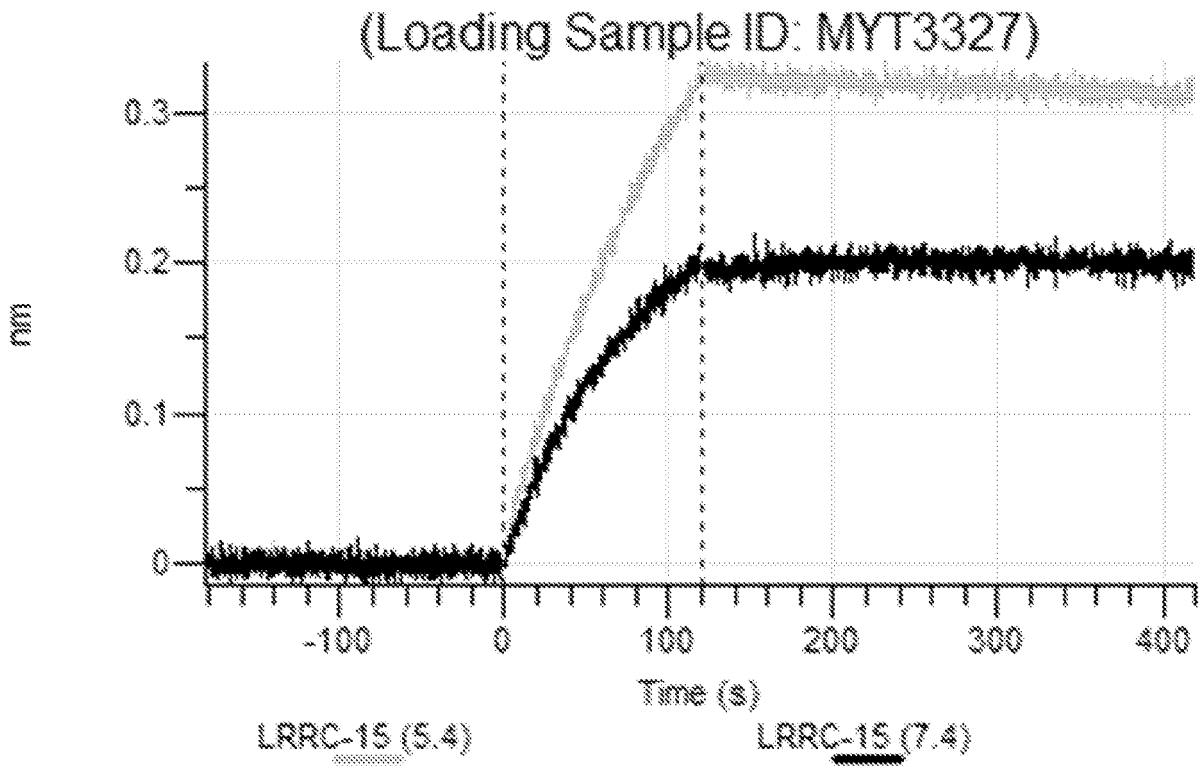

(Loading Sample ID: MYT3327)
0.3
0.2
0.1
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23C

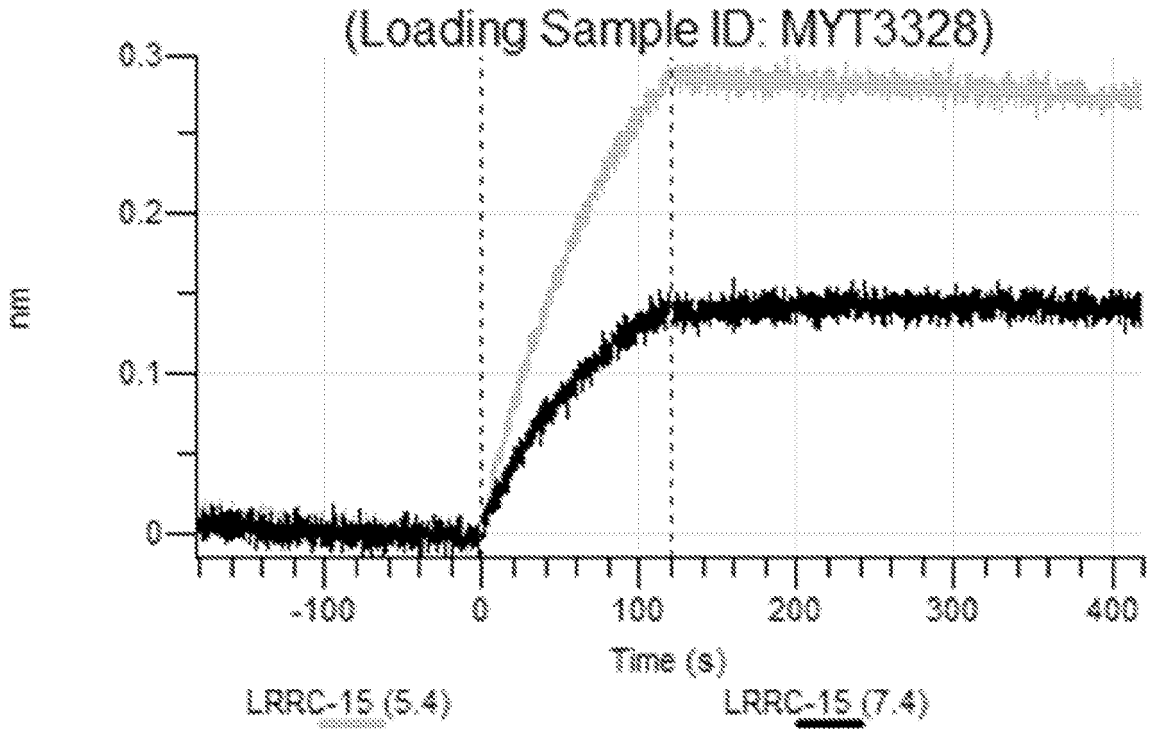

(Loading Sample ID: MYT3328)
0.3
0.2
0.1
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23D

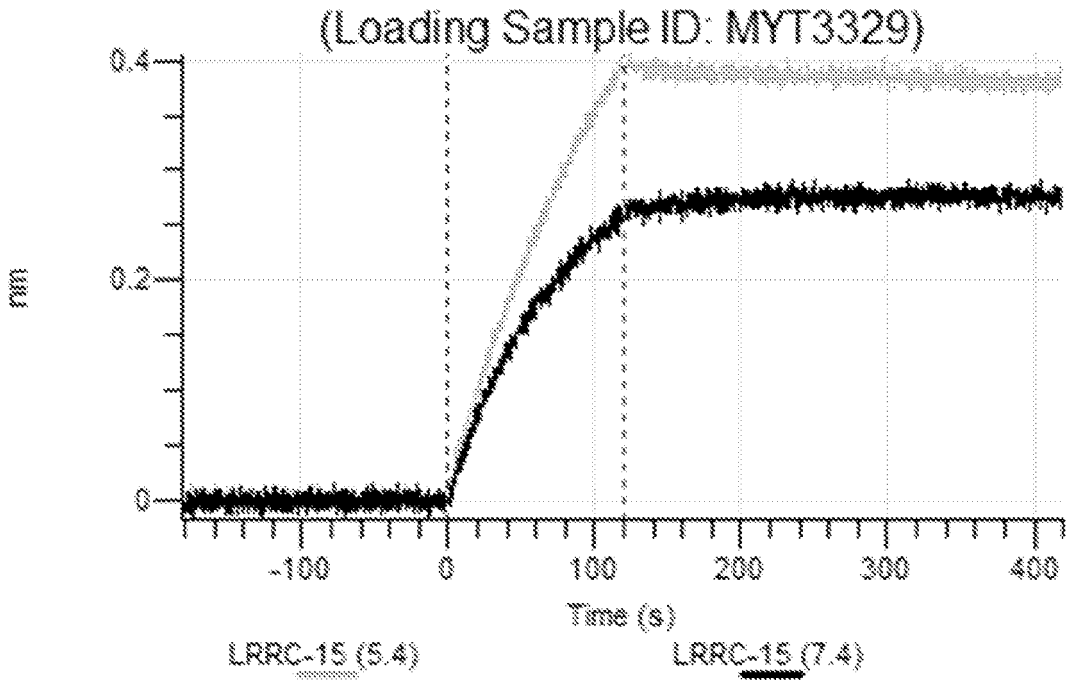

(Loading Sample ID: MYT3329)
0.4
0.2
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23E

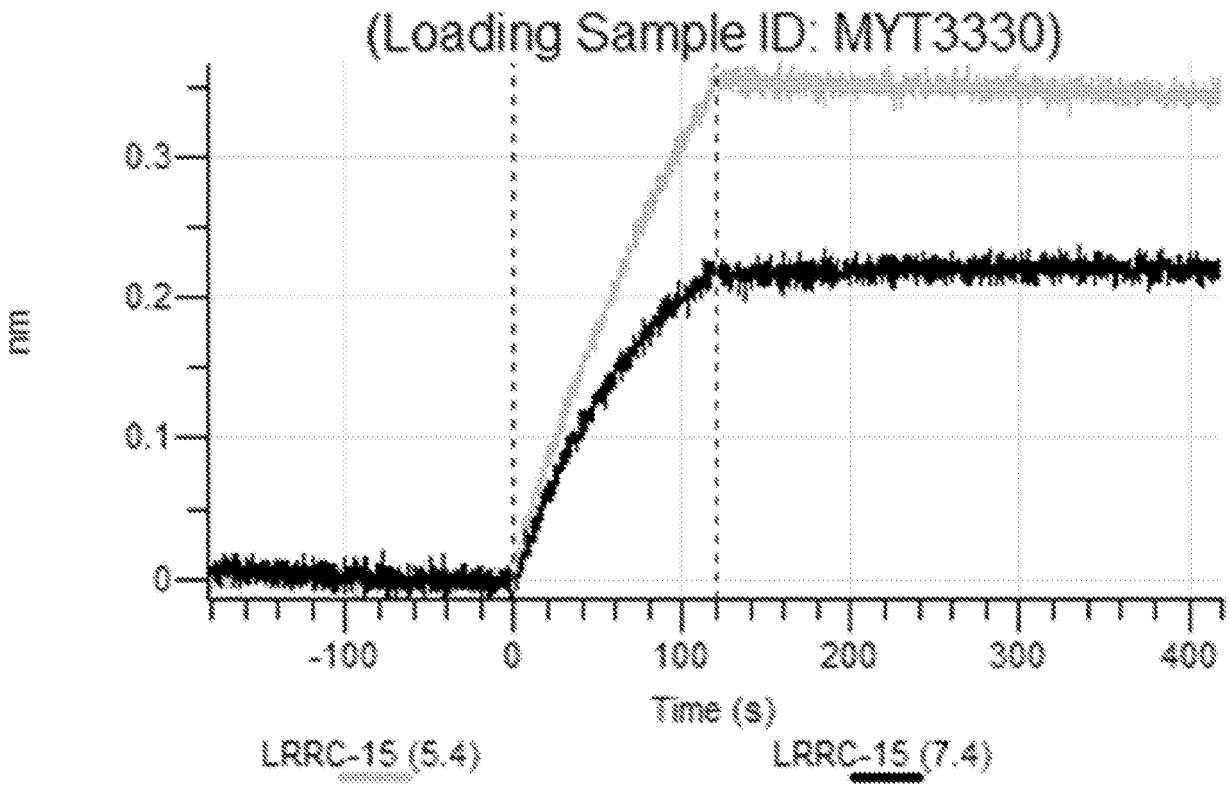

(Loading Sample ID: MYT3330)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23F

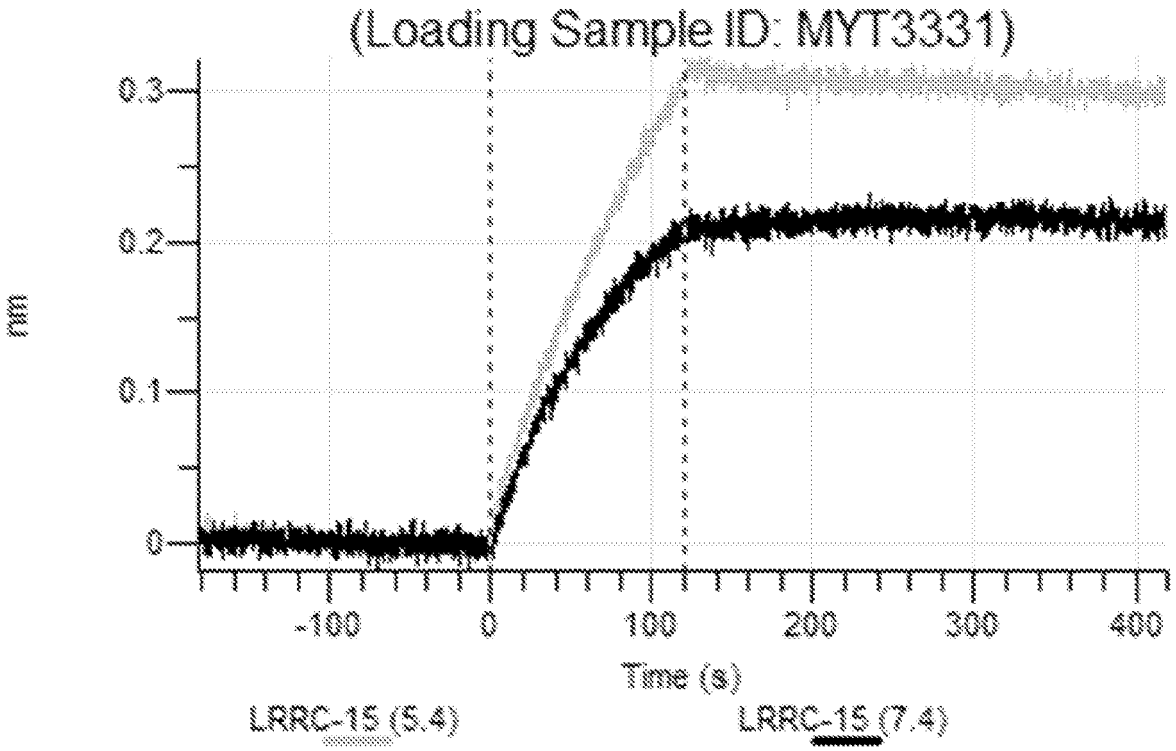

(Loading Sample ID: MYT3331)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23G

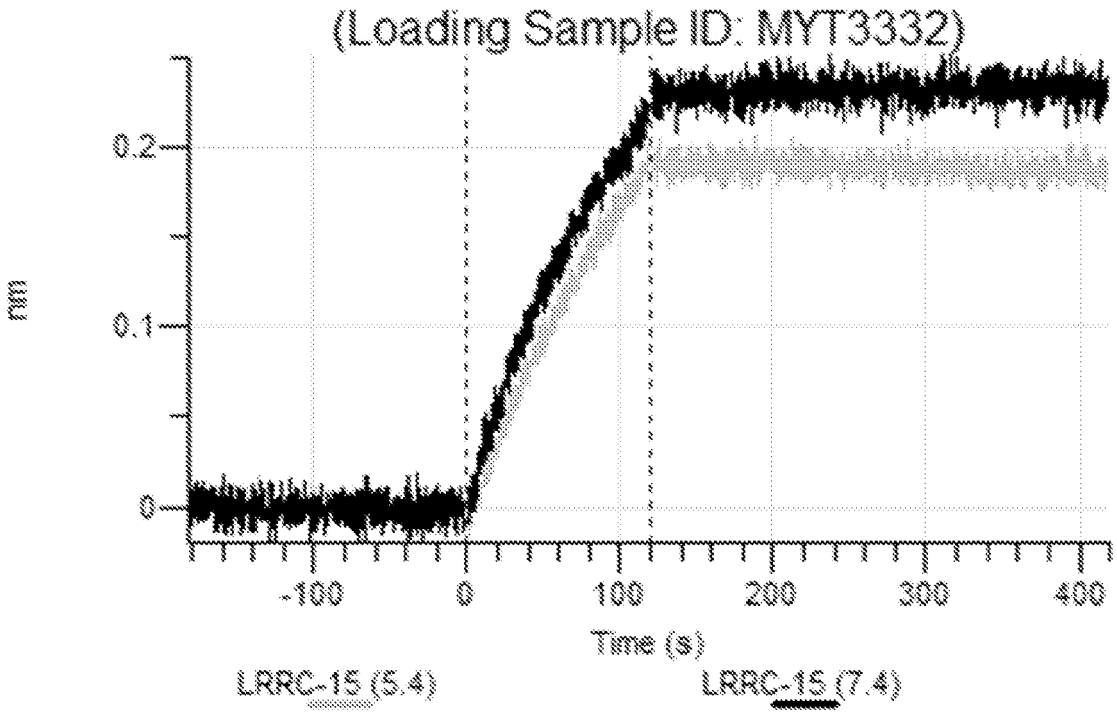

(Loading Sample ID: MYT3332)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23H

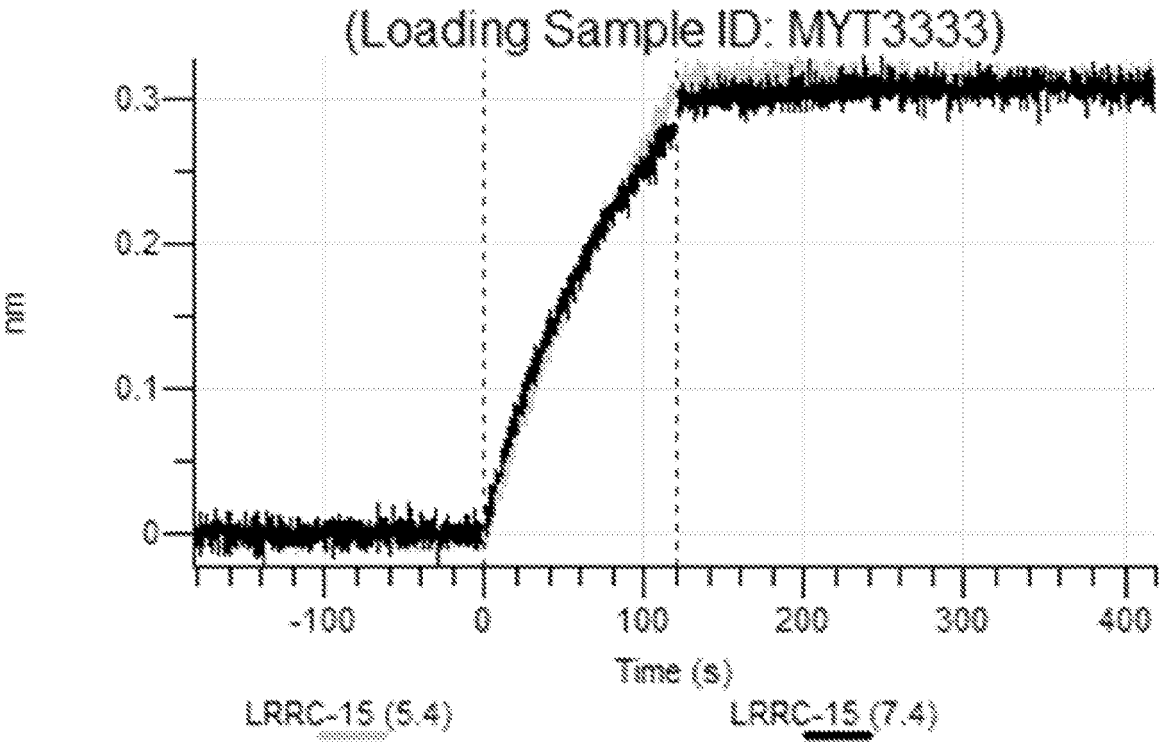

(Loading Sample ID: MYT3333)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23I

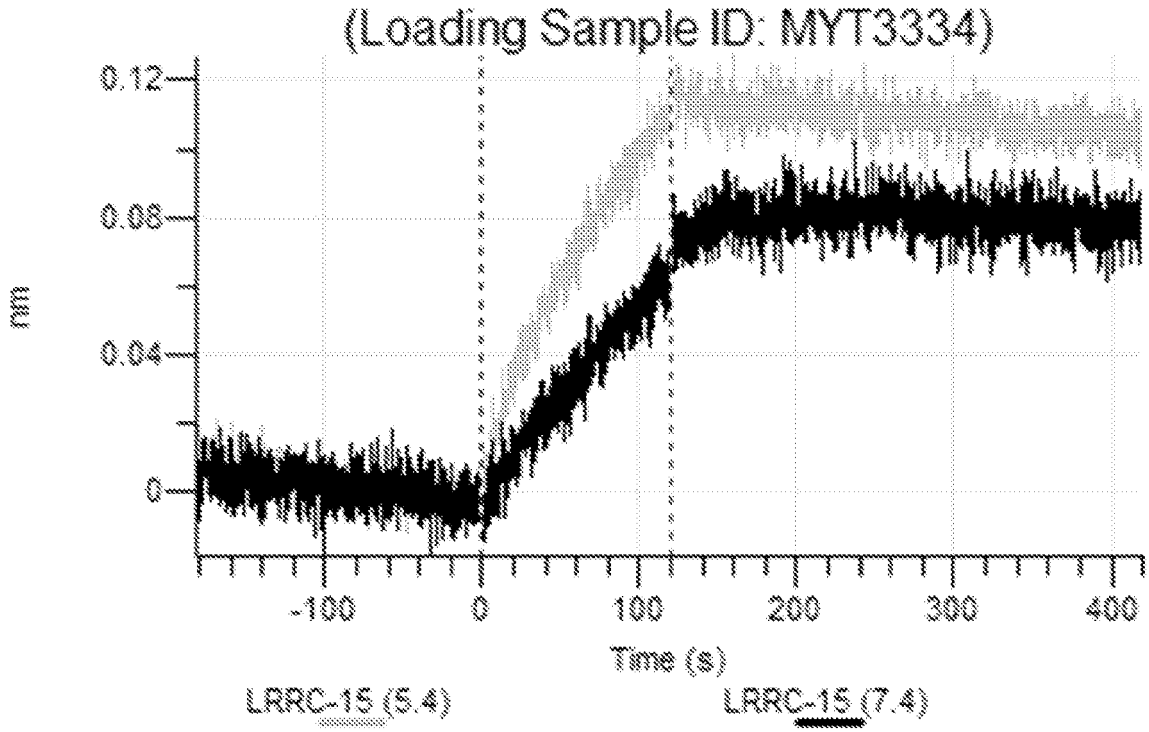

(Loading Sample ID: MYT3334)
0.12
0.08
0.04
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23J

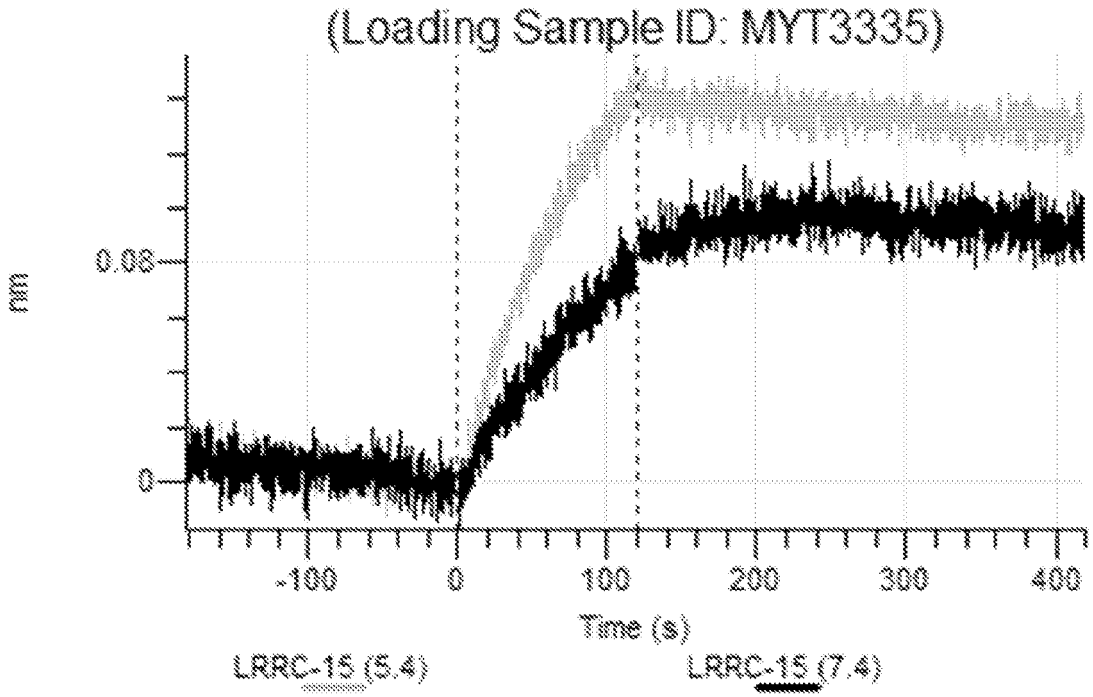

(Loading Sample ID: MYT3335)
nm
0.08
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23K

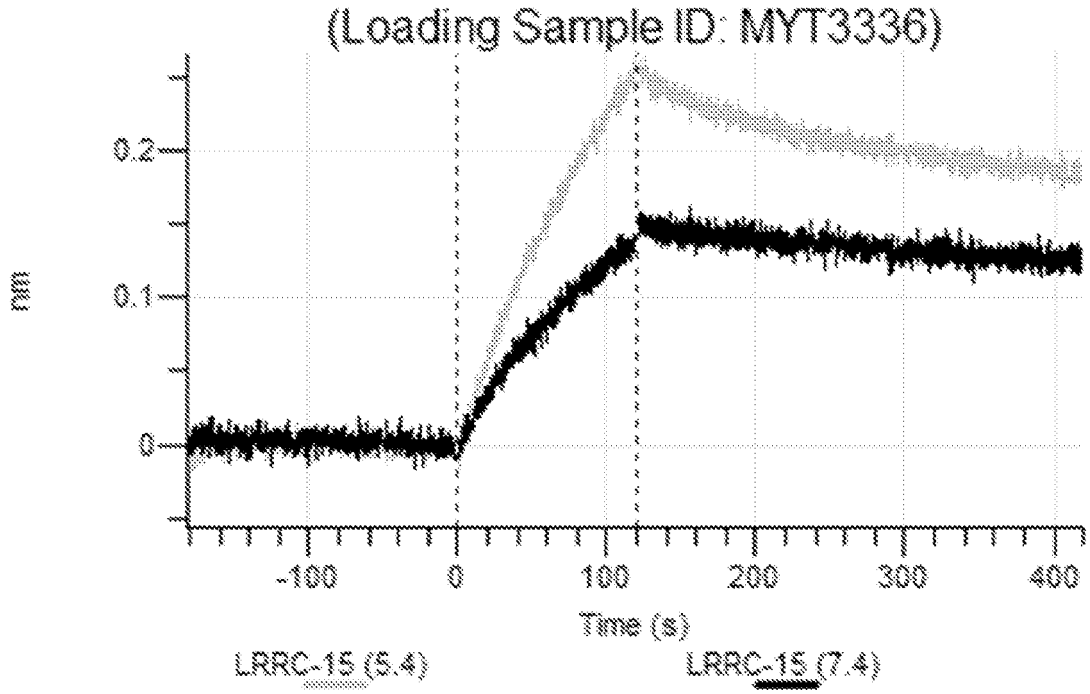

(Loading Sample ID: MYT3336)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23L

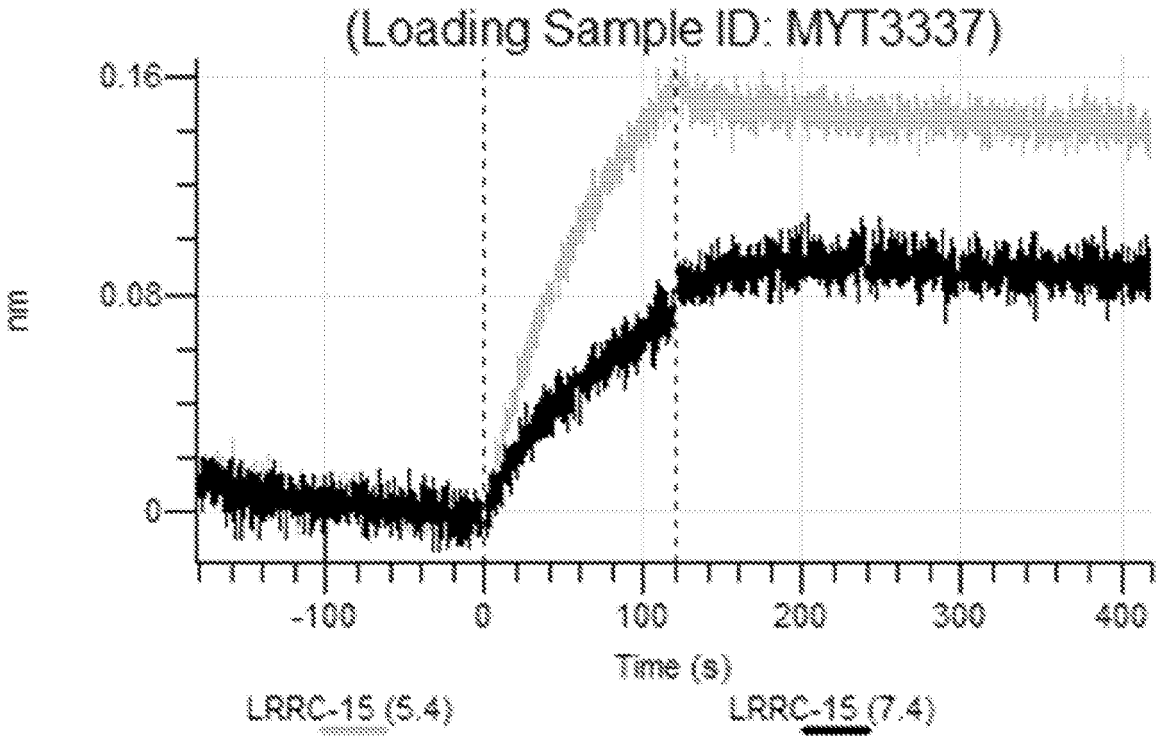

(Loading Sample ID: MYT3337)
0.16
0.08
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23M

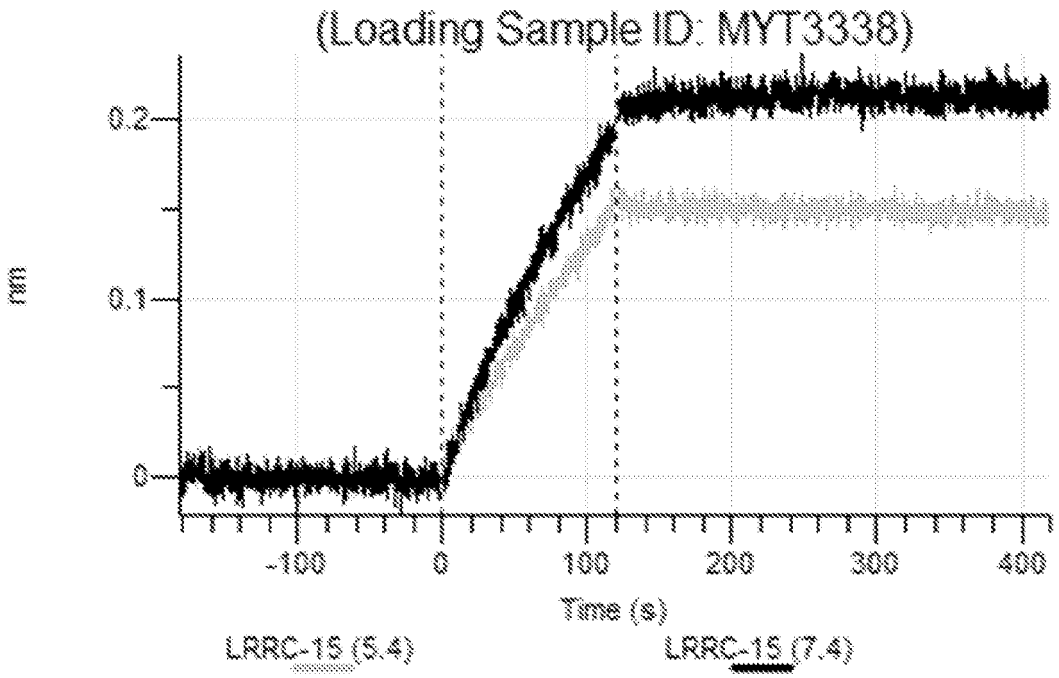

(Loading Sample ID: MYT3338)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23N

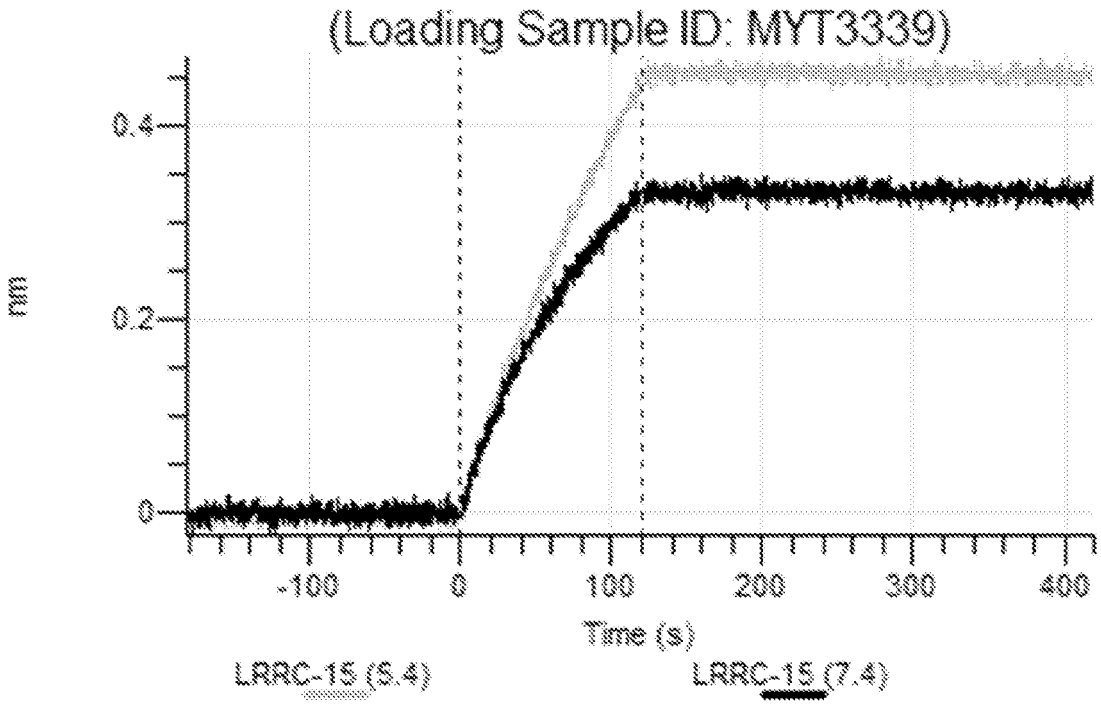

(Loading Sample ID: MYT3339)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23O

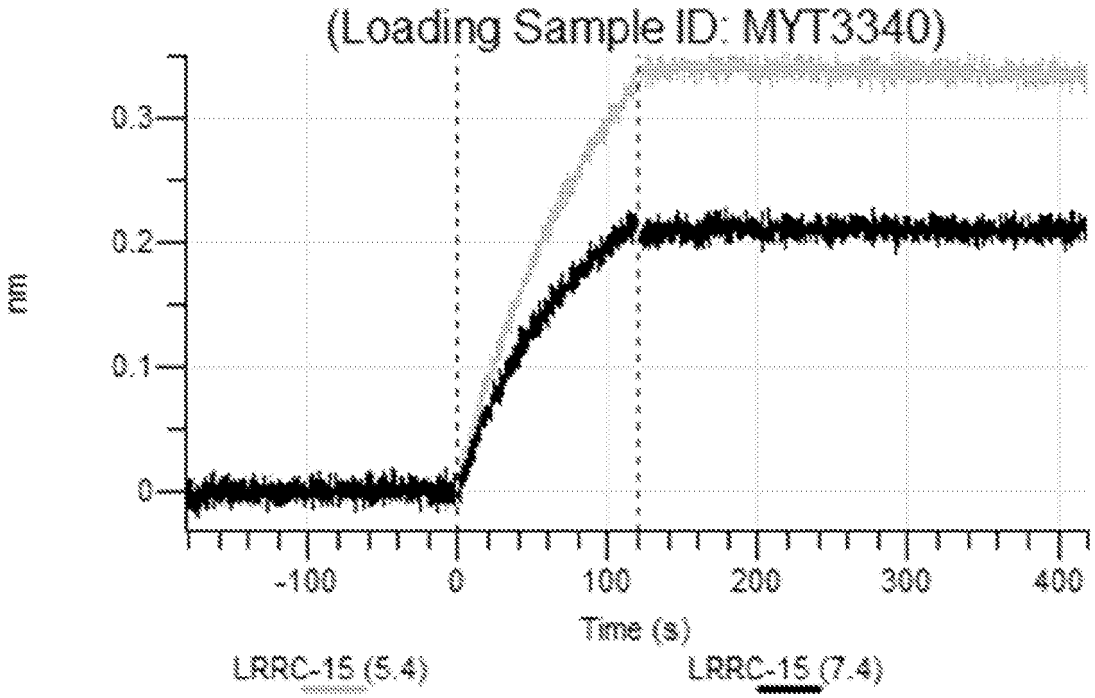

(Loading Sample ID: MYT3340)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23P

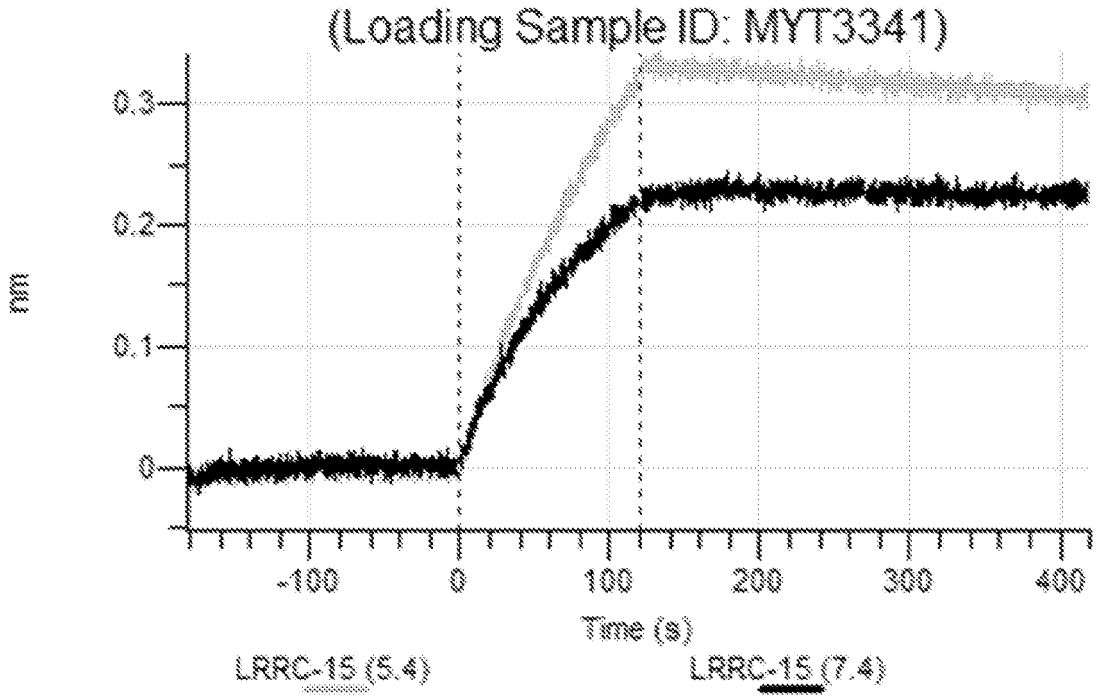

(Loading Sample ID: MYT3341)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23Q

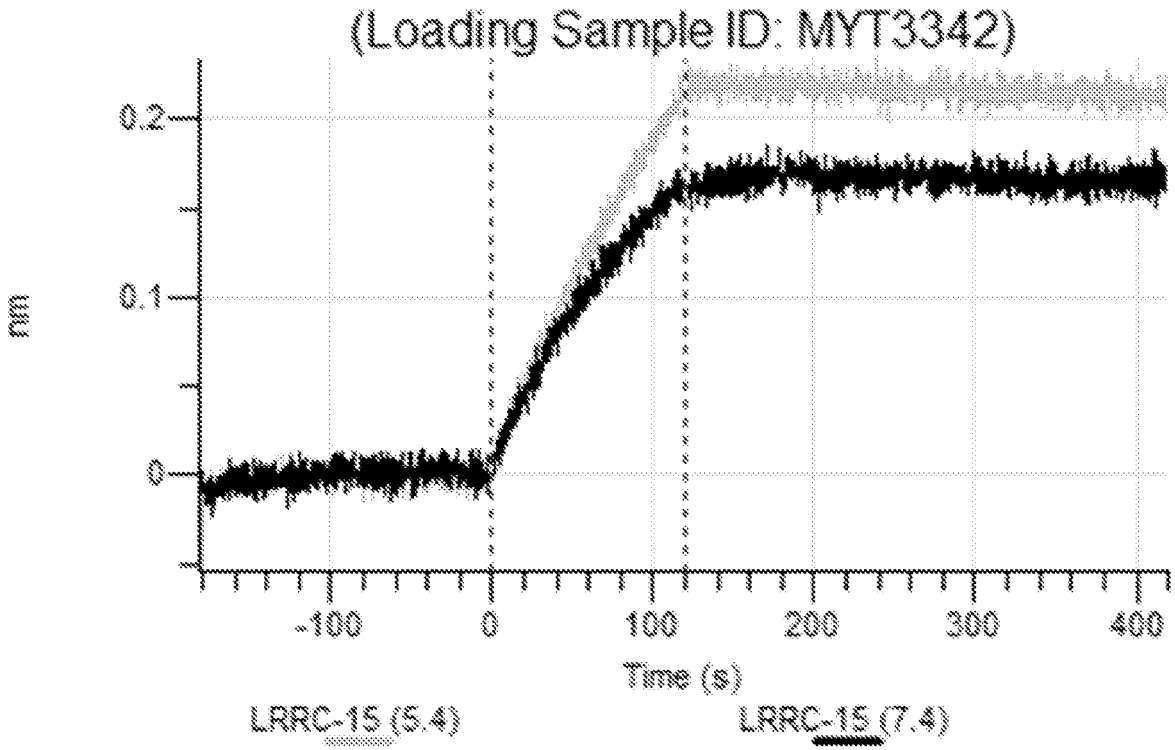

(Loading Sample ID: MYT3342)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23R

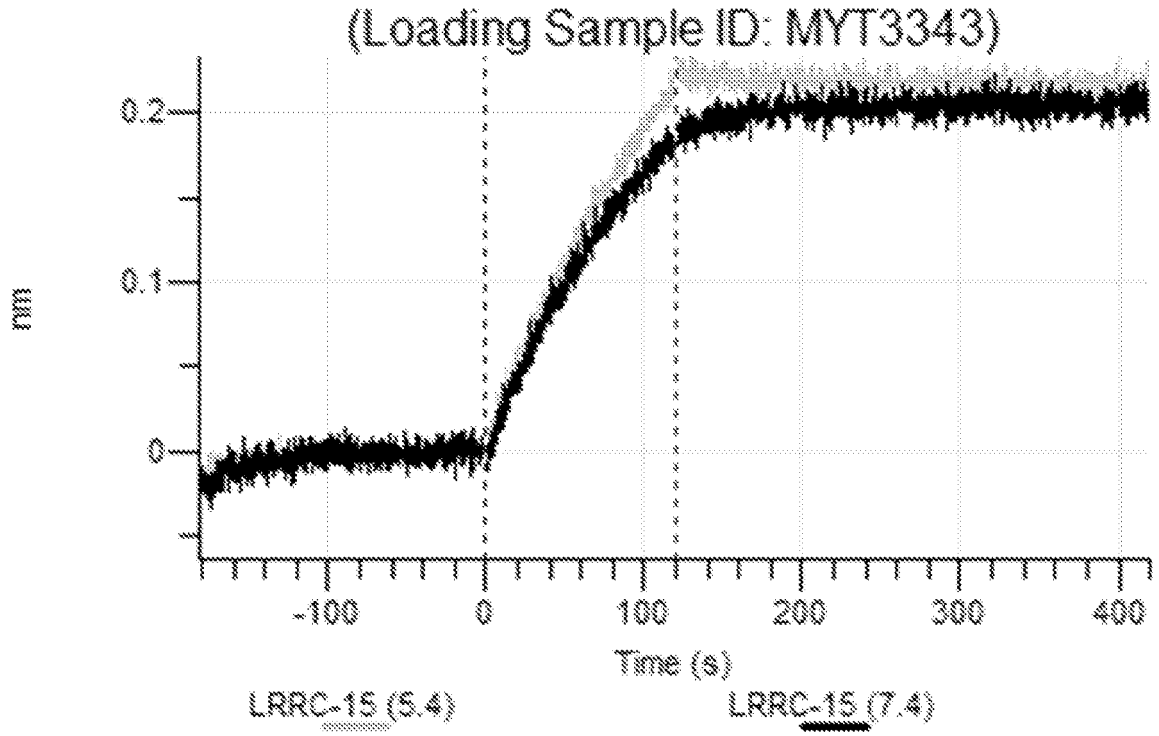

(Loading Sample ID: MYT3343)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23S

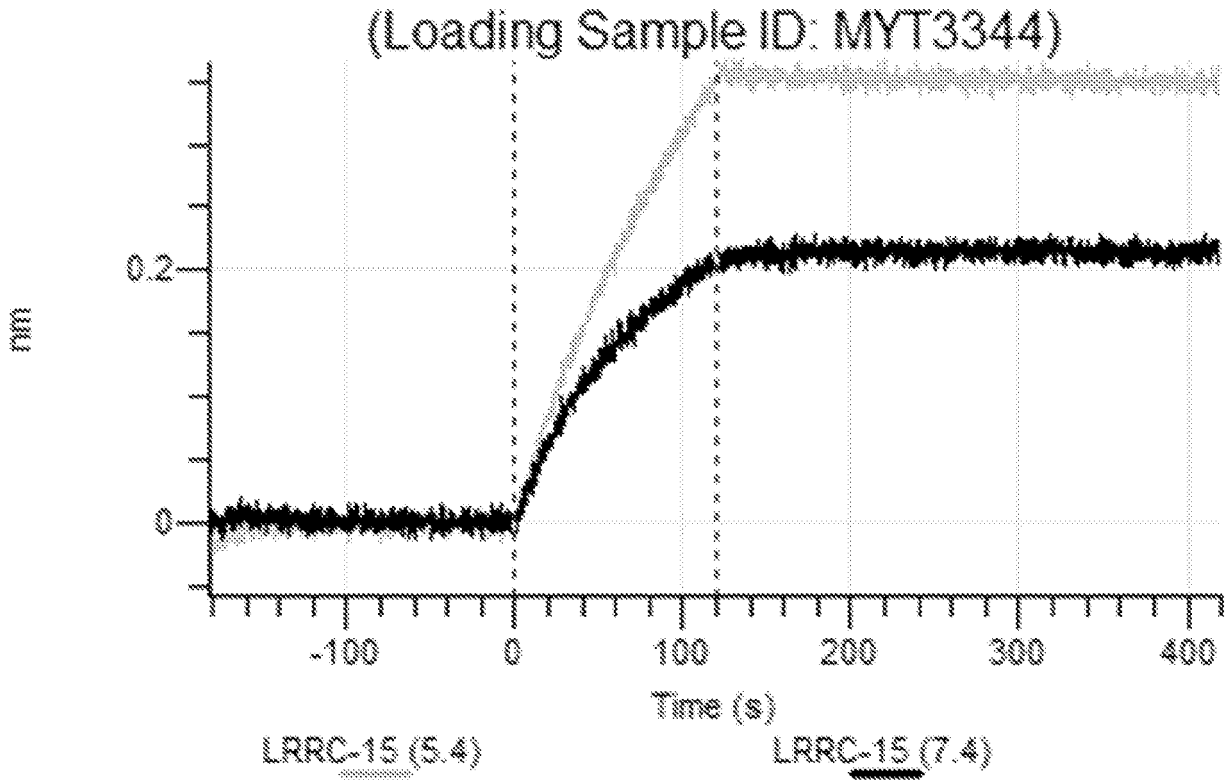

(Loading Sample ID: MYT3344)
nm
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23T

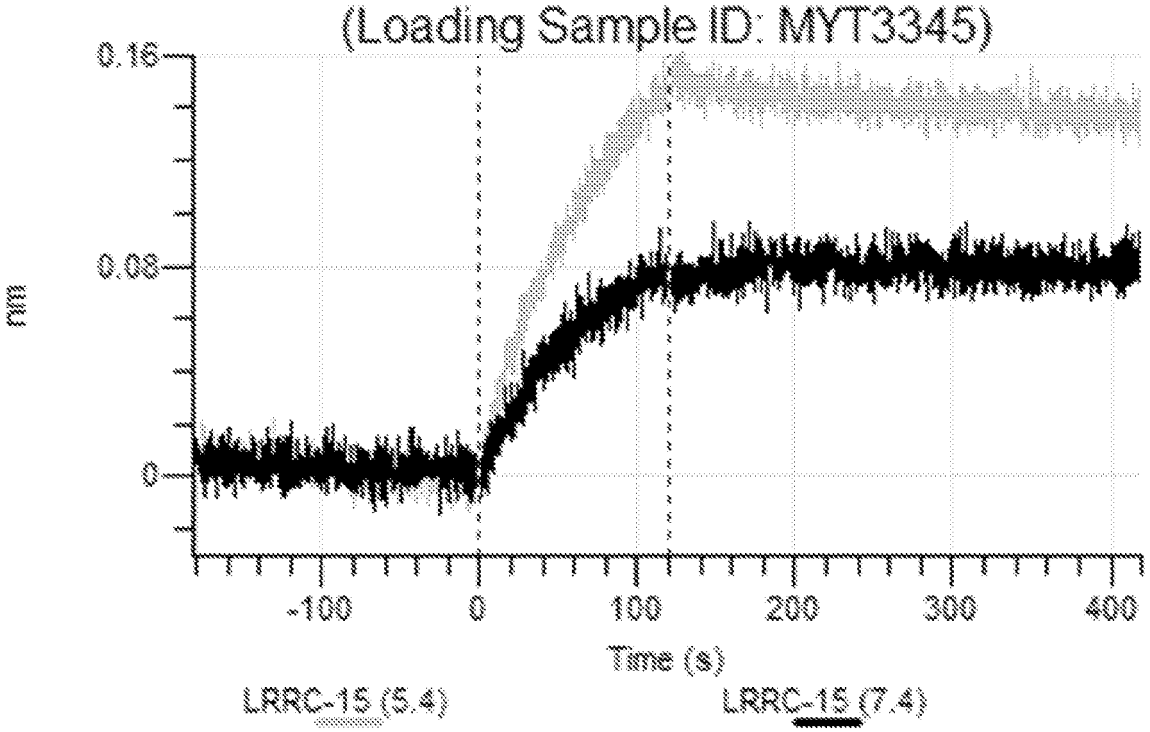

(Loading Sample ID: MYT3345)
0.16
0.08
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23U

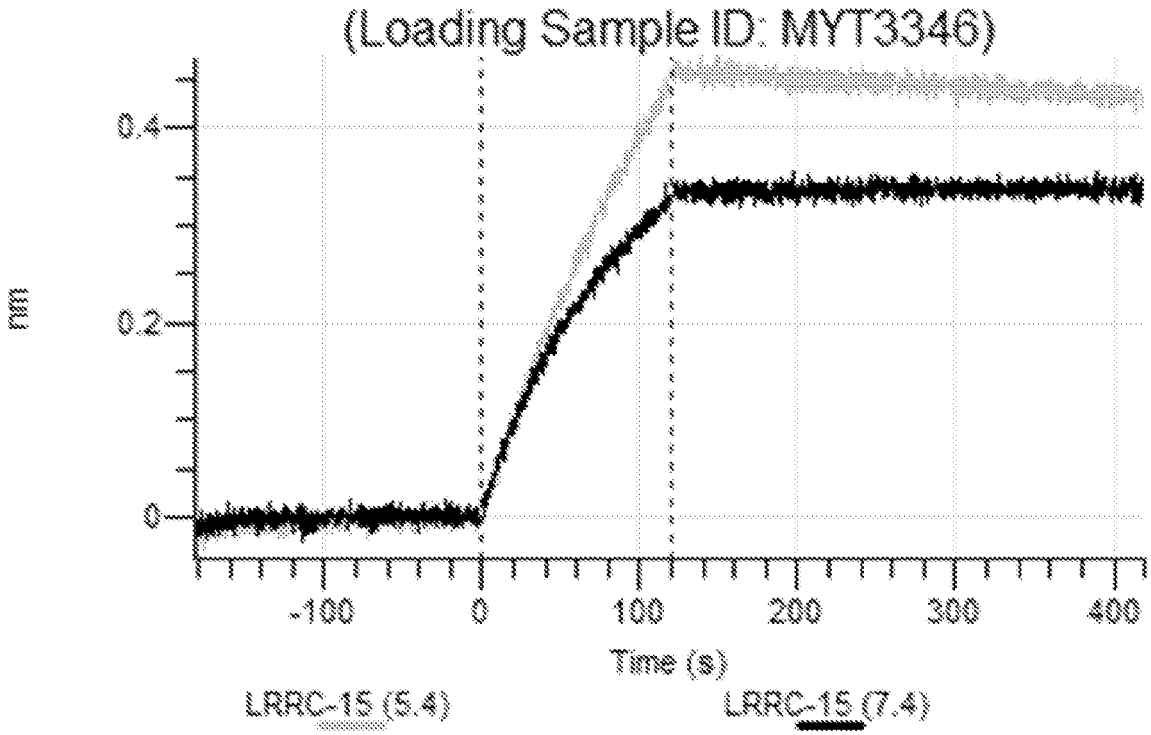

(Loading Sample ID: MYT3346)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23V

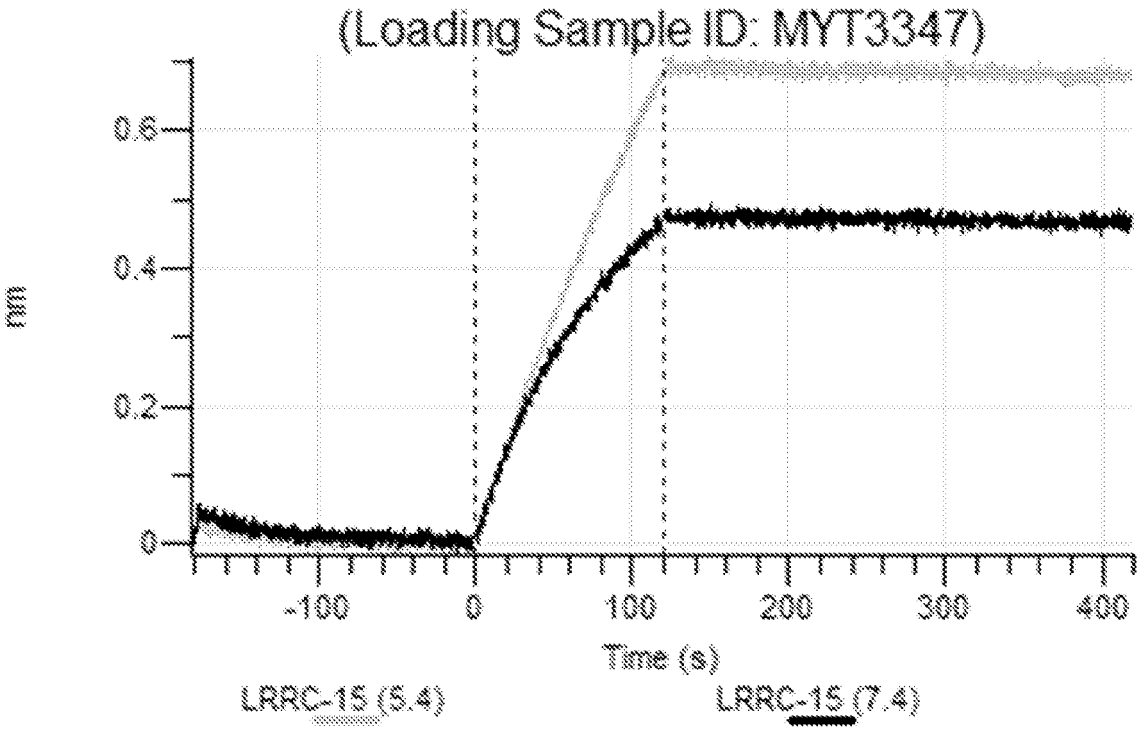

(Loading Sample ID: MYT3347)
nm
0.6
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23W

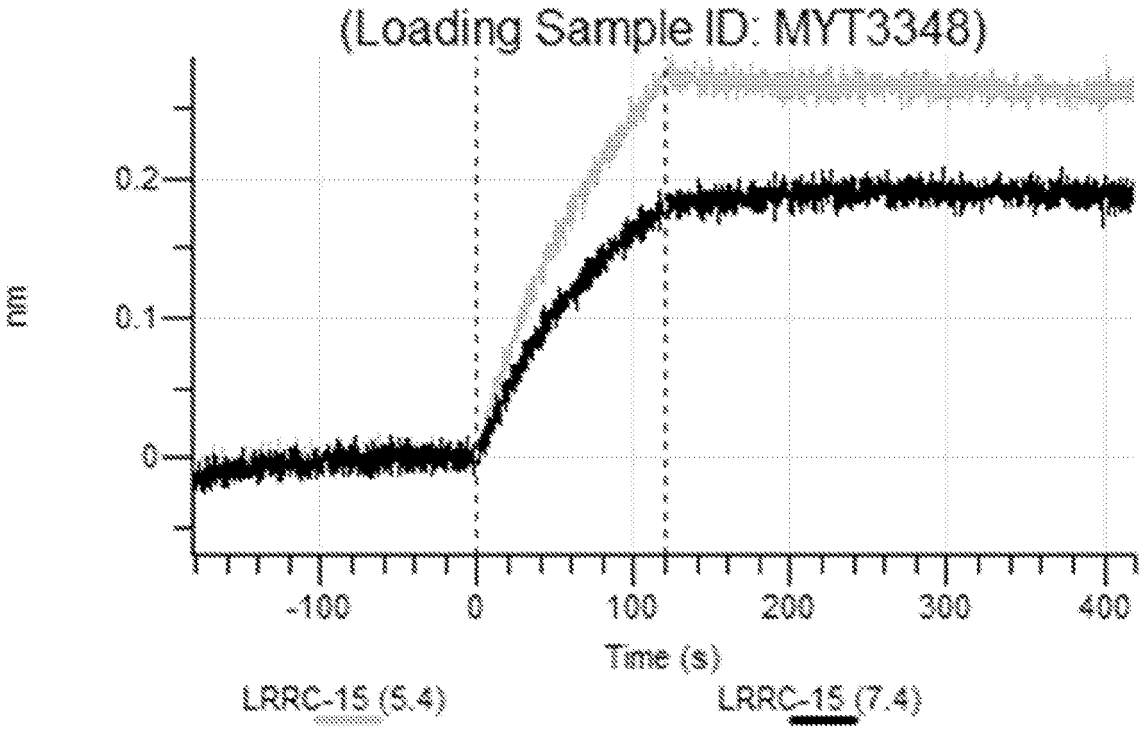

(Loading Sample ID: MYT3348)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23X

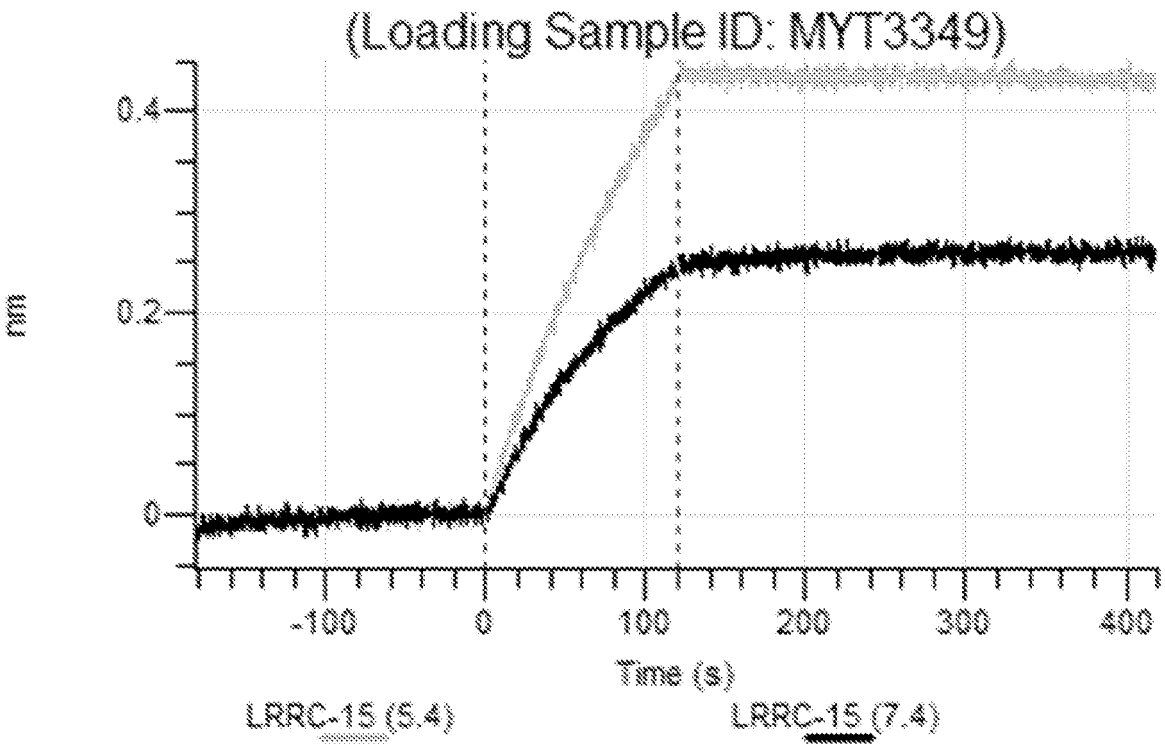

(Loading Sample ID: MYT3349)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23Y

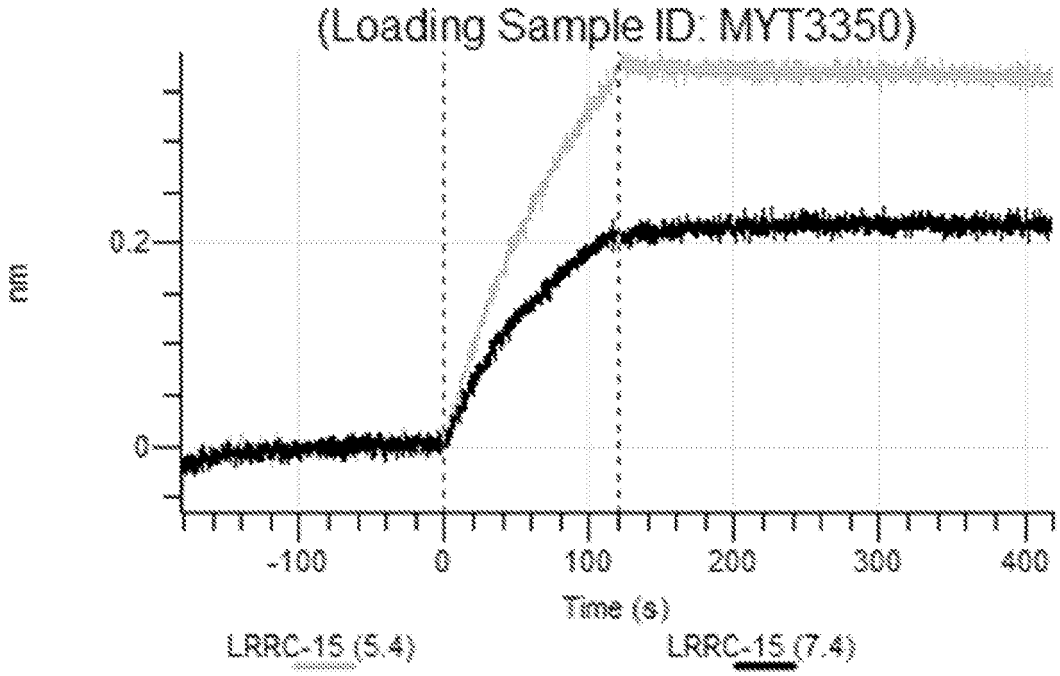

(Loading Sample ID: MYT3350)
nm
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23Z

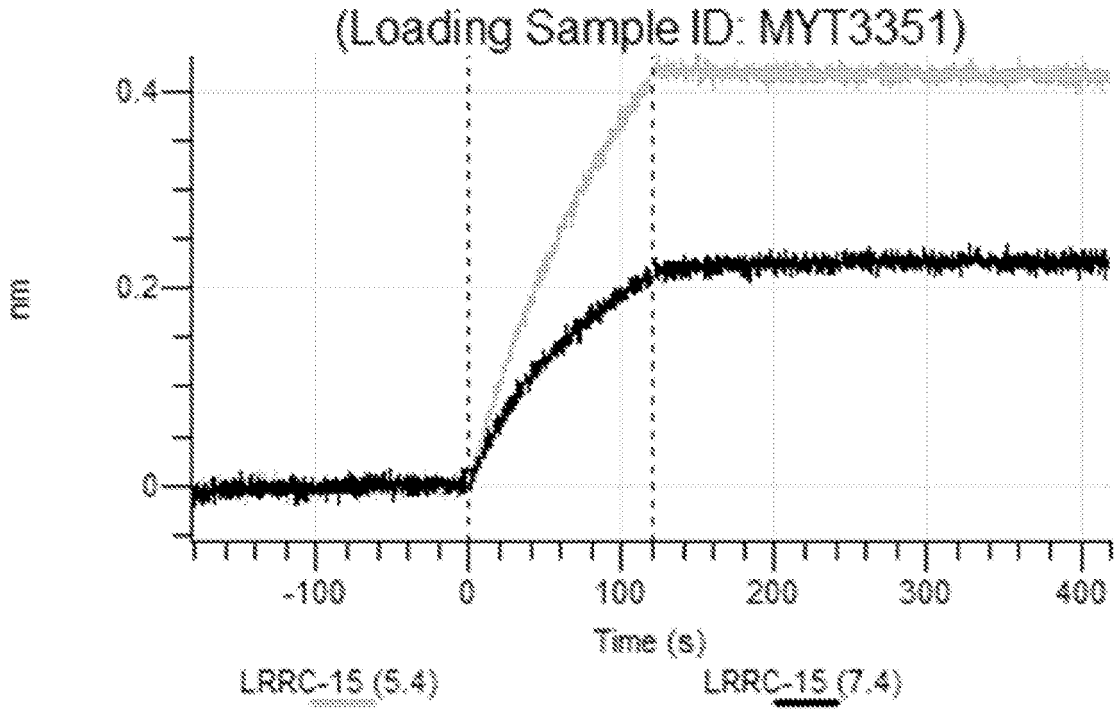

(Loading Sample ID: MYT3351)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AA

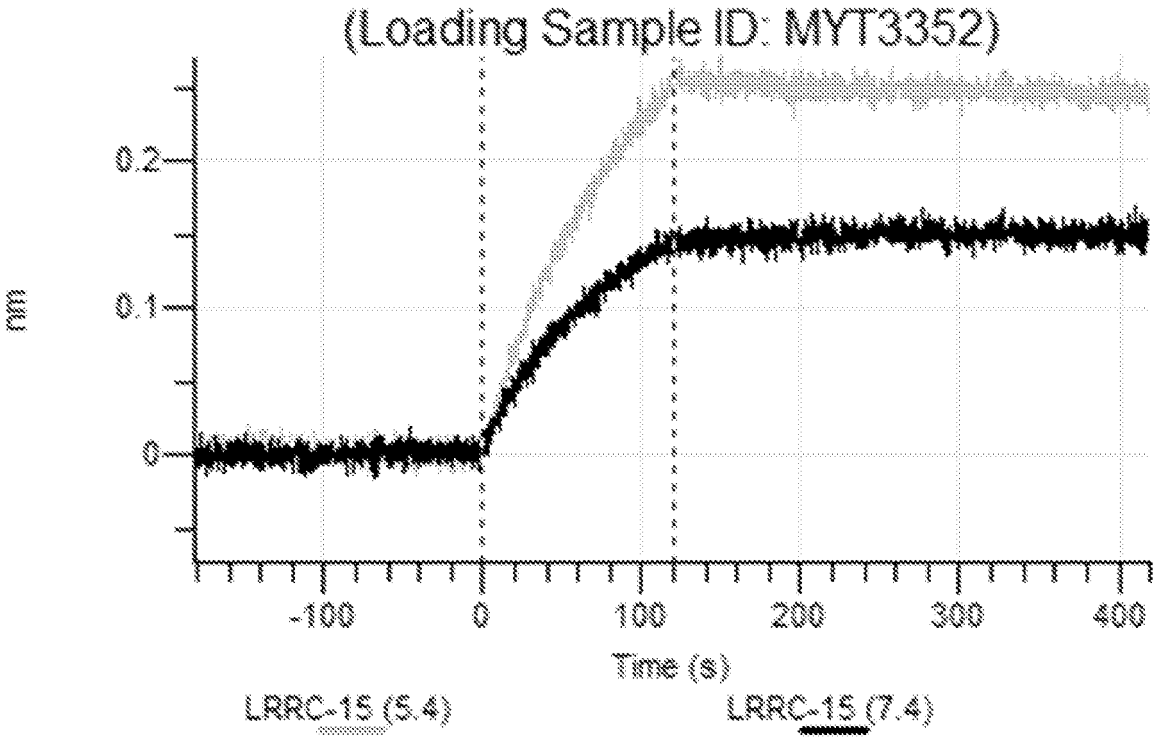

(Loading Sample ID: MYT3352)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AB

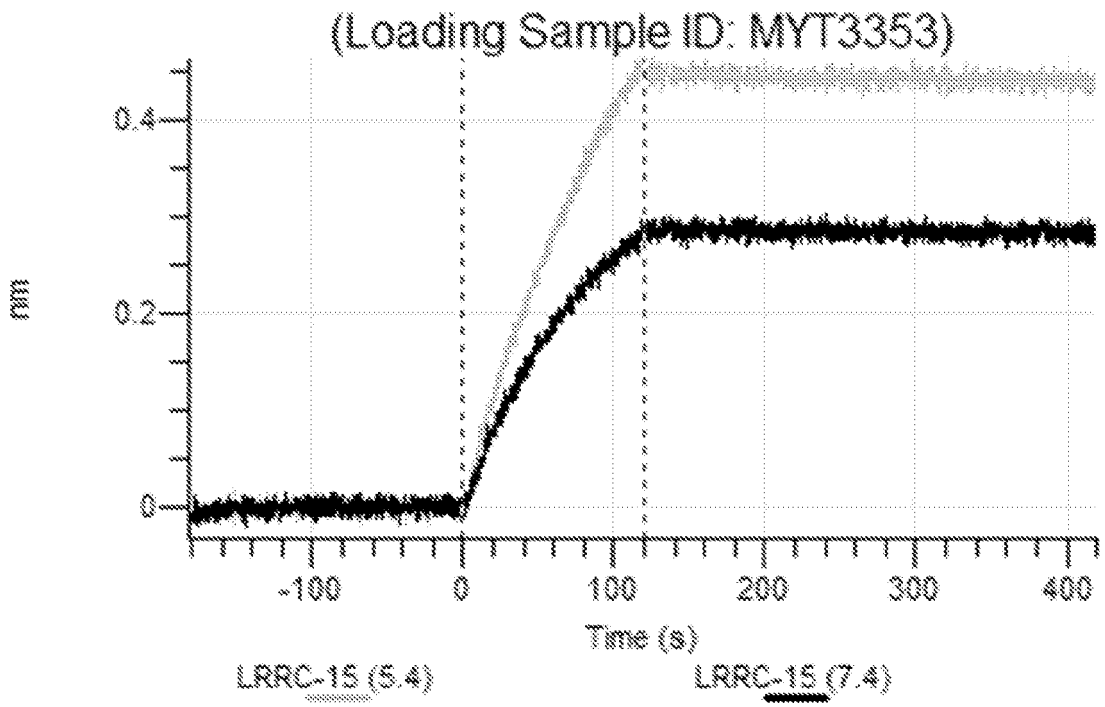

(Loading Sample ID: MYT3353)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AC

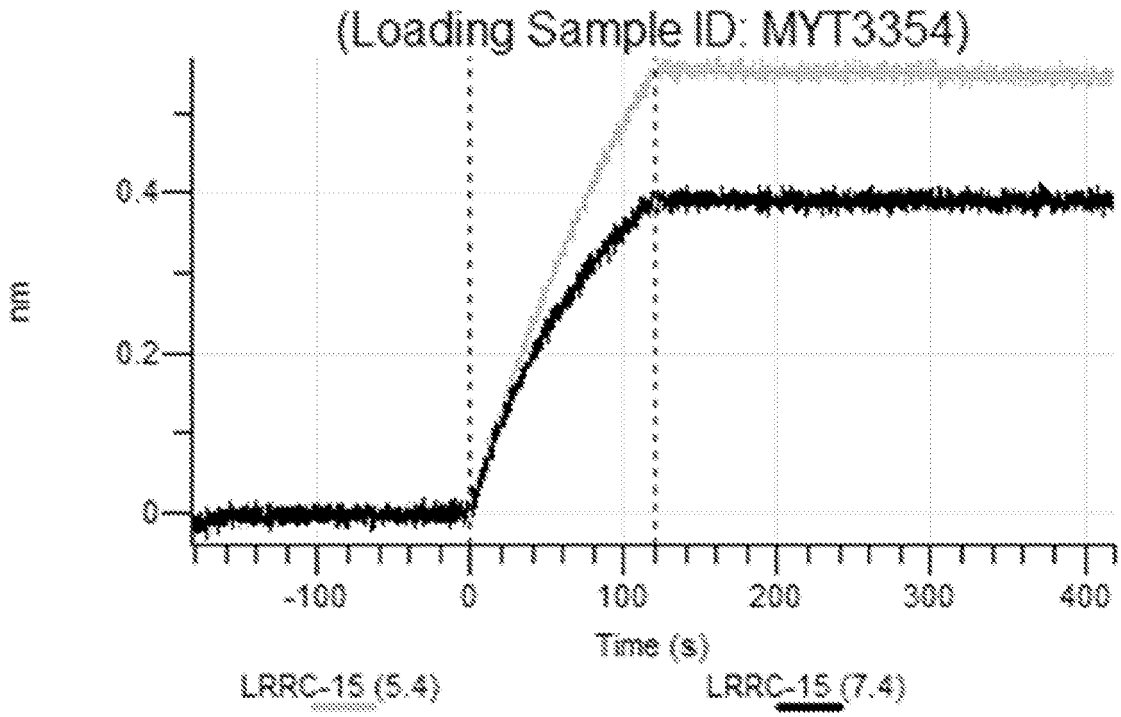

(Loading Sample ID: MYT3354)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AD

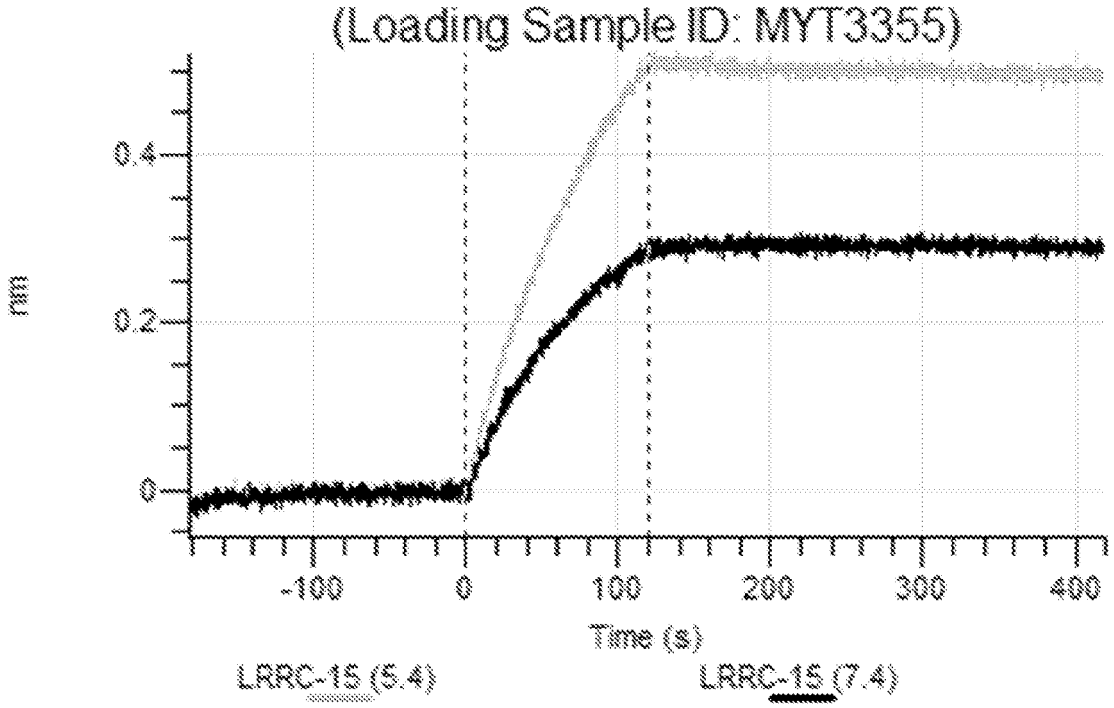

(Loading Sample ID: MYT3355)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AE

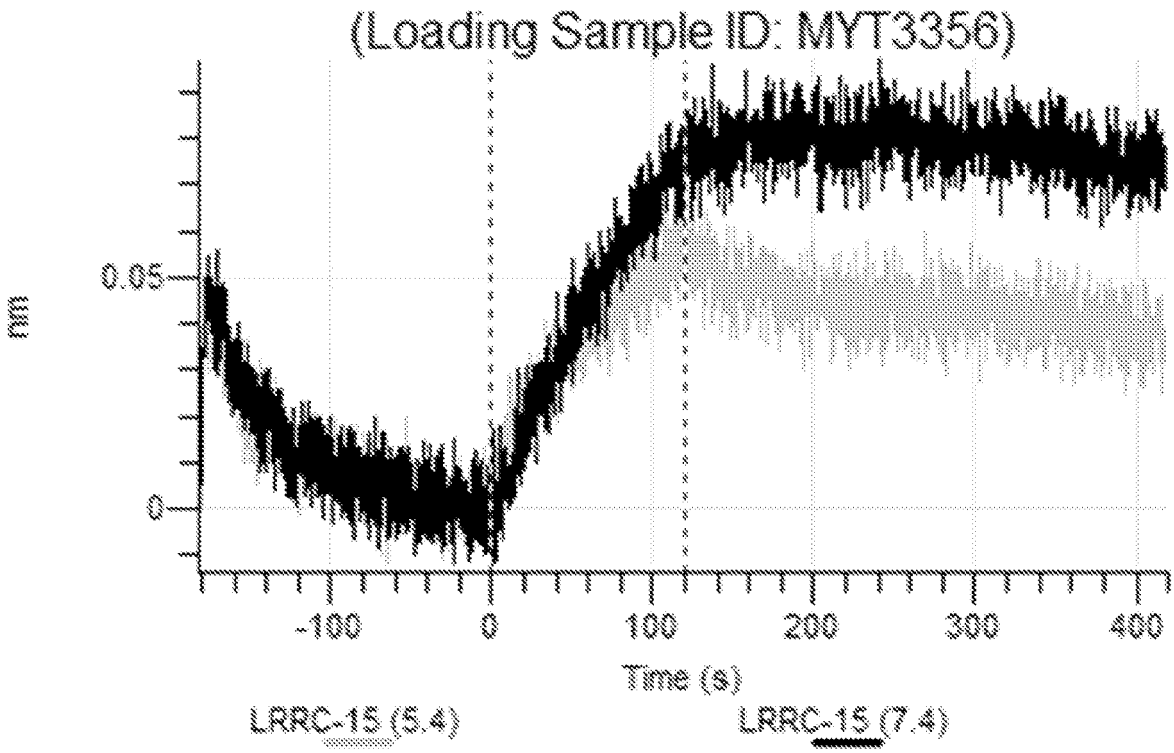

(Loading Sample ID: MYT3356)
nm
0.05
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AF

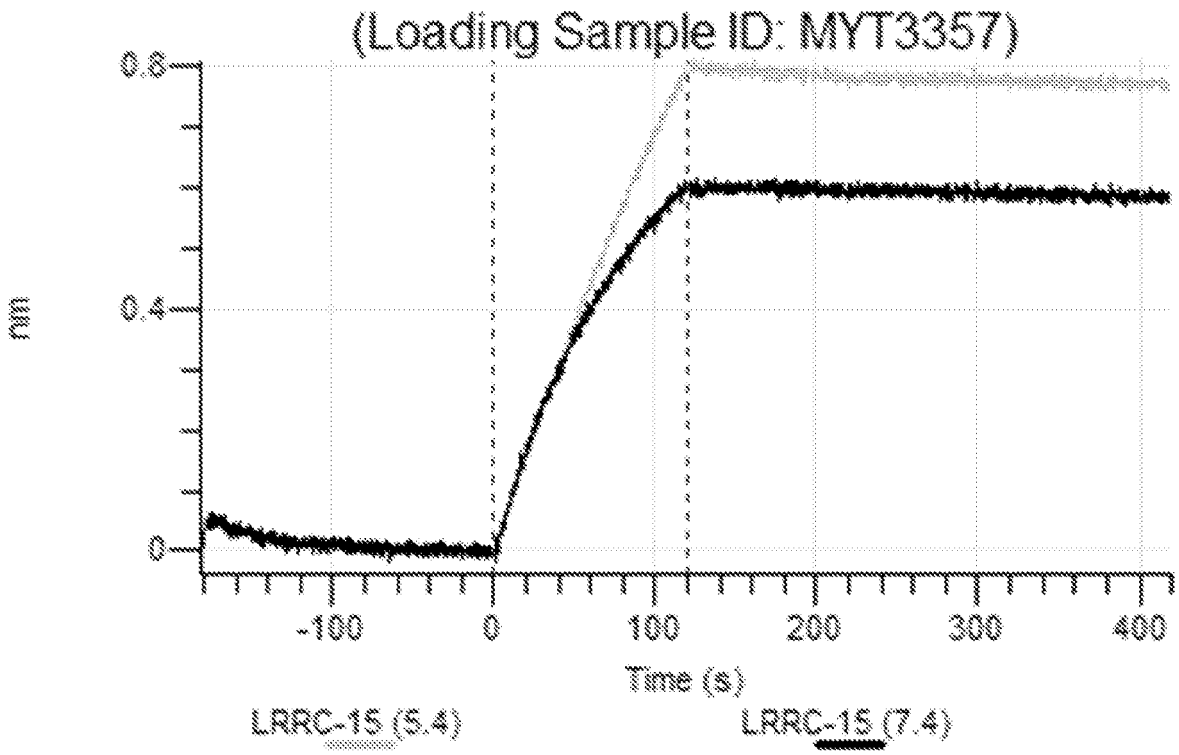

(Loading Sample ID: MYT3357)
nm
0.8
0.4
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AG

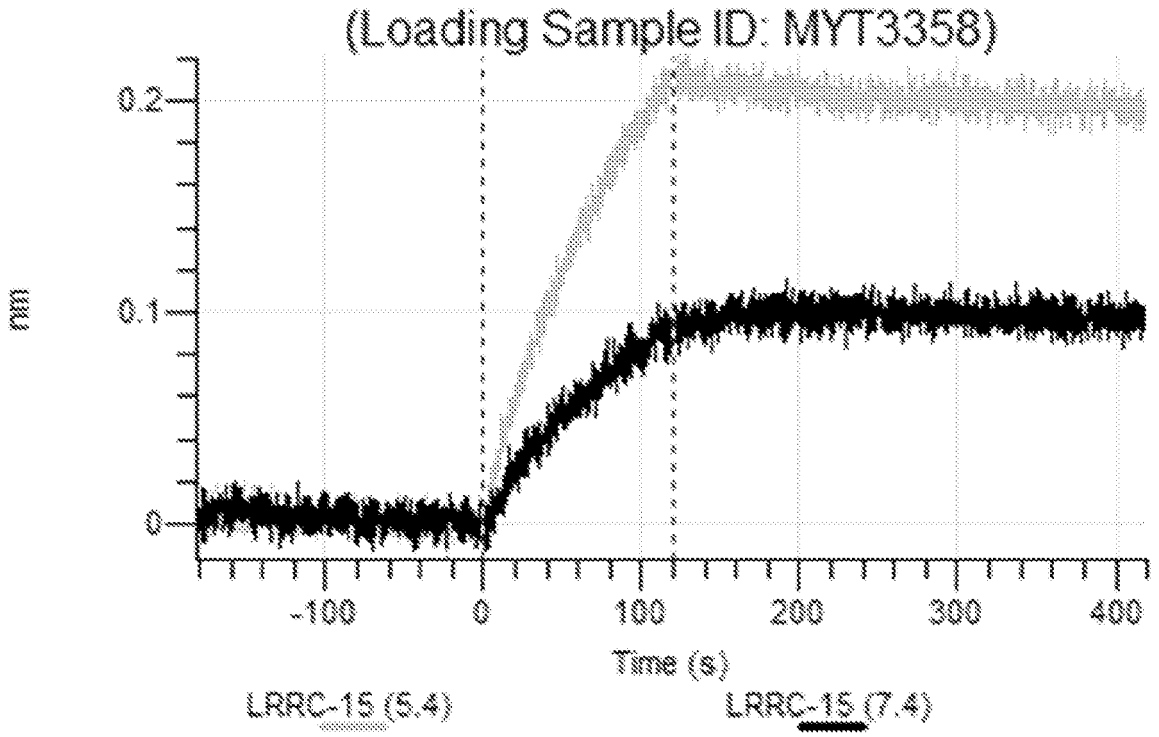

(Loading Sample ID: MYT3358)
0.2
0.1
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AH

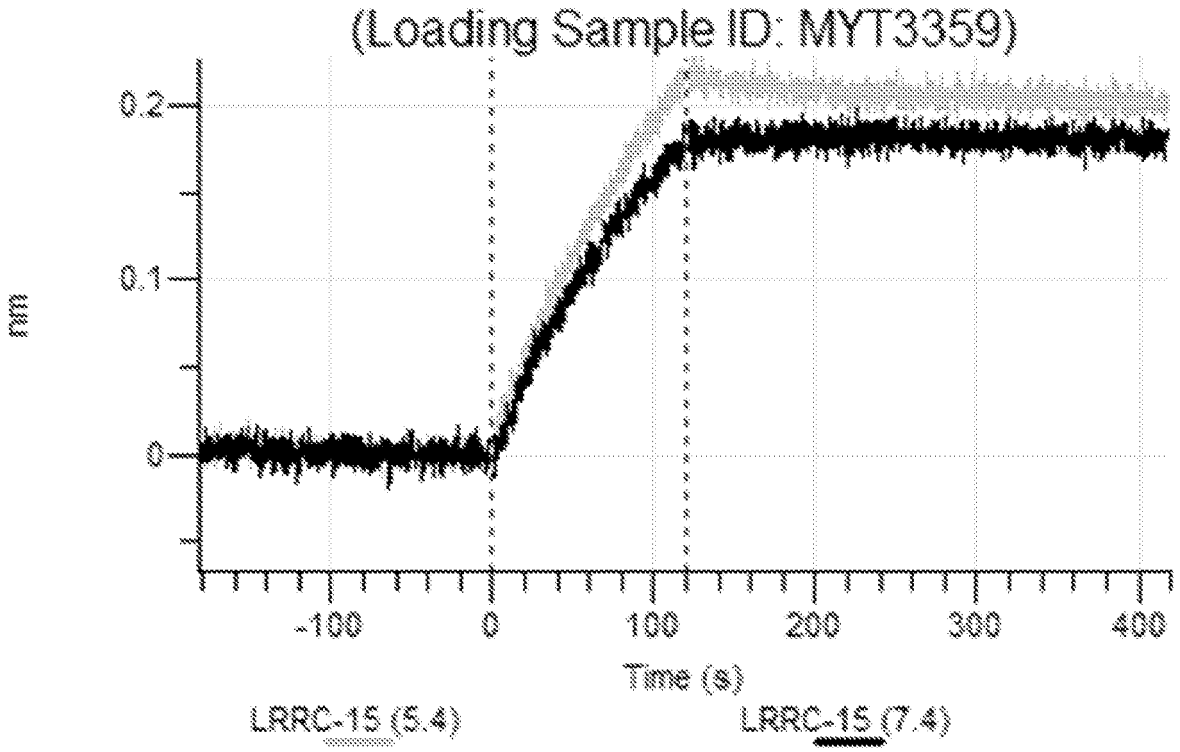

(Loading Sample ID: MYT3359)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AI

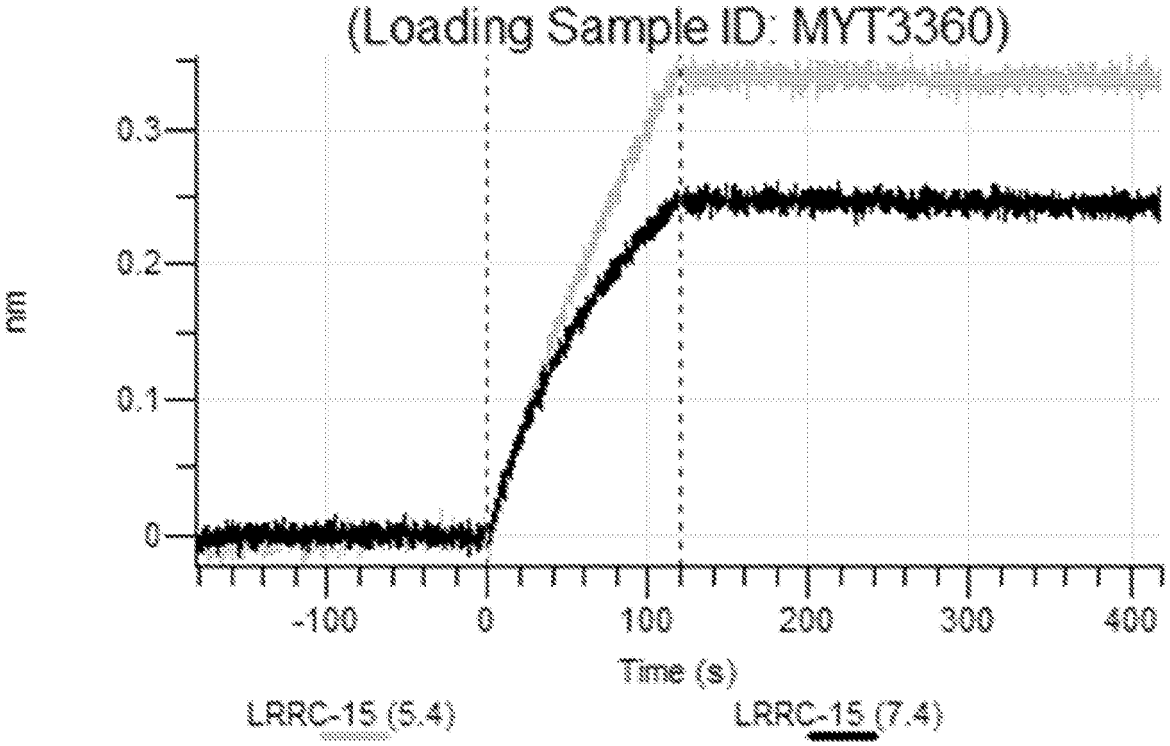

(Loading Sample ID: MYT3360)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AJ

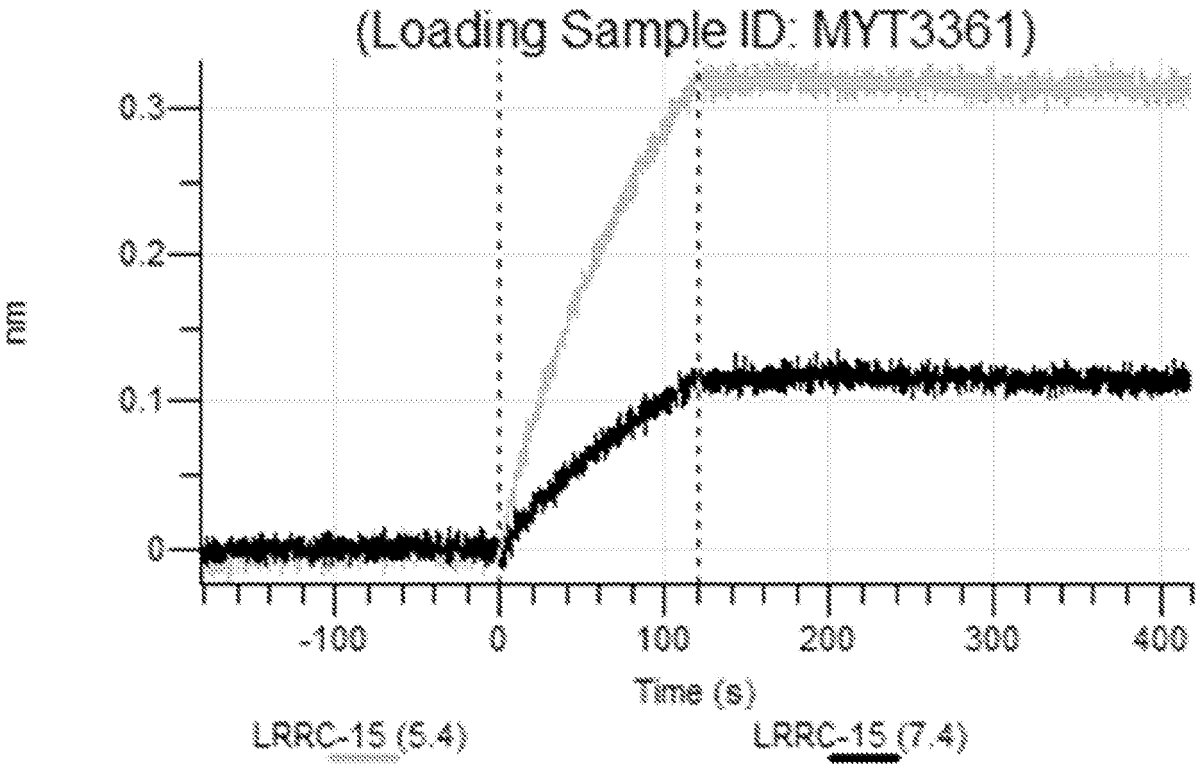

(Loading Sample ID: MYT3361)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AK

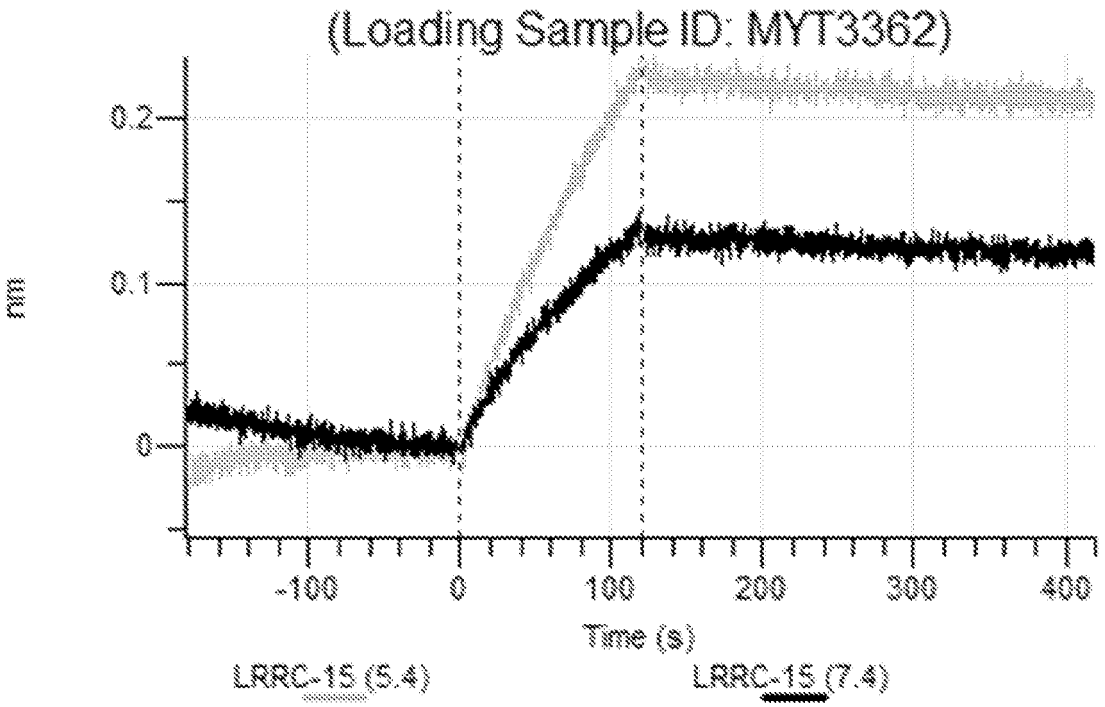

(Loading Sample ID: MYT3362)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AL

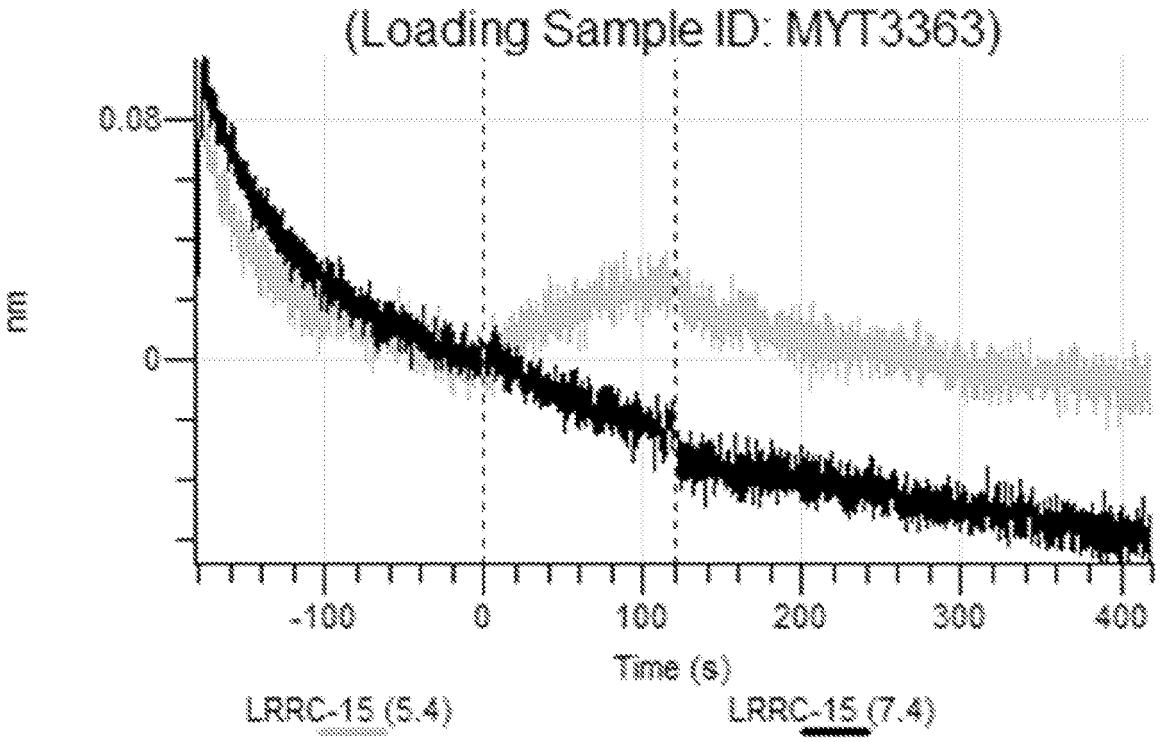

(Loading Sample ID: MYT3363)
0.08
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AM

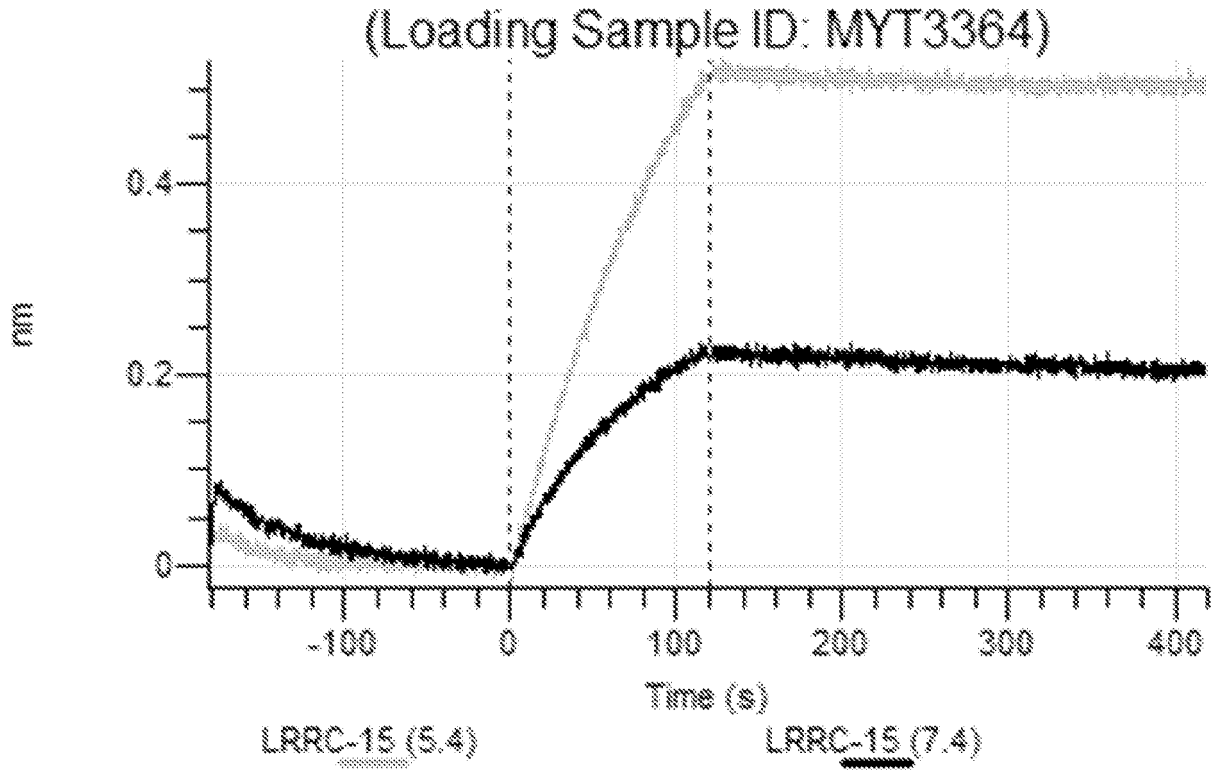

(Loading Sample ID: MYT3364)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AN

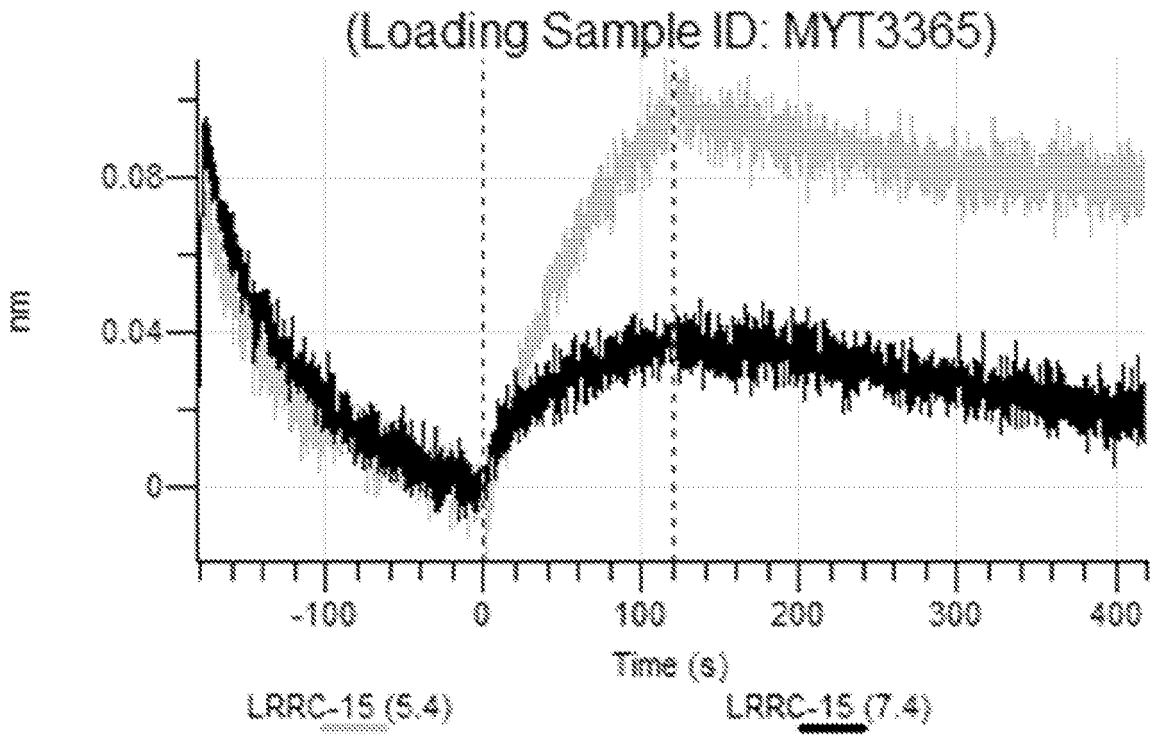

(Loading Sample ID: MYT3365)
nm
0.08
0.04
0
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AO

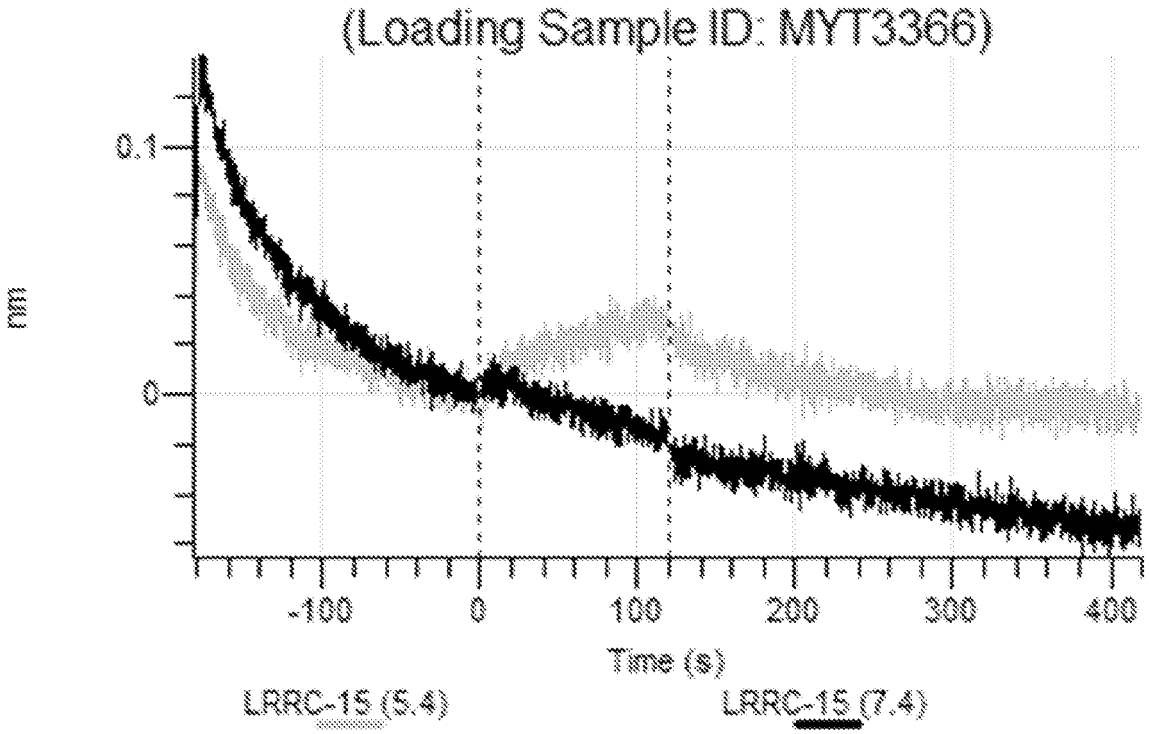

(Loading Sample ID: MYT3366)
0.1
0
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AP

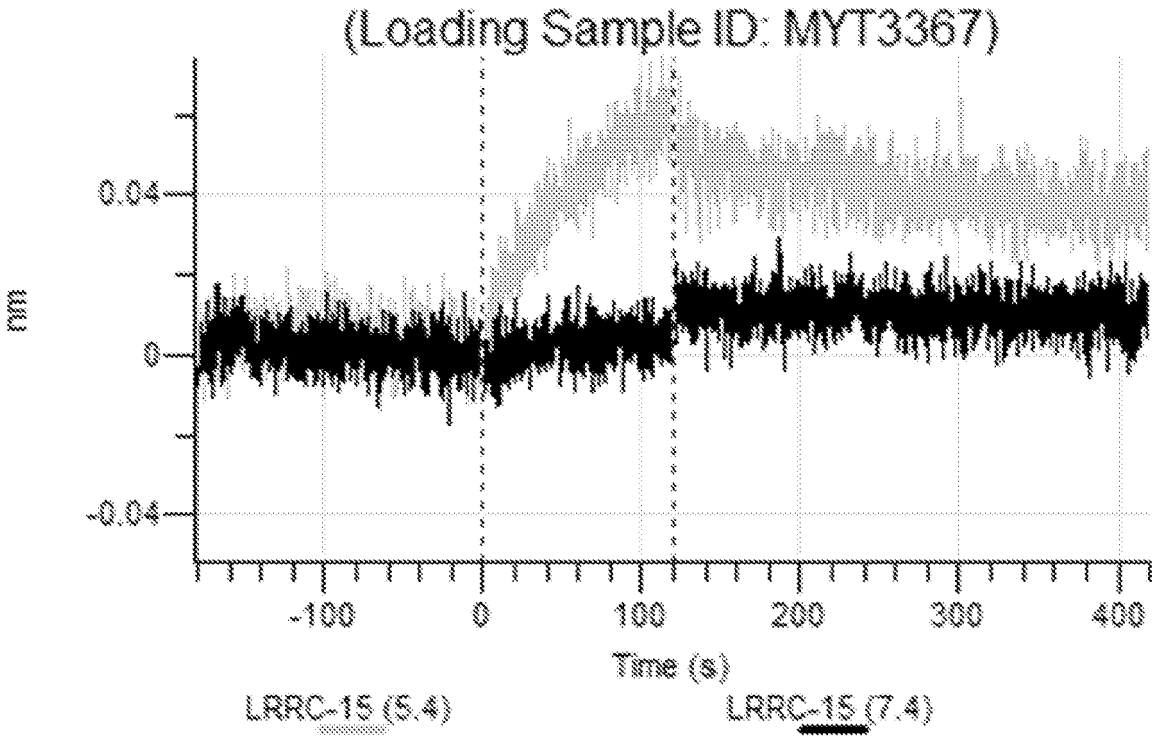

(Loading Sample ID: MYT3367)
0.04
0
-0.04
nm
-100
0
100
200
300
400
Time (s)
LRRC-15 (5.4)
LRRC-15 (7.4)

FIG. 23AQ

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
MYT3325 (huAD208.4.1)	178	179	180	181	182	183	184	185
MYT3326	186	179						
MYT3327	187	179						
MYT3328	188	179						
MYT3329	189	179						
MYT3330	190	179						
MYT3331	191	179						
MYT3332	192	179						
MYT3333	193	179						
MYT3334	194	179						
MYT3335	195	179						
MYT3336	196	179						
MYT3337	197	179						
MYT3338	198	179						
MYT3339	199	179						
MYT3340	200	179						
MYT3341	201	179						
MYT3342	202	179						
MYT3343	203	179						
MYT3344	204	179						
MYT3345	205	179						
MYT3346	206	179						
MYT3347	207	179						
MYT3348	208	179						
MYT3349	209	179						
MYT3350	210	179						
MYT3351	211	179						
MYT3352	212	179						
MYT3353	213	179						
MYT3354	214	179						
MYT3355	215	179						
MYT3356	216	179						
MYT3357	217	179						
MYT3358	218	179						
MYT3359	219	179						
MYT3360	220	179						
MYT3361	221	179						
MYT3362	222	179						
MYT3363	223	179						
MYT3364	224	179						
MYT3365	225	179						
MYT3366	226	179						
MYT3367	227	179						

FIG. 24

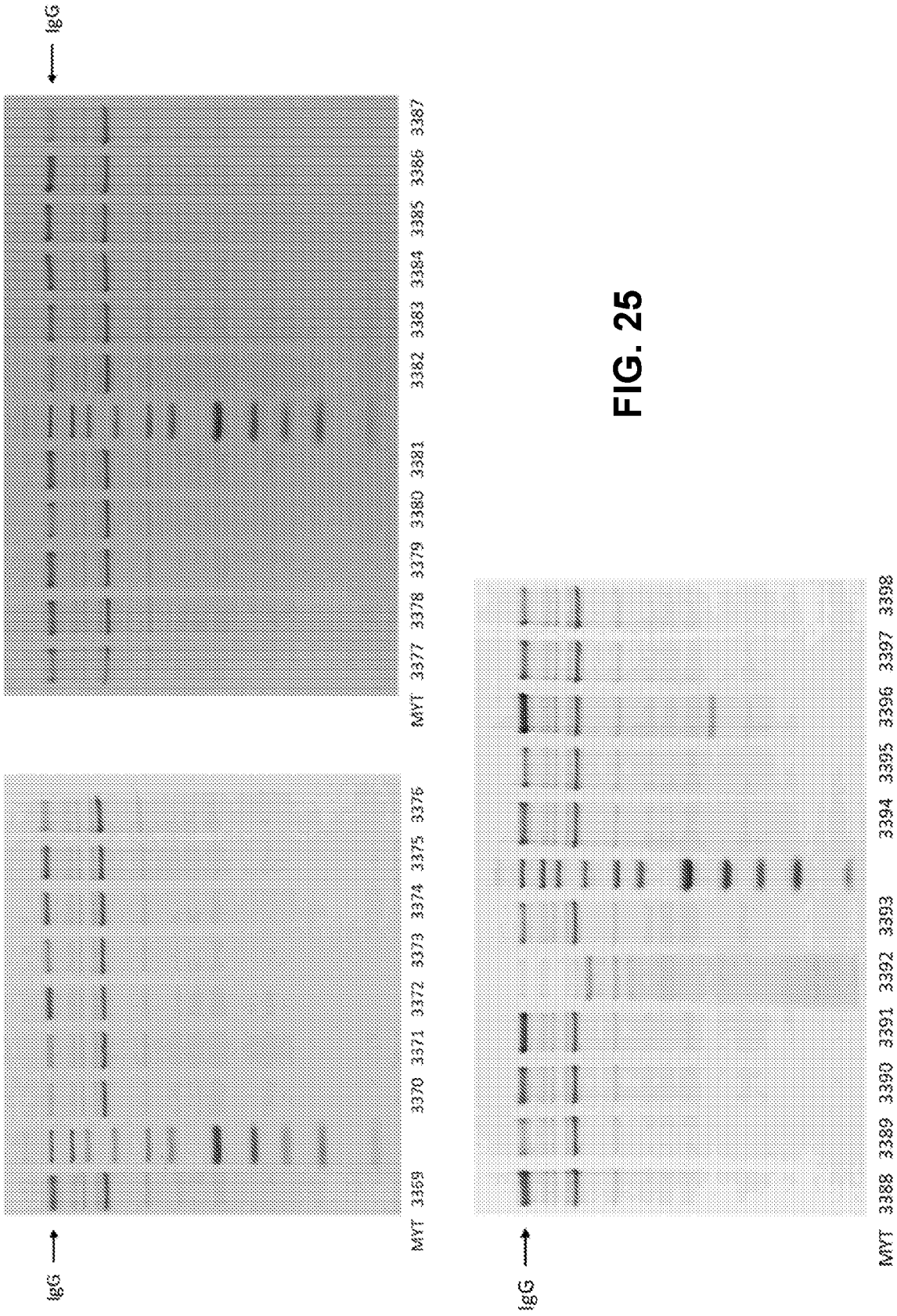

IgG
MYT 3369 3370 3371 3372 3373 3374 3375 3376
IgG
MYT 3377 3378 3379 3380 3381 3382 3383 3384 3385 3386 3387
IgG
MYT 3388 3389 3390 3391 3392 3393 3394 3395 3396 3397 3398

FIG. 25

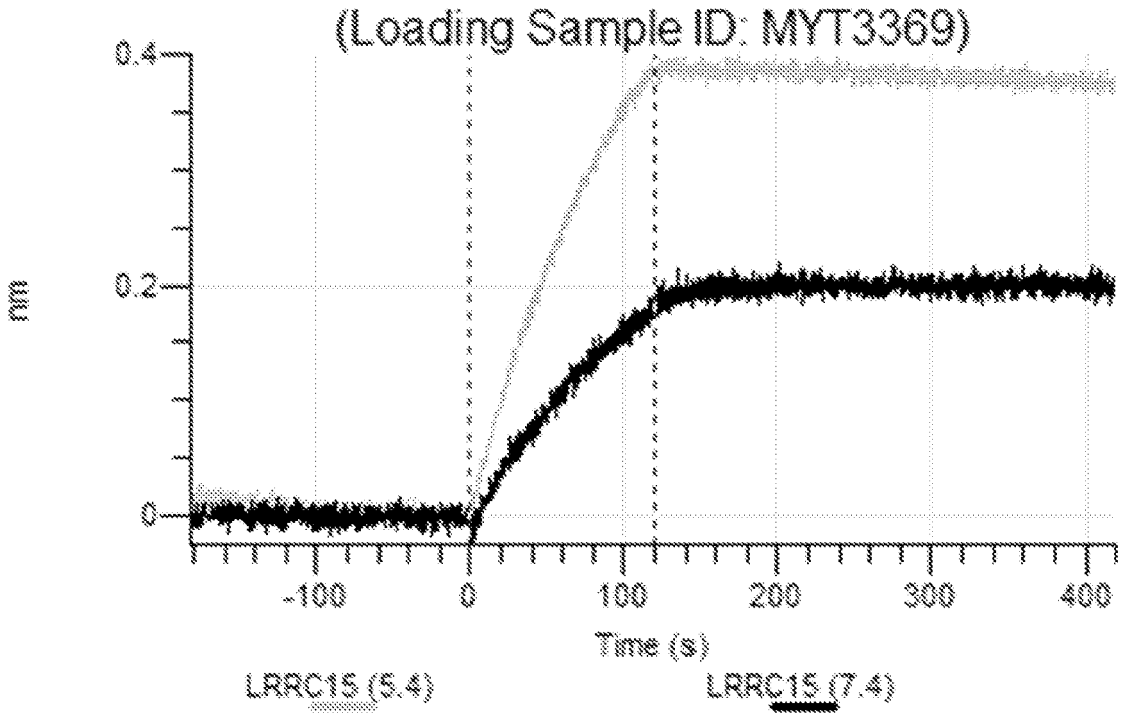

(Loading Sample ID: MYT3369)
0.4
0.2
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26A

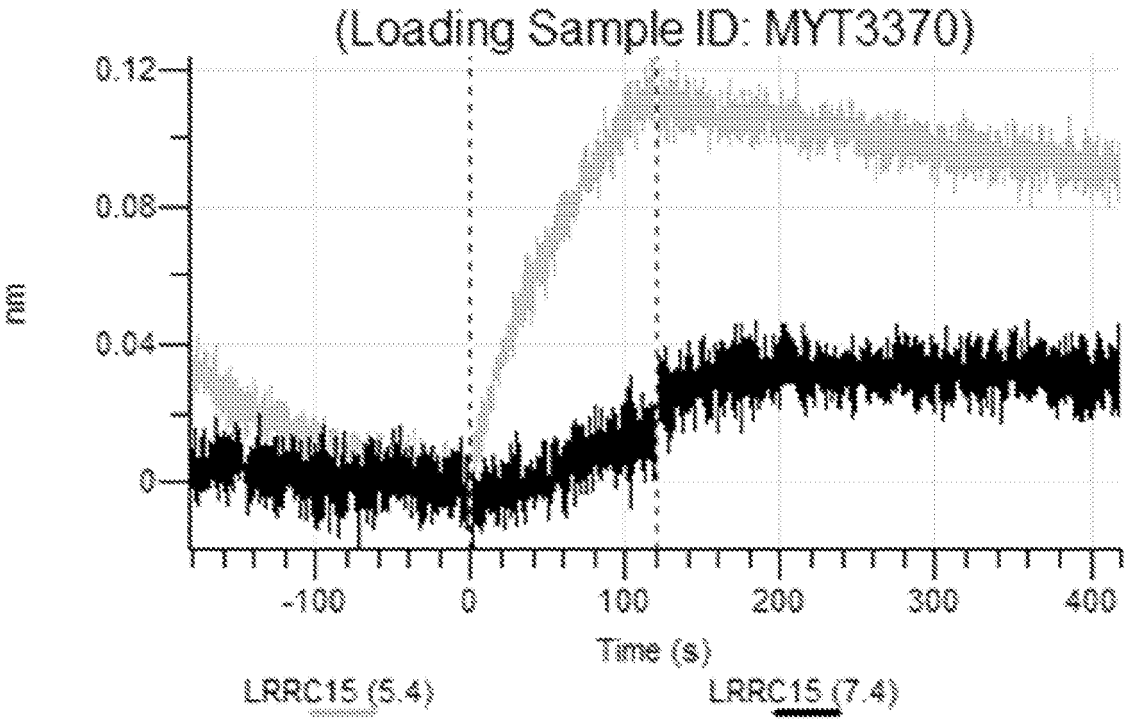

(Loading Sample ID: MYT3370)
0.12
0.08
0.04
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26B

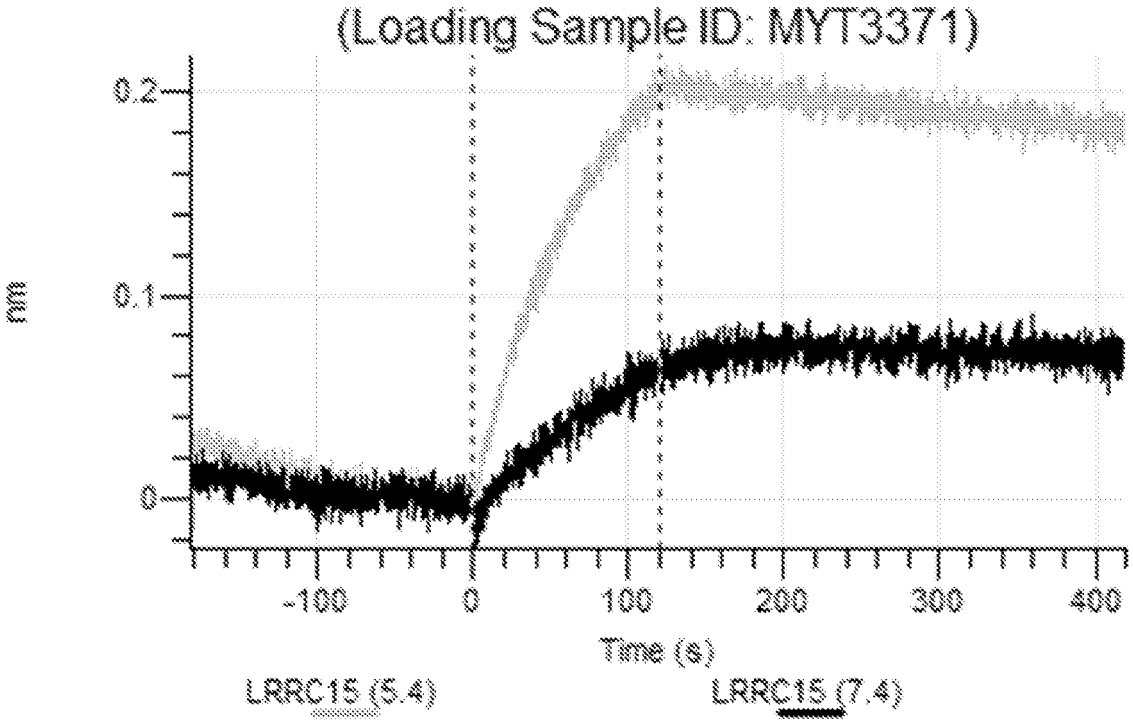

(Loading Sample ID: MYT3371)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26C

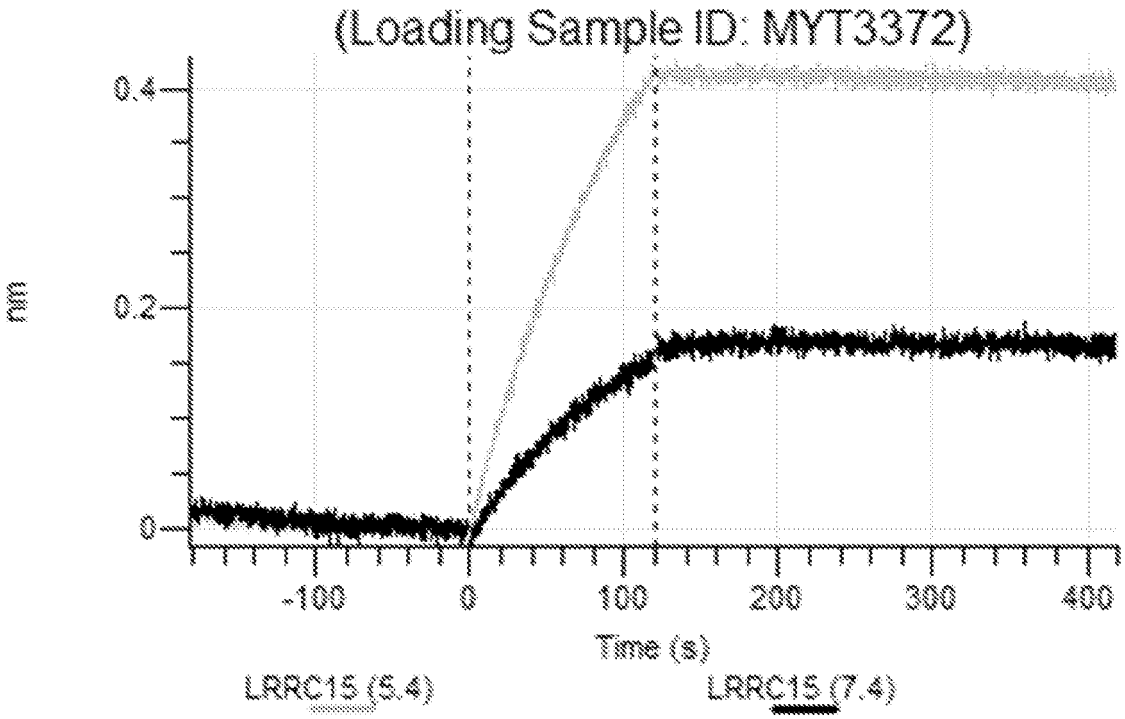

(Loading Sample ID: MYT3372)
0.4
0.2
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26D

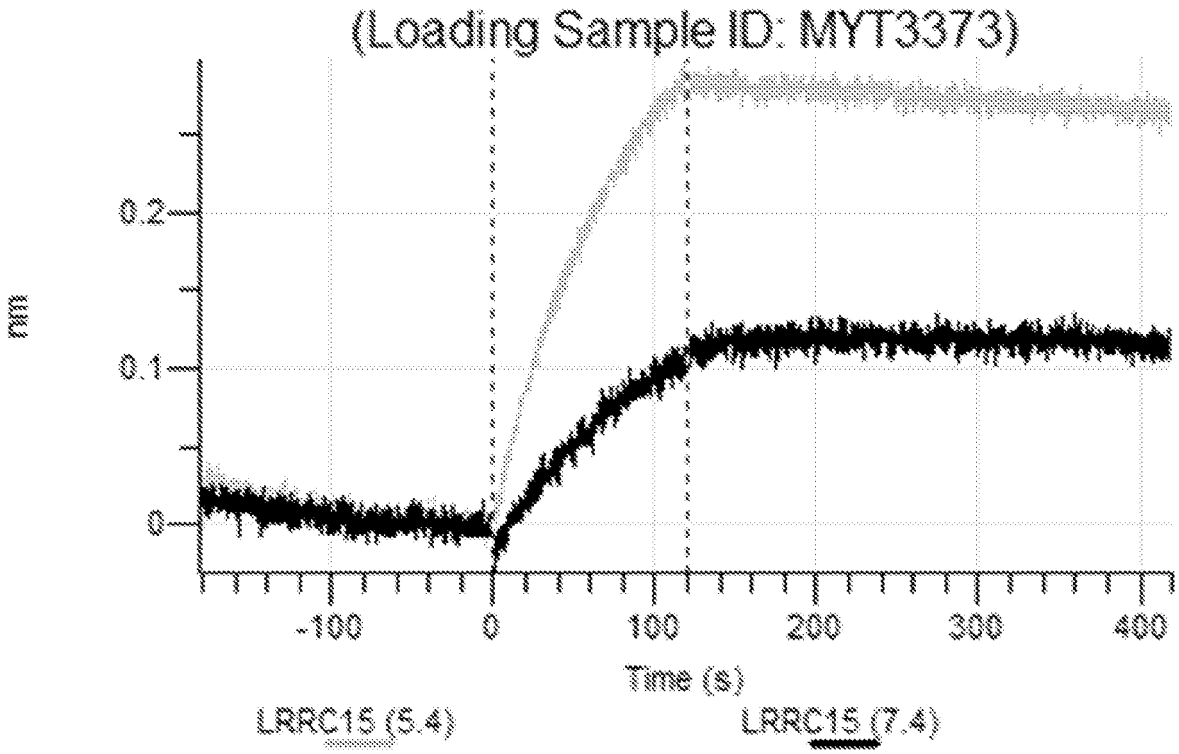

(Loading Sample ID: MYT3373)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26E

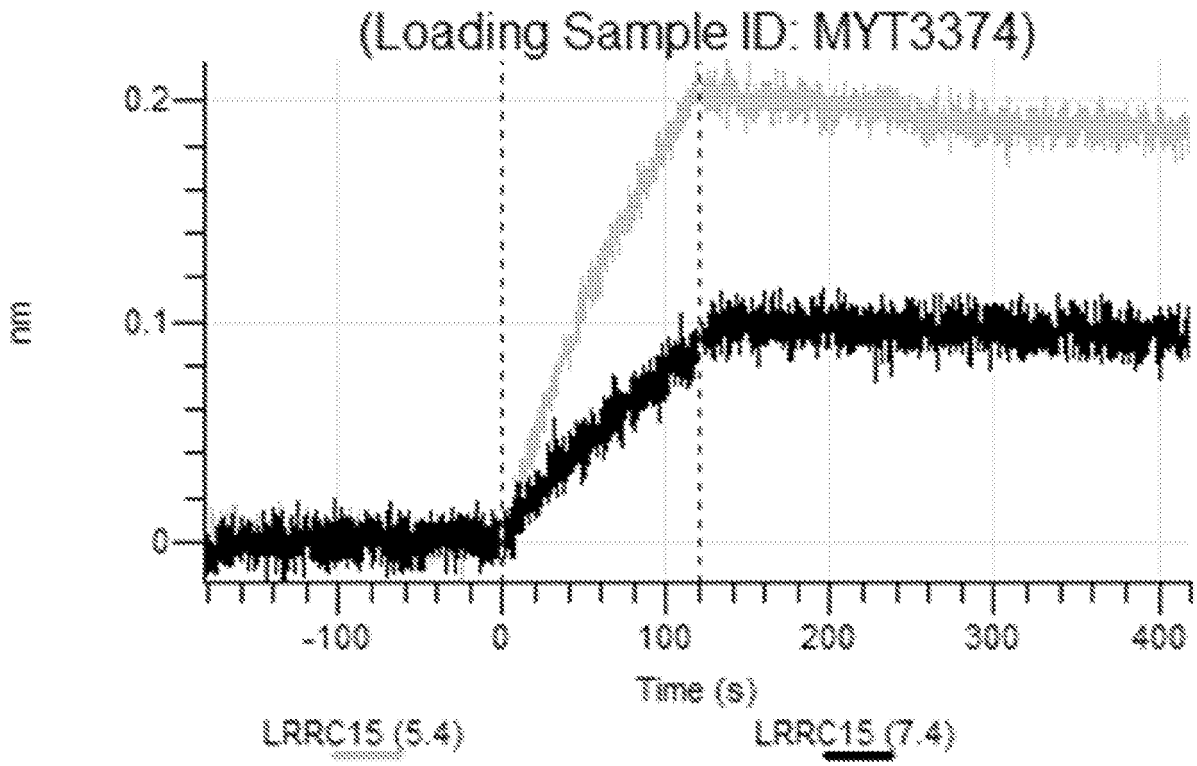

(Loading Sample ID: MYT3374)
0.2
0.1
0
(nm)
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26F

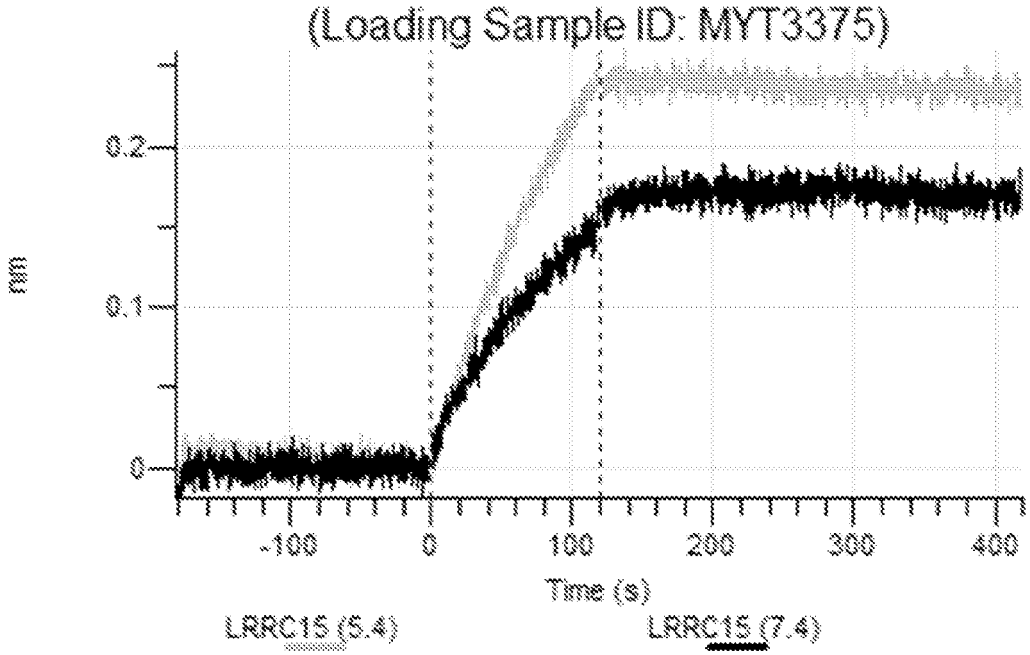

(Loading Sample ID: MYT3375)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26G

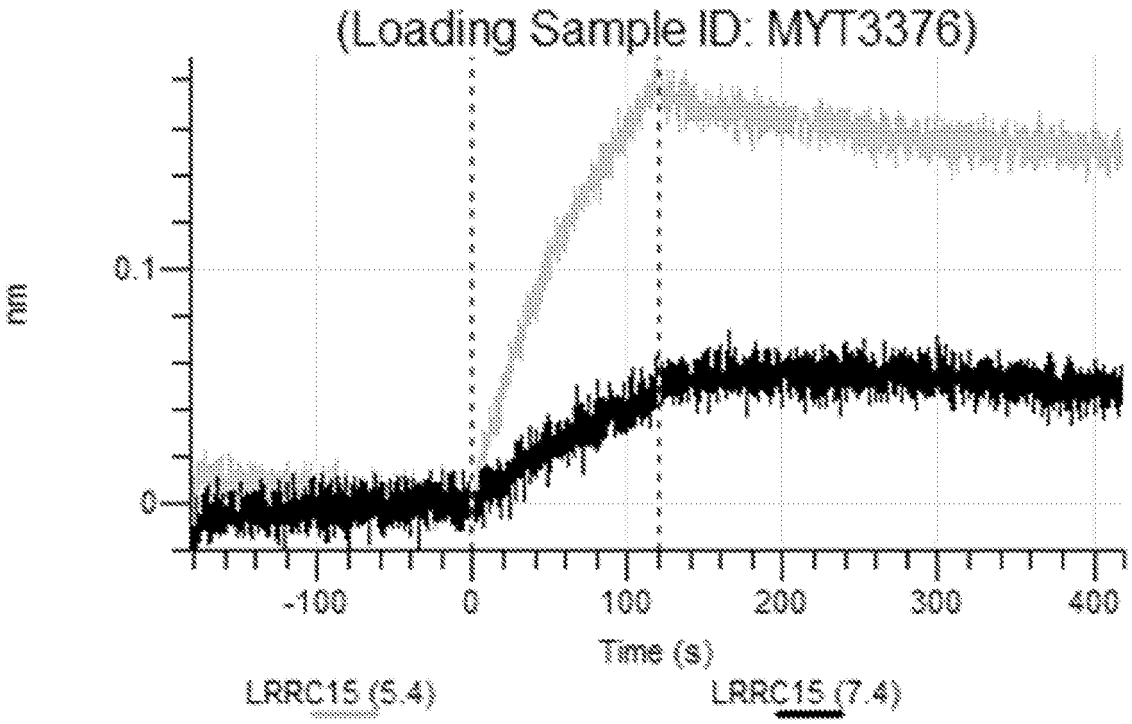

(Loading Sample ID: MYT3376)
nm
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26H

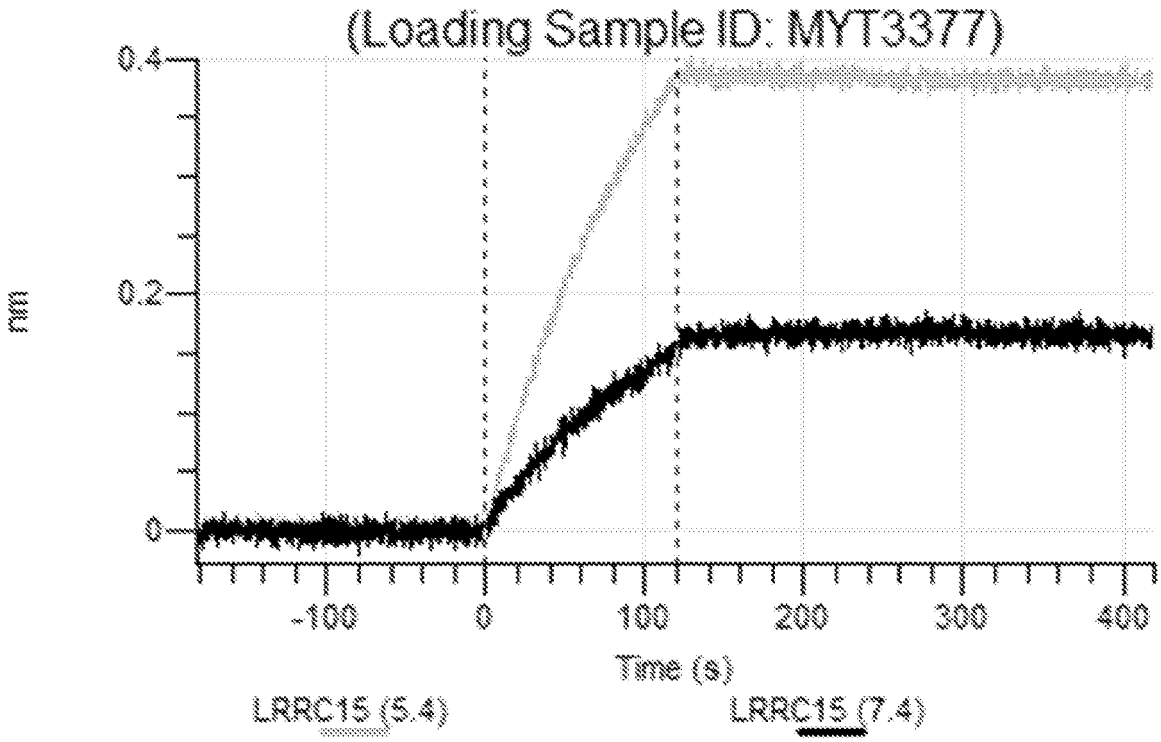

(Loading Sample ID: MYT3377)
0.4
0.2
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26I

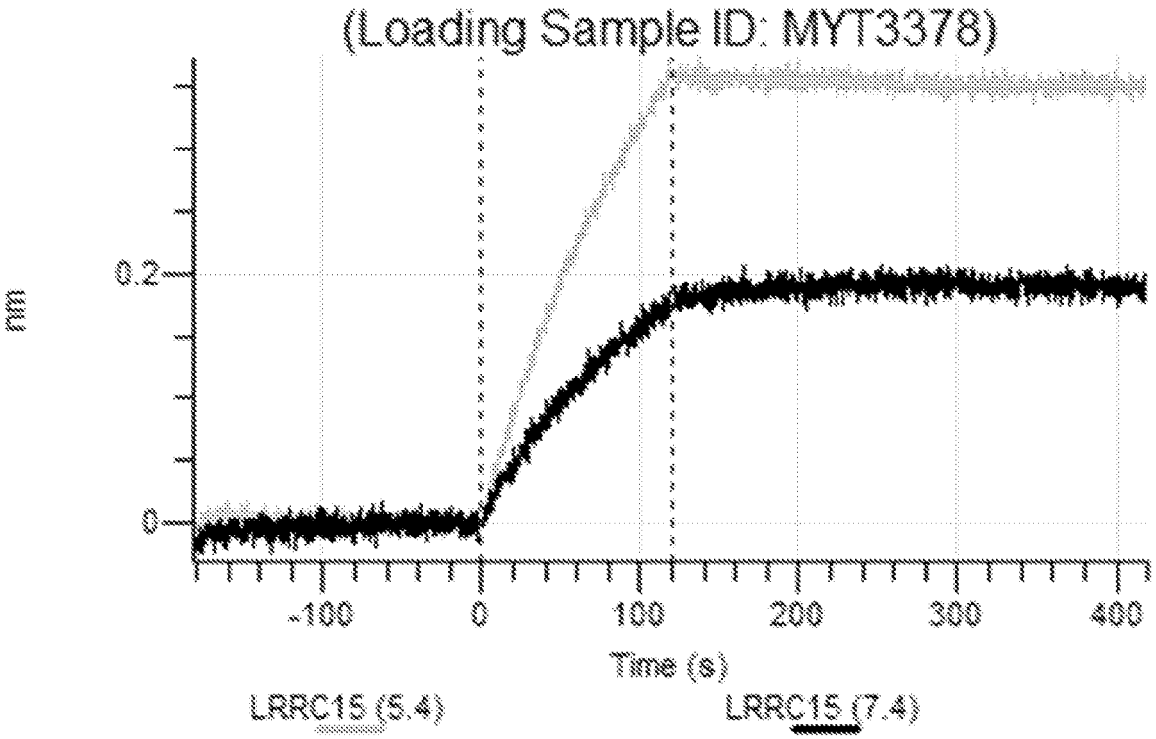

(Loading Sample ID: MYT3378)
nm
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26J

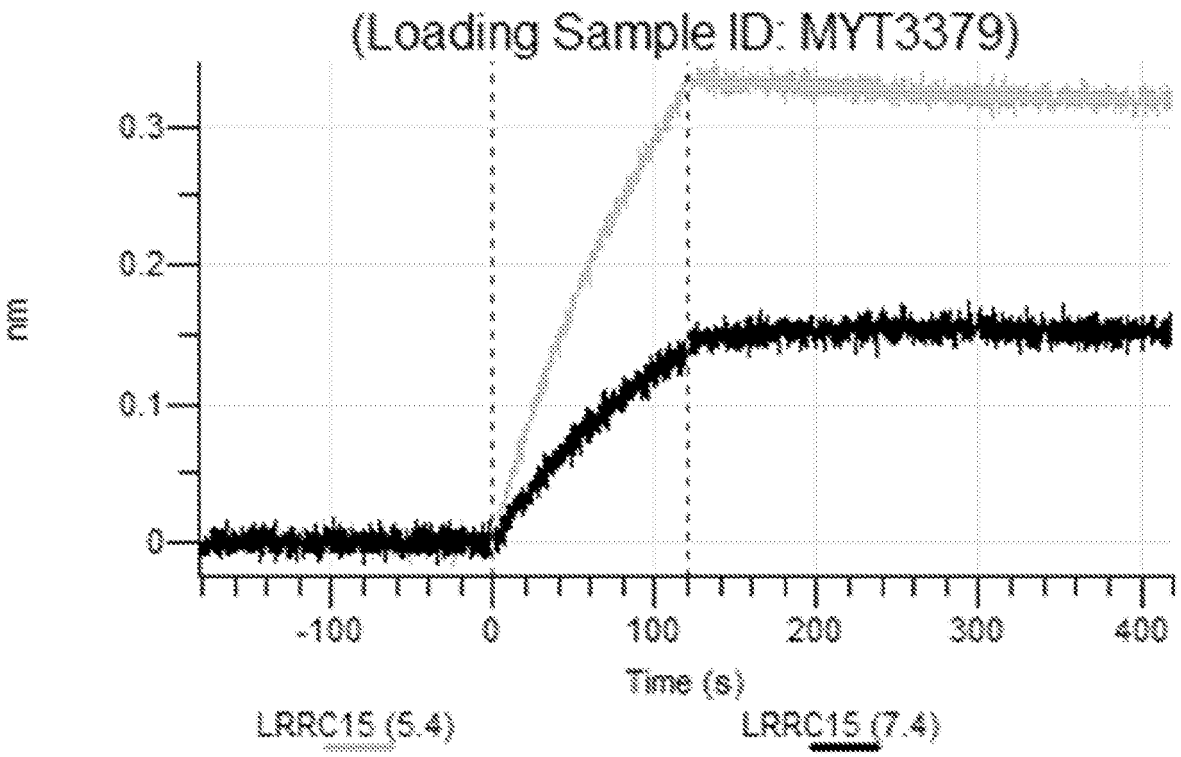

(Loading Sample ID: MYT3379)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26K

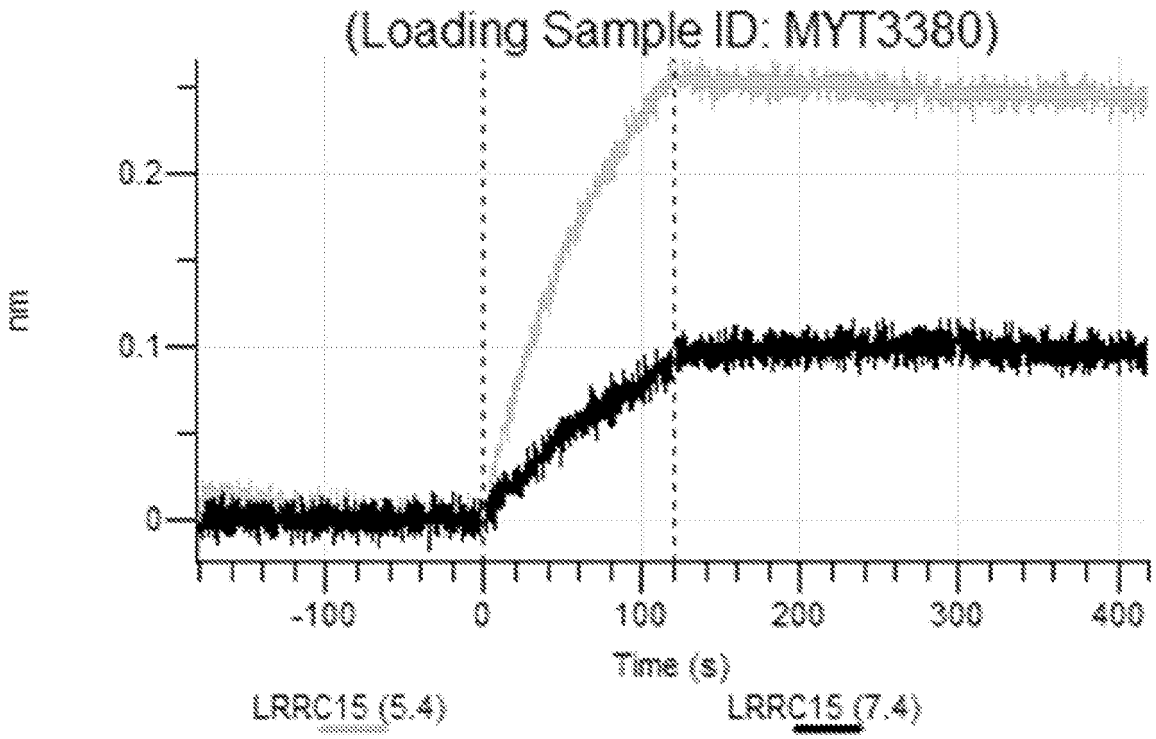

(Loading Sample ID: MYT3380)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26L

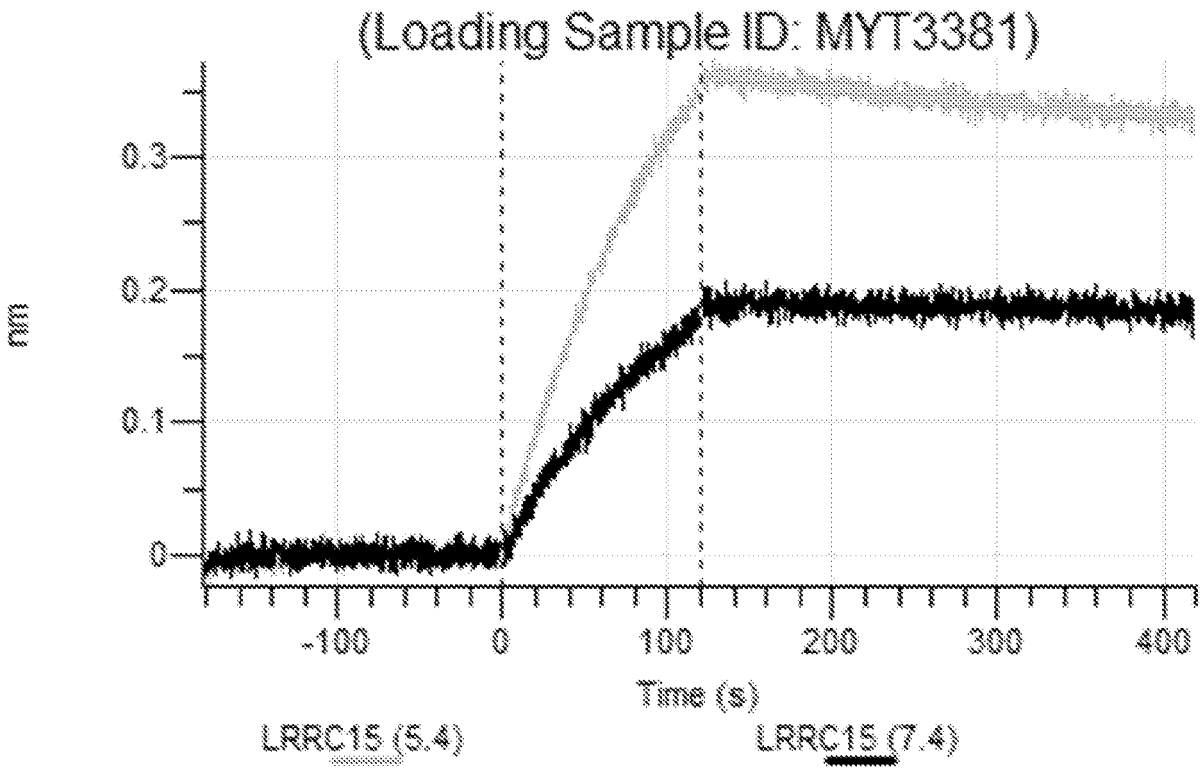

(Loading Sample ID: MYT3381)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26M

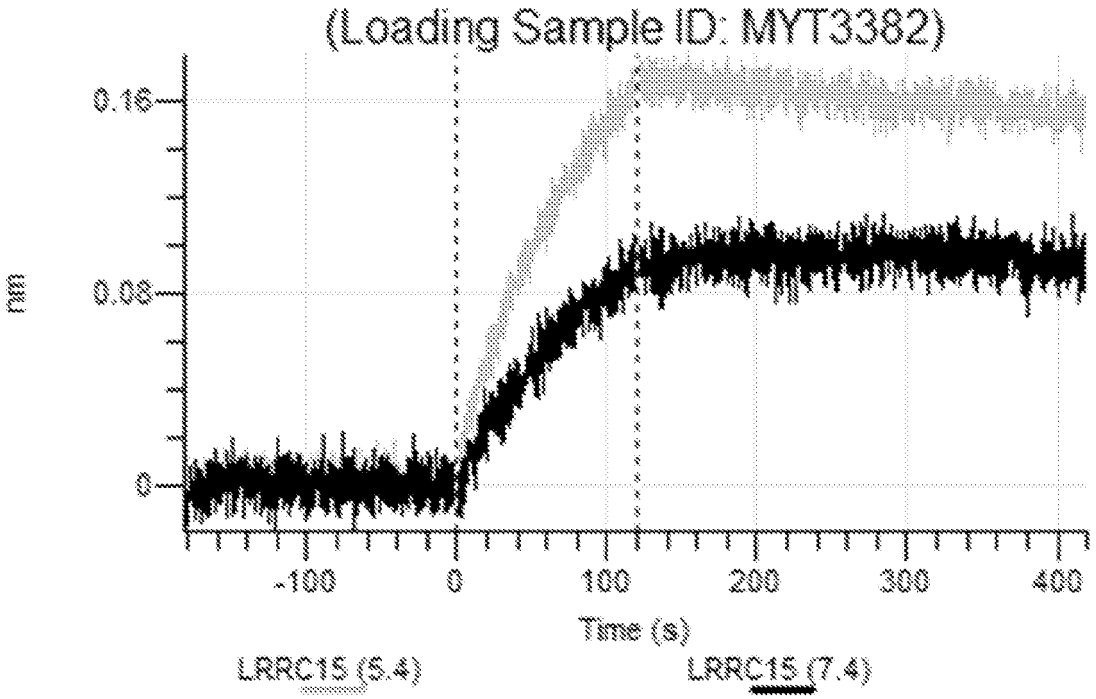

(Loading Sample ID: MYT3382)
0.16
0.08
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26N

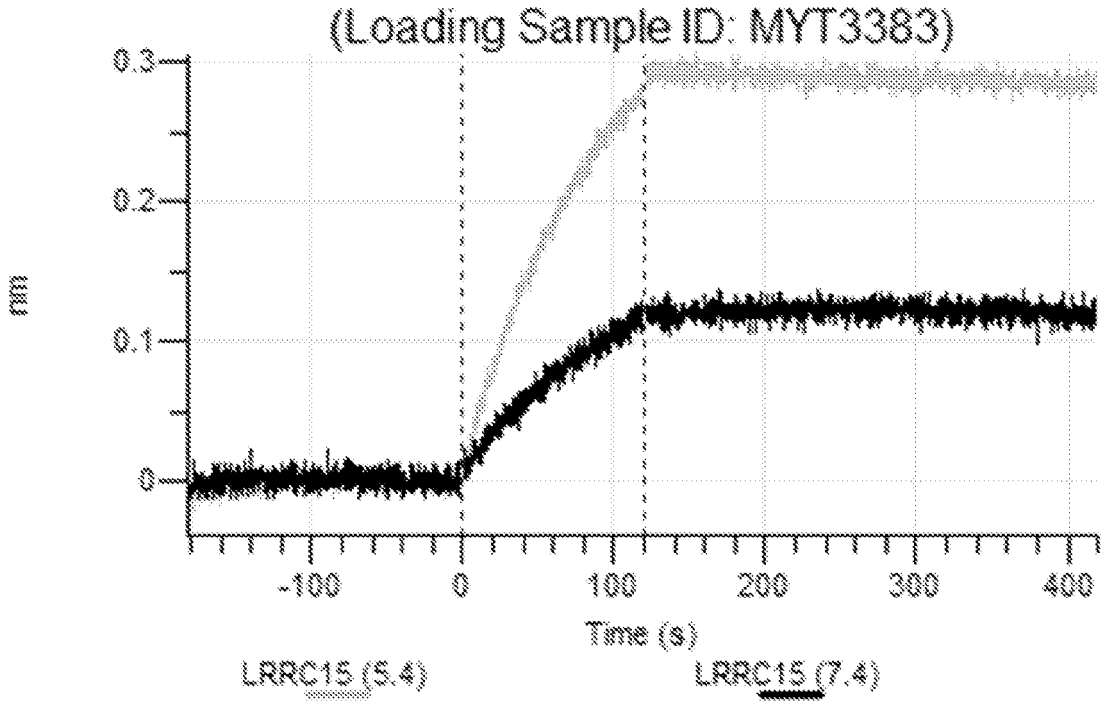

(Loading Sample ID: MYT3383)
0.3
0.2
0.1
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26O

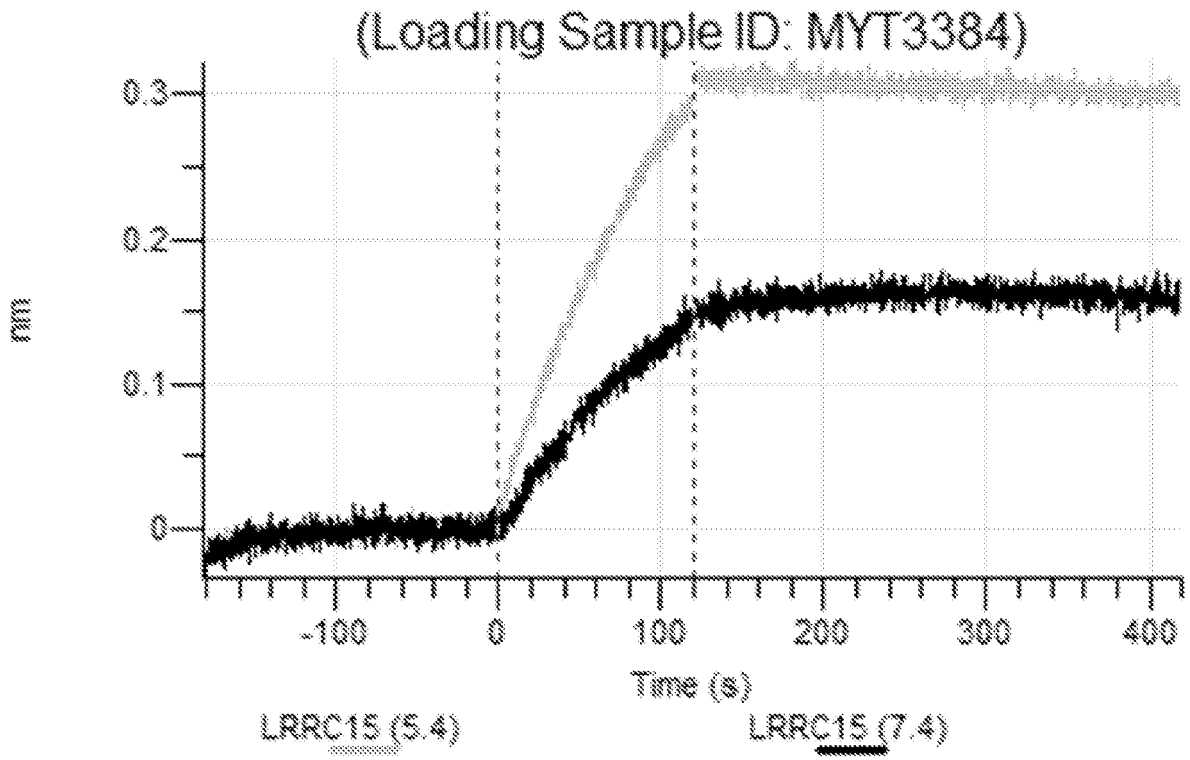

(Loading Sample ID: MYT3384)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26P

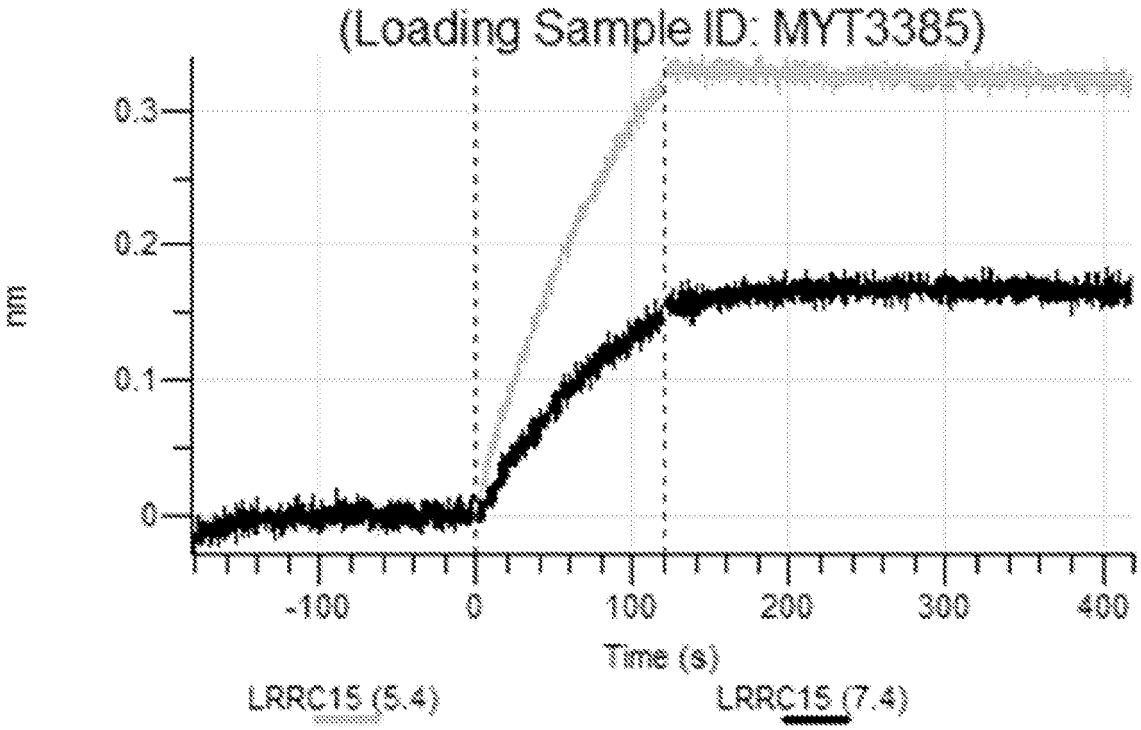

(Loading Sample ID: MYT3385)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26Q

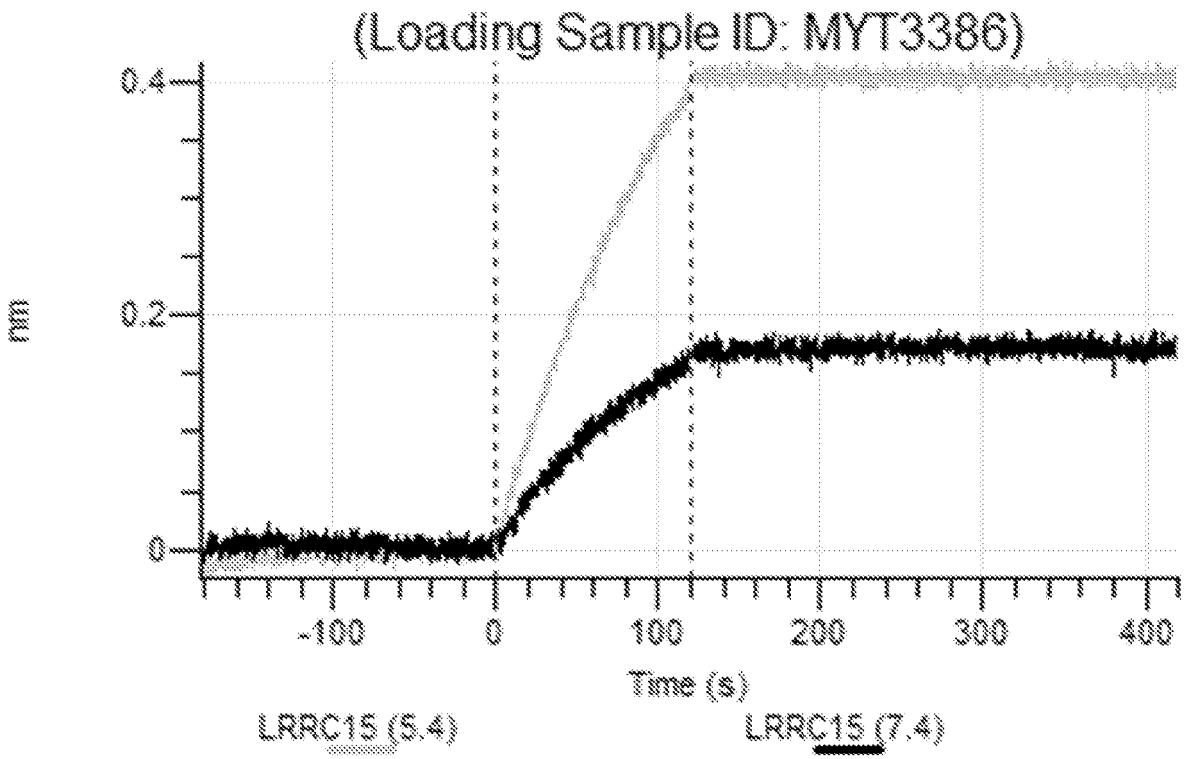

(Loading Sample ID: MYT3386)
0.4
0.2
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26R

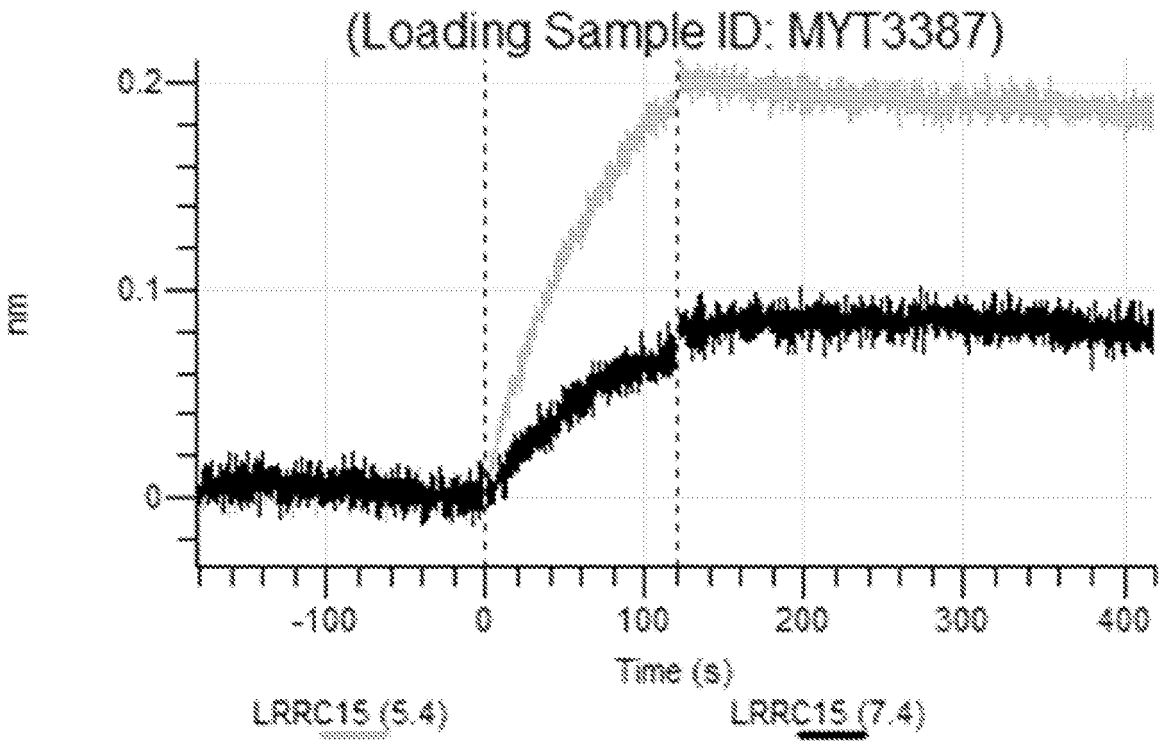

(Loading Sample ID: MYT3387)
0.2
0.1
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26S

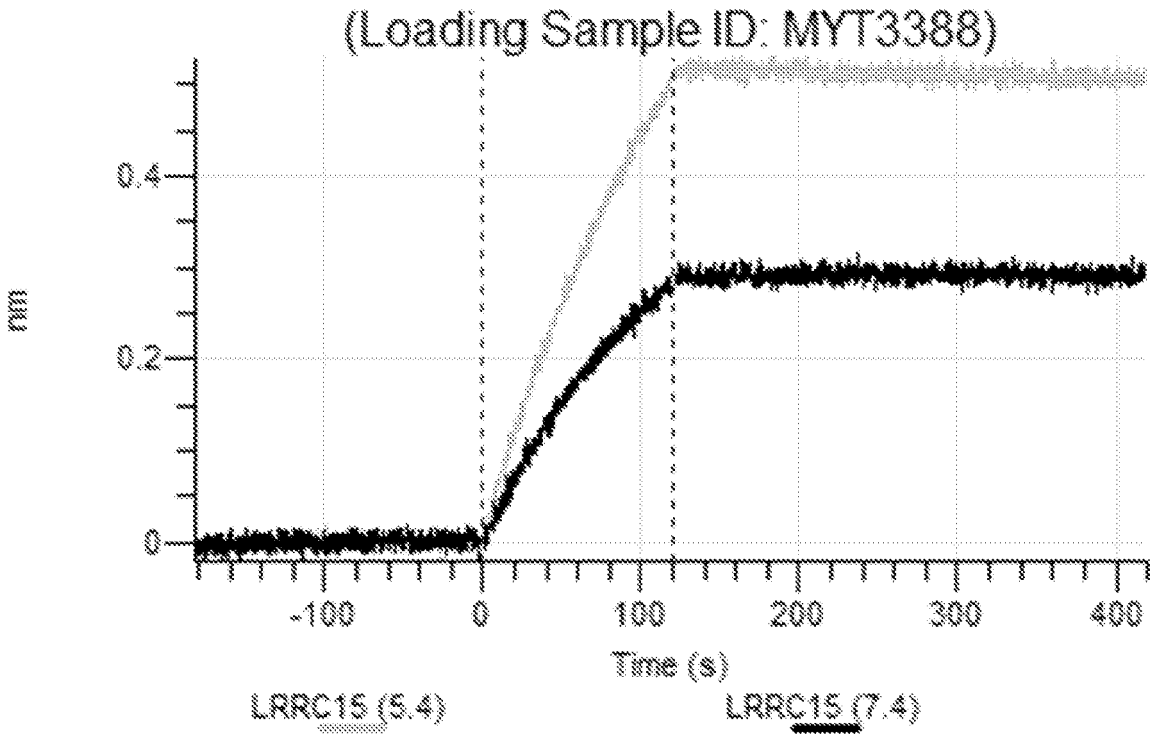

(Loading Sample ID: MYT3388)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26T

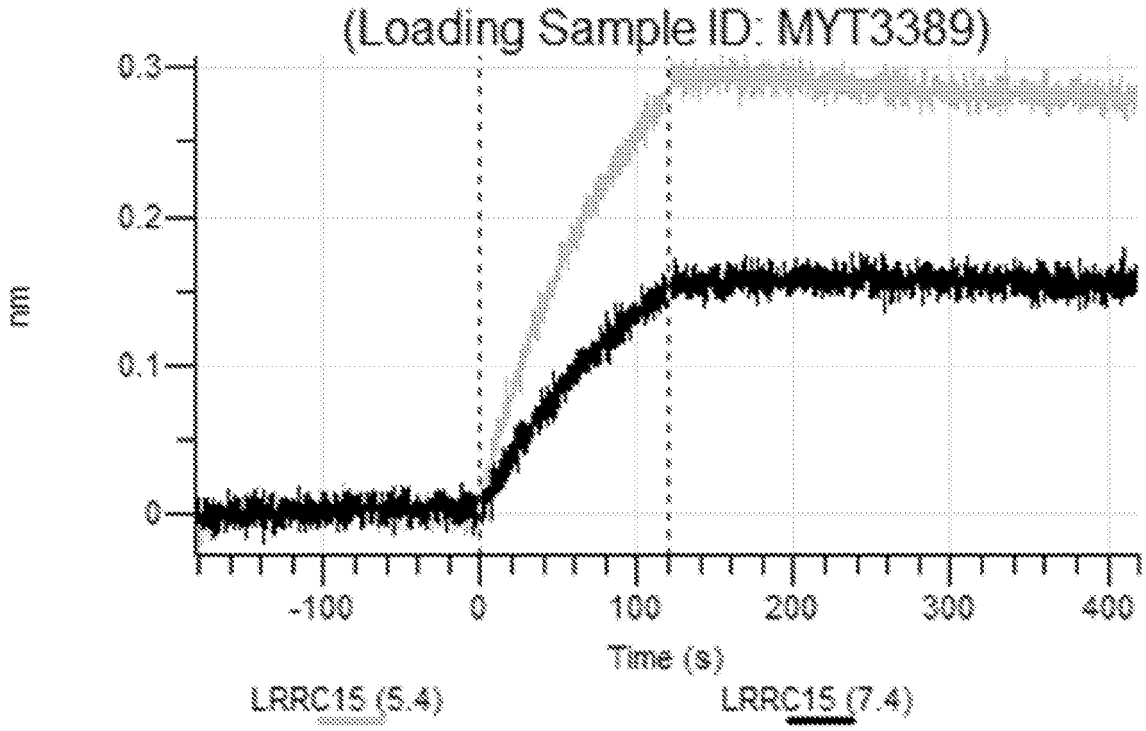

(Loading Sample ID: MYT3389)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26U

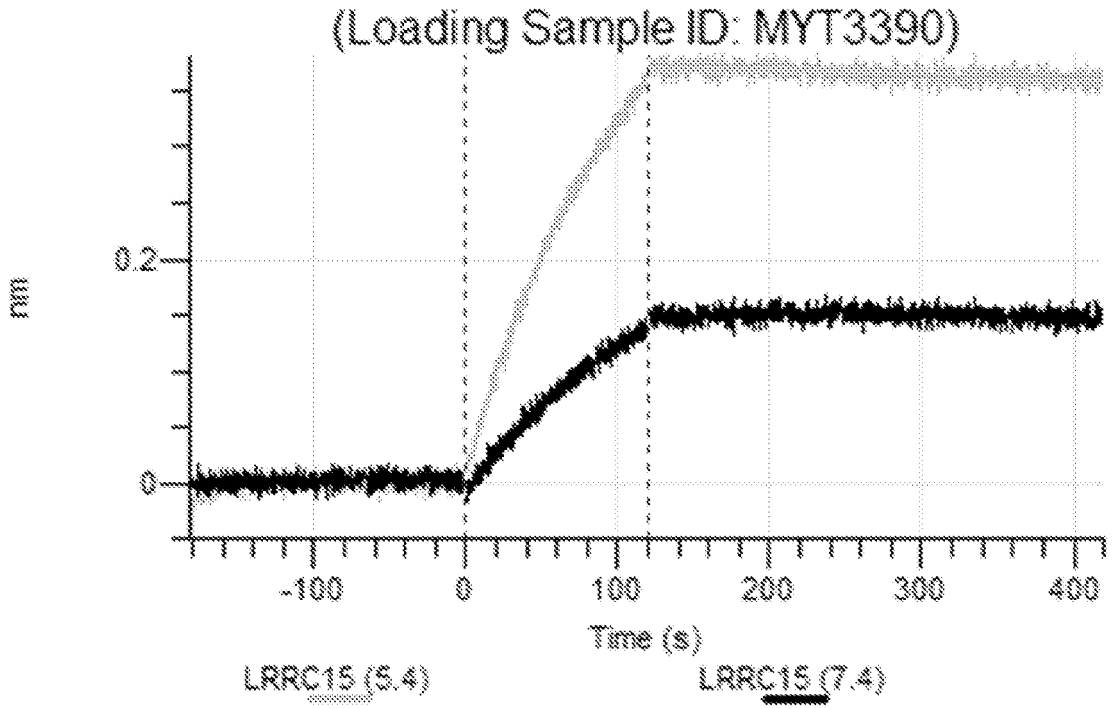

(Loading Sample ID: MYT3390)
nm
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26V

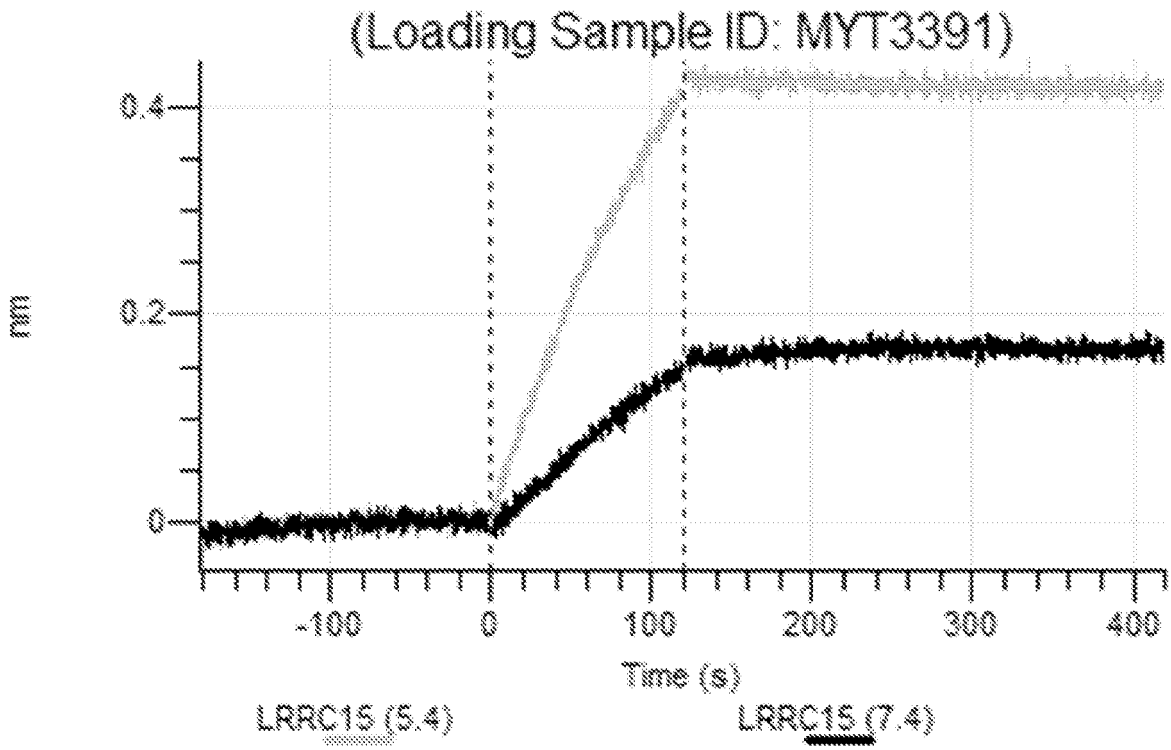

(Loading Sample ID: MYT3391)
nm
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26W

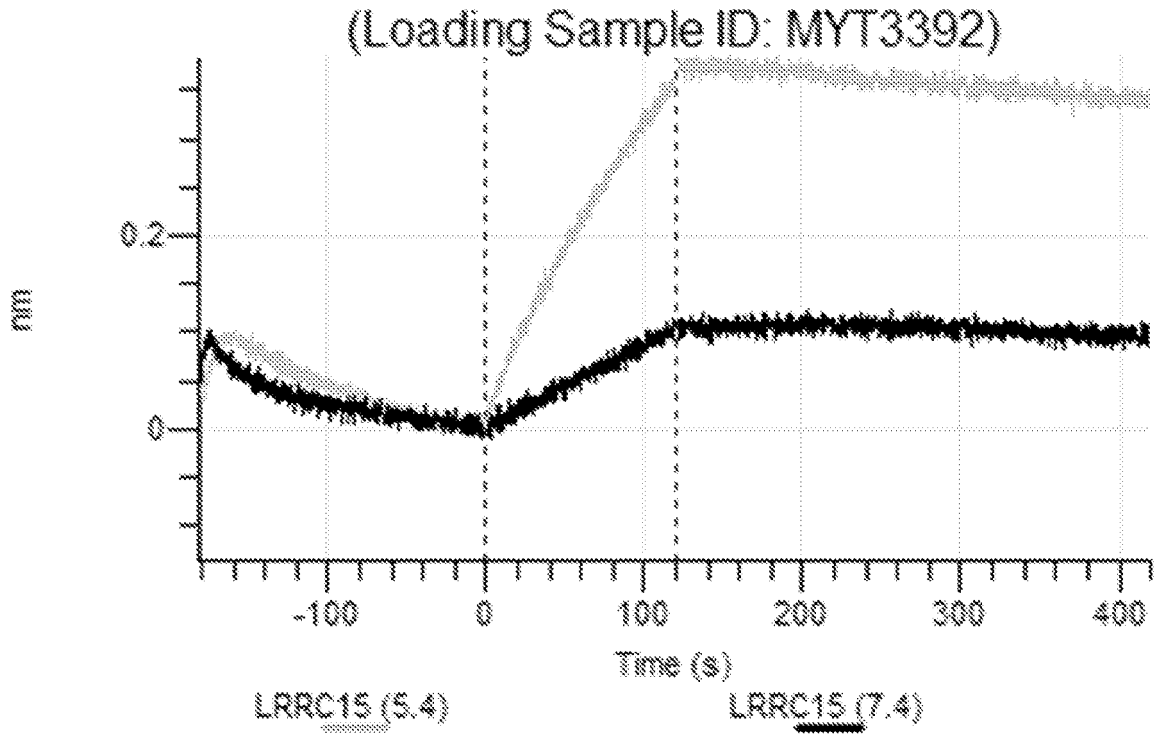

(Loading Sample ID: MYT3392)
nm
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26X

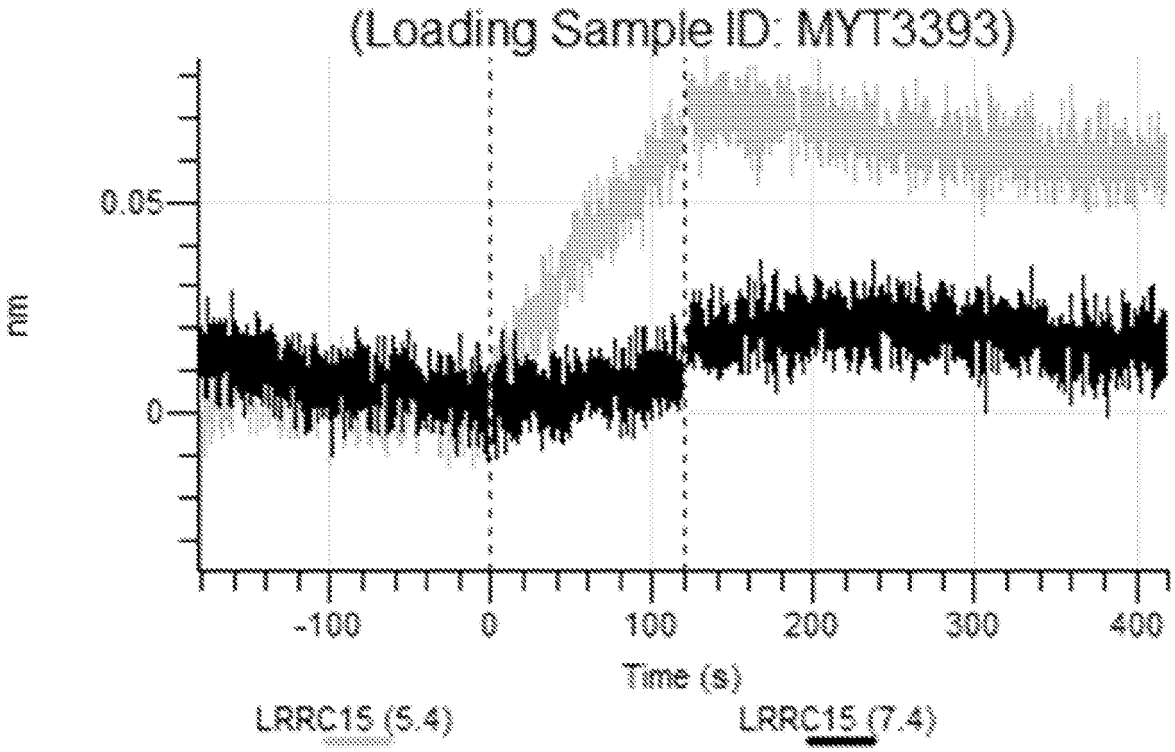

(Loading Sample ID: MYT3393)
nm
0.05
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26Y

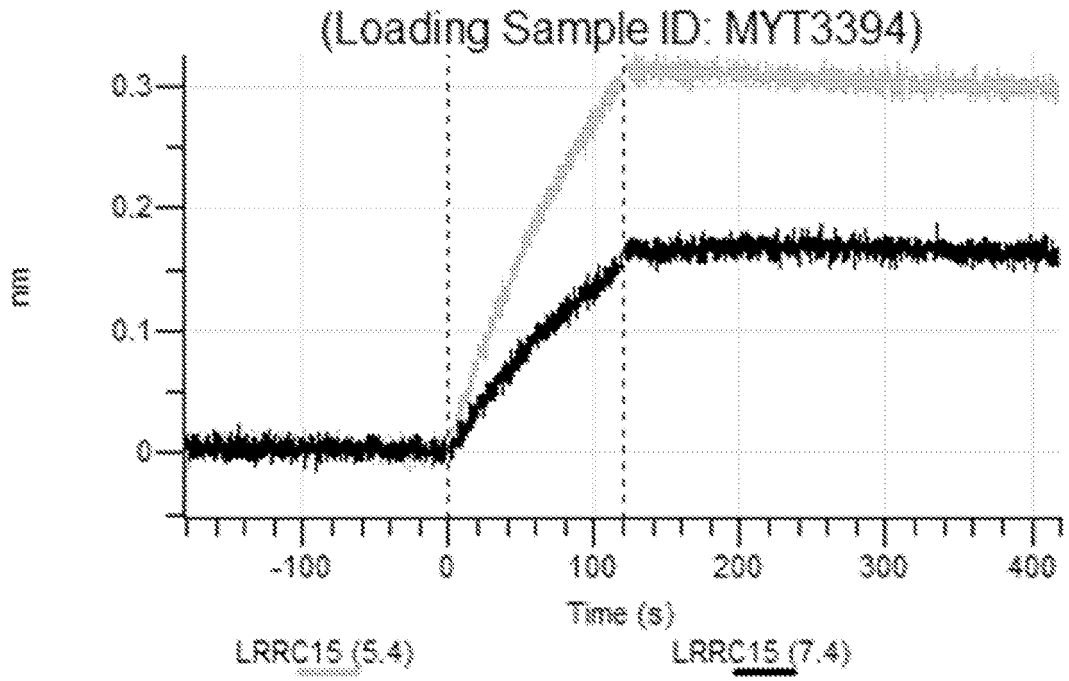

(Loading Sample ID: MYT3394)
nm
0.3
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26Z

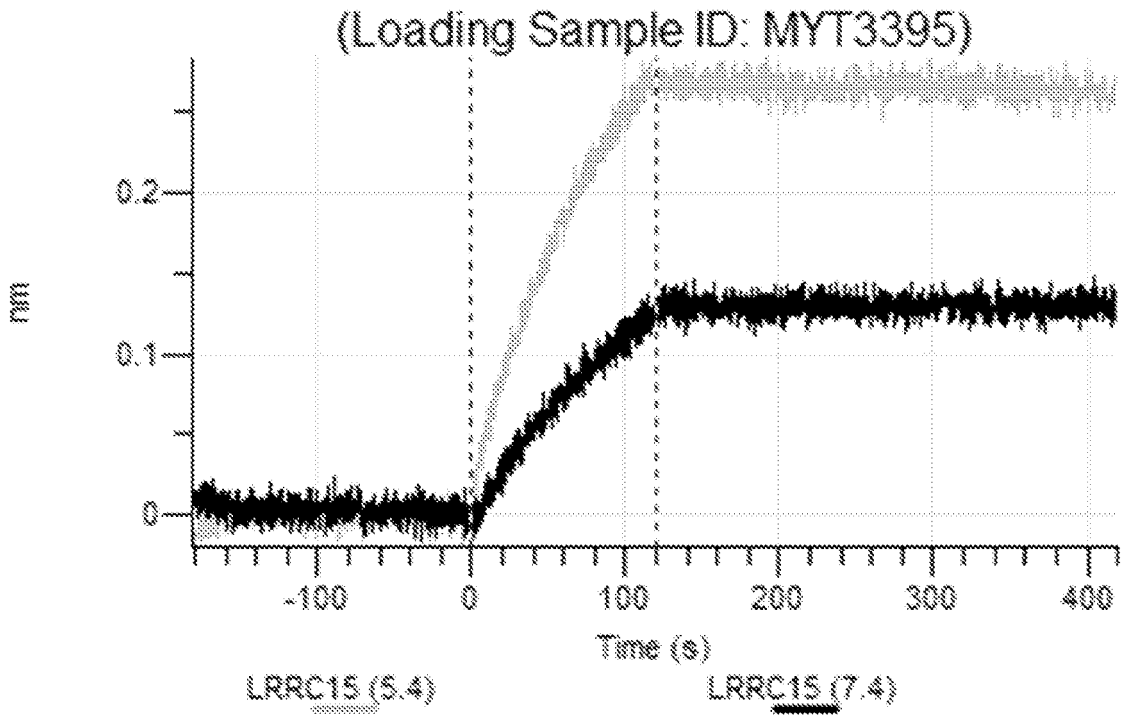

(Loading Sample ID: MYT3395)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26AA

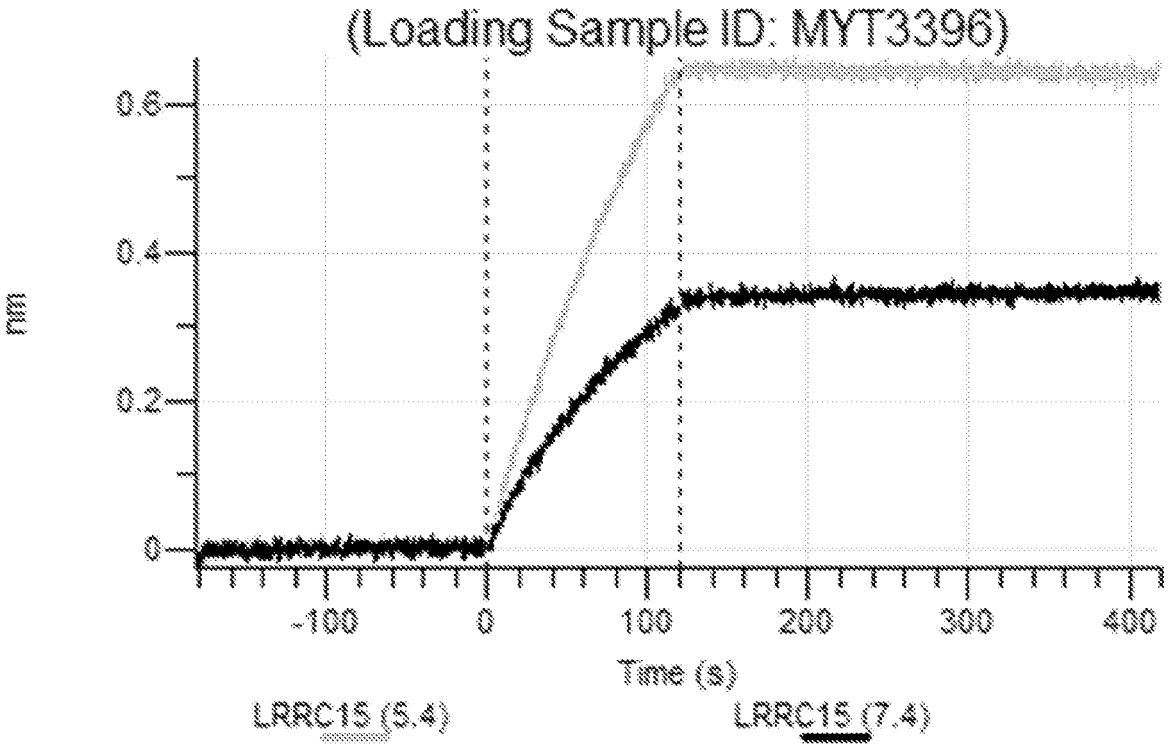

(Loading Sample ID: MYT3396)
nm
0.6
0.4
0.2
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26AB

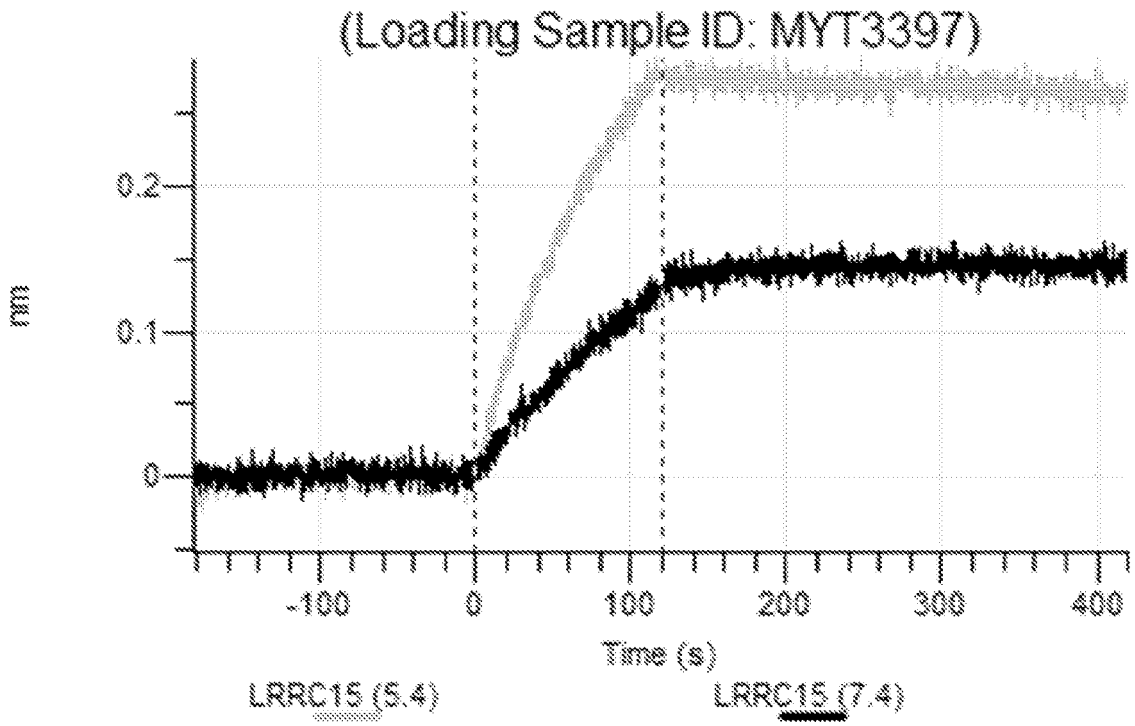

(Loading Sample ID: MYT3397)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26AC

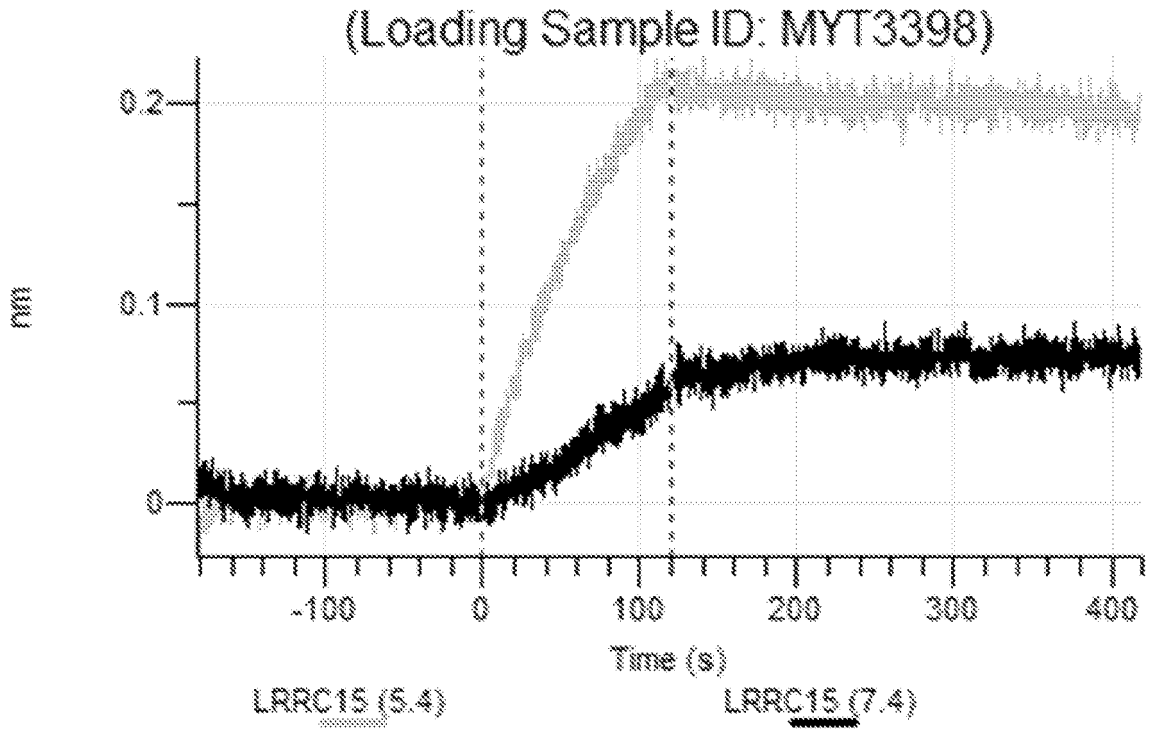

(Loading Sample ID: MYT3398)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 26AD

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
MYT3325 (huAD208.4.1)	178	179	180	181	182	183	184	185
MYT3369	178	228						
MYT3370	178	229						
MYT3371	178	230						
MYT3372	178	231						
MYT3373	178	232						
MYT3374	178	233						
MYT3375	178	234						
MYT3376	178	235						
MYT3377	178	236						
MYT3378	178	237						
MYT3379	178	238						
MYT3380	178	239						
MYT3381	178	240						
MYT3382	178	241						
MYT3383	178	242						
MYT3384	178	243						
MYT3385	178	244						
MYT3386	178	245						
MYT3387	178	246						
MYT3388	178	247						
MYT3389	178	248						
MYT3390	178	249						
MYT3391	178	250						
MYT3392	178	251						
MYT3393	178	252						
MYT3394	178	253						
MYT3395	178	254						
MYT3396	178	255						
MYT3397	178	256						
MYT3398	178	257						

FIG. 27

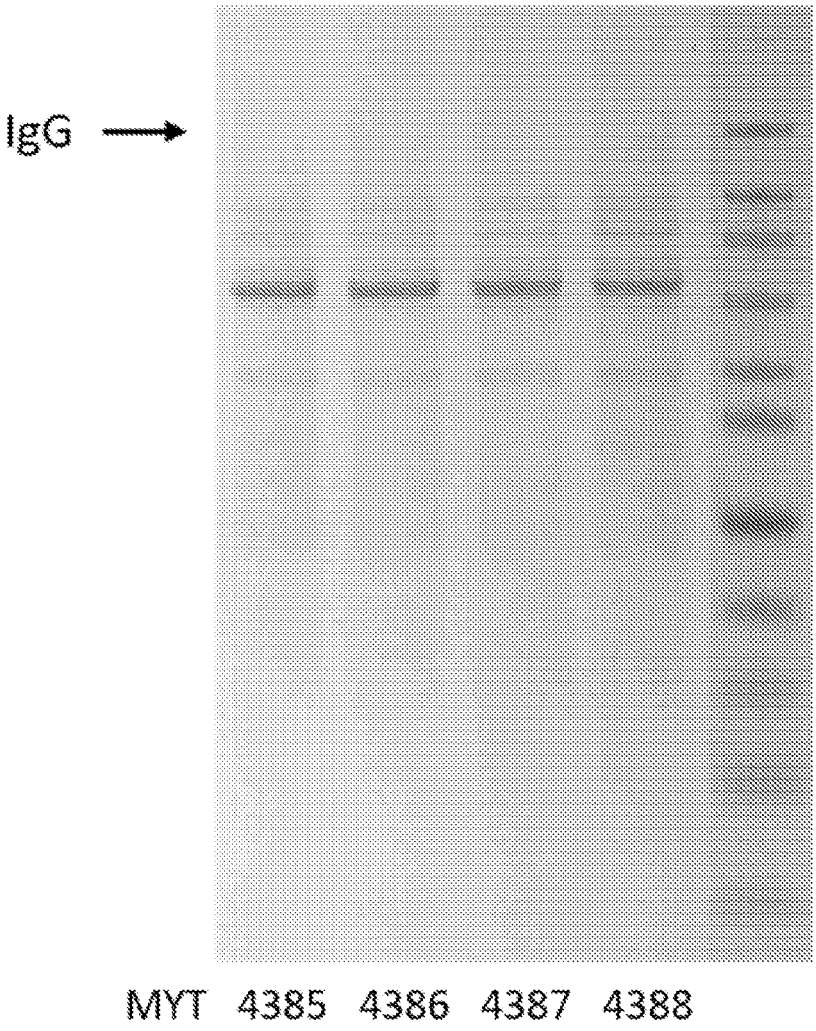


FIG. 28

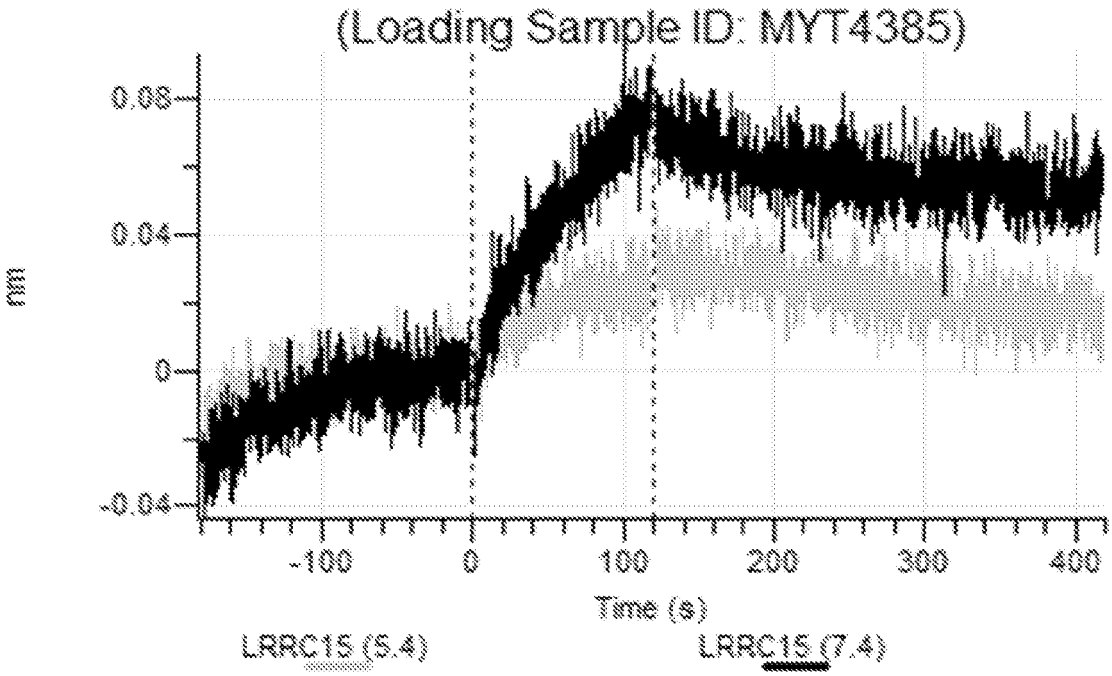

(Loading Sample ID: MYT4385)
0.08
0.04
0
-0.04
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 29A

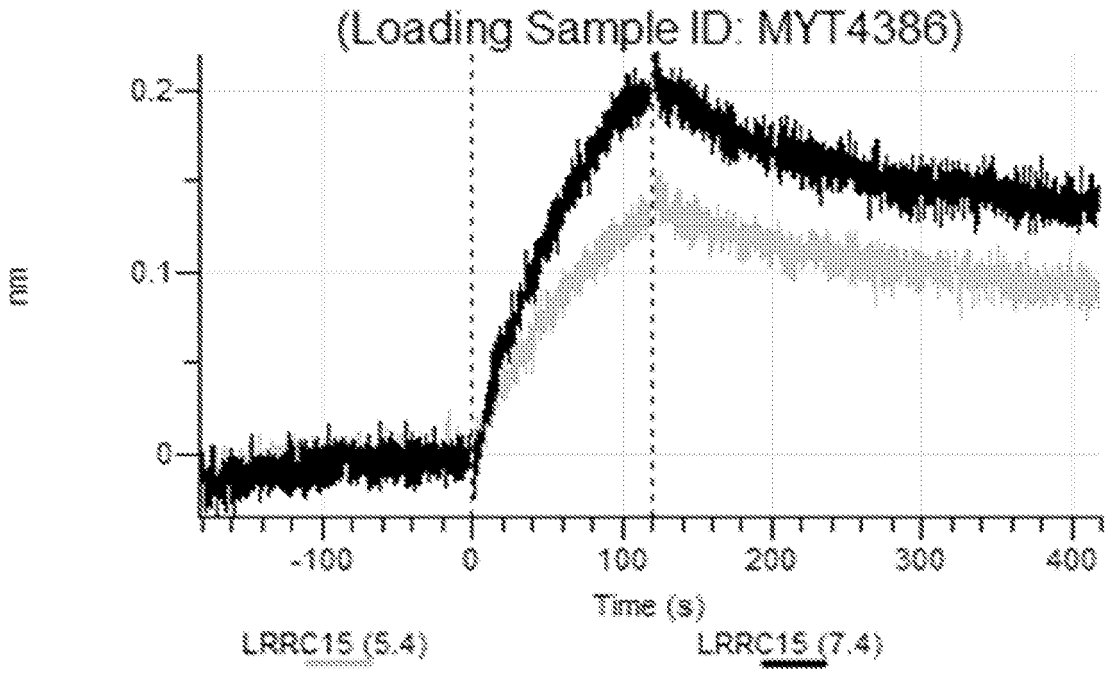

(Loading Sample ID: MYT4386)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 29B

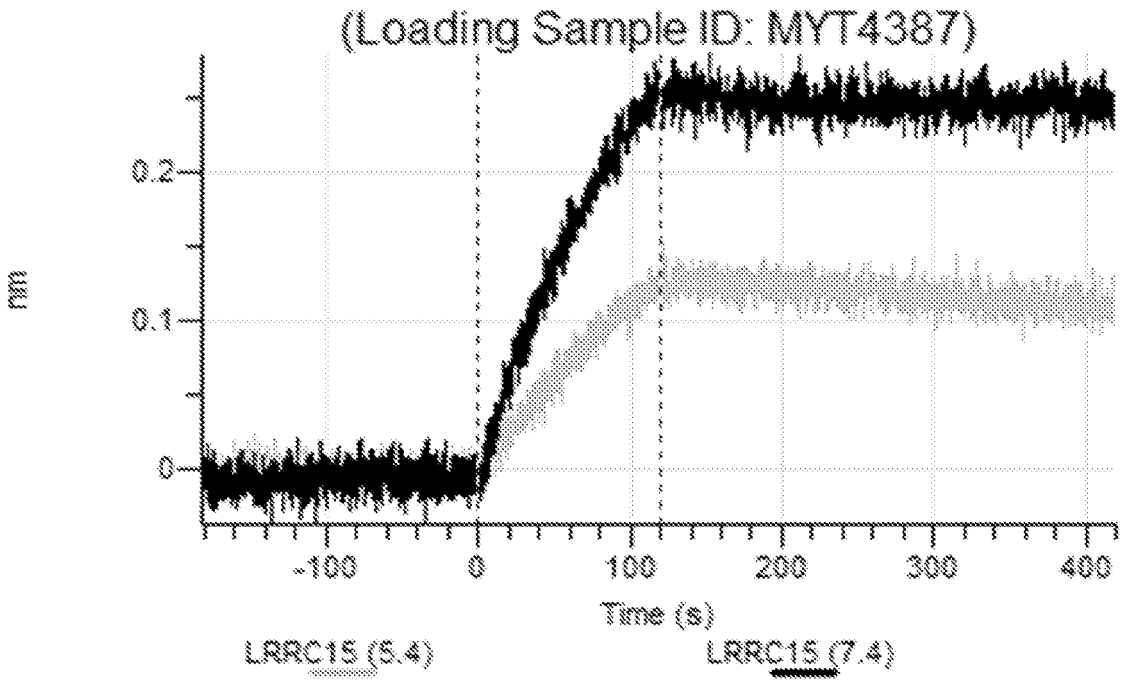

(Loading Sample ID: MYT4387)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 29C

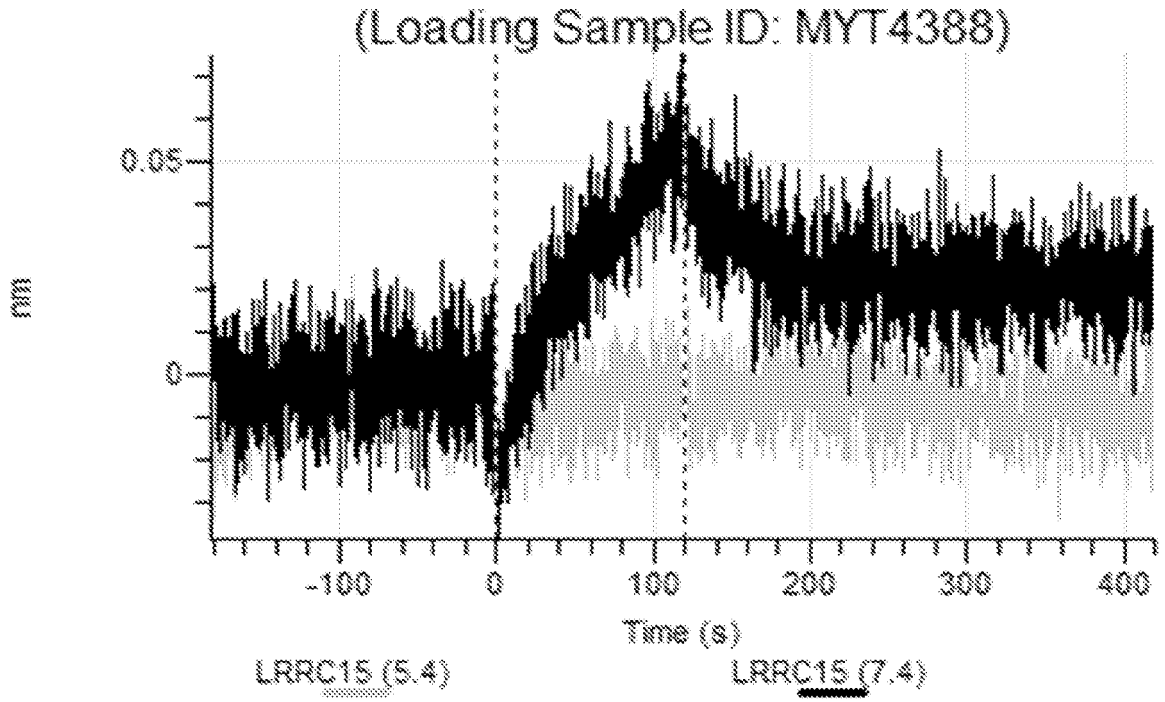

(Loading Sample ID: MYT4388)
0.05
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 29D

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
MYT3325 (huAD208.4.1)	178	179	180	181	182	183	184	185
MYT4385	258	179						
MYT4386	259	179						
MYT4387	260	179						
MYT4388	261	179						

FIG. 30

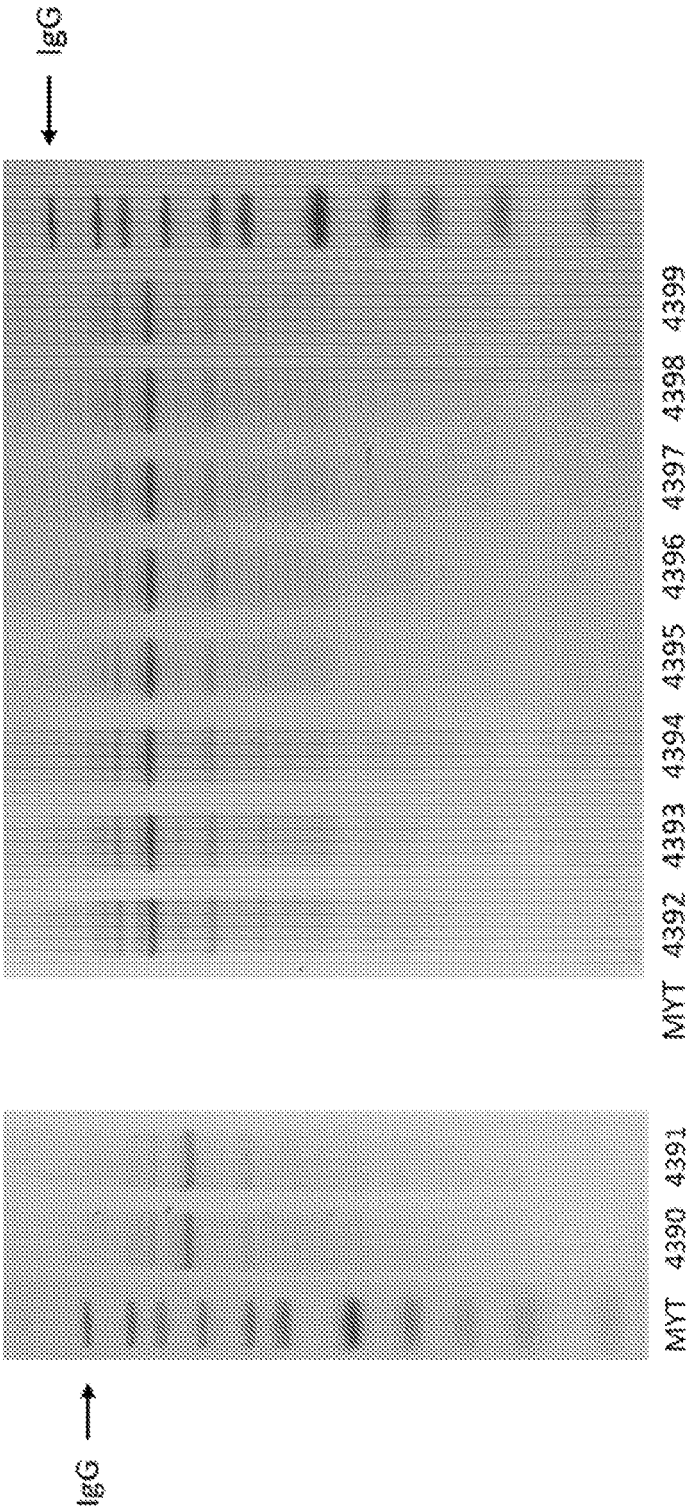

IgG
MYT 4392 4393 4394 4395 4396 4397 4398 4399
MYT 4390 4391
IgG

FIG. 31

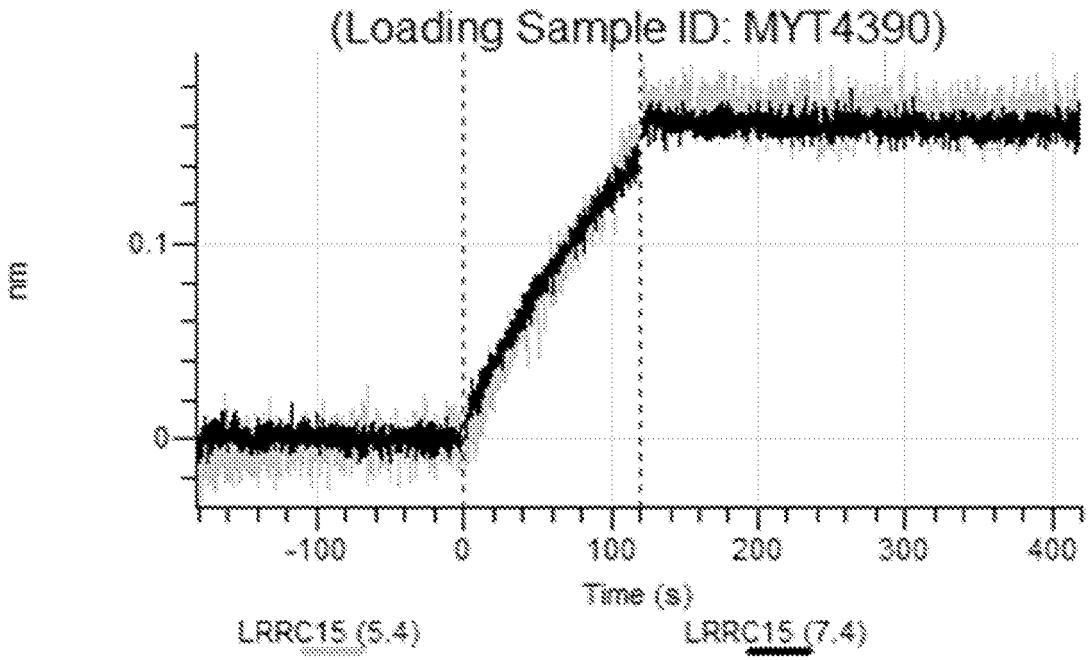

(Loading Sample ID: MYT4390)
nm
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 32A

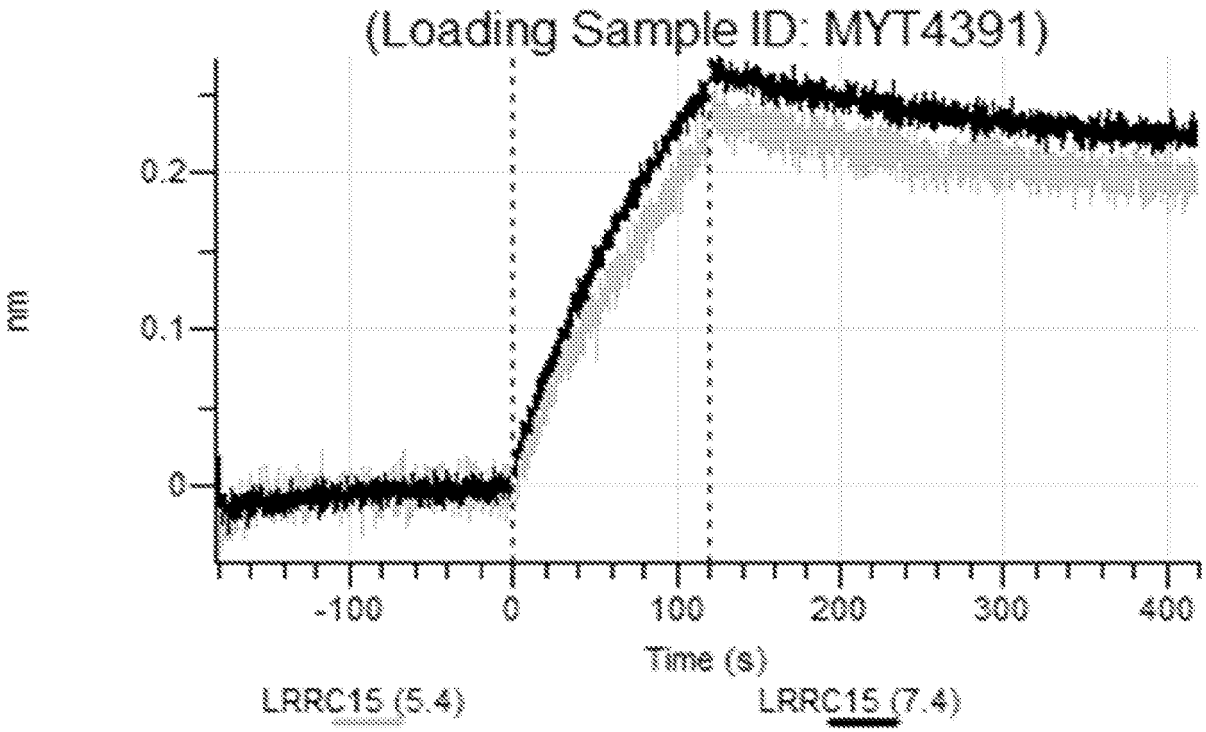

(Loading Sample ID: MYT4391)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 32B

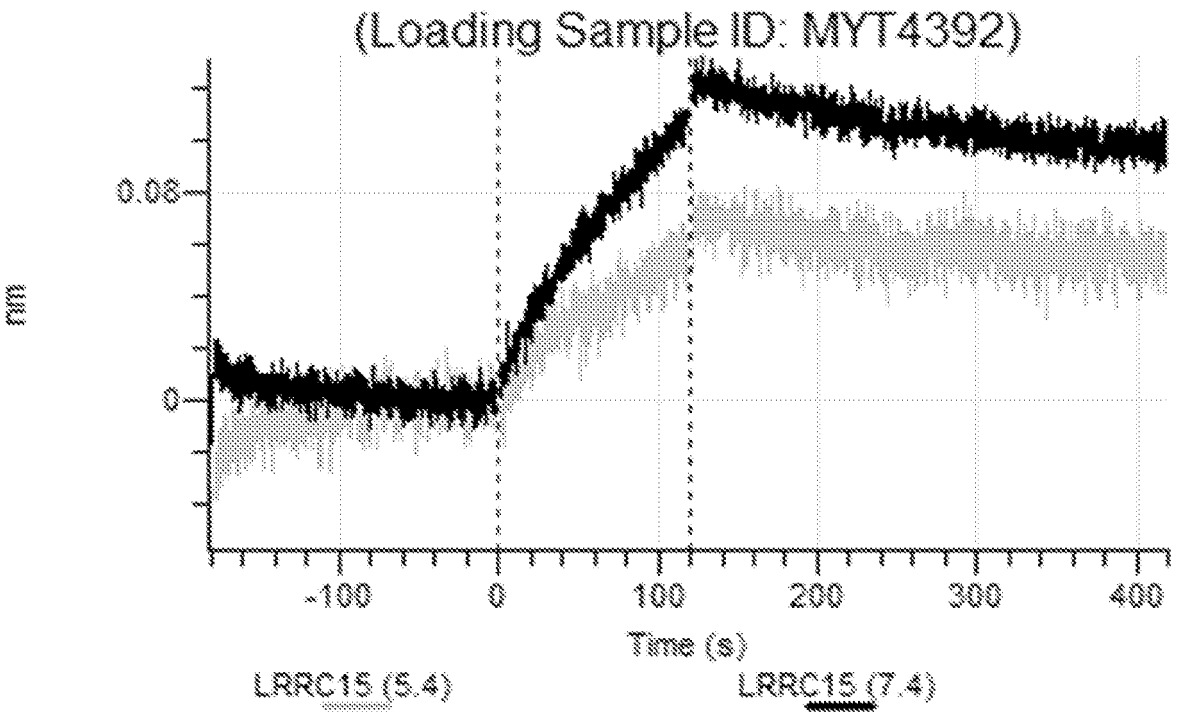

(Loading Sample ID: MYT4392)
nm
0.08
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 32C

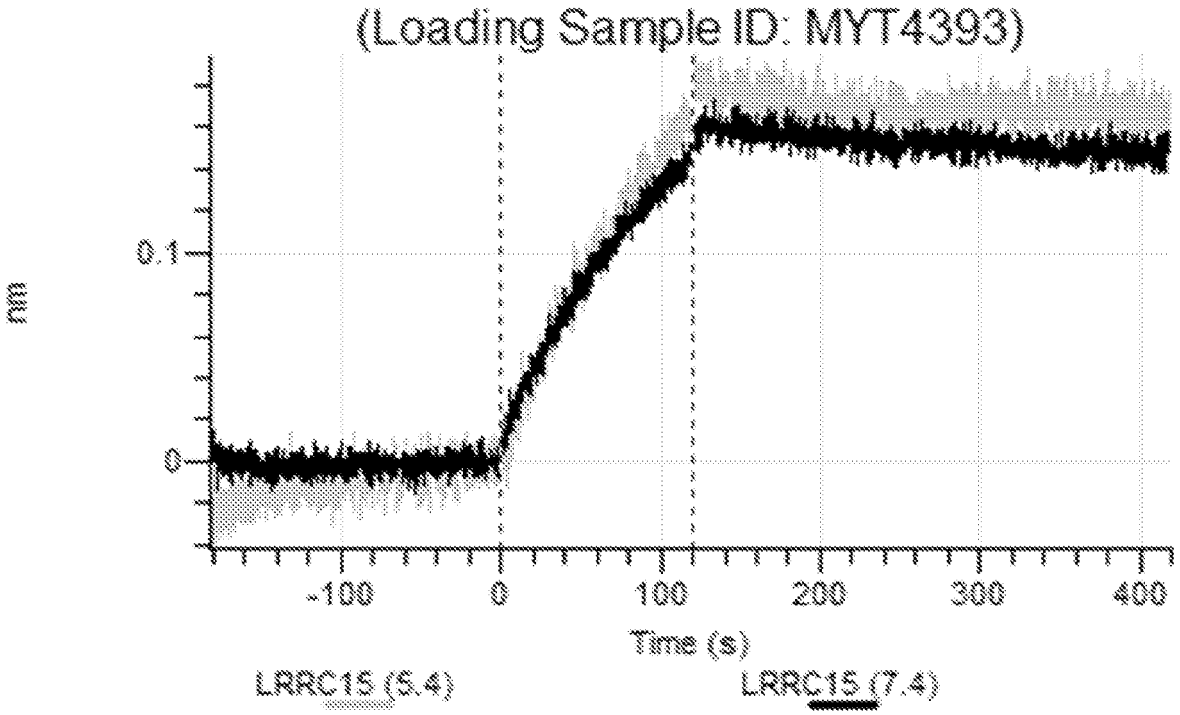

(Loading Sample ID: MYT4393)
nm
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 32D

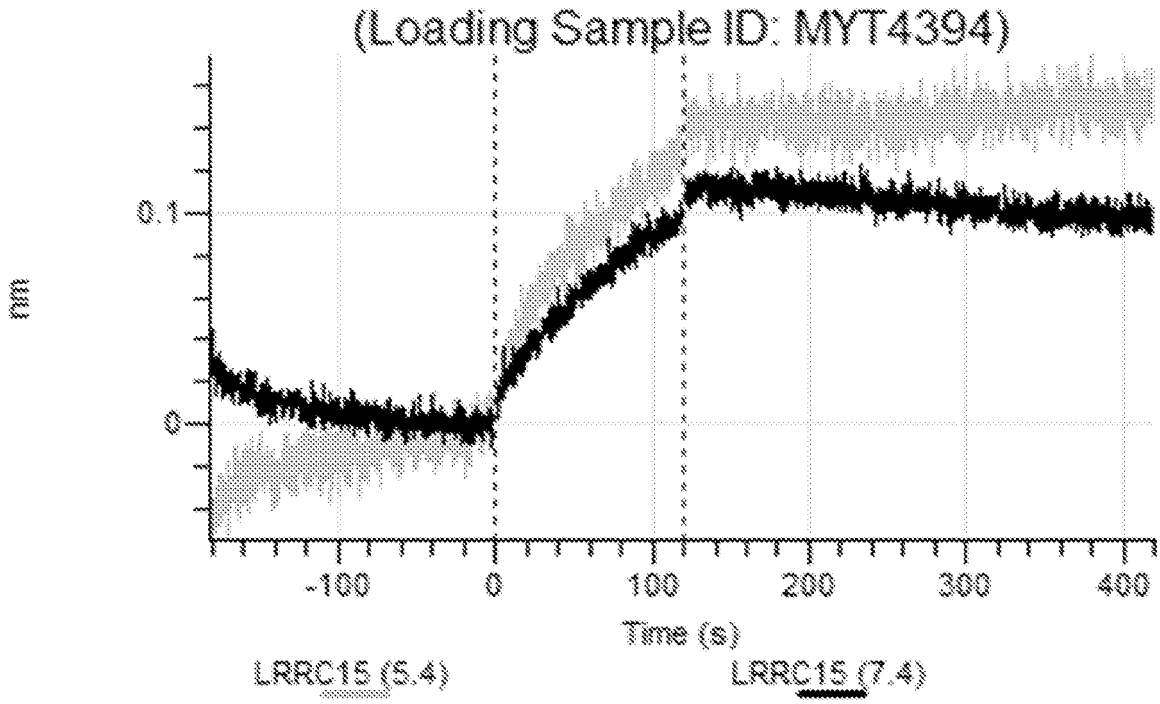

(Loading Sample ID: MYT4394)
nm
0.1
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 32E

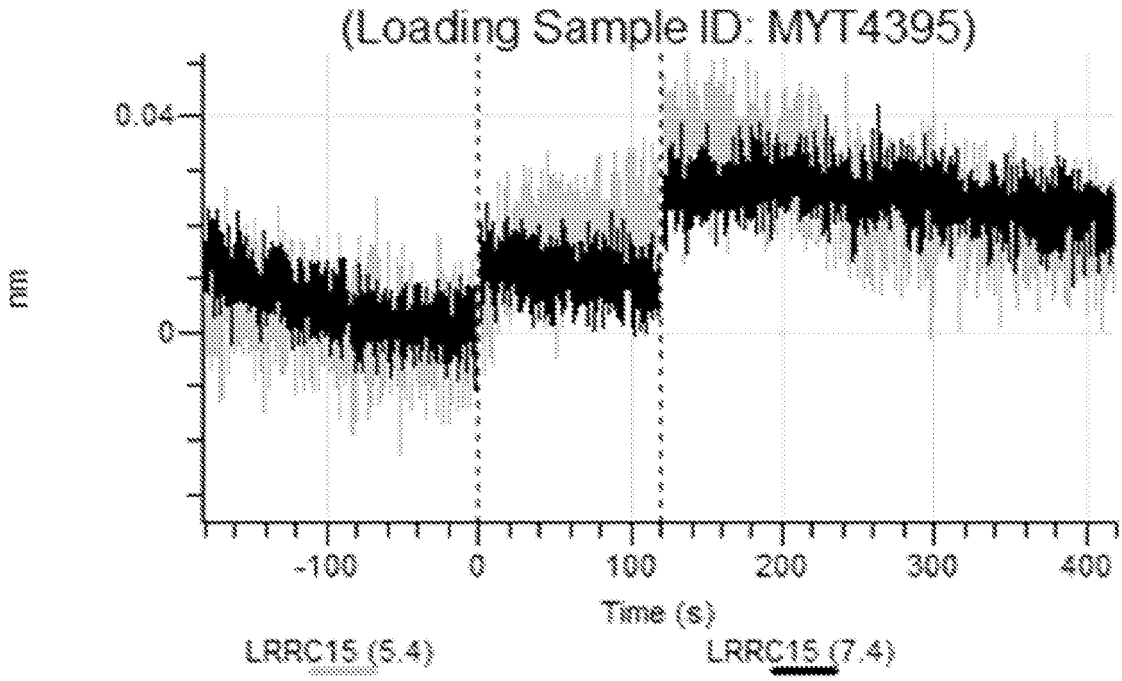

(Loading Sample ID: MYT4395)
0.04
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 32F

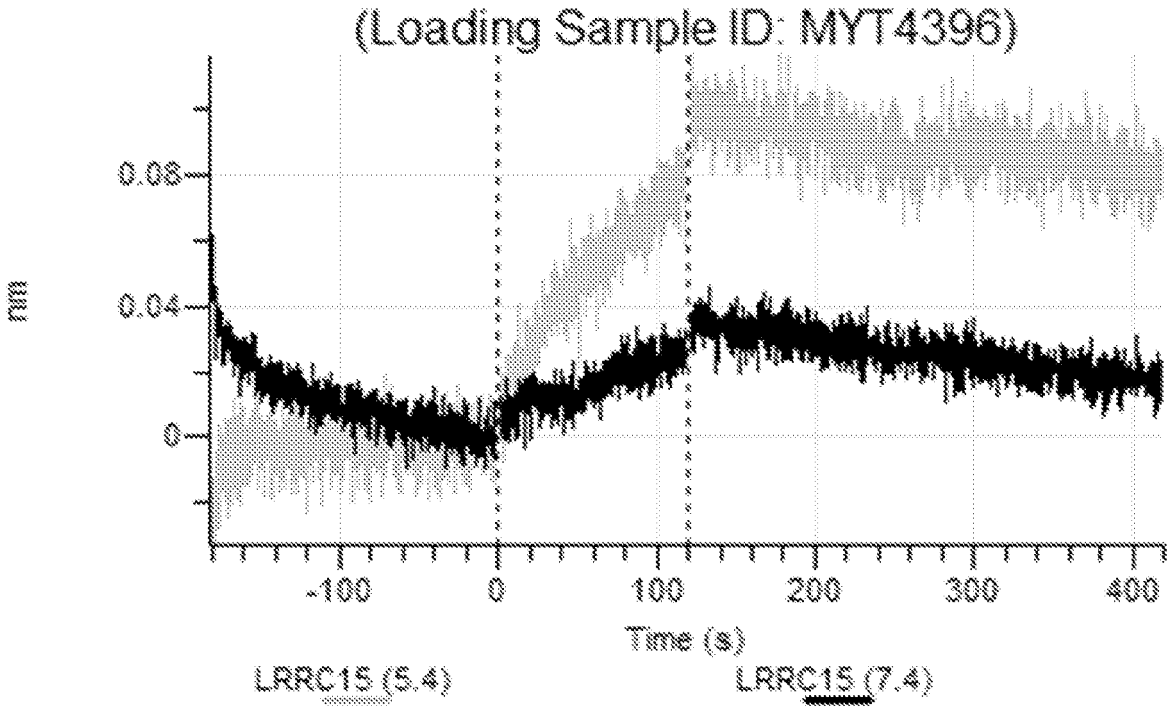

(Loading Sample ID: MYT4396)
nm
0.08
0.04
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 32G

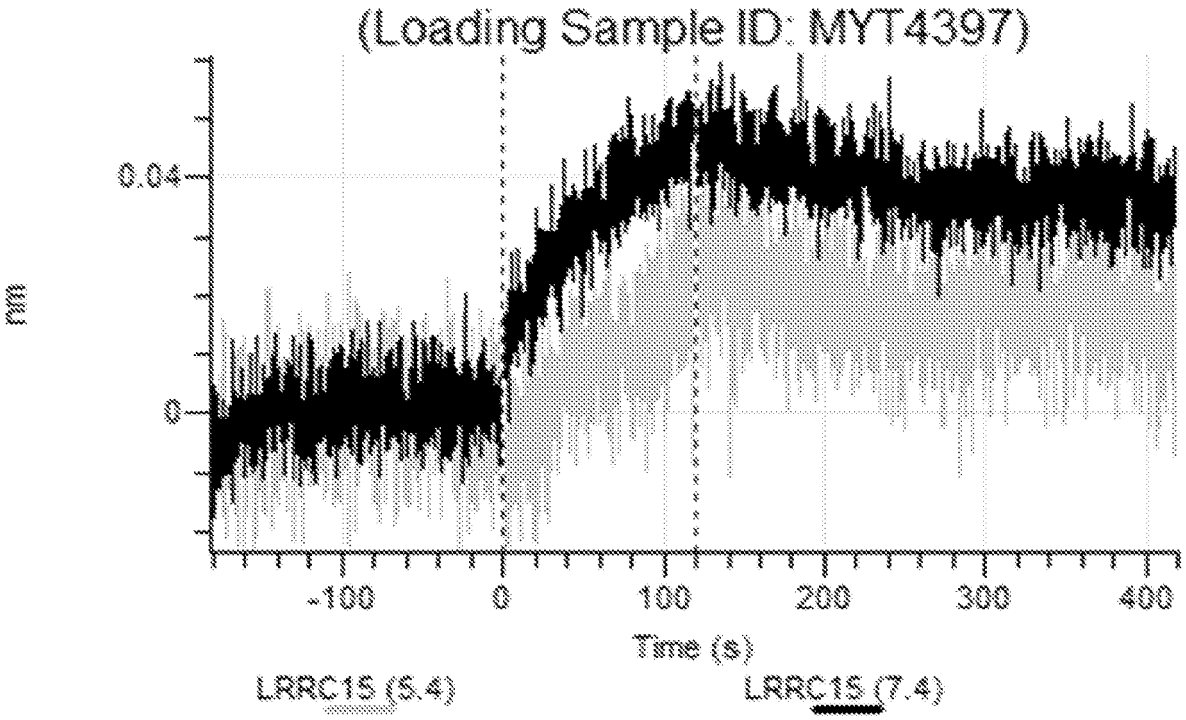

(Loading Sample ID: MYT4397)
nm
0.04
0
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 32H

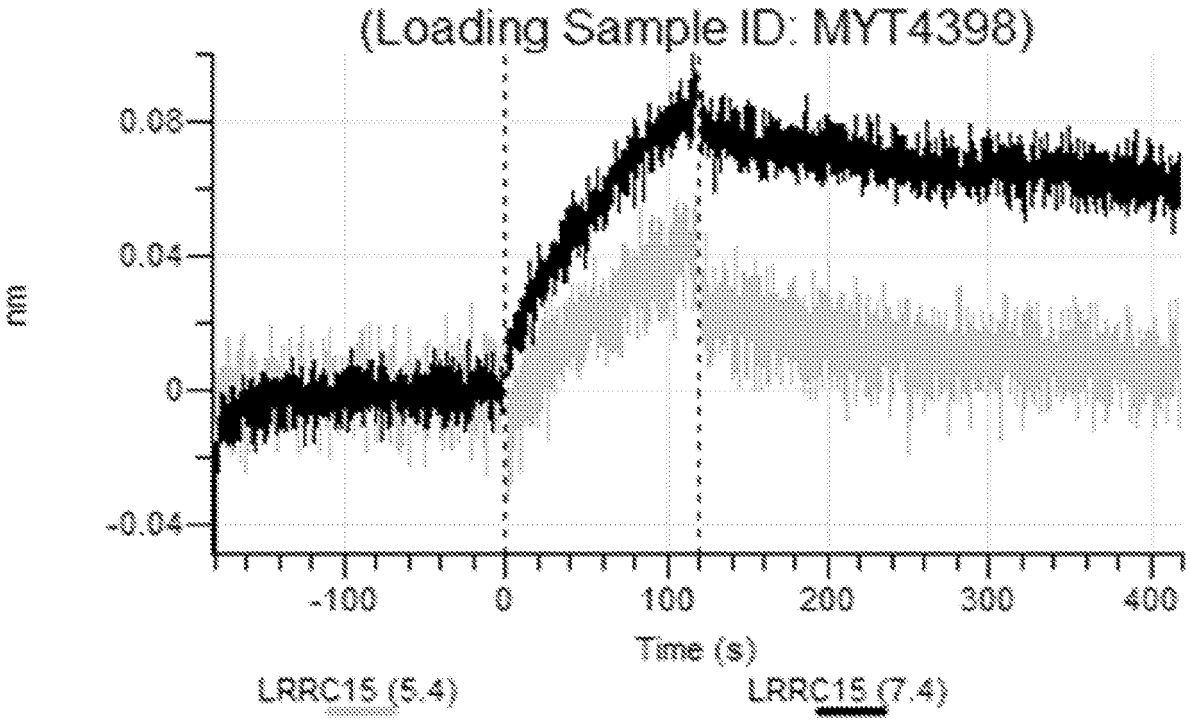

(Loading Sample ID: MYT4398)
nm
0.08
0.04
0
-0.04
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 32I

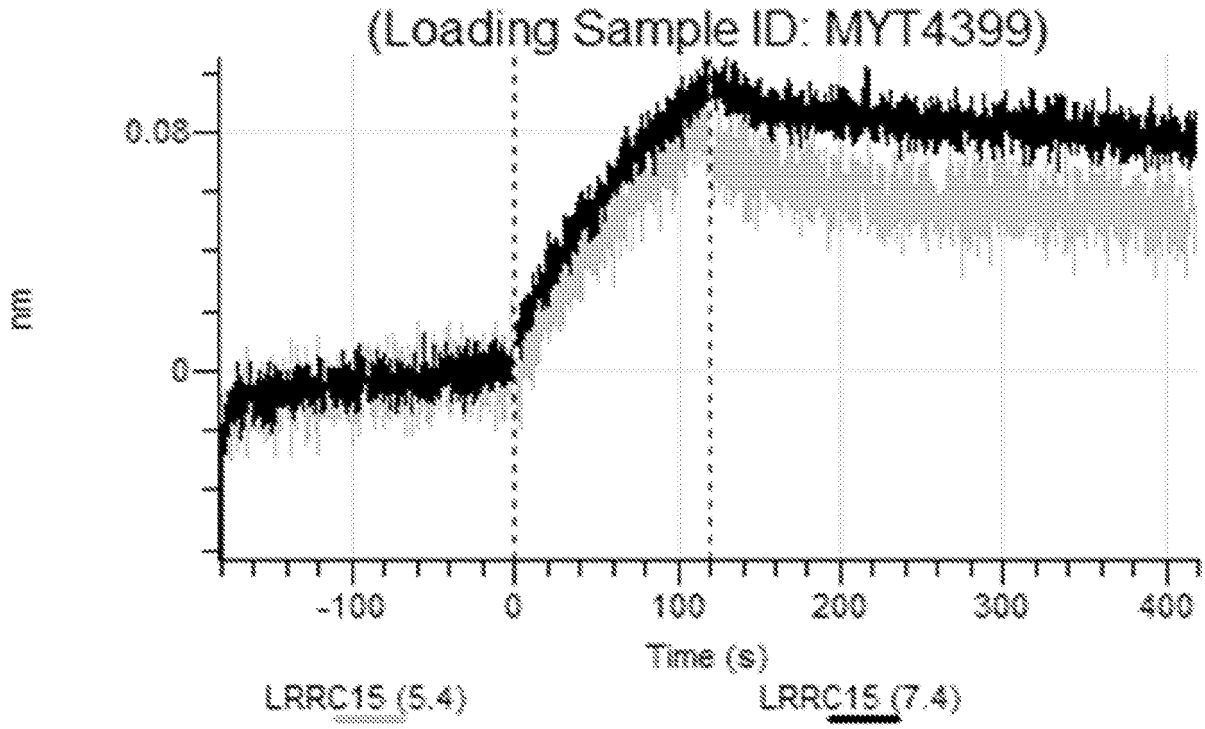

(Loading Sample ID: MYT4399)
0.08
0
nm
-100
0
100
200
300
400
Time (s)
LRRC15 (5.4)
LRRC15 (7.4)

FIG. 32J

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	
MYT3325 (huAD208.4.1)	178	179	180	181	182	183	184	
MYT4390	178	262						
MYT4391	178	263						
MYT4392	178	264						
MYT4393	178	265						
MYT4394	178	266						
MYT4395	178	267						
MYT4396	178	268						
MYT4397	178	269						
MYT4398	178	270						
MYT4399	178	271						

FIG. 33

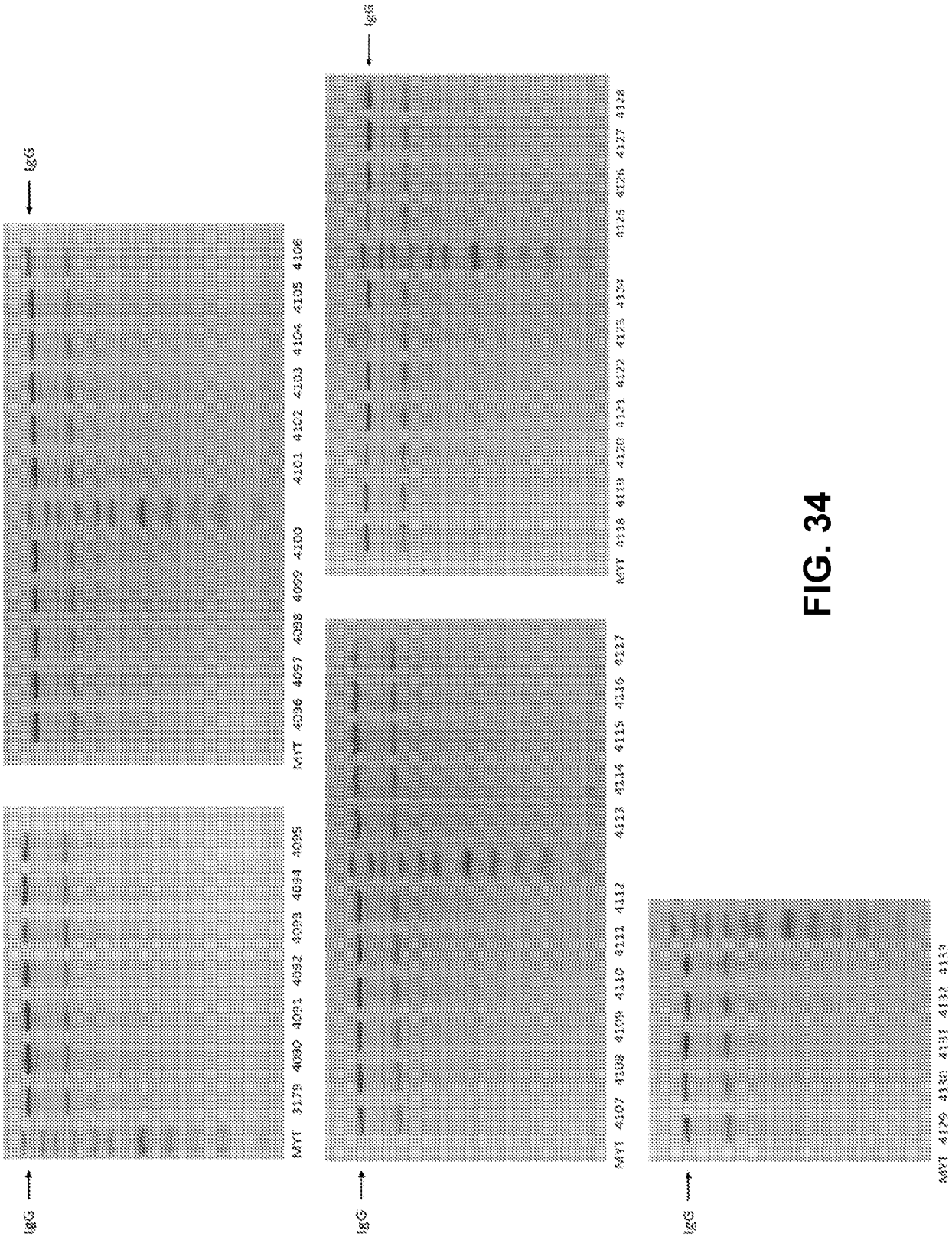


FIG. 34

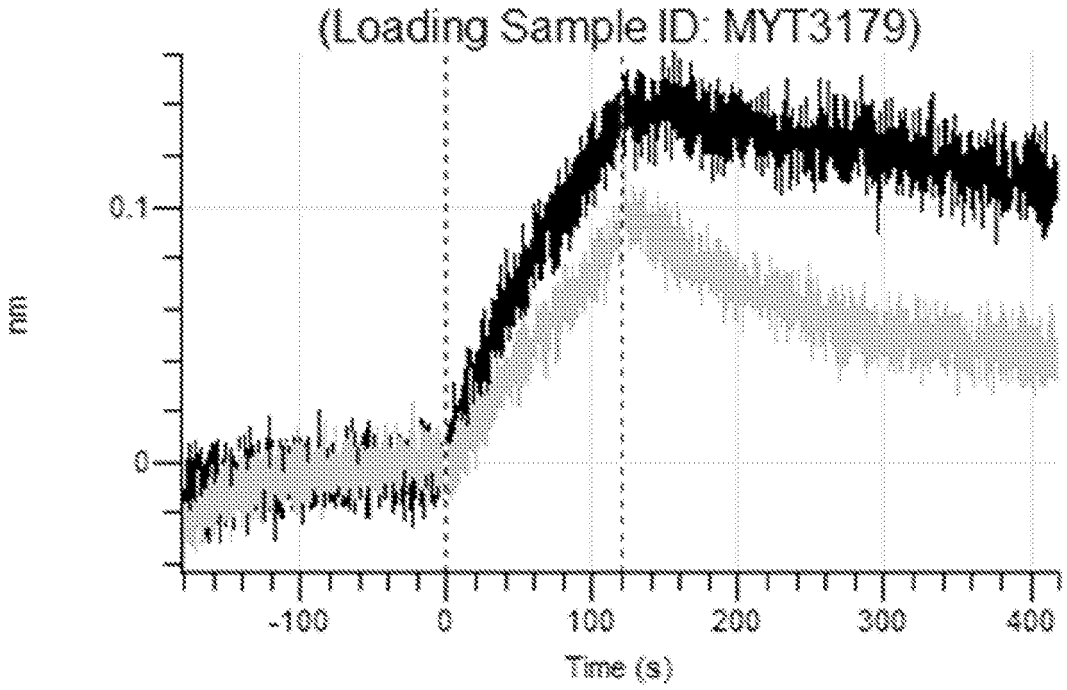


FIG. 35A

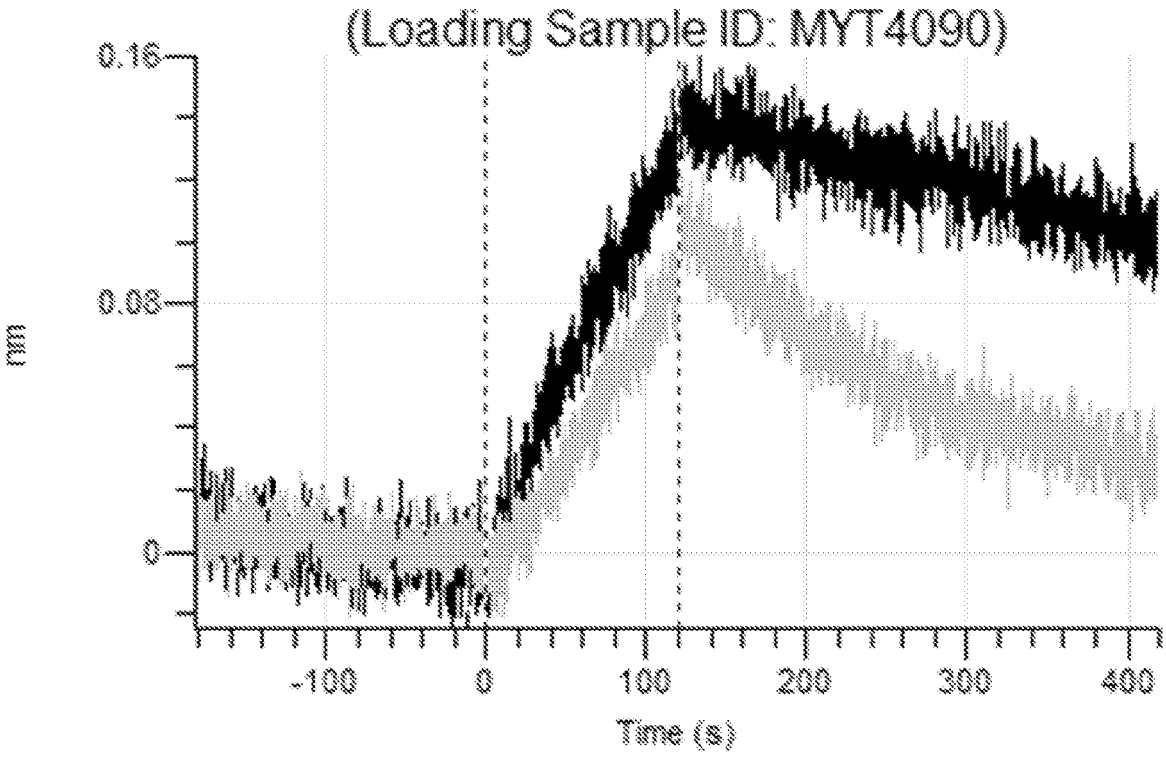

(Loading Sample ID: MYT4090)
0.16
0.08
0
nm
-100
0
100
200
300
400
Time (s)

FIG. 35B

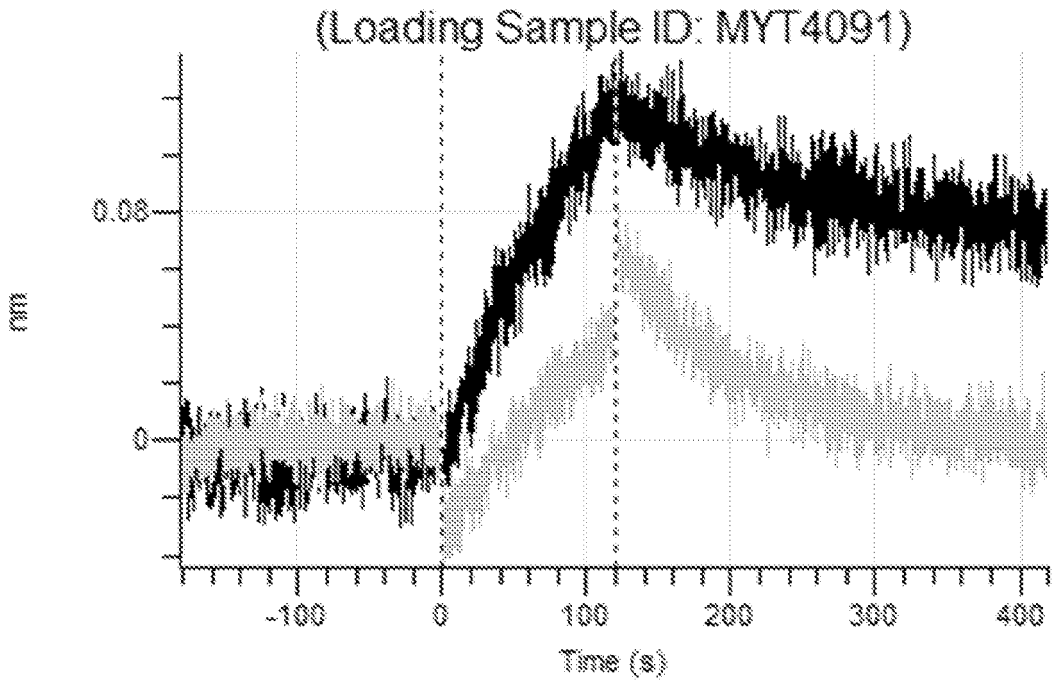


FIG. 35C

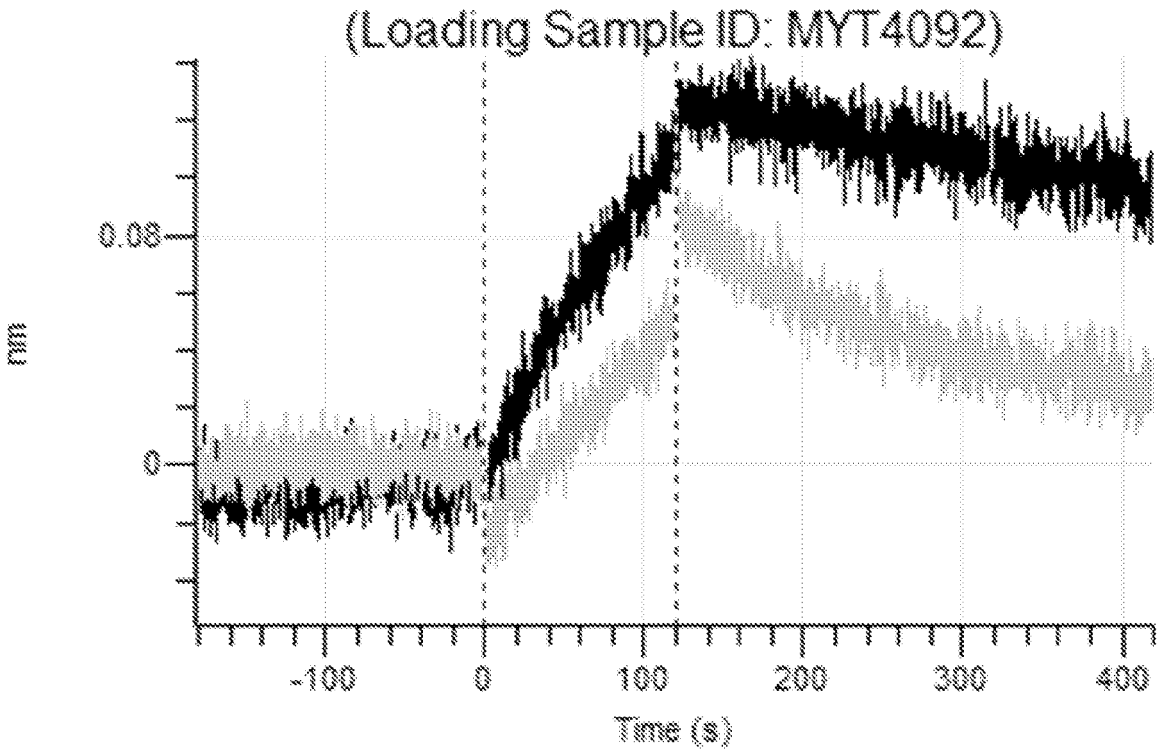


FIG. 35D

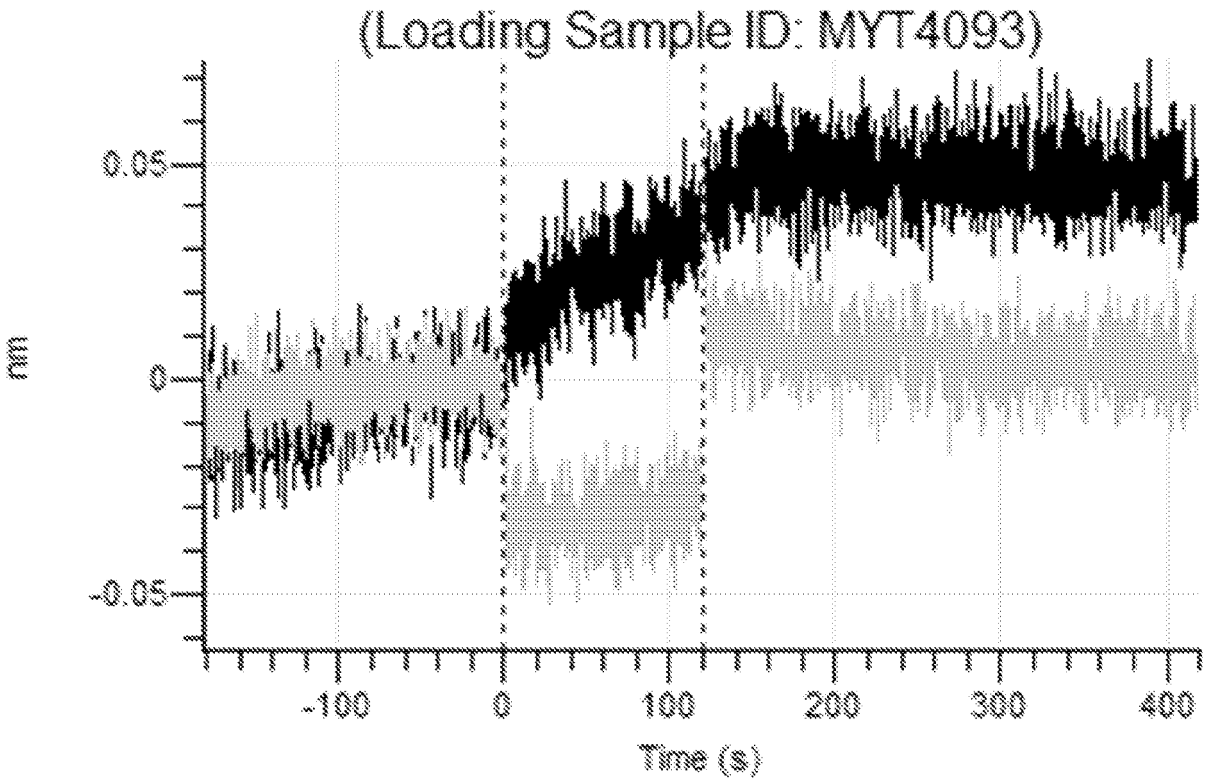

(Loading Sample ID: MYT4093)
0.05
0
-0.05
nm
-100
0
100
200
300
400
Time (s)

FIG. 35E

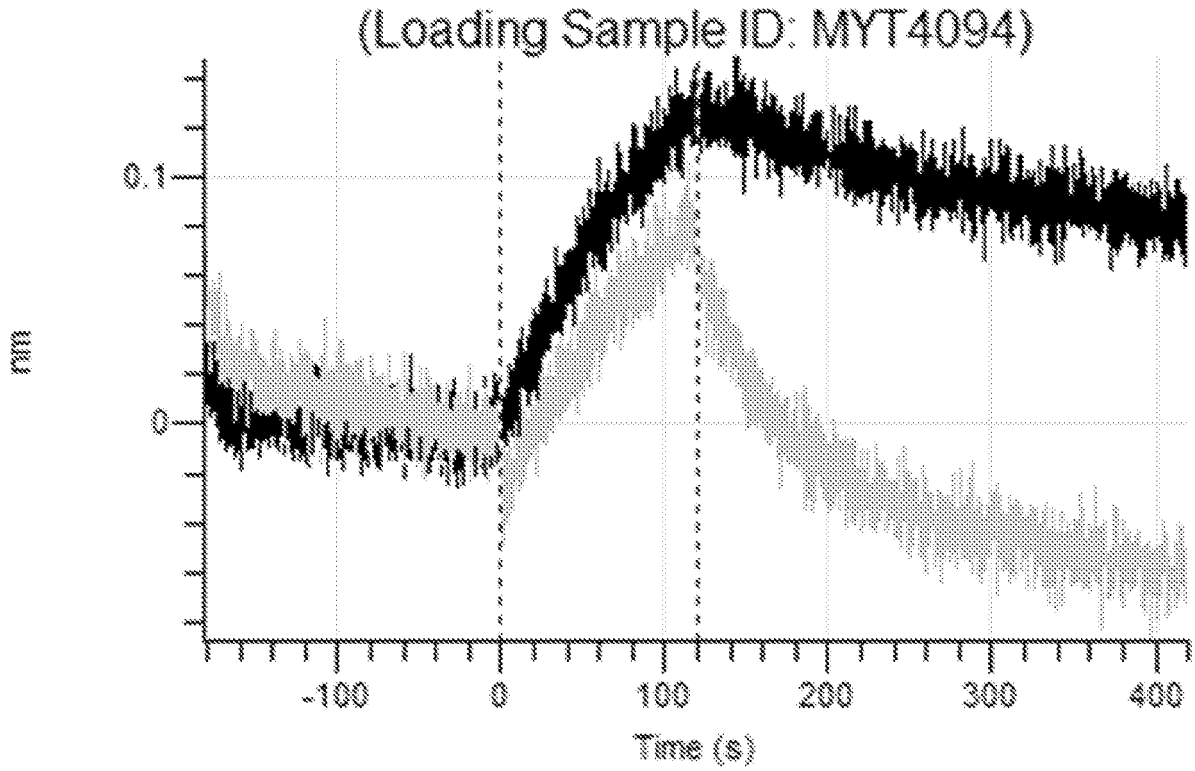


FIG. 35F

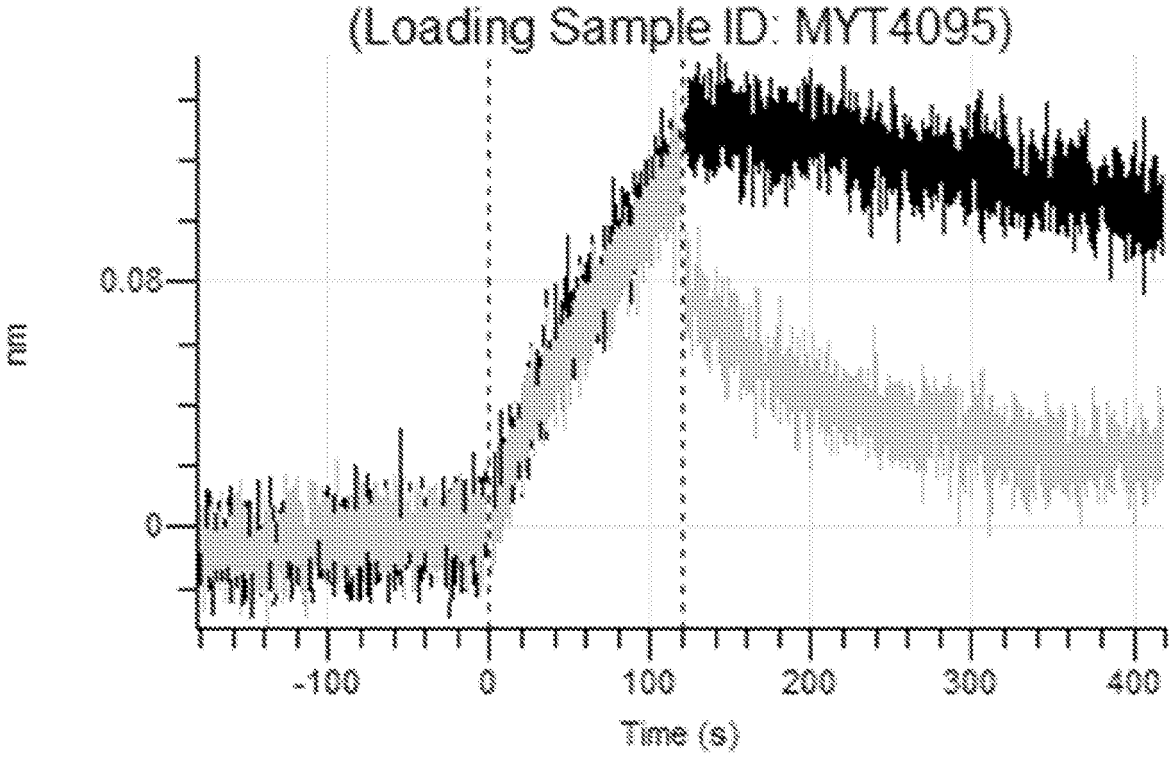


FIG. 35G

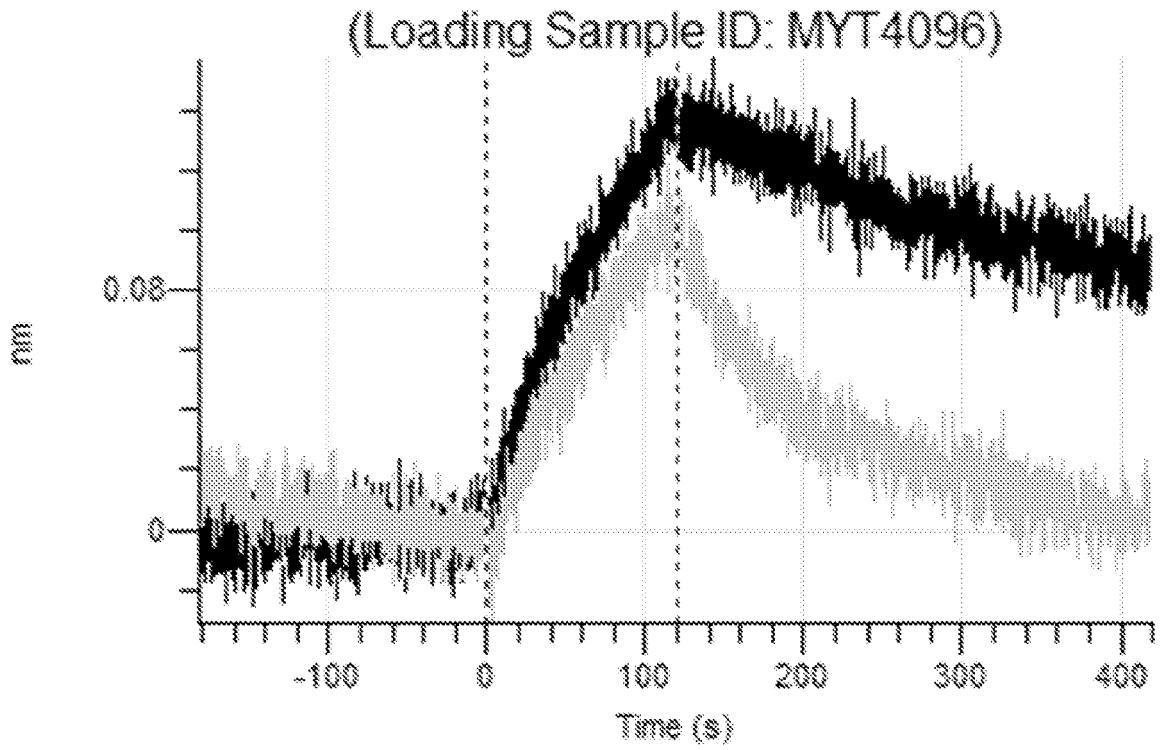


FIG. 35H

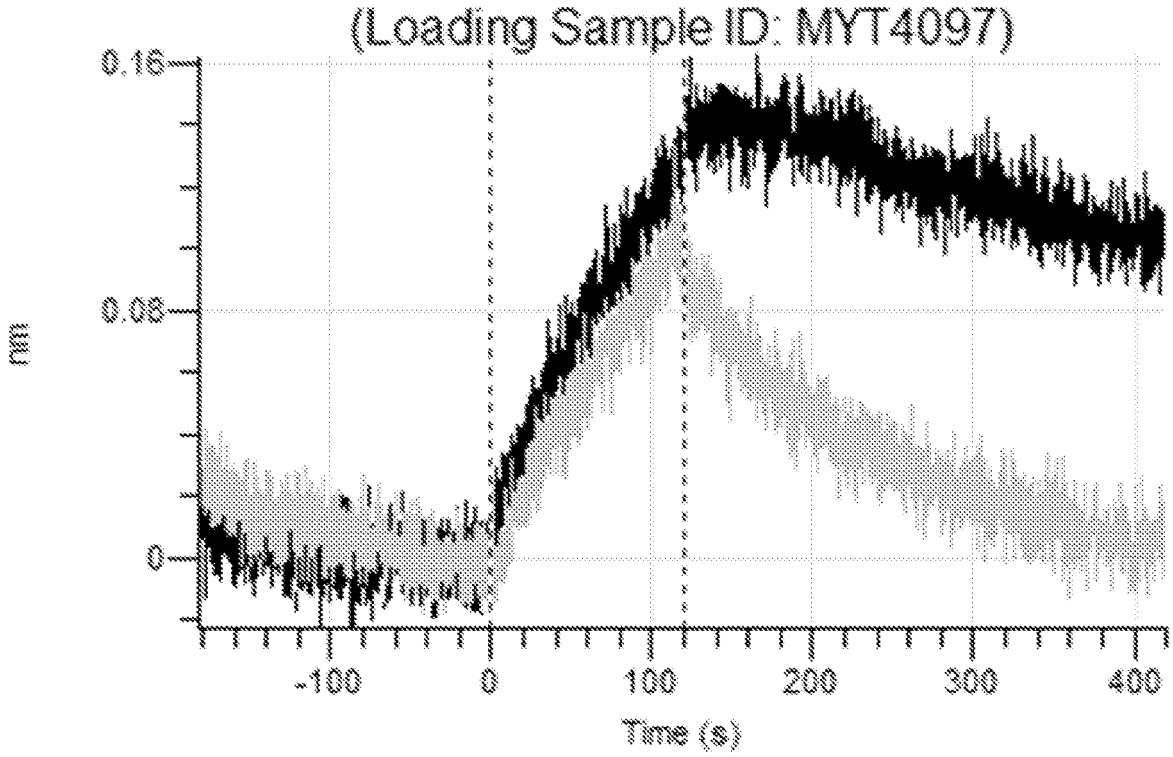

(Loading Sample ID: MYT4097)
0.16
0.08
0
nm
-100
0
100
200
300
400
Time (s)

FIG. 35I

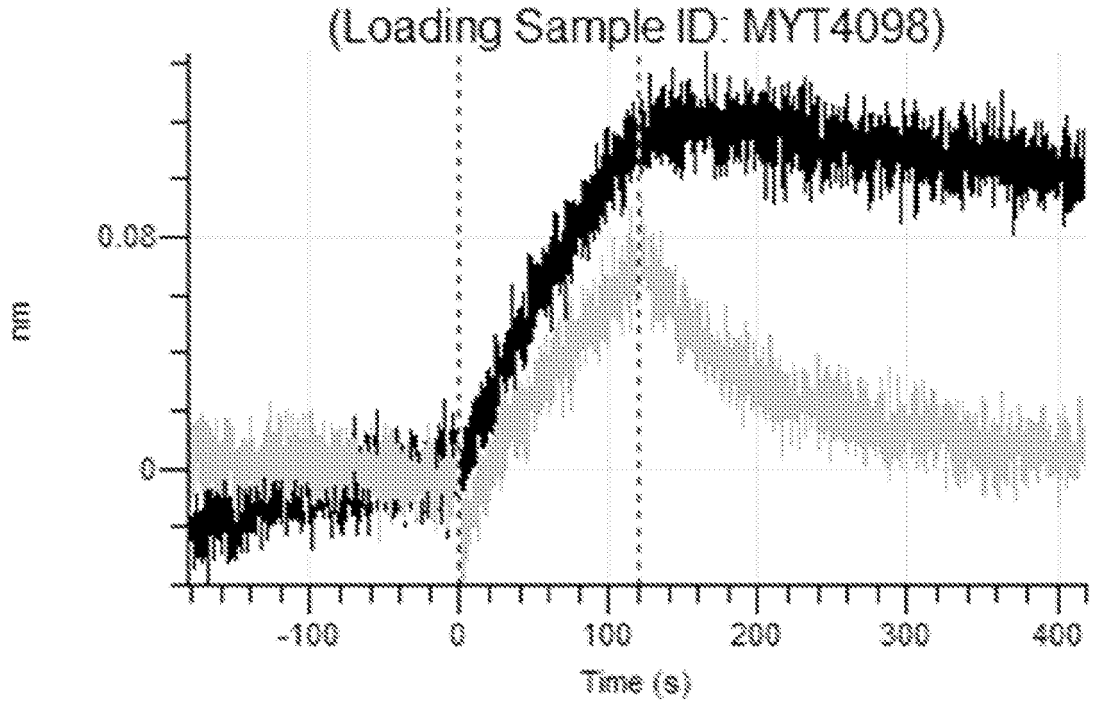


FIG. 35J

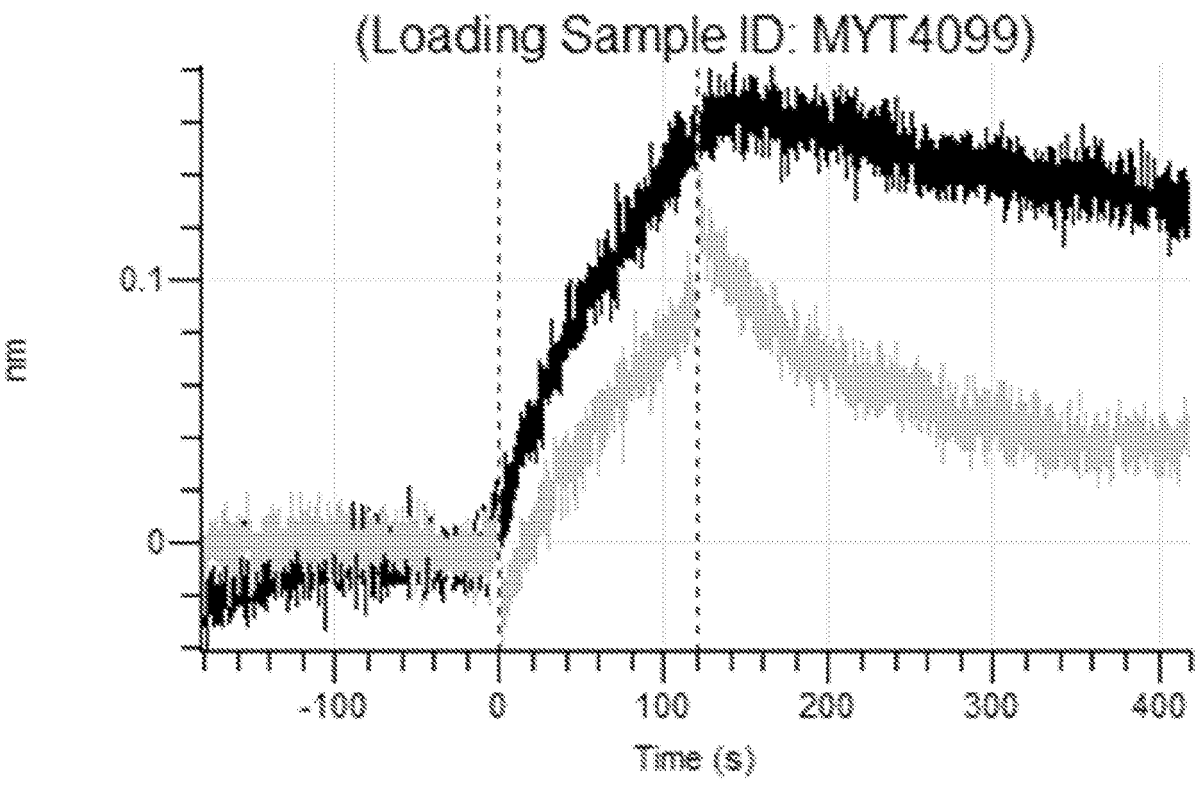


FIG. 35K

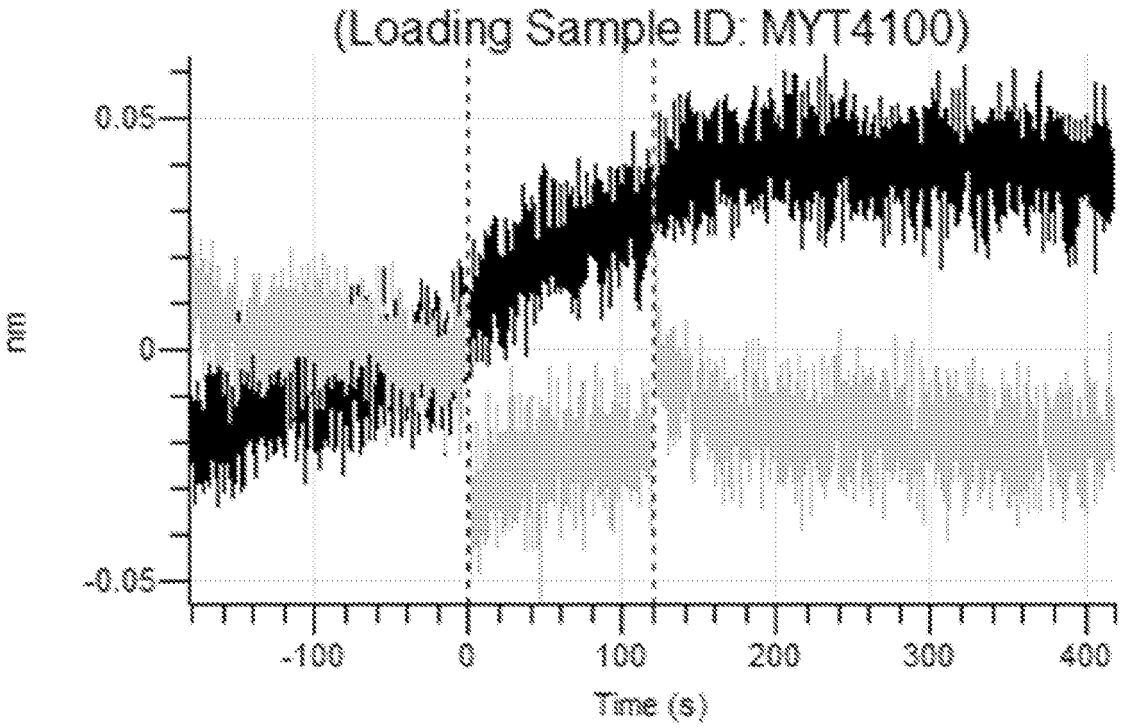

(Loading Sample ID: MYT4100)
nm
0.05
0
-0.05
-100
0
100
200
300
400
Time (s)

FIG. 35L

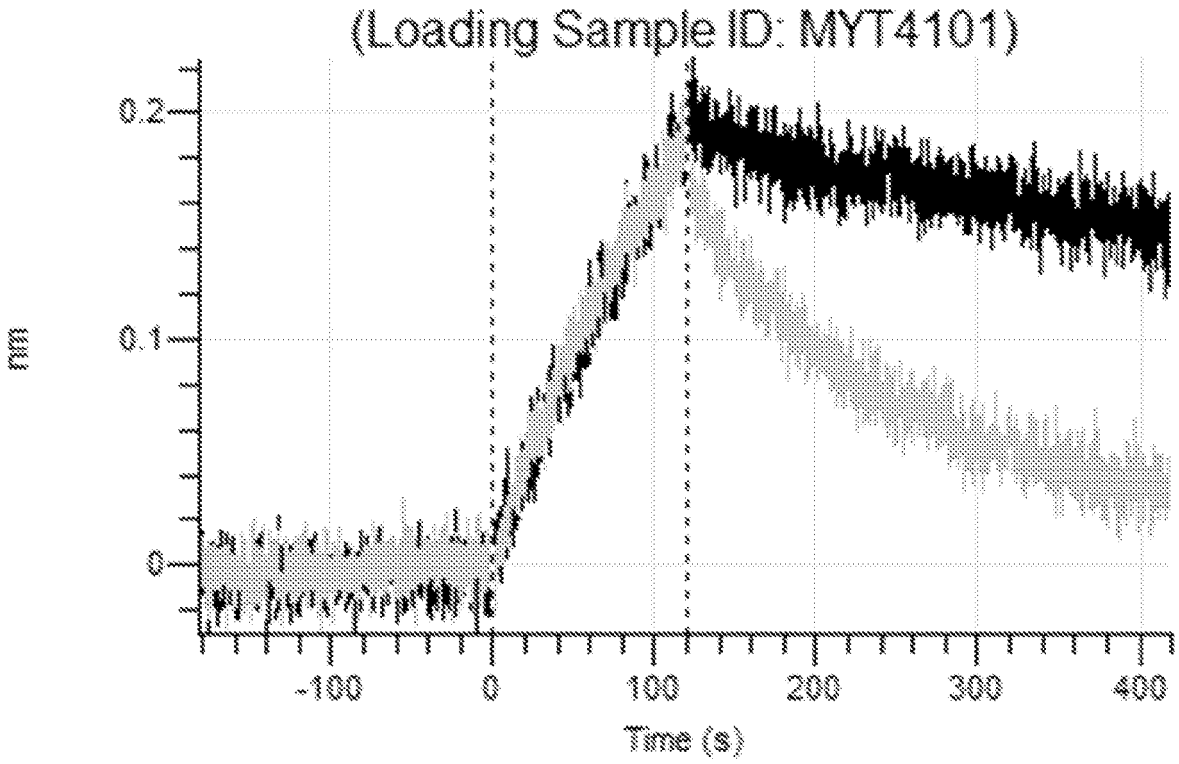

(Loading Sample ID: MYT4101)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)

FIG. 35M

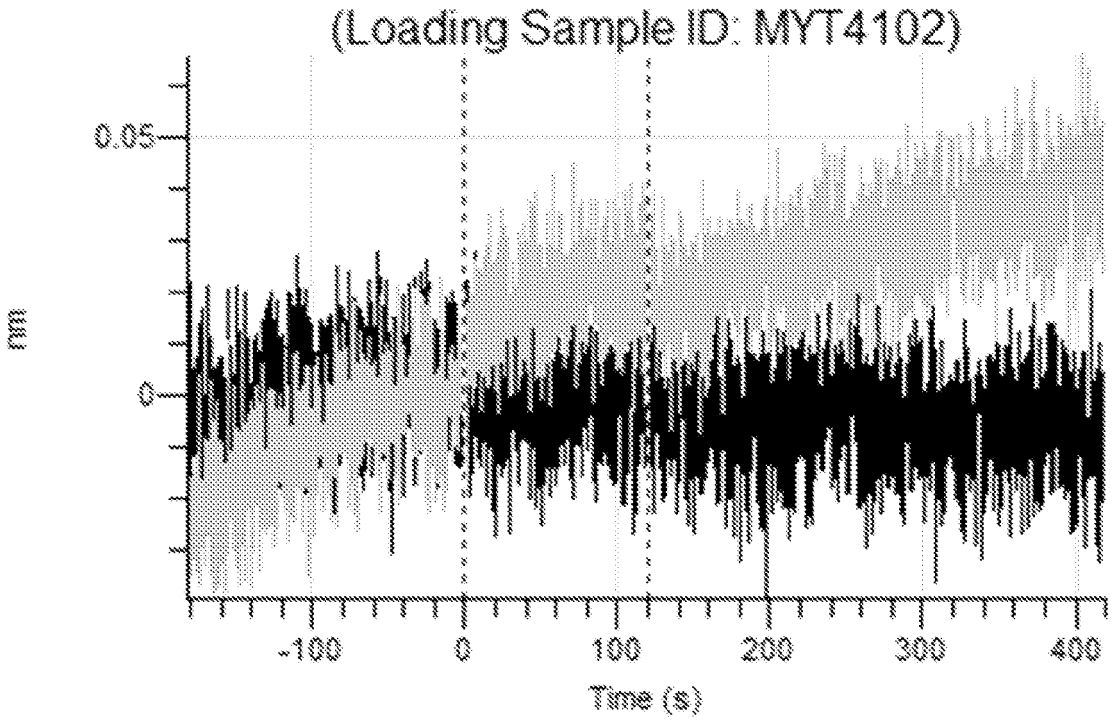


FIG. 35N

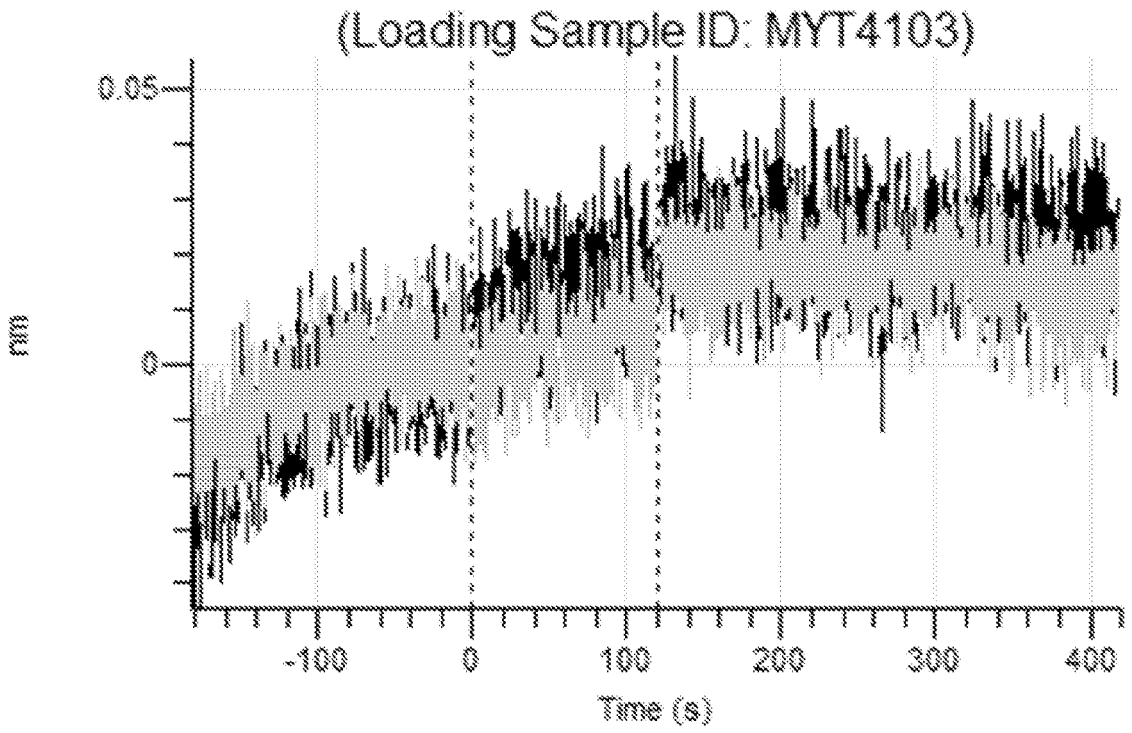


FIG. 35O

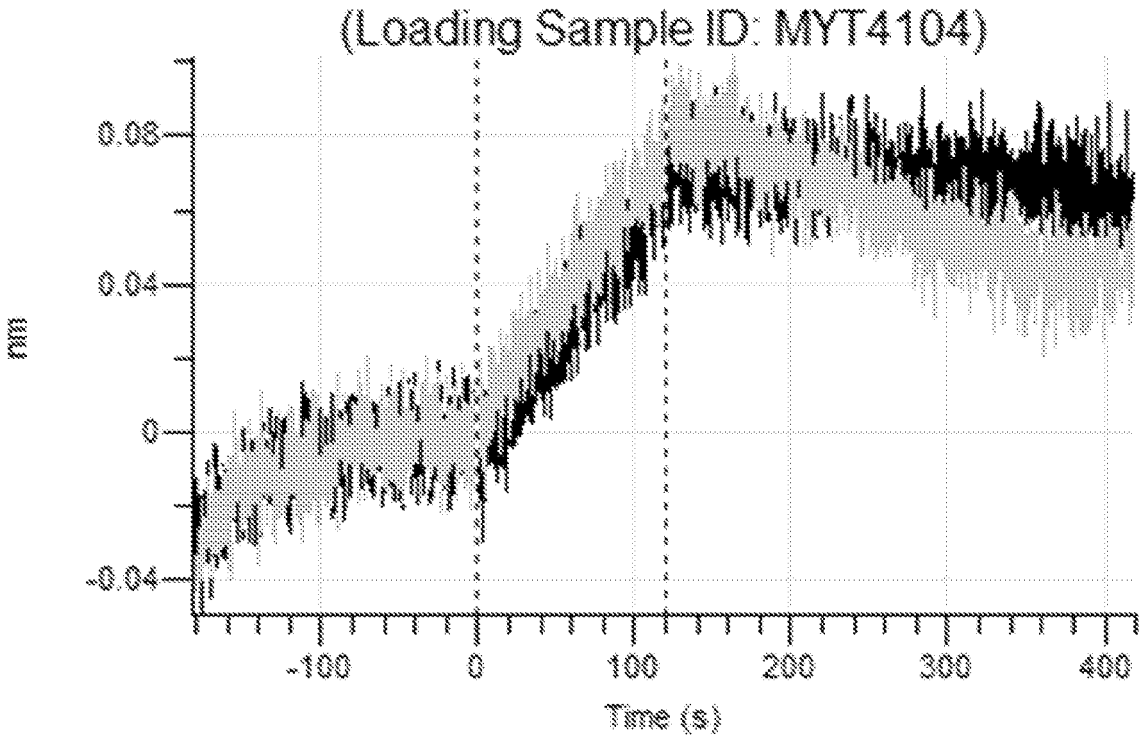

(Loading Sample ID: MYT4104)
nm
0.08
0.04
0
-0.04
-100
0
100
200
300
400
Time (s)

FIG. 35P

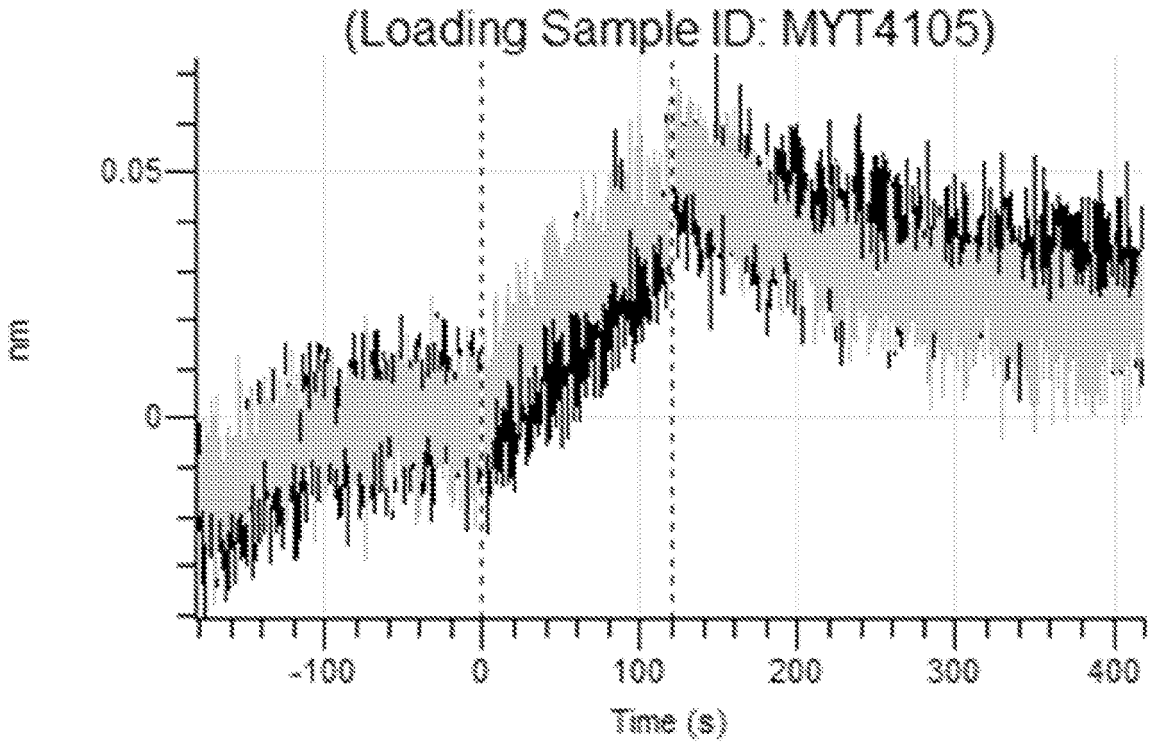


FIG. 35Q

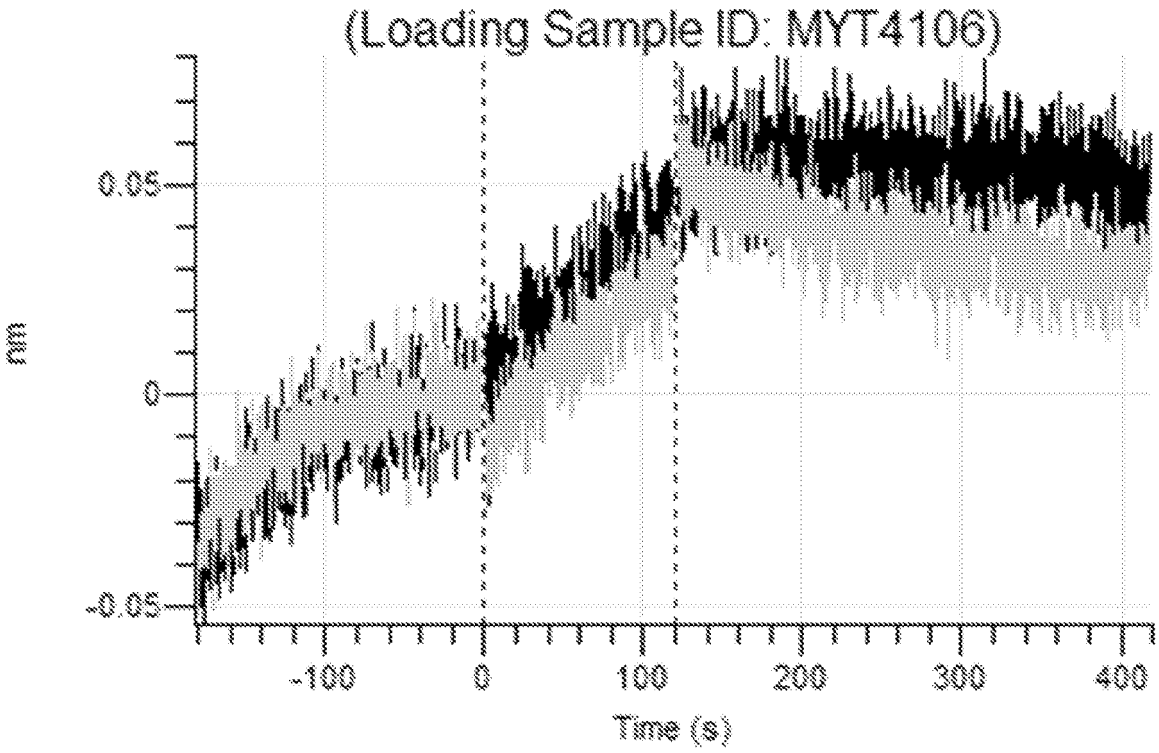

(Loading Sample ID: MYT4106)
nm
0.05
0
-0.05
-100
0
100
200
300
400
Time (s)

FIG. 35R

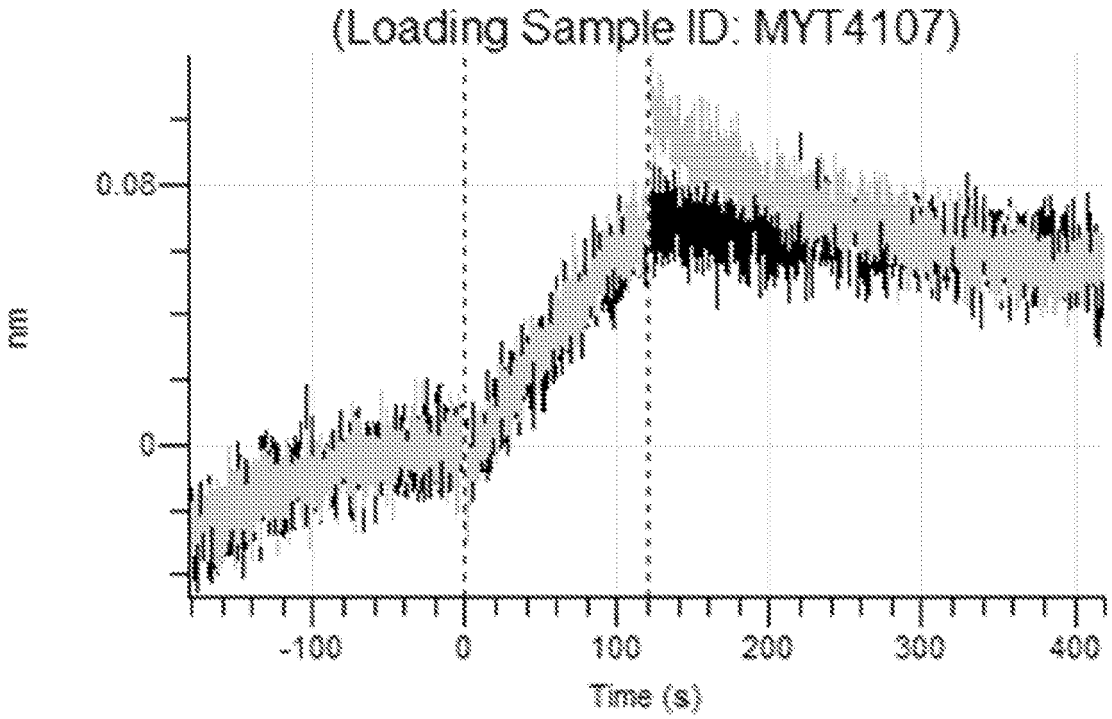


FIG. 35S

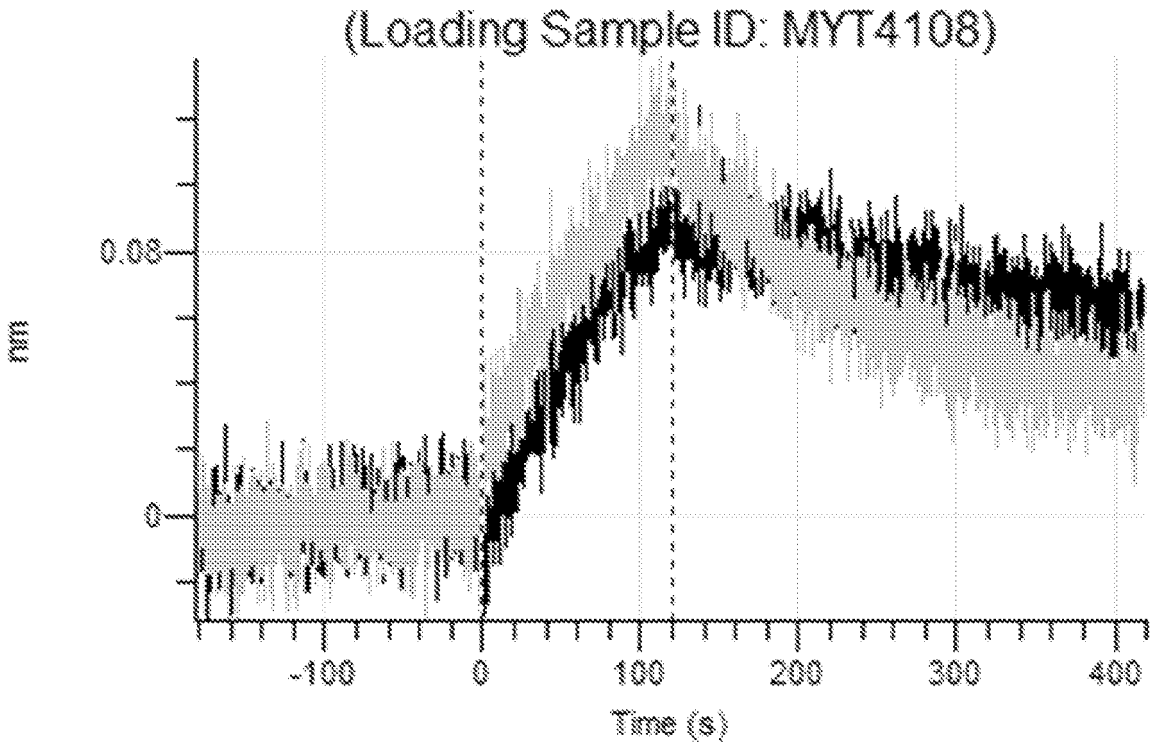


FIG. 35T

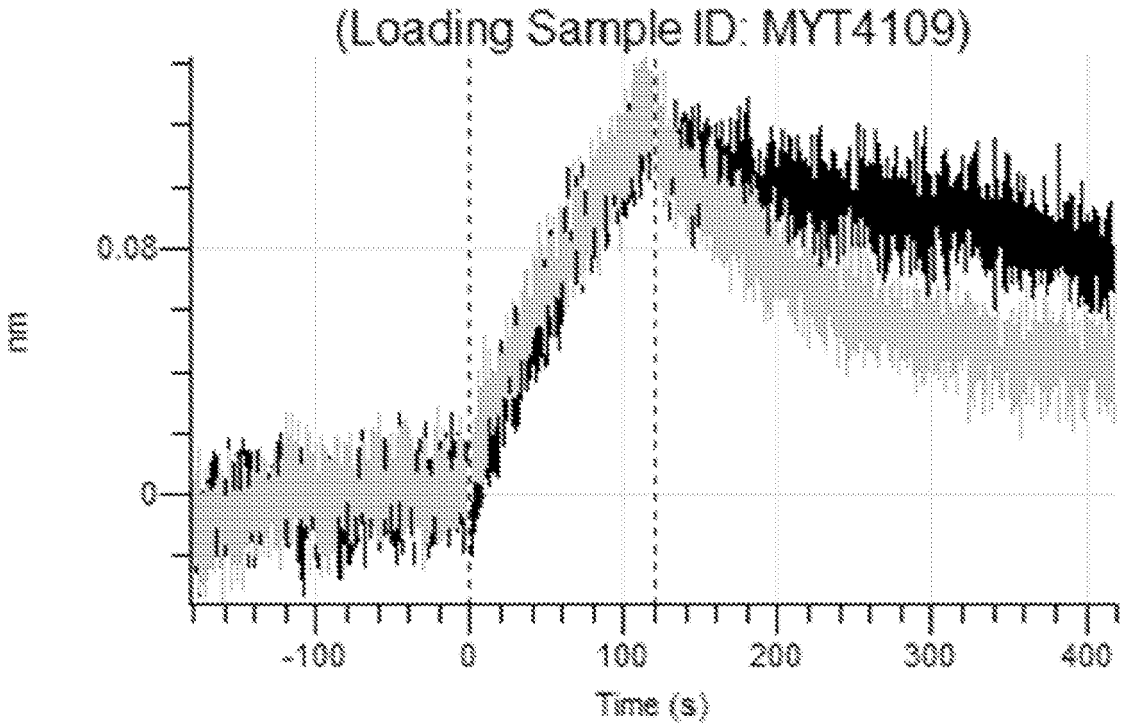


FIG. 35U

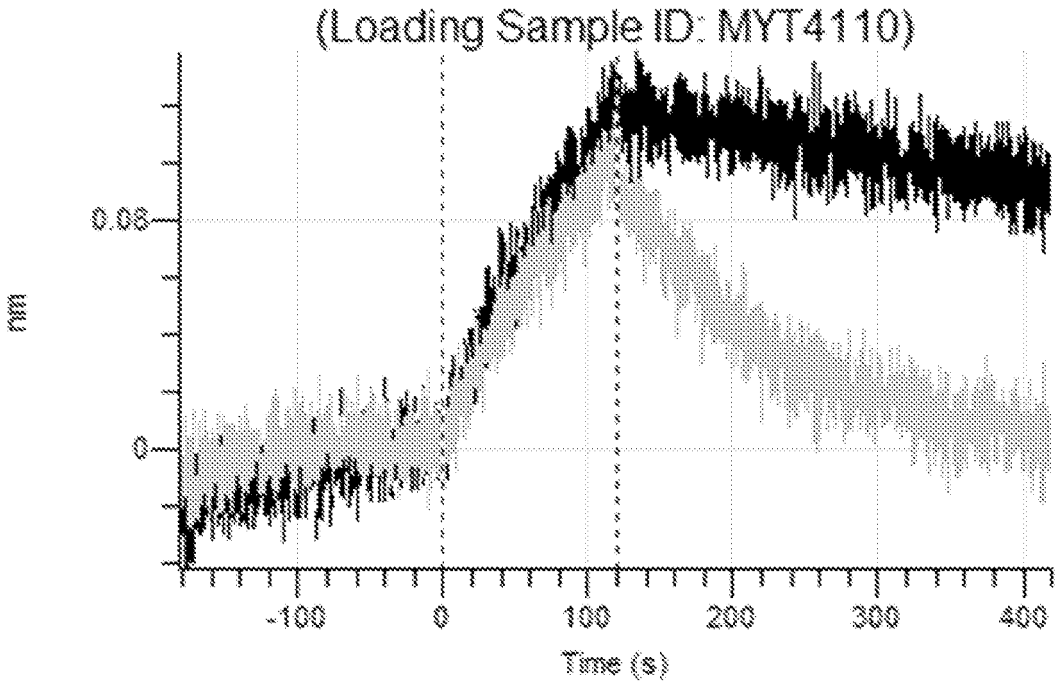


FIG. 35V

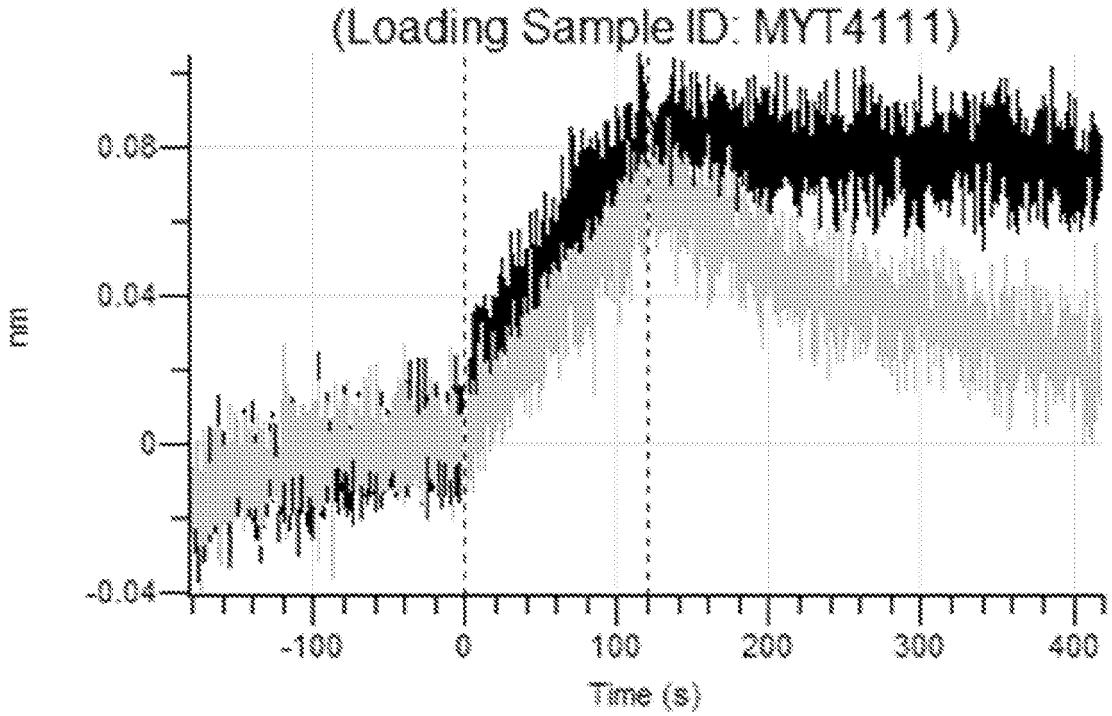

(Loading Sample ID: MYT4111)
0.08
0.04
0
-0.04
nm
-100
0
100
200
300
400
Time (s)

FIG. 35W

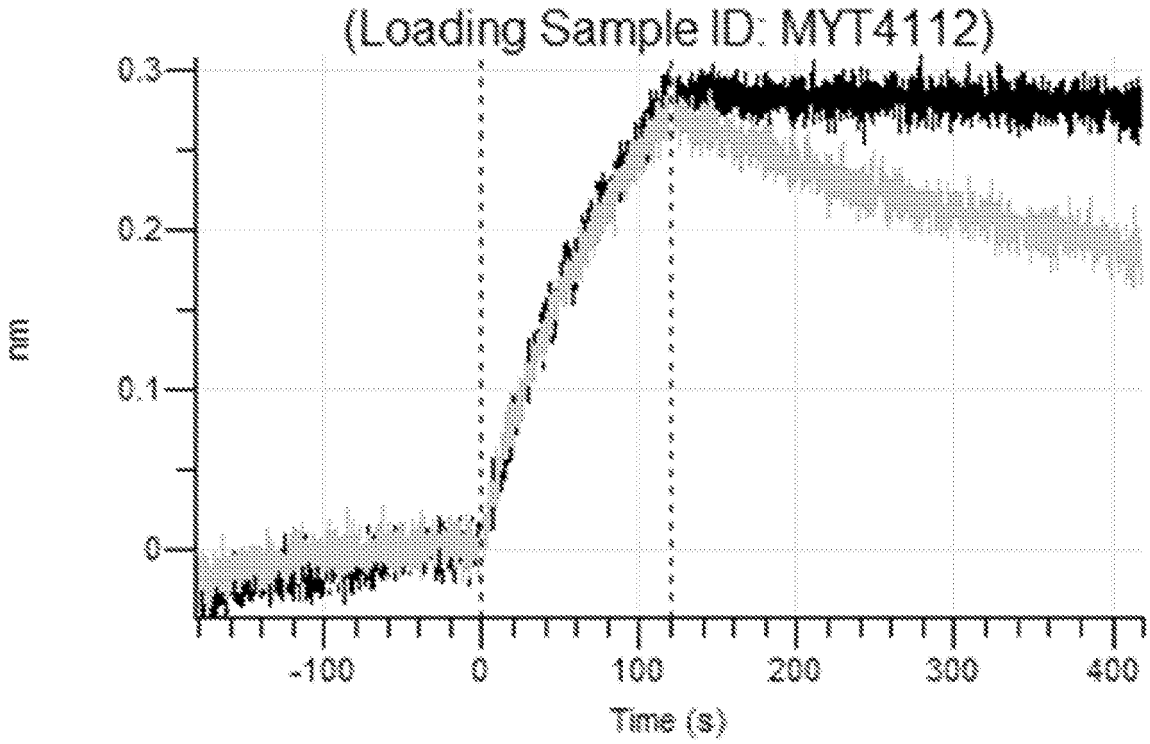

(Loading Sample ID: MYT4112)
0.3
0.2
0.1
0
nm
-100
0
100
200
300
400
Time (s)

FIG. 35X

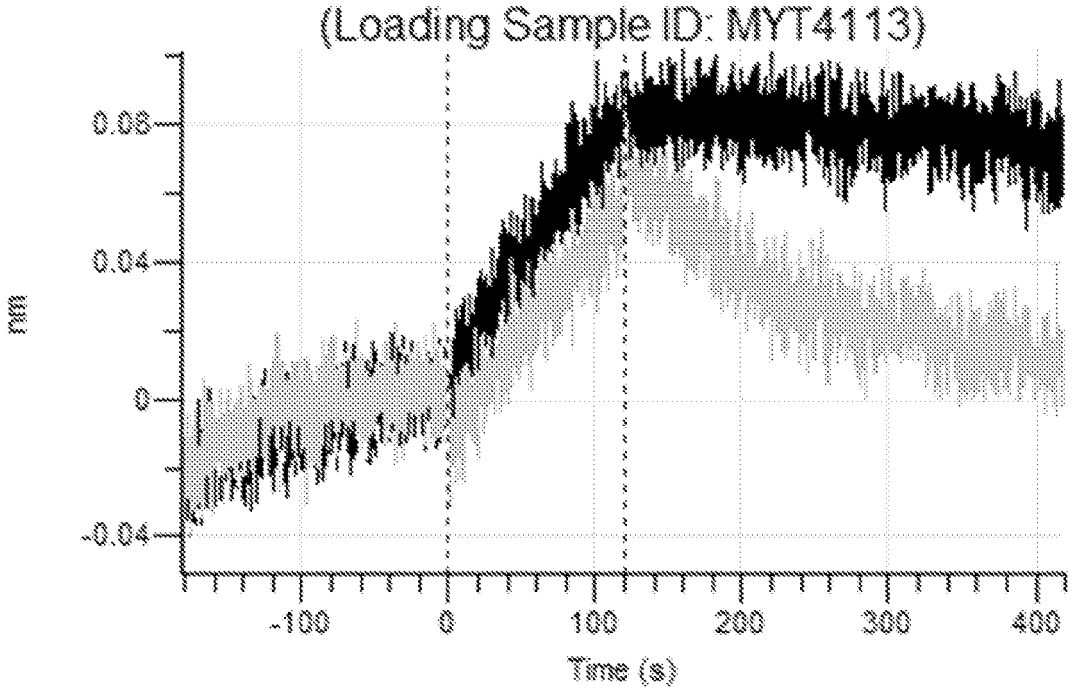

(Loading Sample ID: MYT4113)
0.08
0.04
0
-0.04
nm
-100
0
100
200
300
400
Time (s)

FIG. 35Y

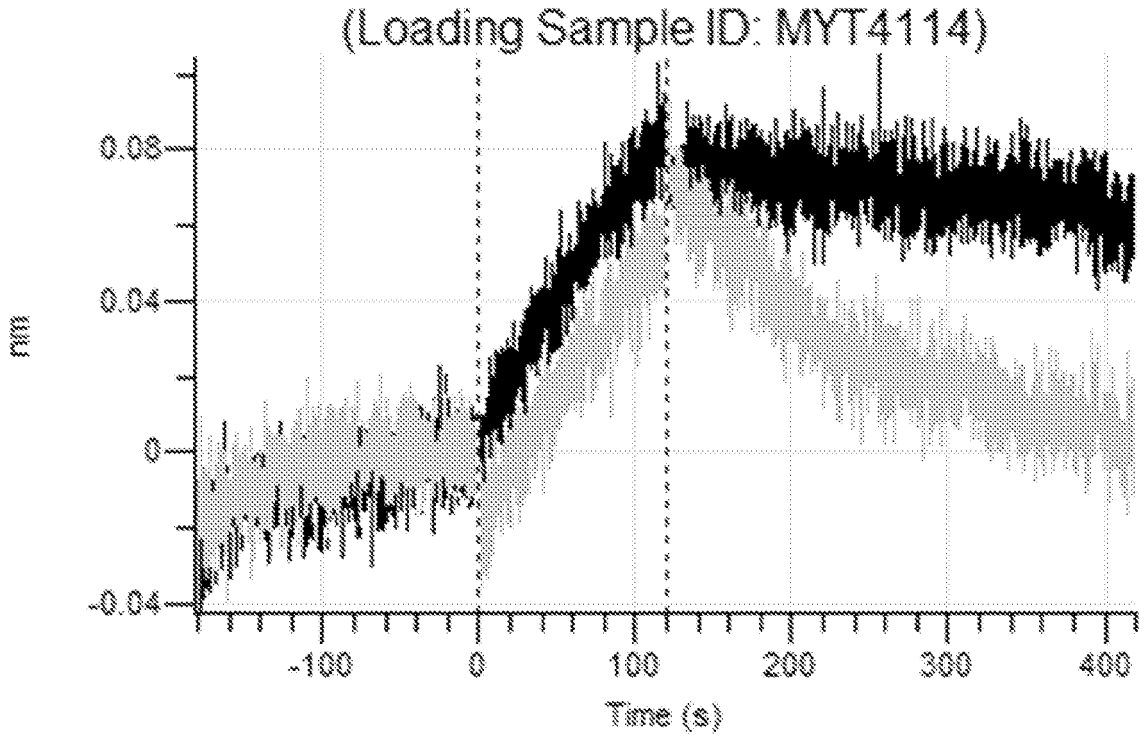

(Loading Sample ID: MYT4114)
nm
0.08
0.04
0
-0.04
-100
0
100
200
300
400
Time (s)

FIG. 35Z

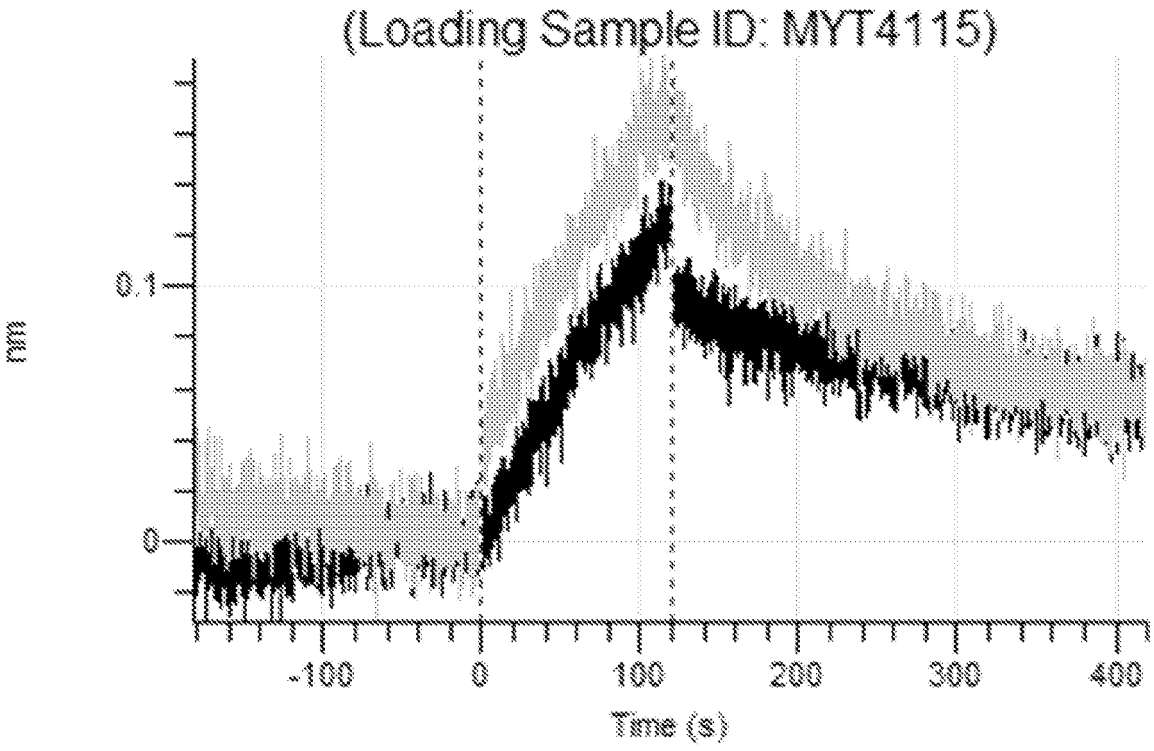


FIG. 35AA

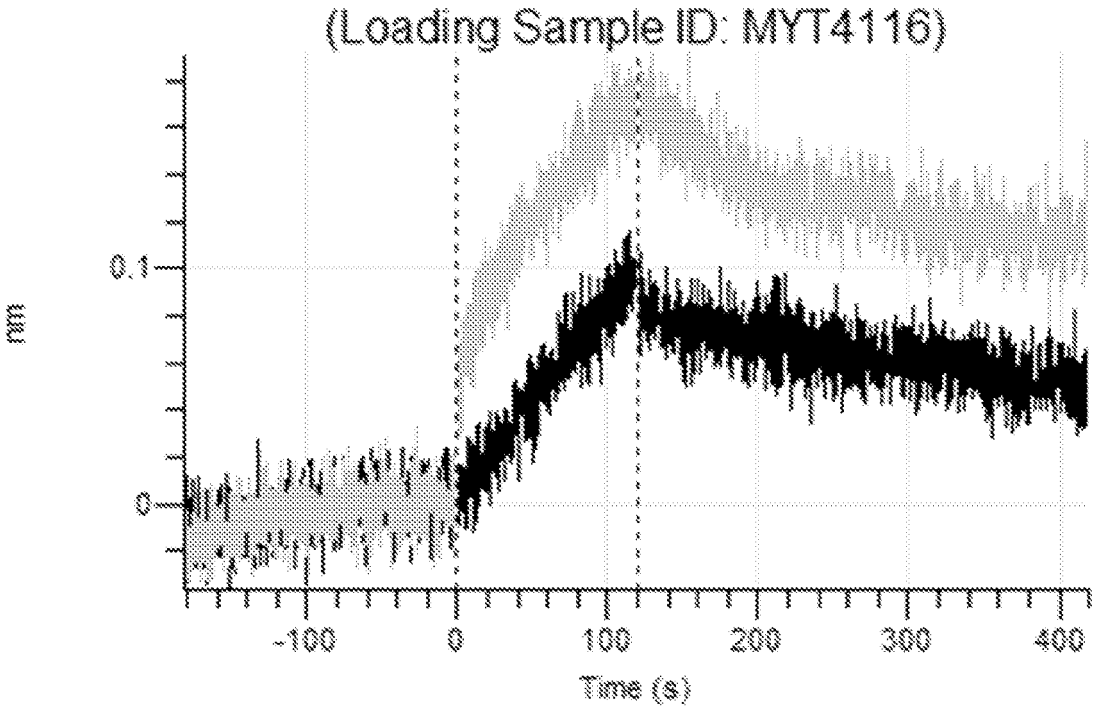


FIG. 35AB

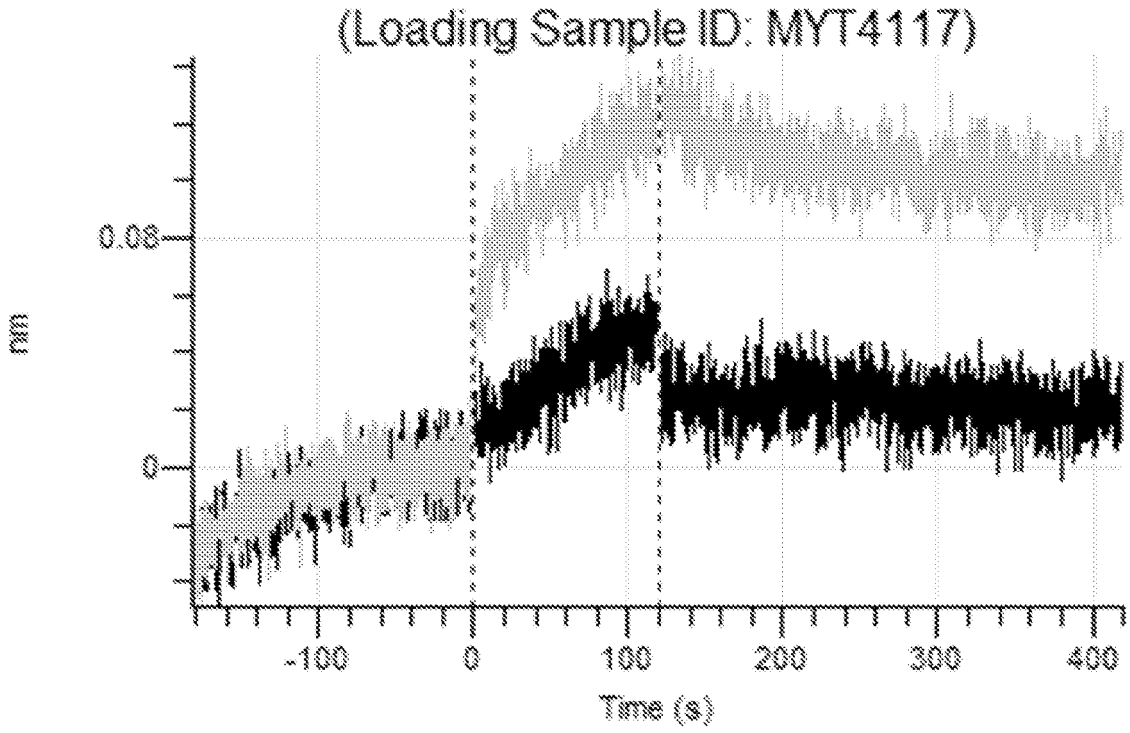


FIG. 35AC

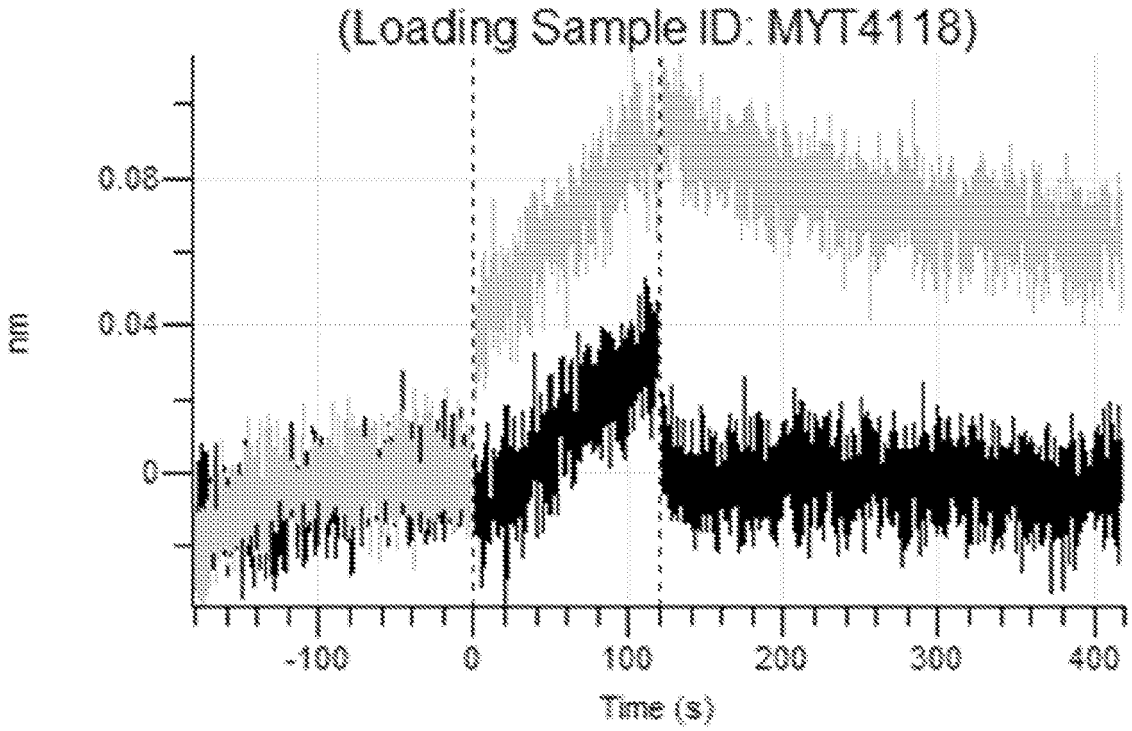

(Loading Sample ID: MYT4118)
nm
0.08
0.04
0
-100
0
100
200
300
400
Time (s)

FIG. 35AD

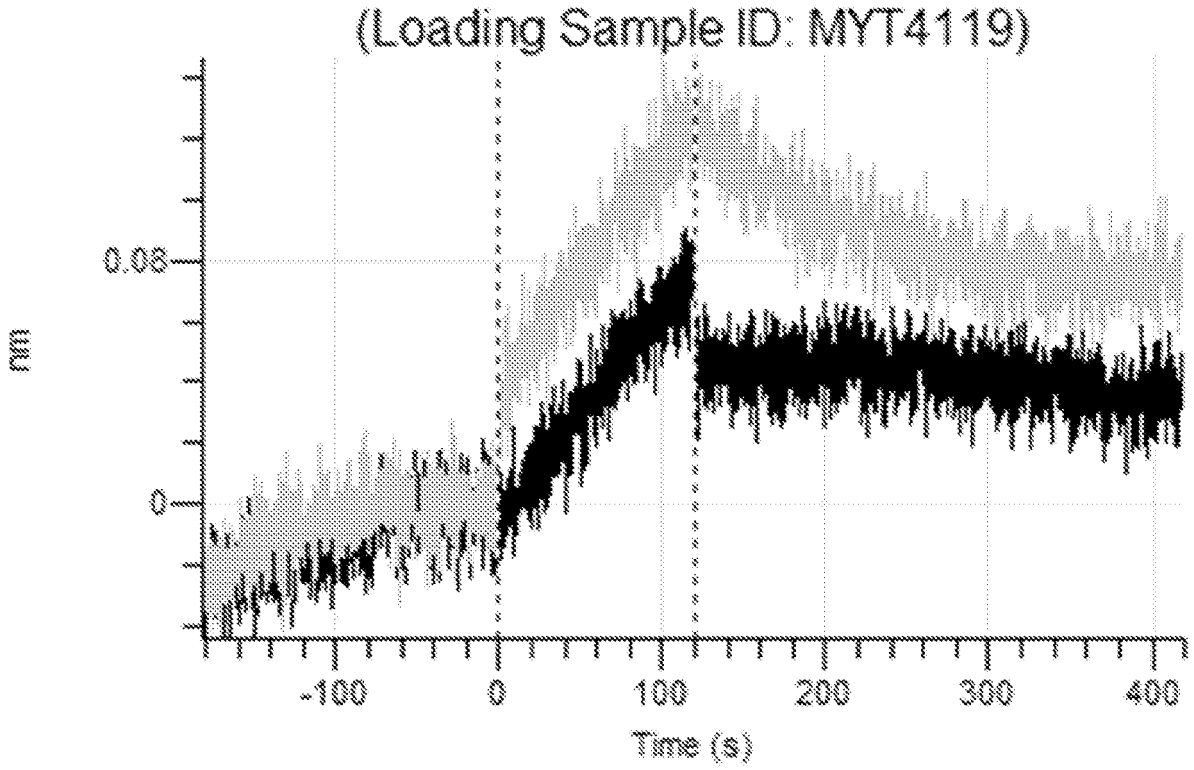


FIG. 35AE

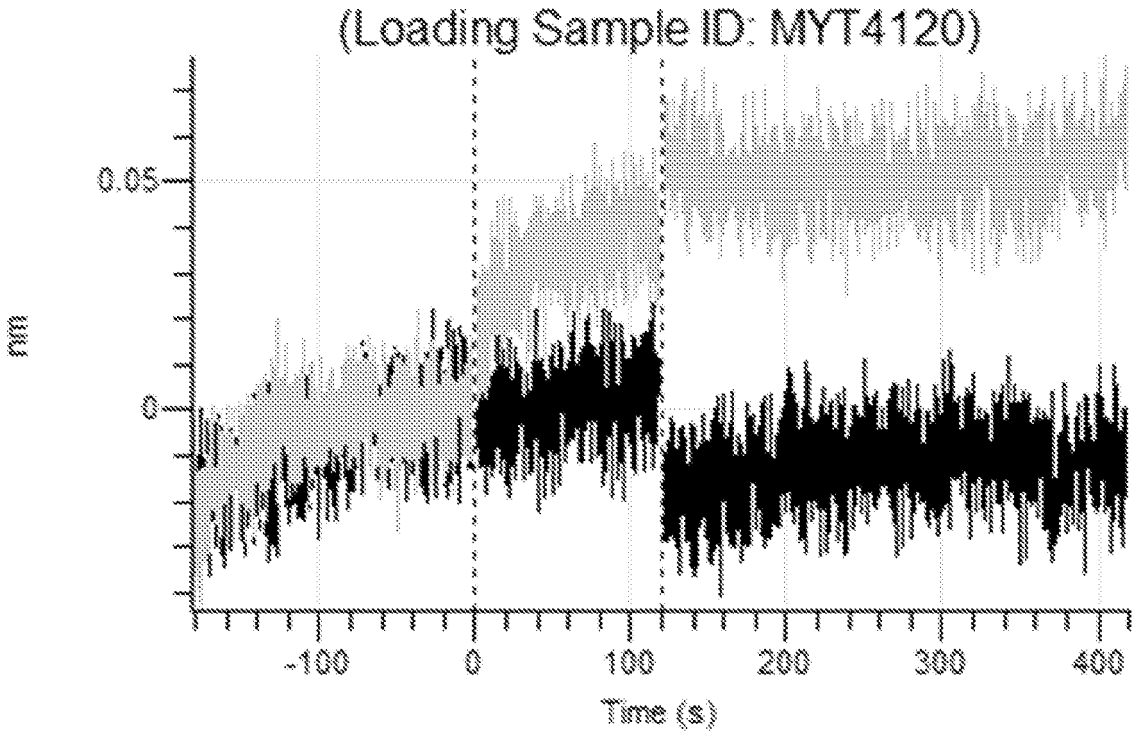


FIG. 35AF

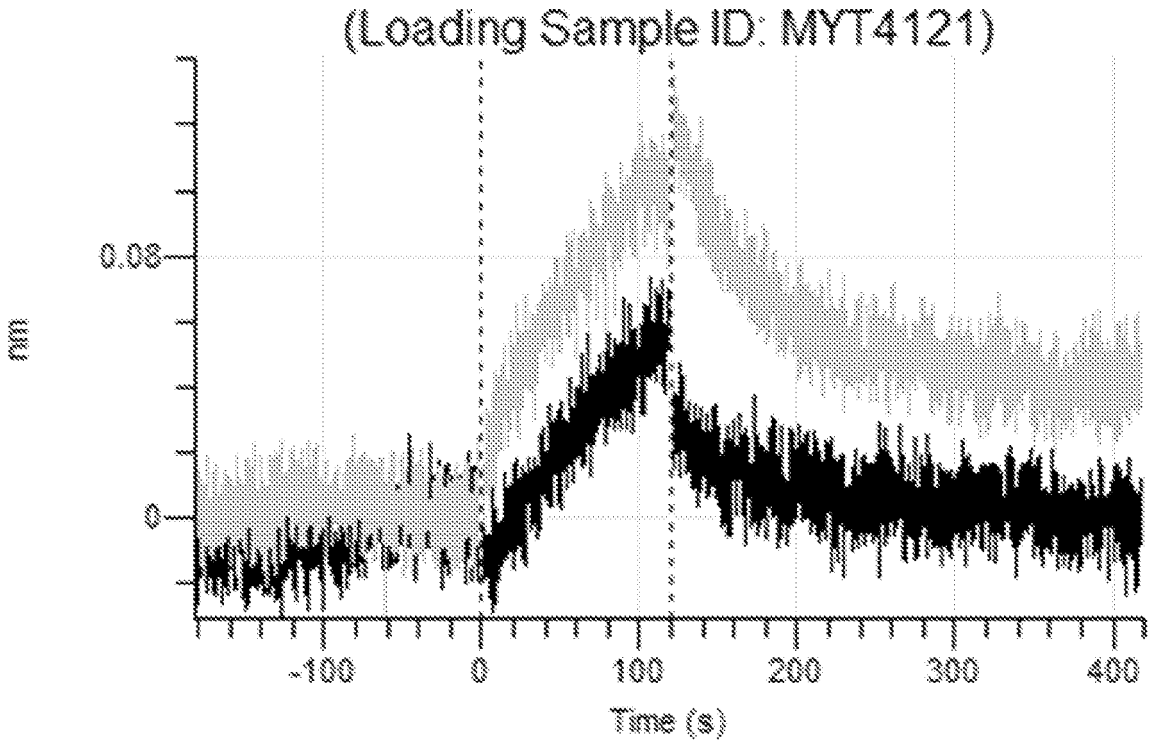


FIG. 35AG

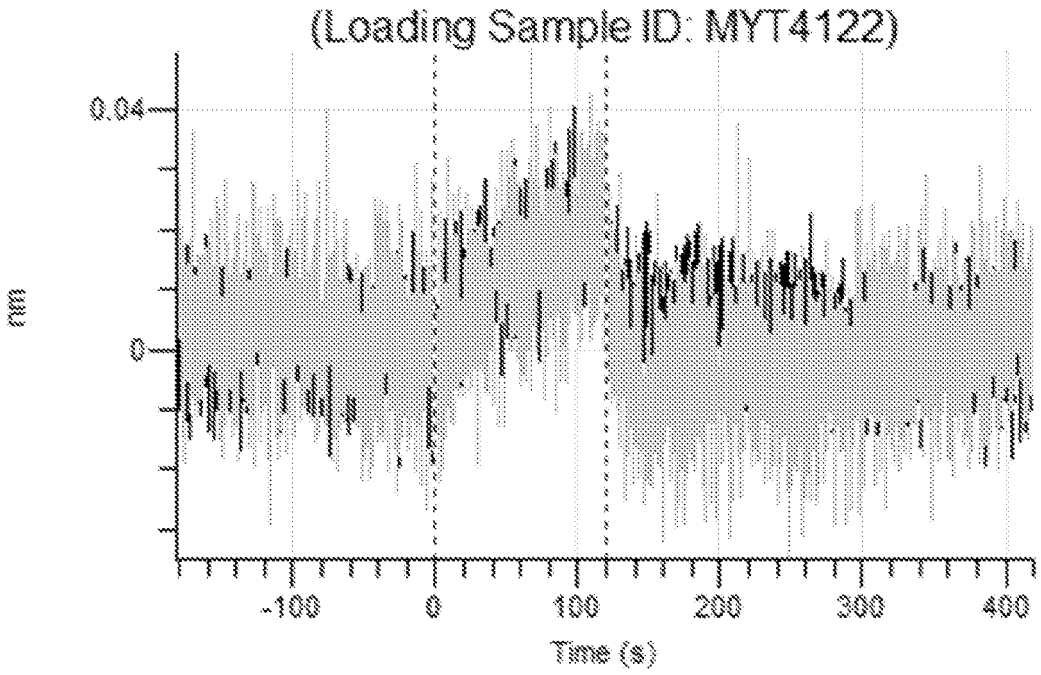


FIG. 35AH

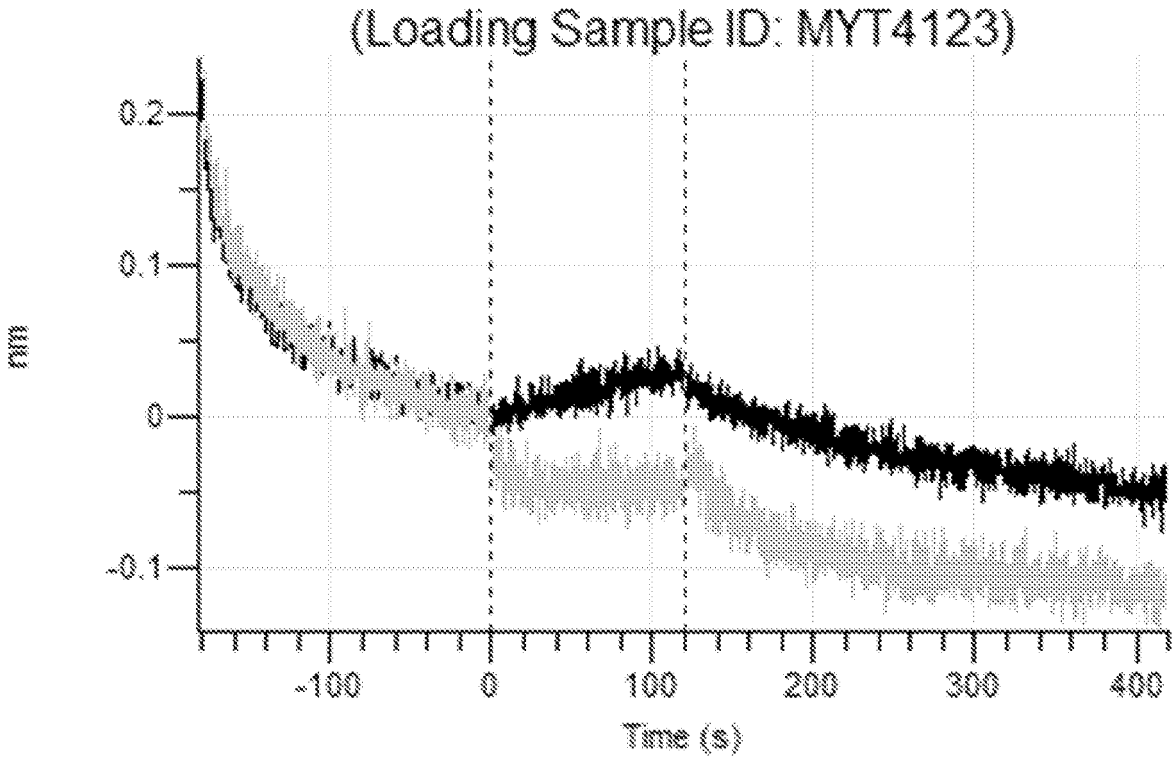

(Loading Sample ID: MYT4123)
nm
0.2
0.1
0
-0.1
-100
0
100
200
300
400
Time (s)

FIG. 35AI

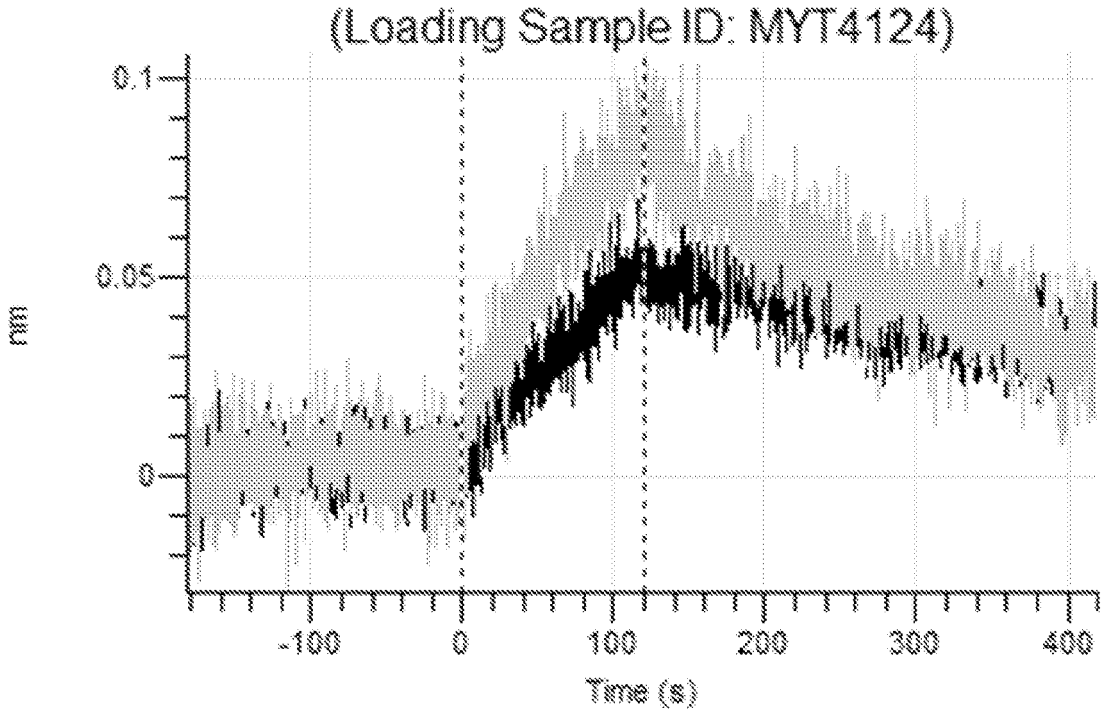

(Loading Sample ID: MYT4124)
0.1
0.05
0
EMG
-100
0
100
200
300
400
Time (s)

FIG. 35AJ

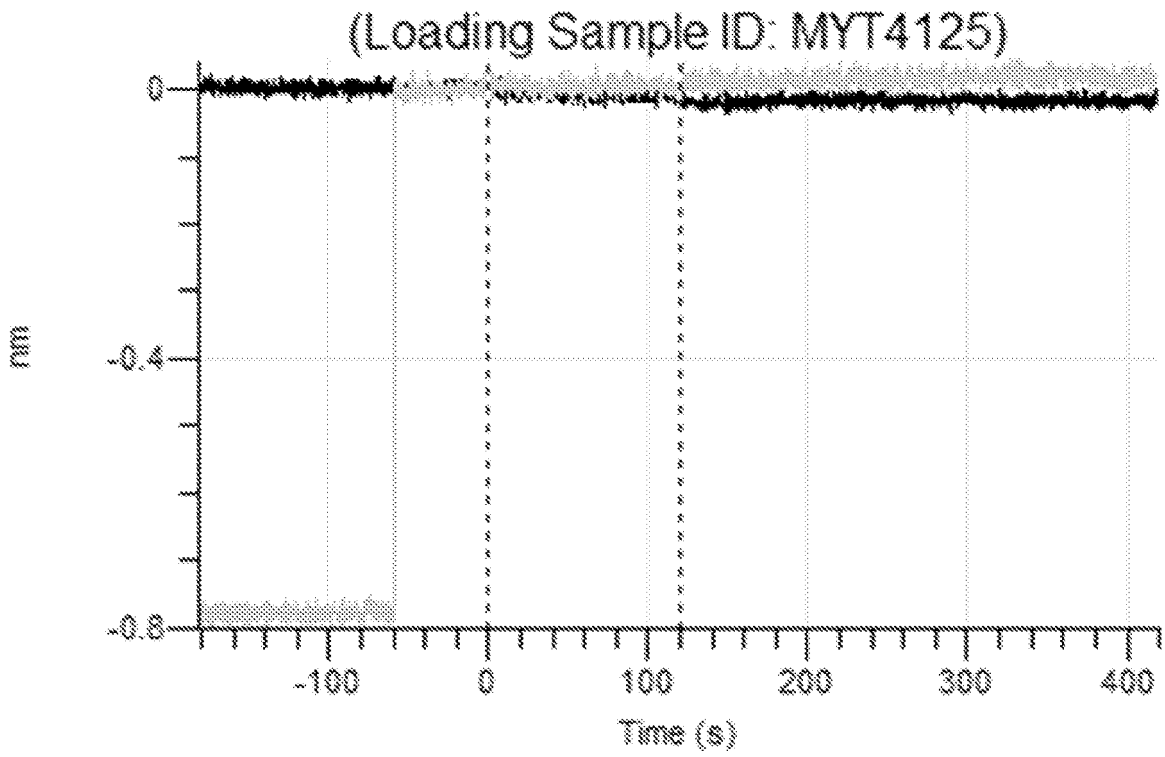

(Loading Sample ID: MYT4125)
0
-0.4
-0.8
nm
-100
0
100
200
300
400
Time (s)

FIG. 35AK

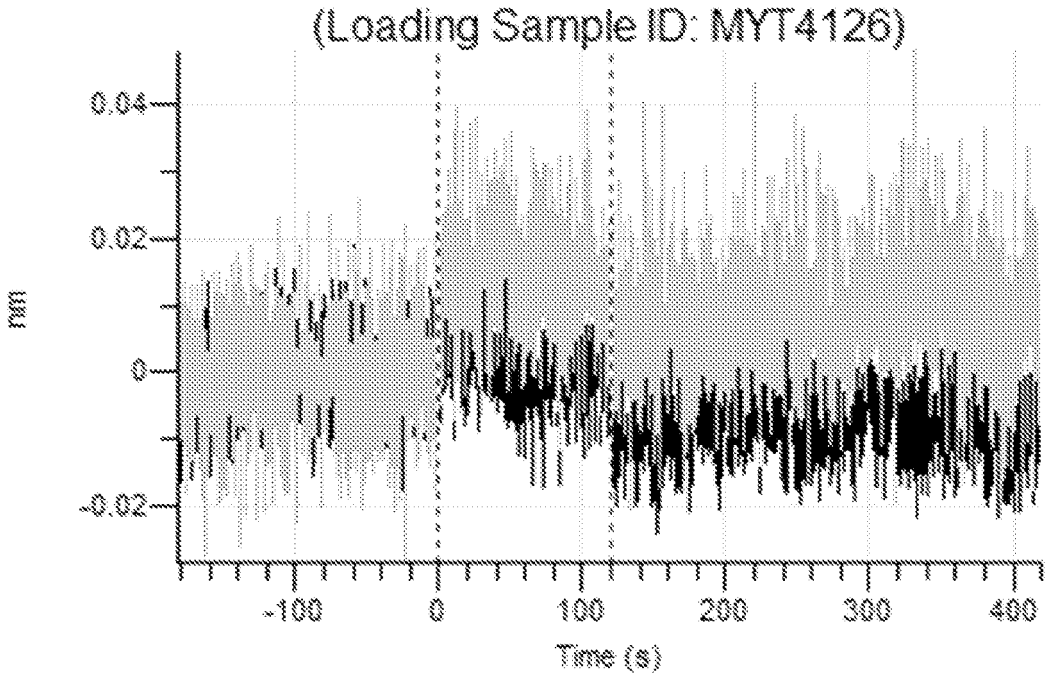

(Loading Sample ID: MYT4126)
0.04
0.02
0
-0.02
mm
-100
0
100
200
300
400
Time (s)

FIG. 35AL

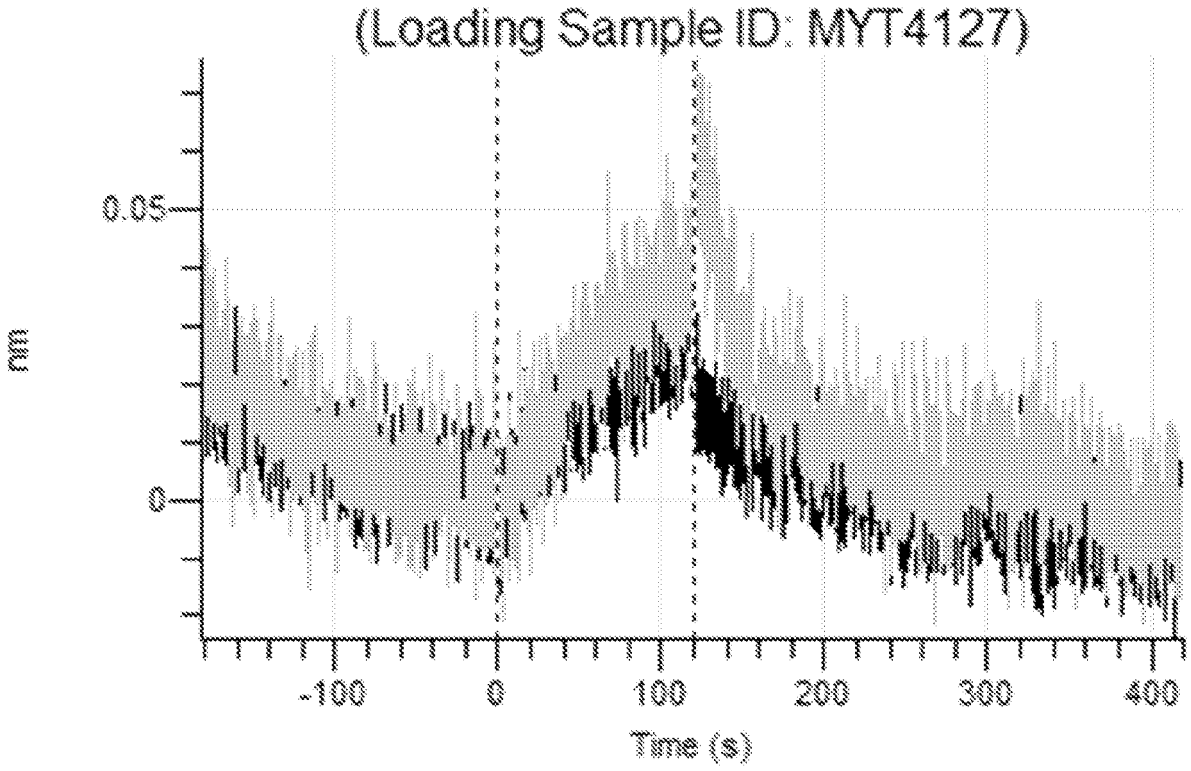


FIG. 35AM

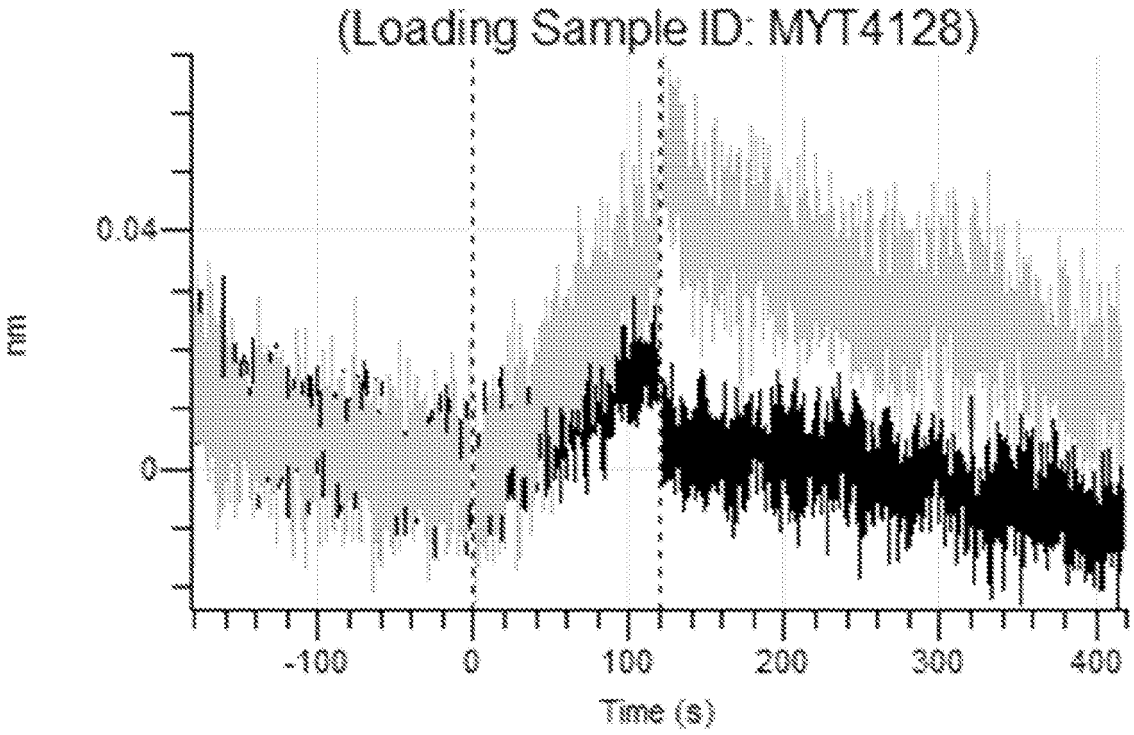


FIG. 35AN

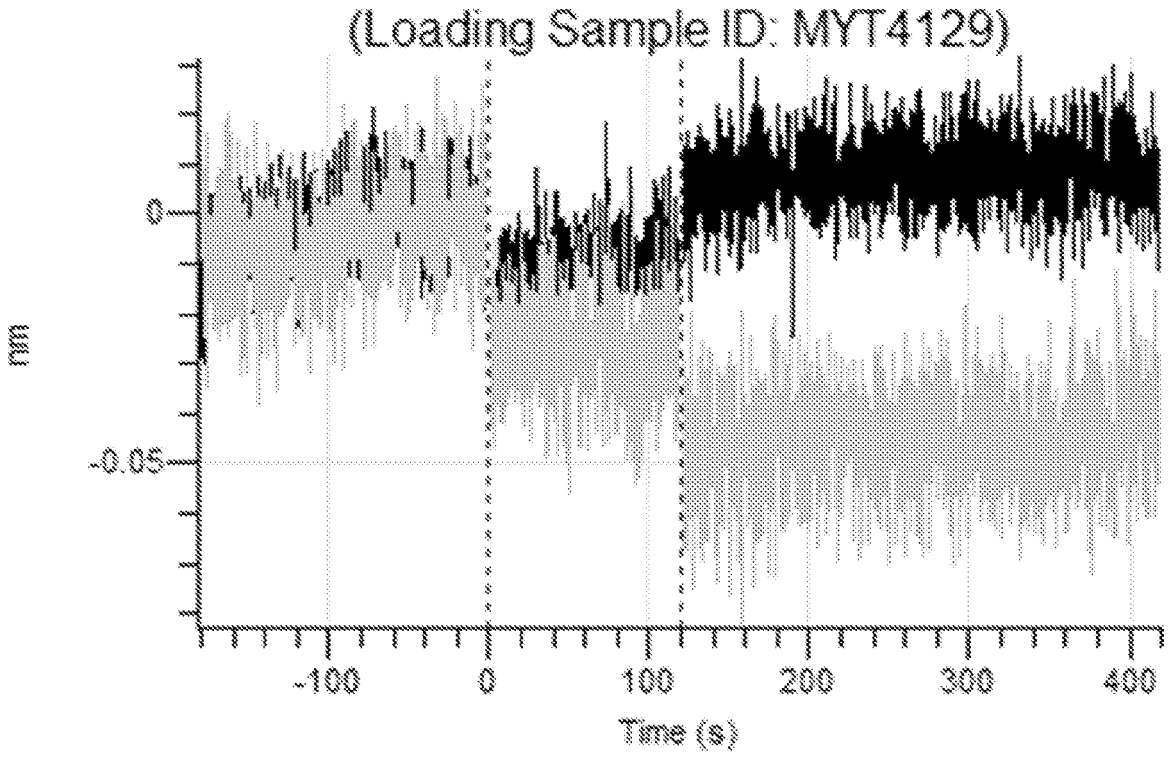


FIG. 35AO

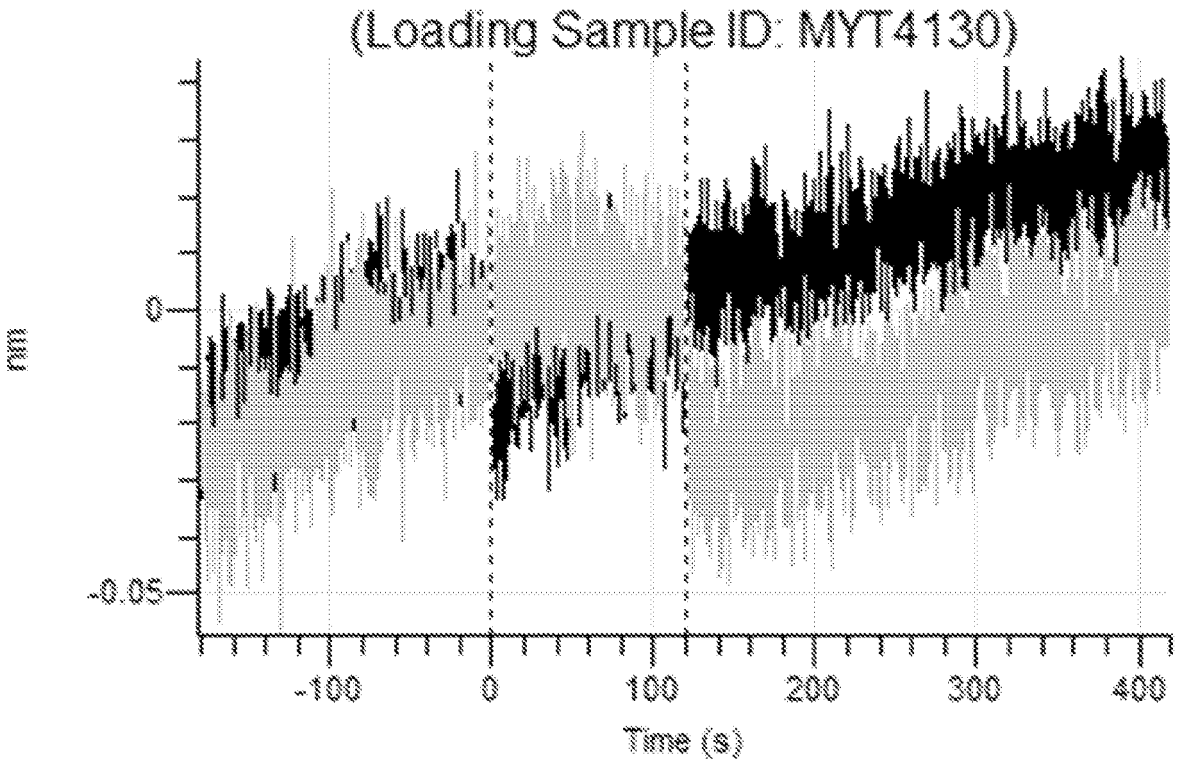


FIG. 35AP

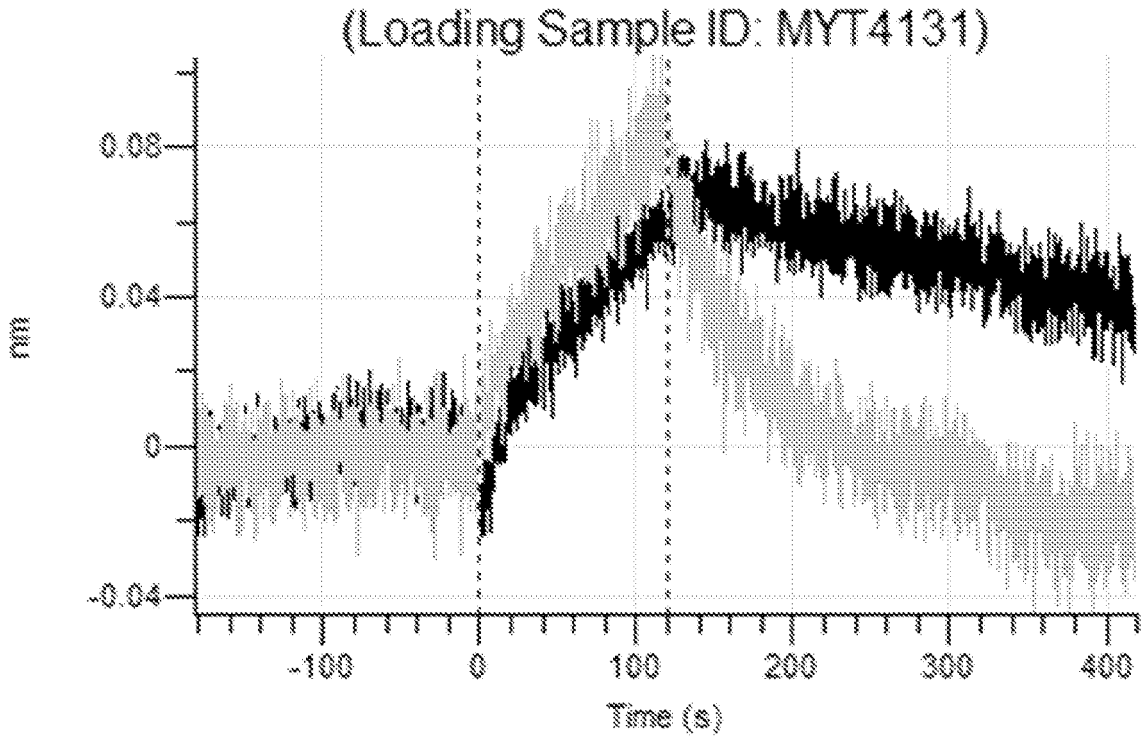

(Loading Sample ID: MYT4131)
nm
0.08
0.04
0
-0.04
-100
0
100
200
300
400
Time (s)

FIG. 35AQ

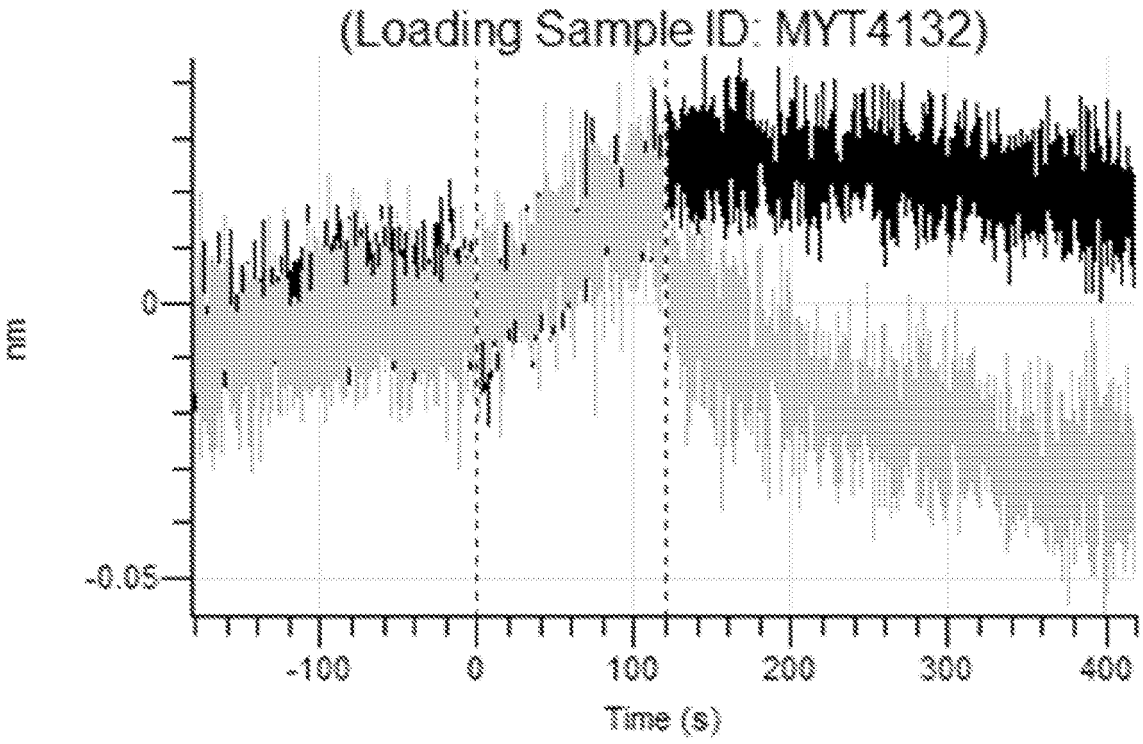


FIG. 35AR

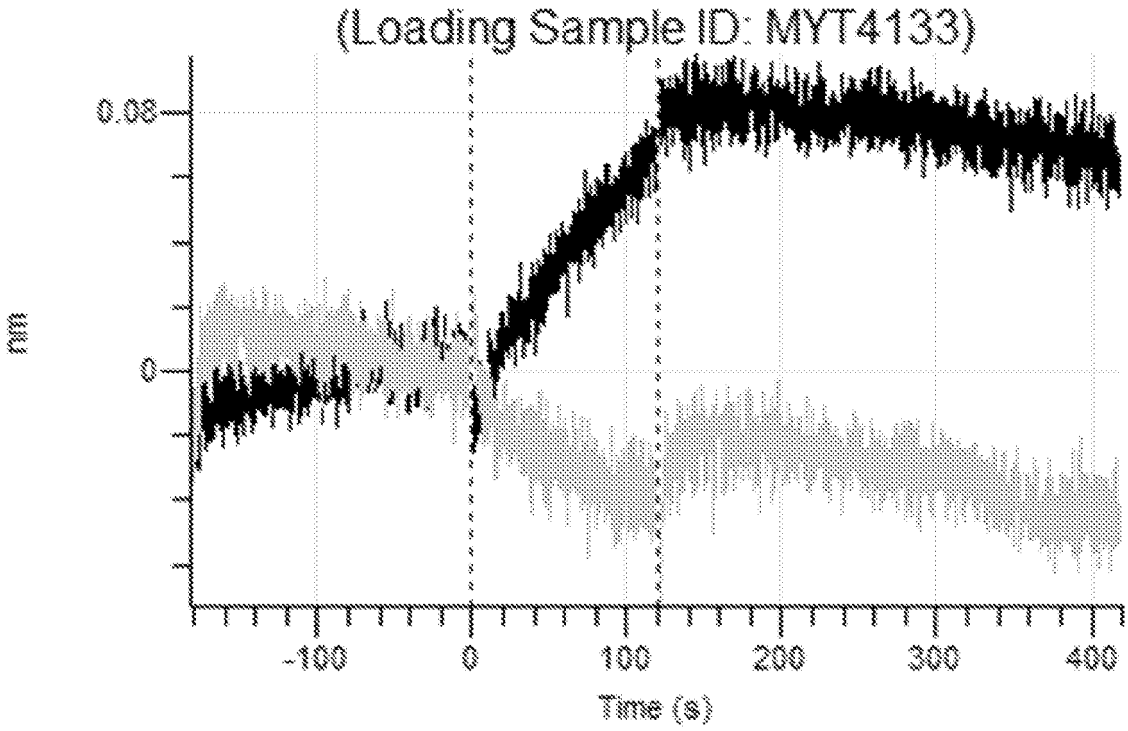


FIG. 35AS

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
MYT3179 (huAD208.12.1)	272	273	274	275	276	277	278	279
MYT4090	280	273						
MYT4091	281	273						
MYT4092	282	273						
MYT4093	283	273						
MYT4094	284	273						
MYT4095	285	273						
MYT4096	286	273						
MYT4097	287	273						
MYT4098	288	273						
MYT4099	289	273						
MYT4100	290	273						
MYT4101	291	273						
MYT4102	292	273						
MYT4103	293	273						
MYT4104	294	273						
MYT4105	295	273						
MYT4106	296	273						
MYT4107	297	273						
MYT4108	298	273						
MYT4109	299	273						
MYT4110	300	273						
MYT4111	301	273						
MYT4112	302	273						
MYT4113	303	273						
MYT4114	304	273						
MYT4115	305	273						
MYT4116	306	273						
MYT4117	307	273						
MYT4118	308	273						
MYT4119	309	273						
MYT4120	310	273						
MYT4121	311	273						
MYT4122	312	273						
MYT4123	313	273						
MYT4124	314	273						
MYT4125	315	273						
MYT4126	316	273						
MYT4127	317	273						
MYT4128	318	273						
MYT4129	319	273						
MYT4130	320	273						
MYT4131	321	273						
MYT4132	322	273						
MYT4133	323	273						

FIG. 36

SUBSTITUTE SHEET (RULE 26)

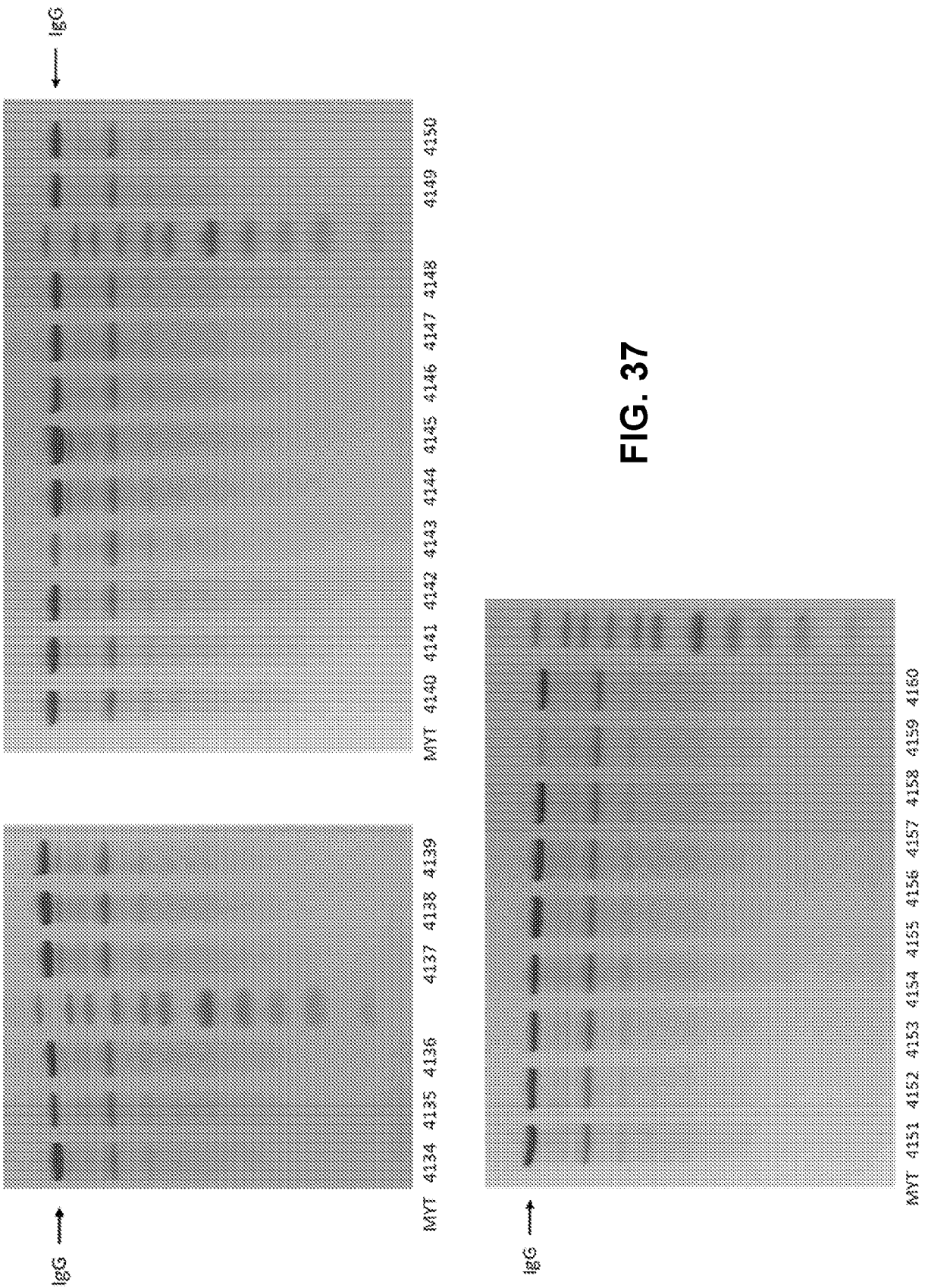

IgG
MYT 4134 4135 4136 4137 4138 4139
IgG
MYT 4140 4141 4142 4143 4144 4145 4146 4147 4148 4149 4150
IgG
MYT 4151 4152 4153 4154 4155 4156 4157 4158 4159 4160

FIG. 37

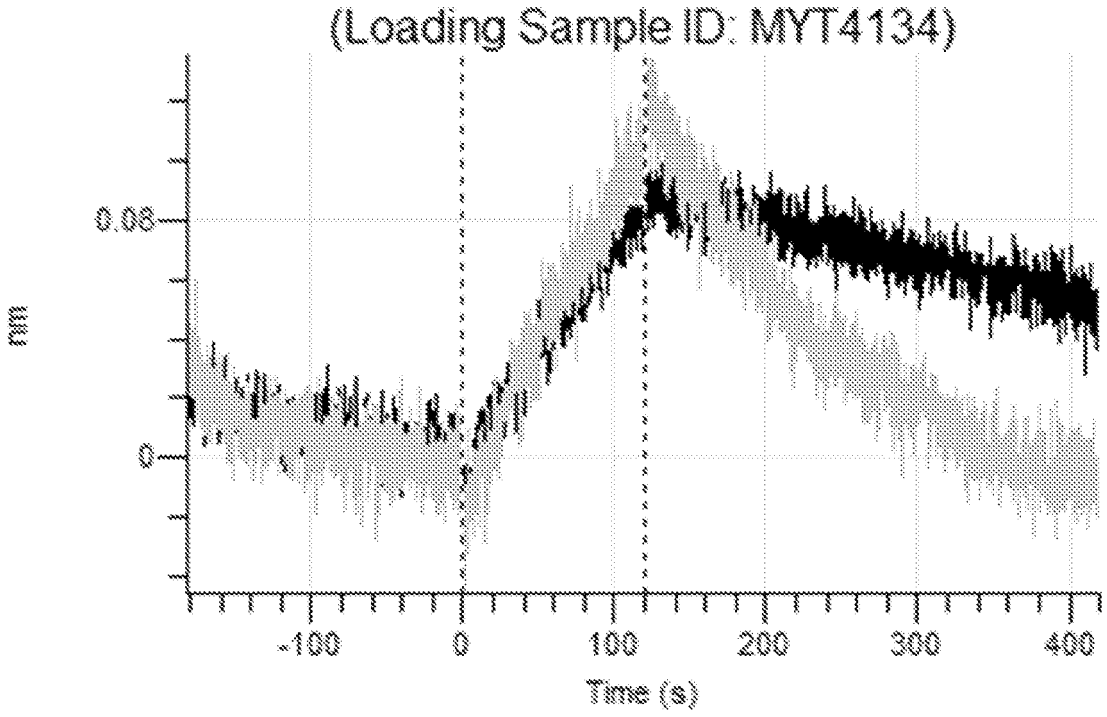


FIG. 38A

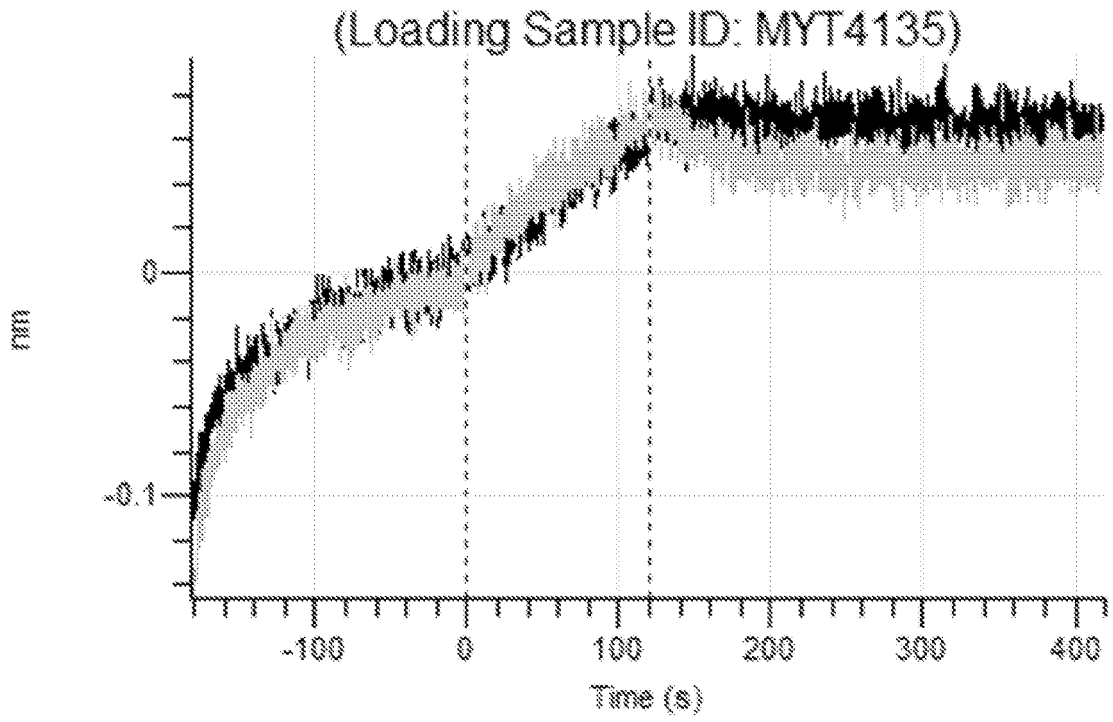


FIG. 38B

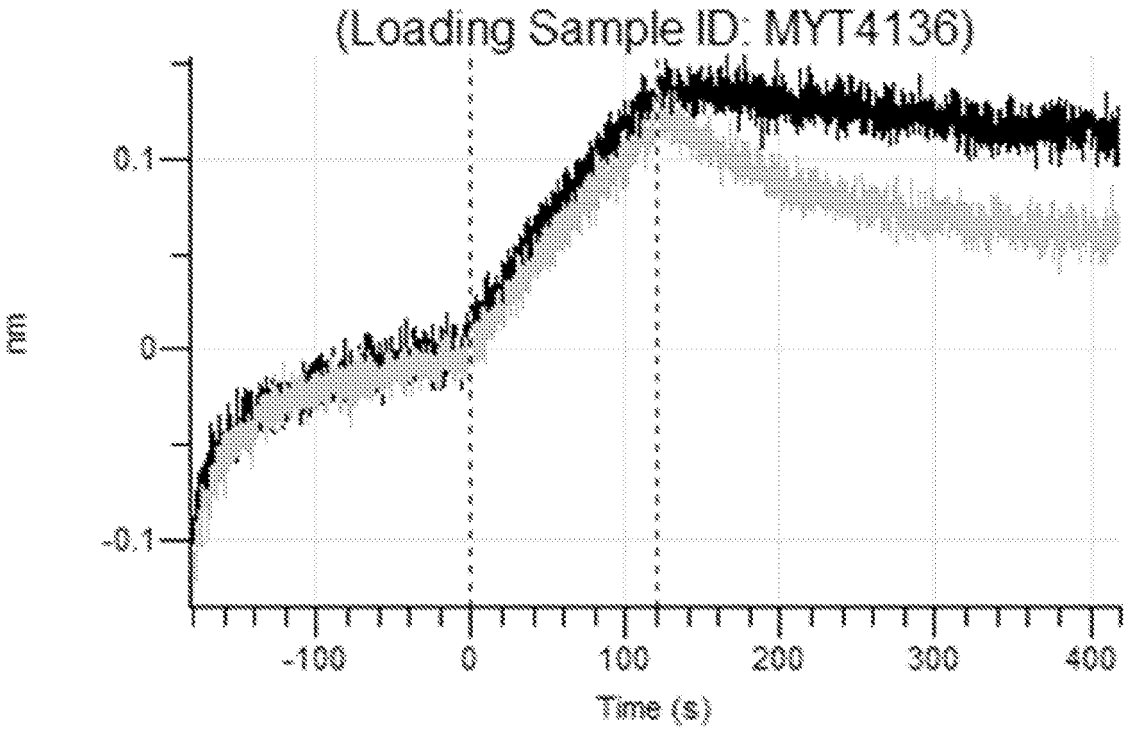

(Loading Sample ID: MYT4136)
nm
0.1
0
-0.1
-100
0
100
200
300
400
Time (s)

FIG. 38C

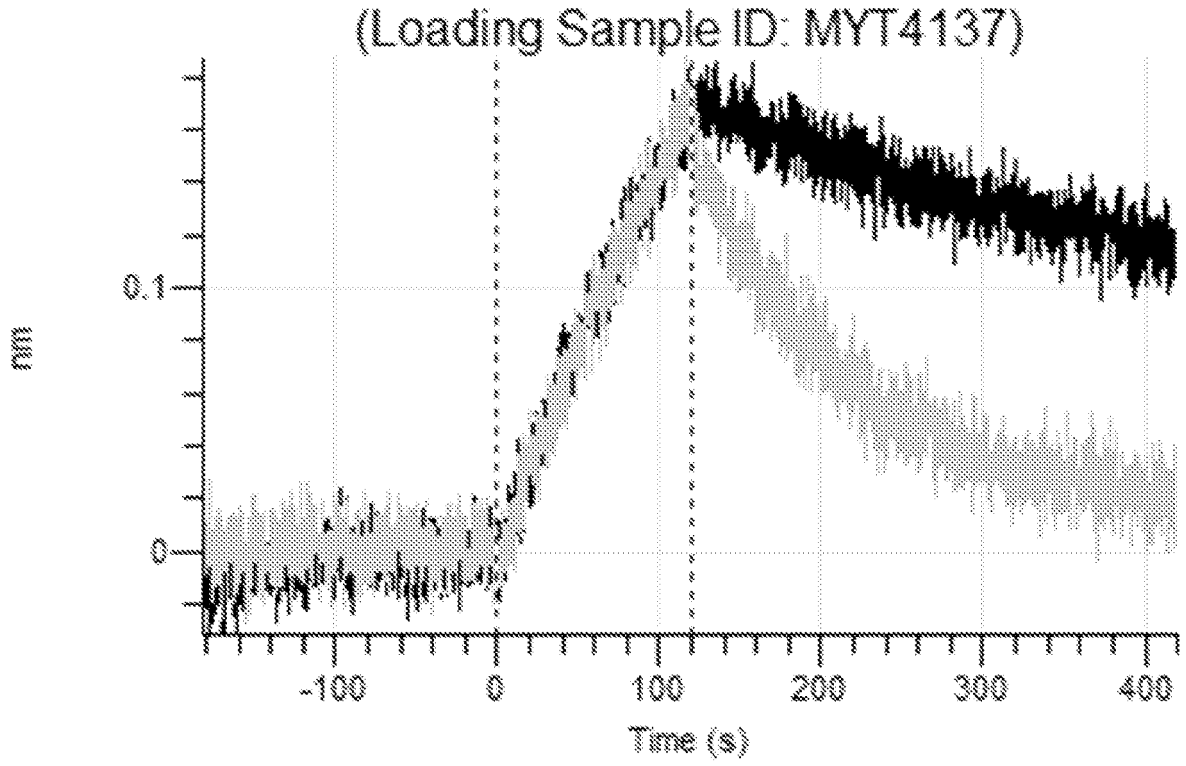


FIG. 38D

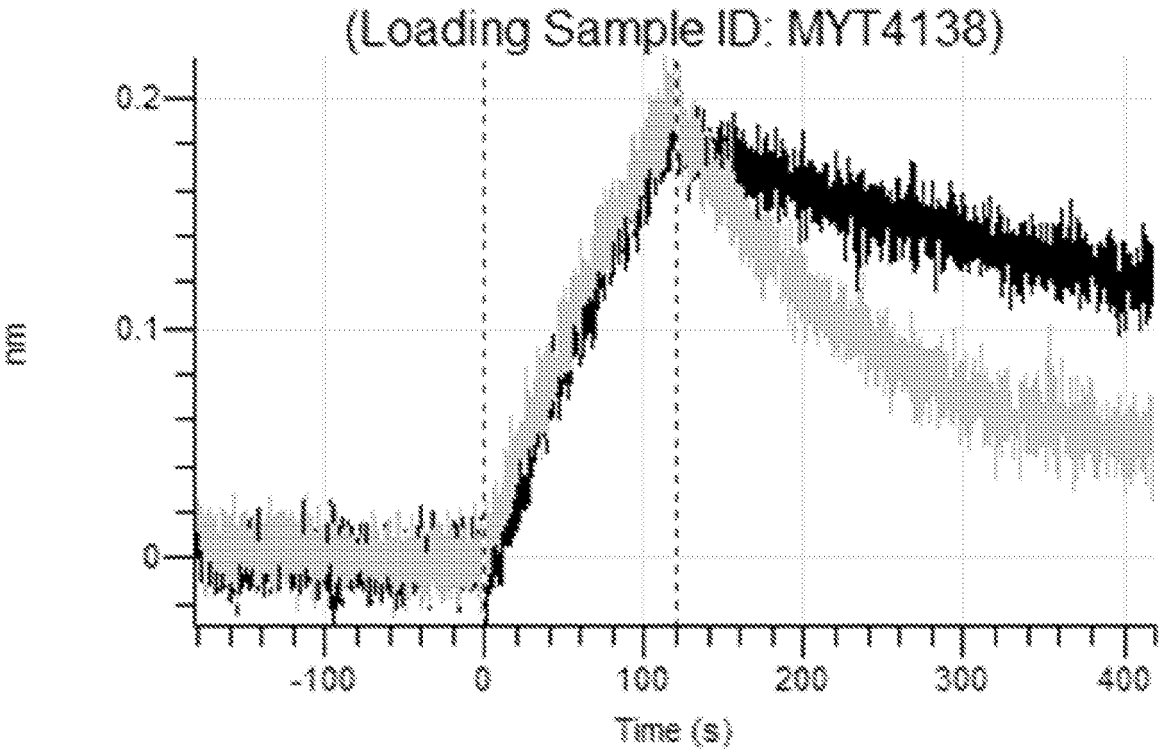

(Loading Sample ID: MYT4138)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)

FIG. 38E

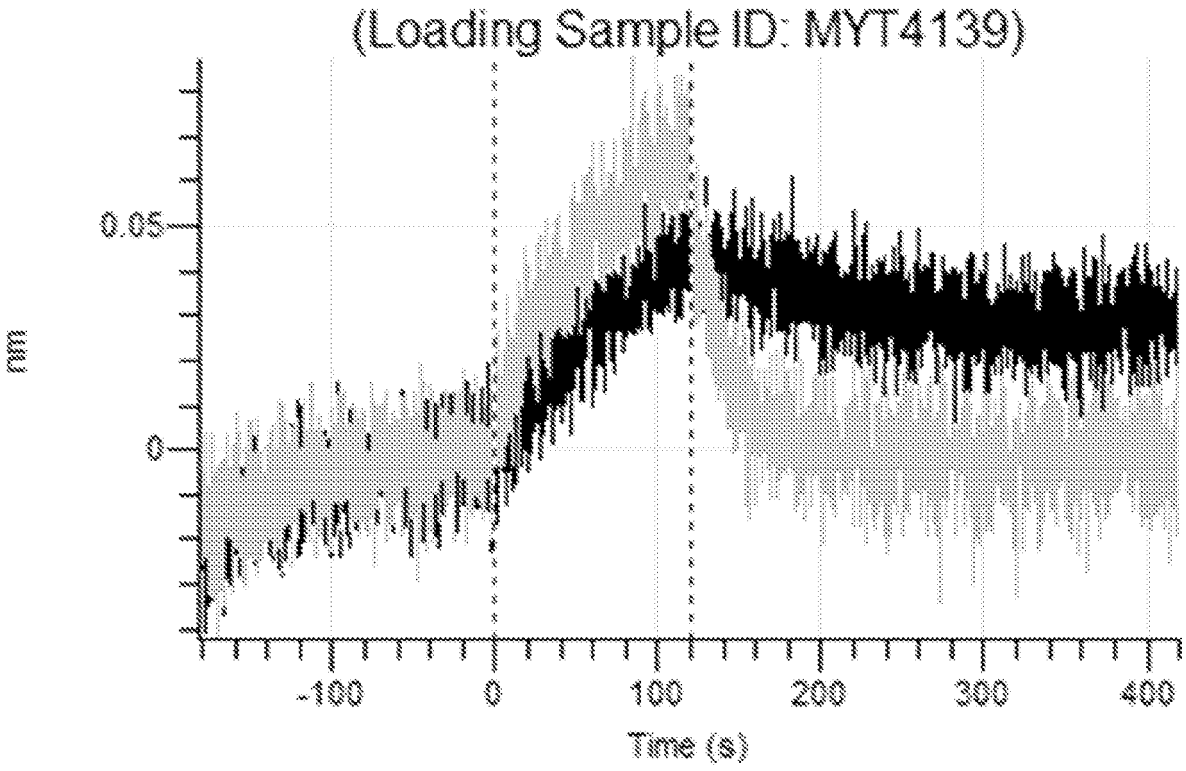


FIG. 38F

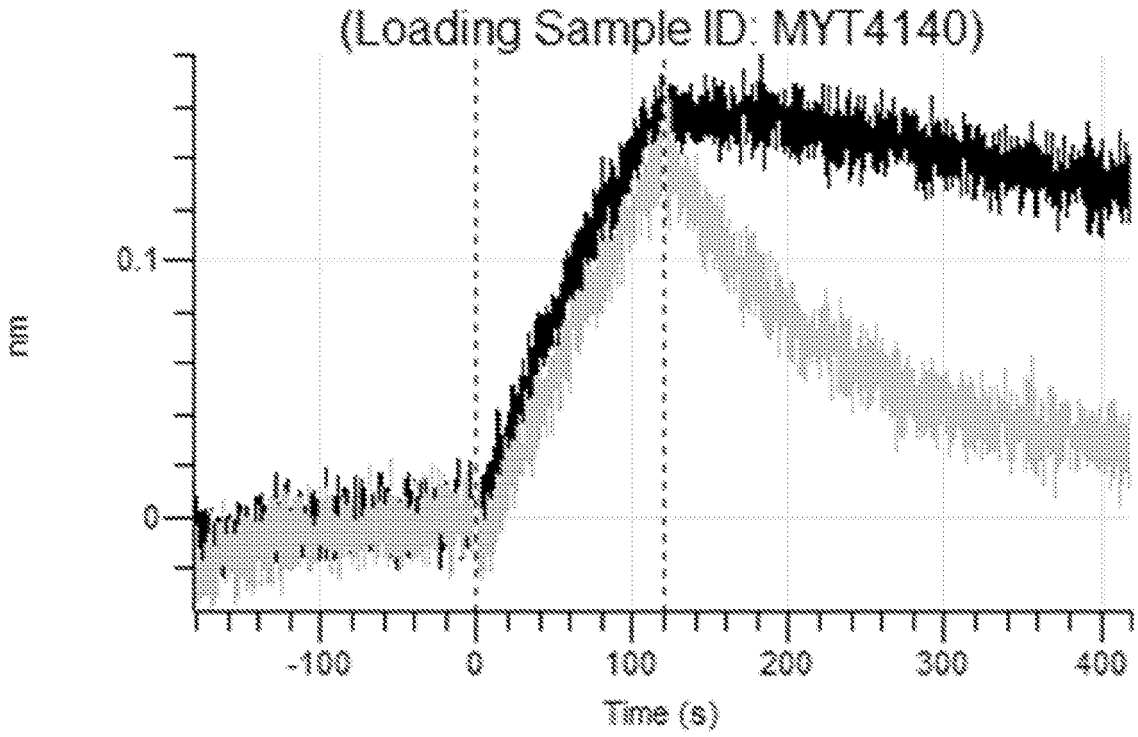


FIG. 38G

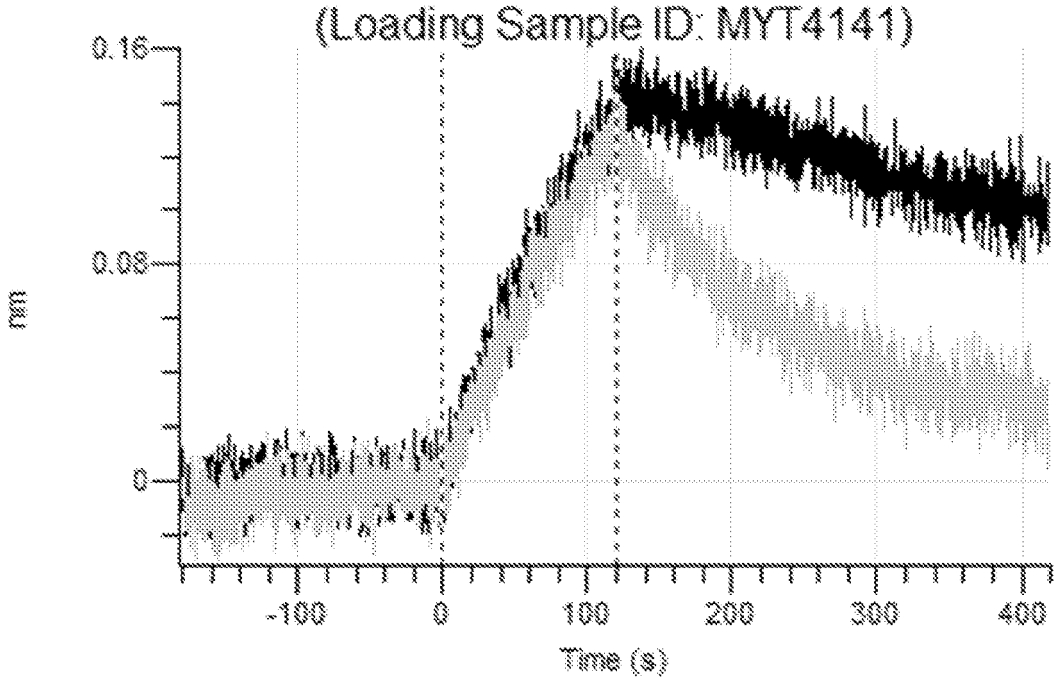

(Loading Sample ID: MYT4141)
0.16
0.08
0
nm
-100
0
100
200
300
400
Time (s)

FIG. 38H

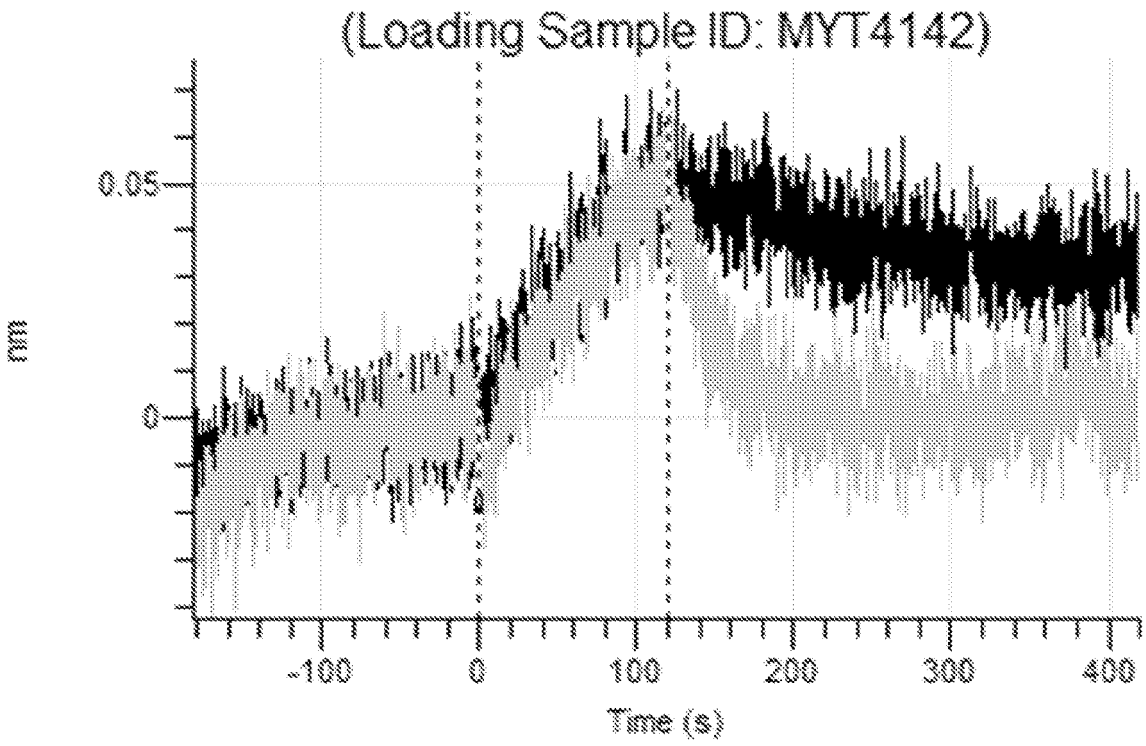


FIG. 38I

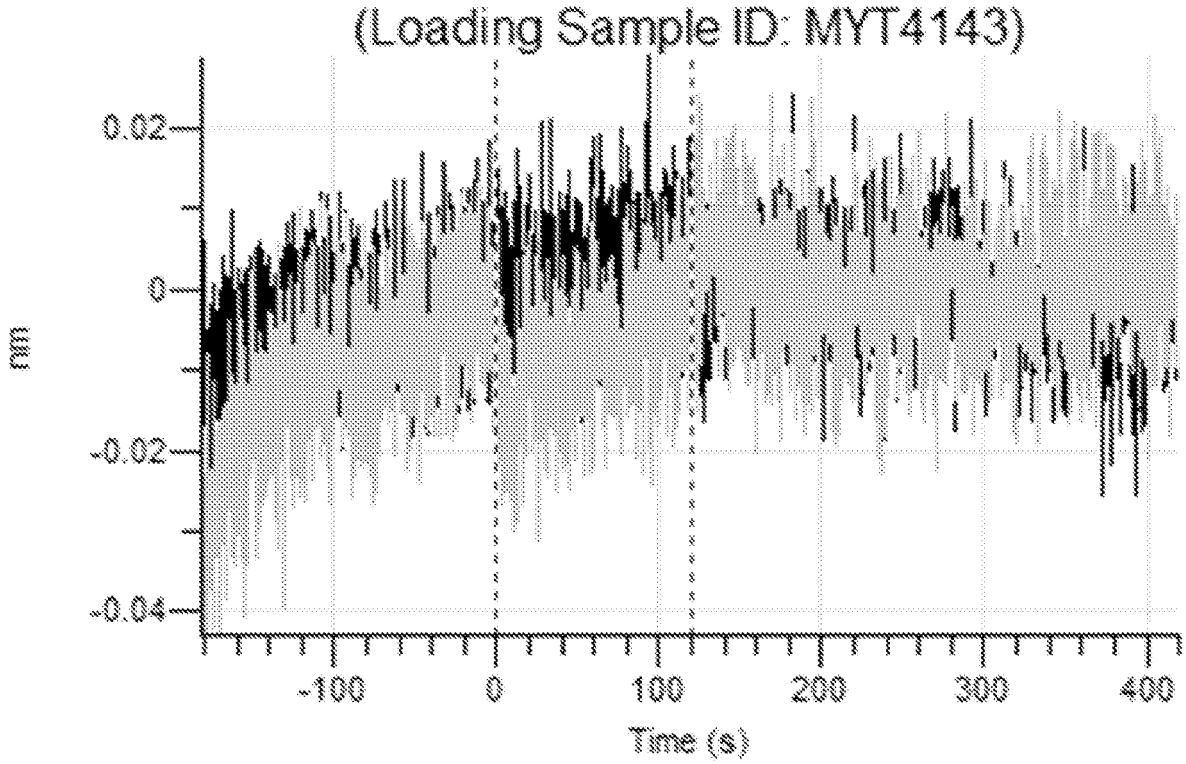

(Loading Sample ID: MYT4143)
0.02
0
-0.02
-0.04
nm
-100
0
100
200
300
400
Time (s)

FIG. 38J

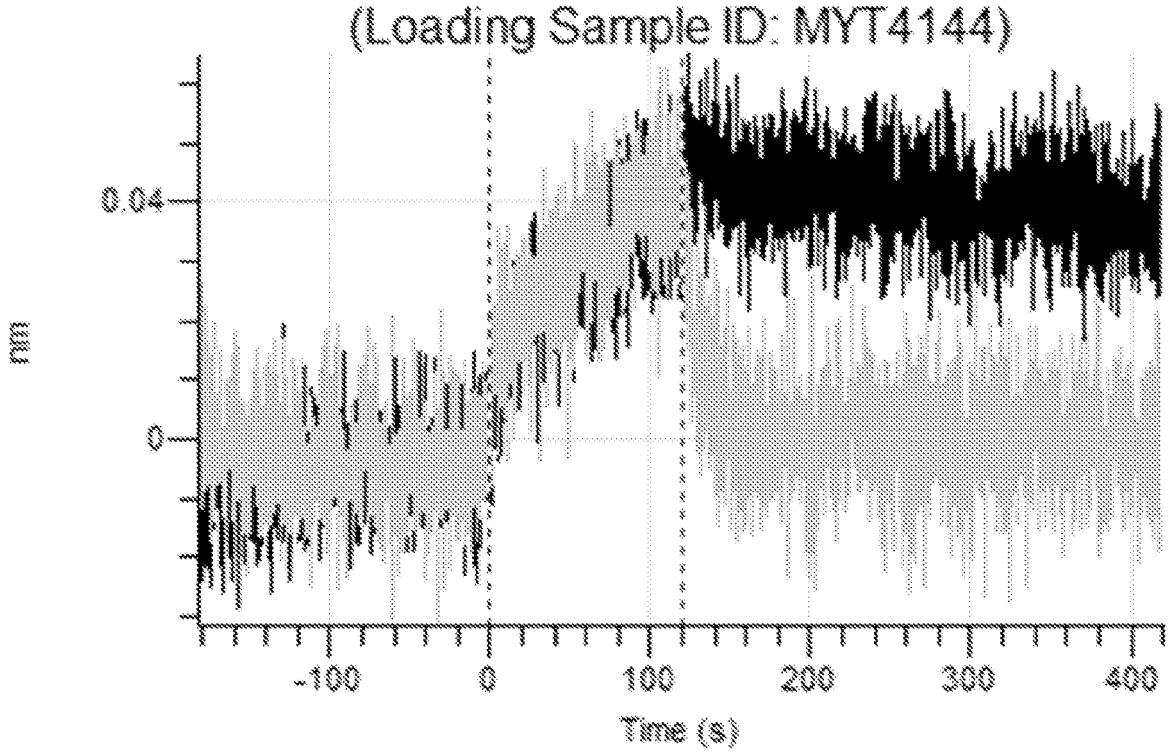


FIG. 38K

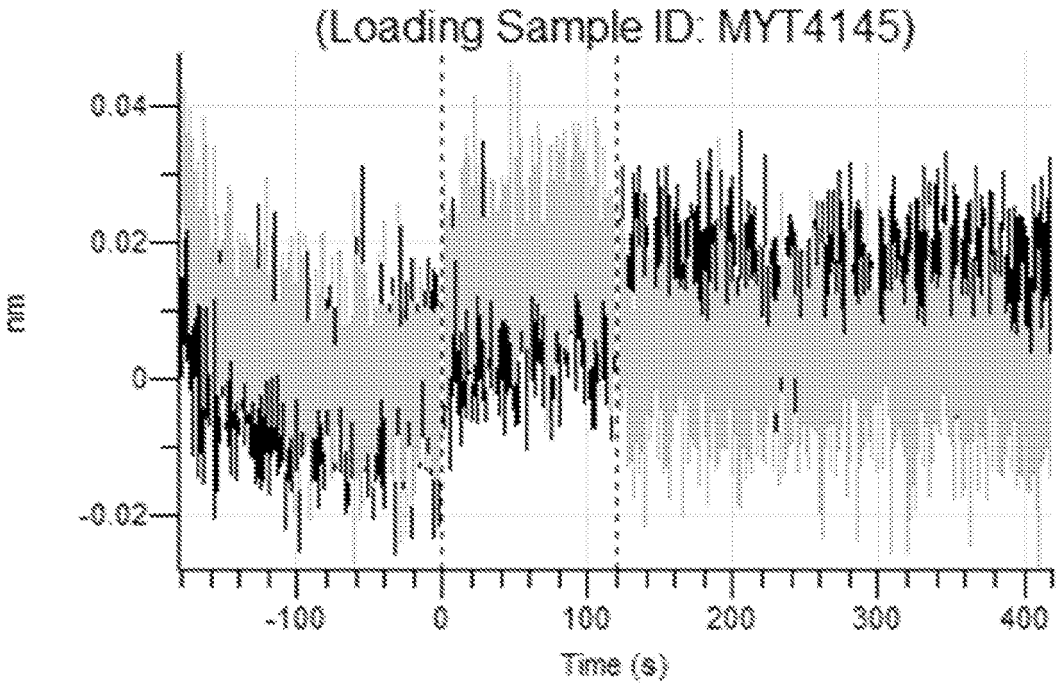

(Loading Sample ID: MYT4145)
0.04
0.02
0
-0.02
cm
-100
0
100
200
300
400
Time (s)

FIG. 38L

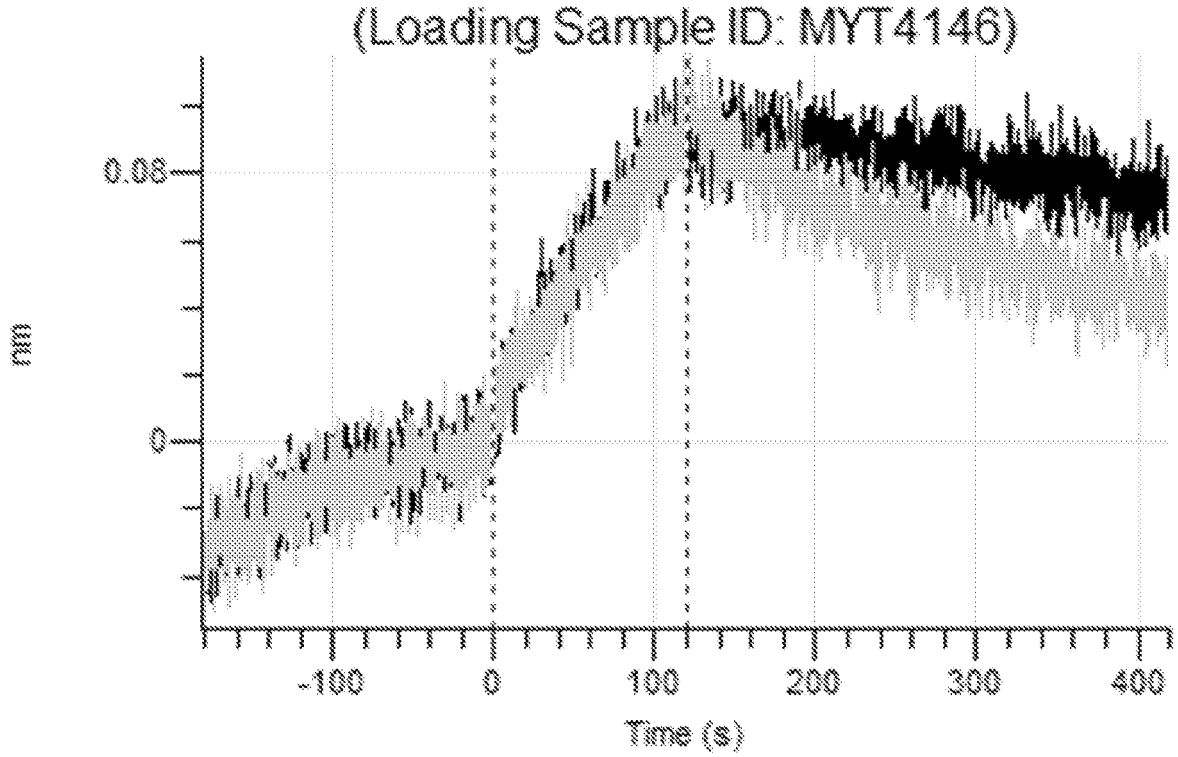


FIG. 38M

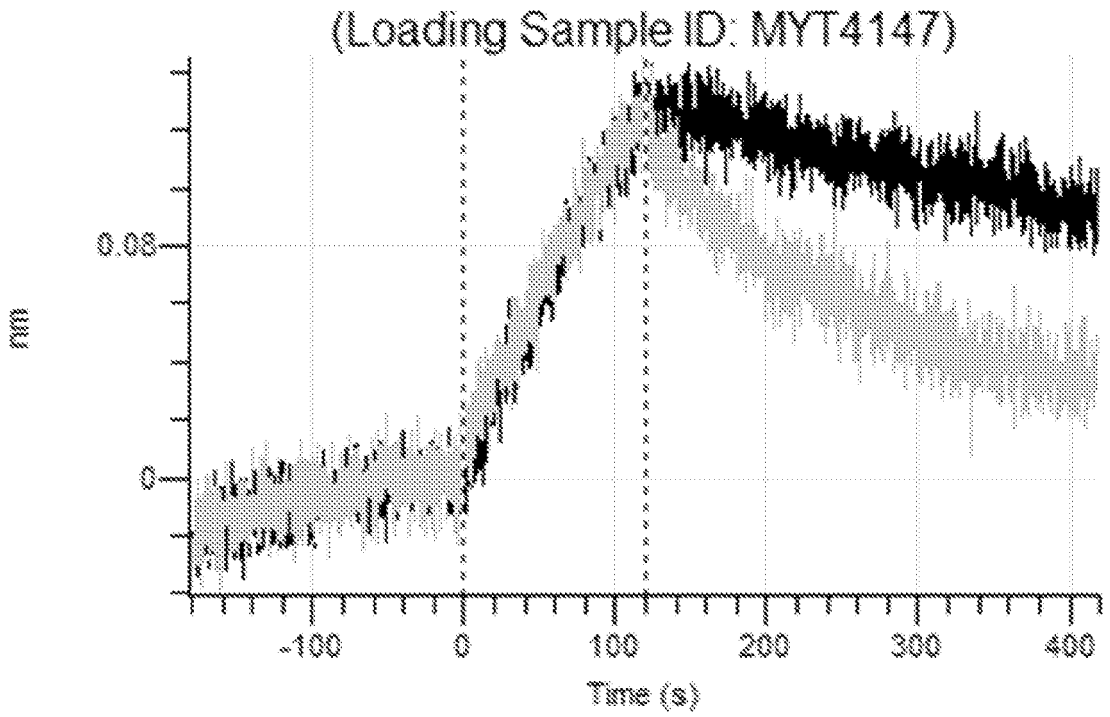


FIG. 38N

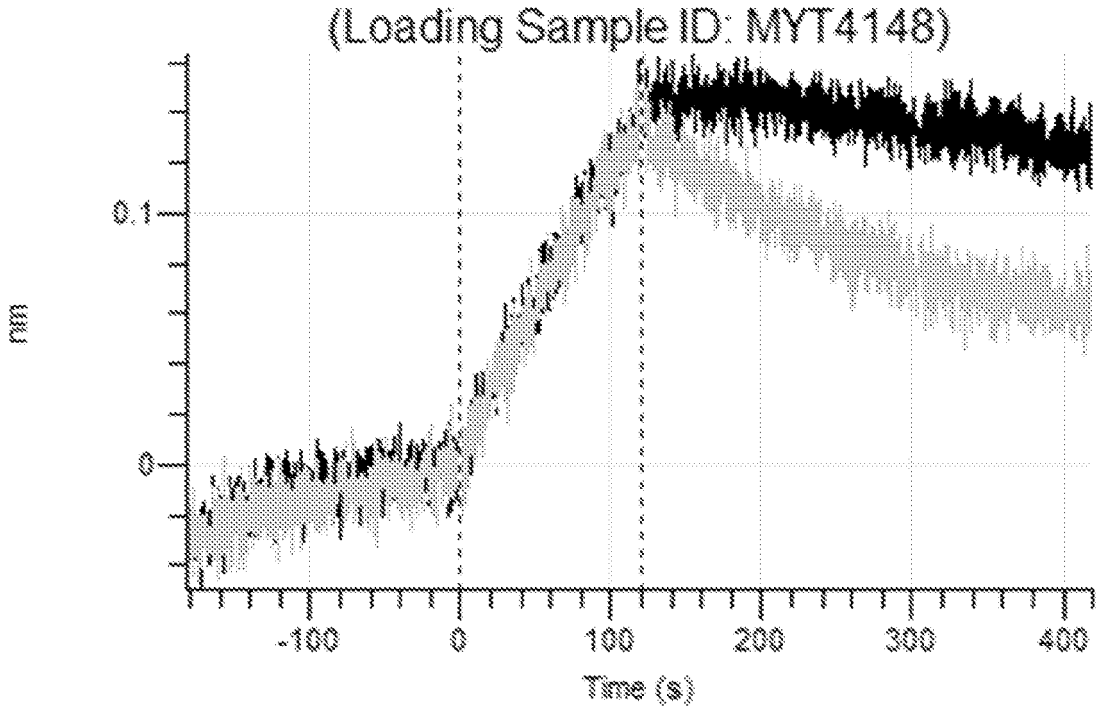


FIG. 38O

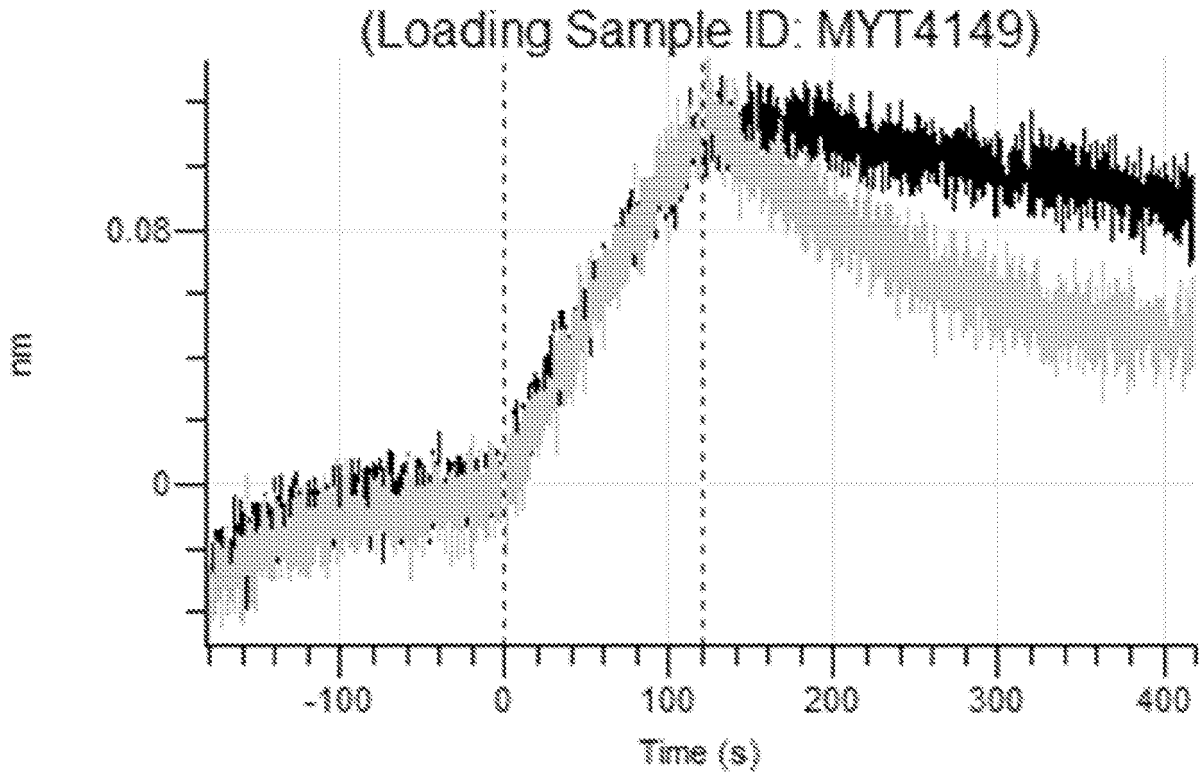


FIG. 38P

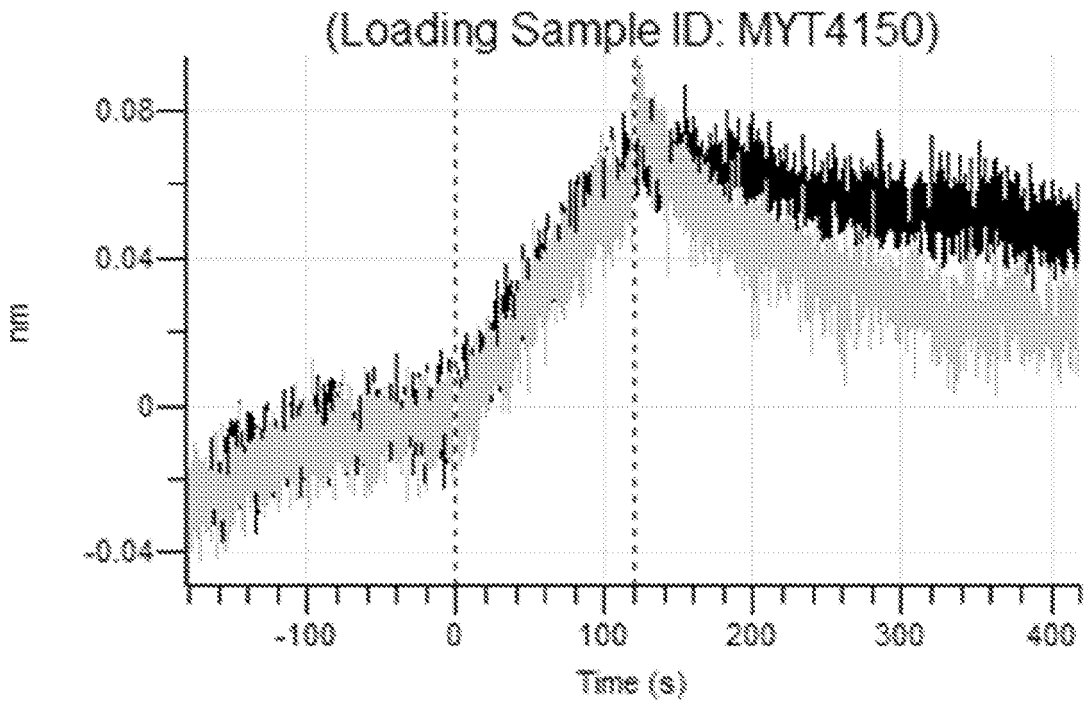

(Loading Sample ID: MYT4150)
0.08
0.04
0
-0.04
EMG
-100
0
100
200
300
400
Time (s)

FIG. 38Q

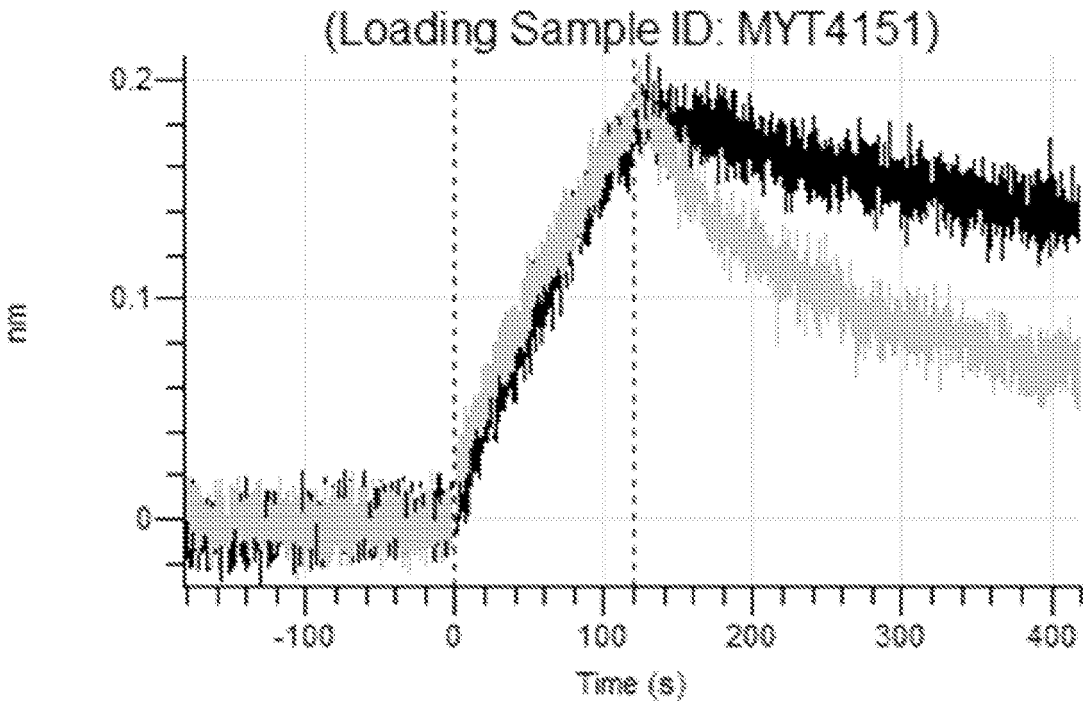

(Loading Sample ID: MYT4151)
0.2
0.1
0
nm
-100
0
100
200
300
400
Time (s)

FIG. 38R

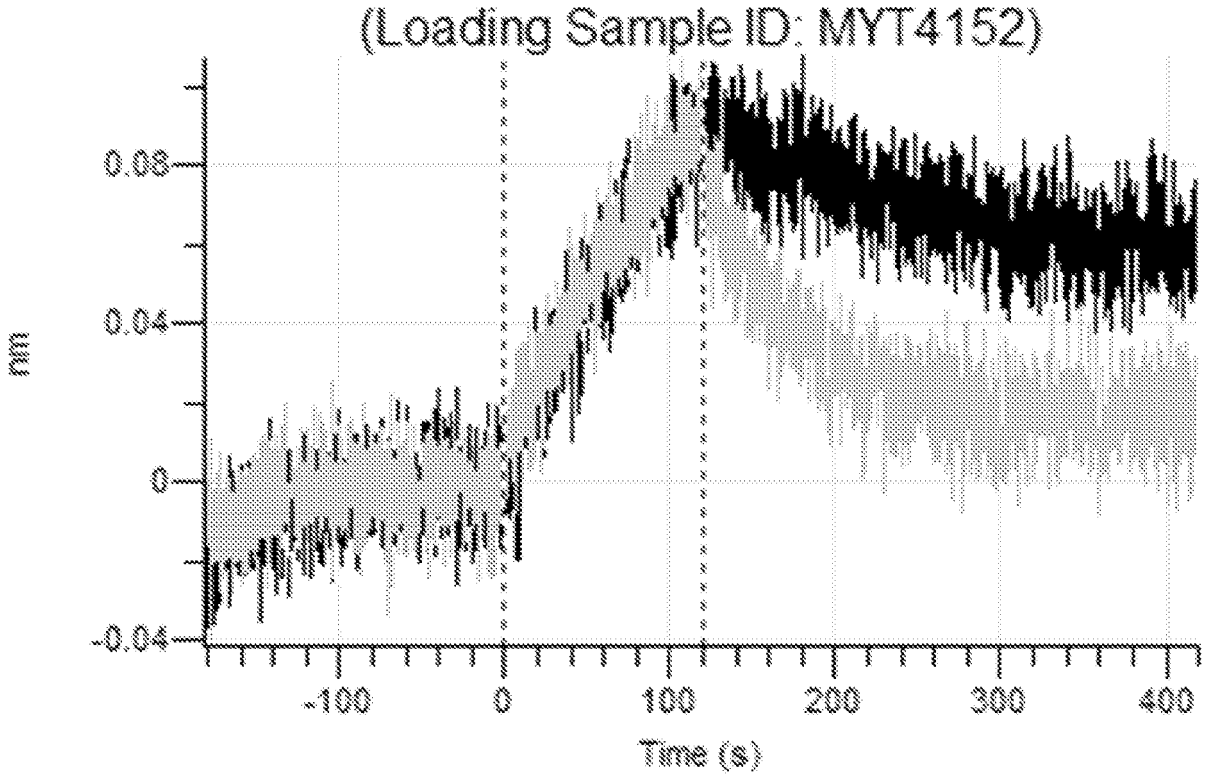

(Loading Sample ID: MYT4152)
0.08
0.04
0
-0.04
nm
-100
0
100
200
300
400
Time (s)

FIG. 38S

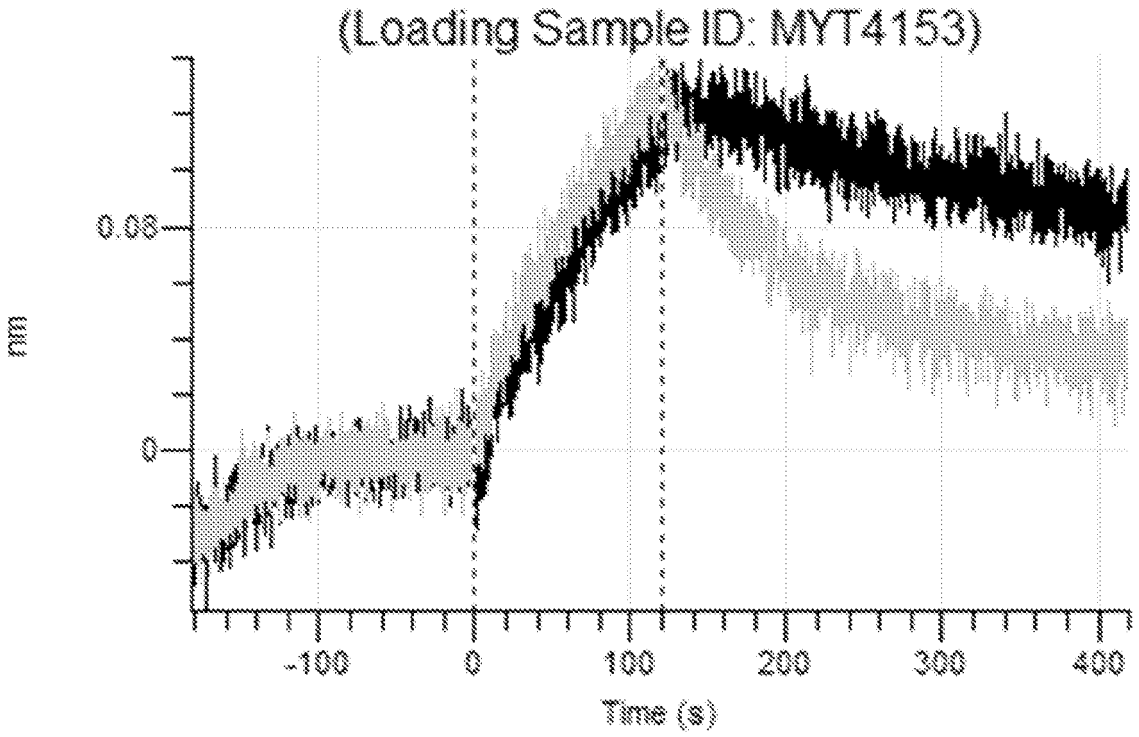


FIG. 38T

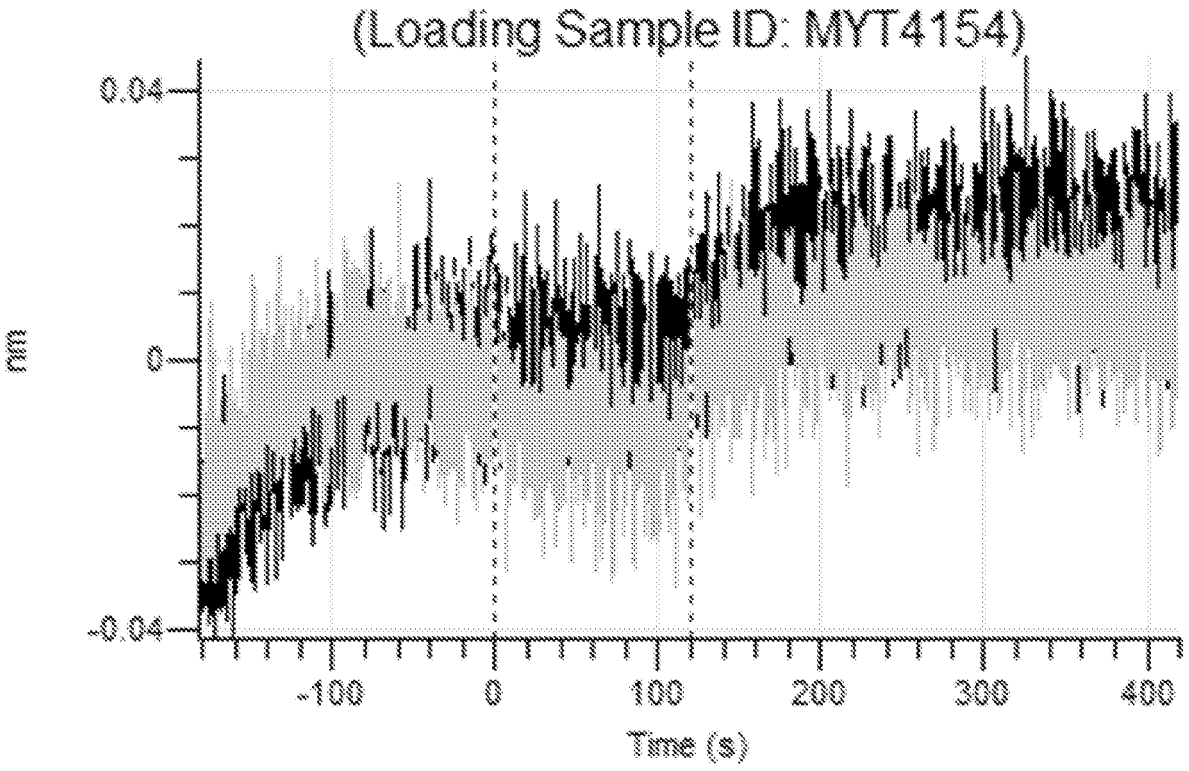

(Loading Sample ID: MYT4154)
0.04
0
-0.04
nm
-100
0
100
200
300
400
Time (s)

FIG. 38U

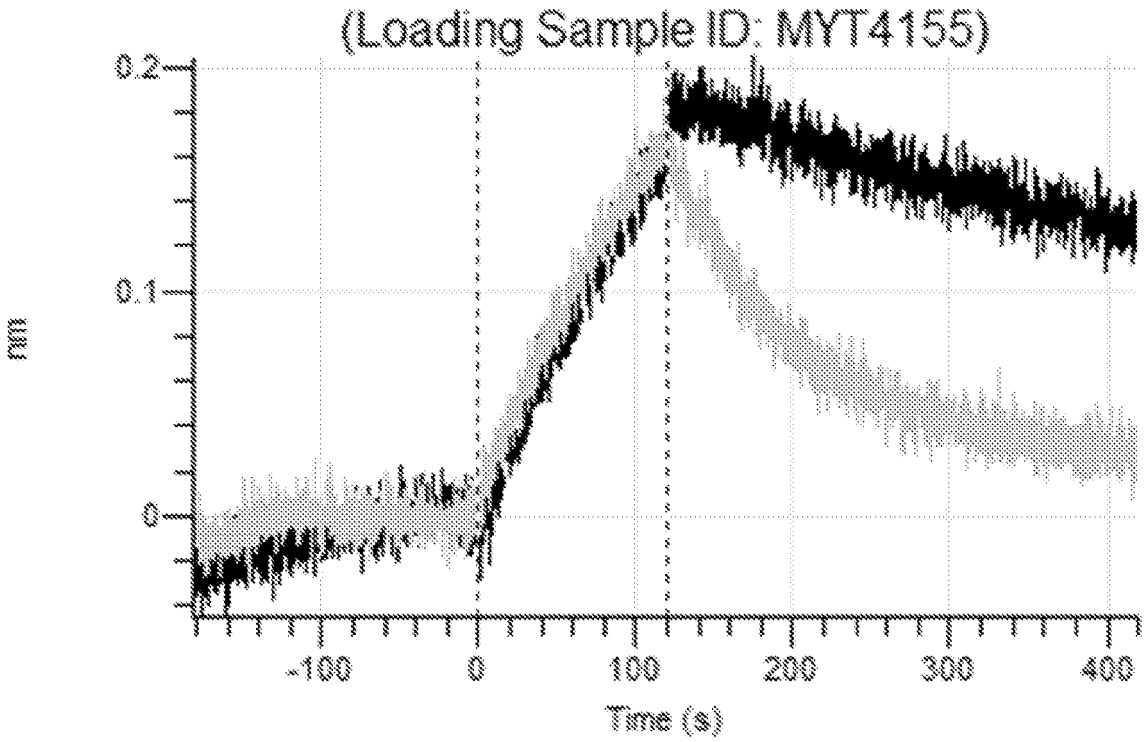

(Loading Sample ID: MYT4155)
nm
0.2
0.1
0
-100
0
100
200
300
400
Time (s)

FIG. 38V

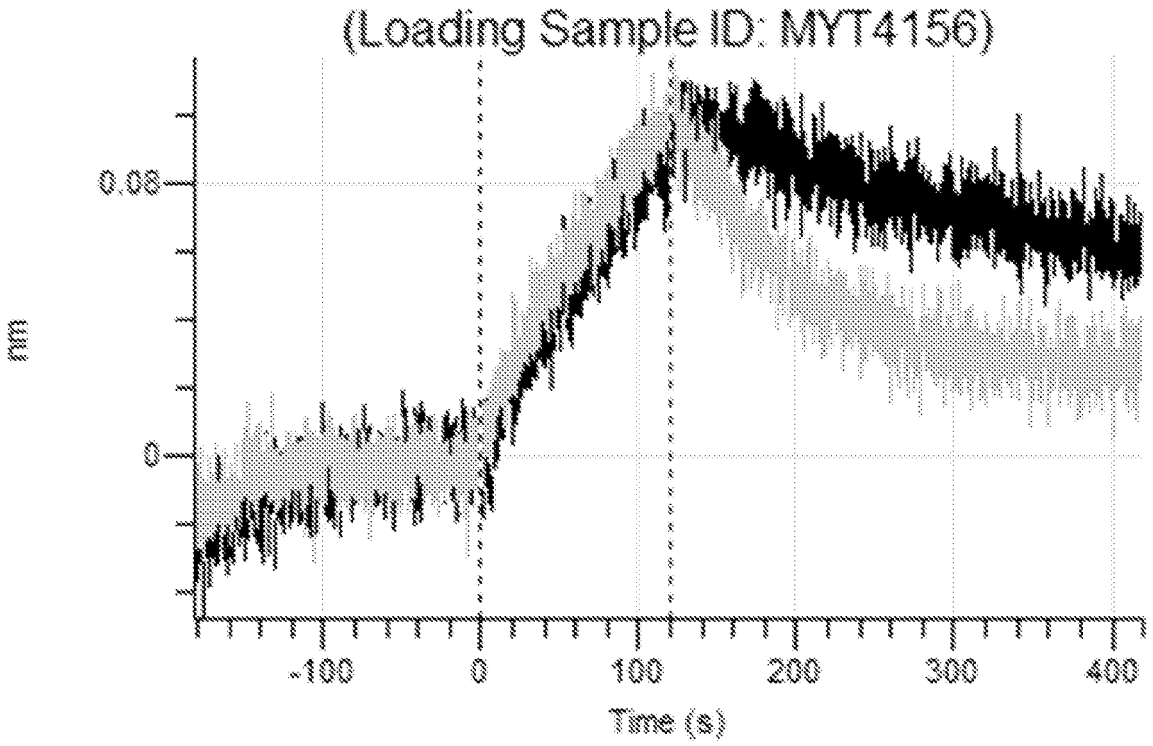


FIG. 38W

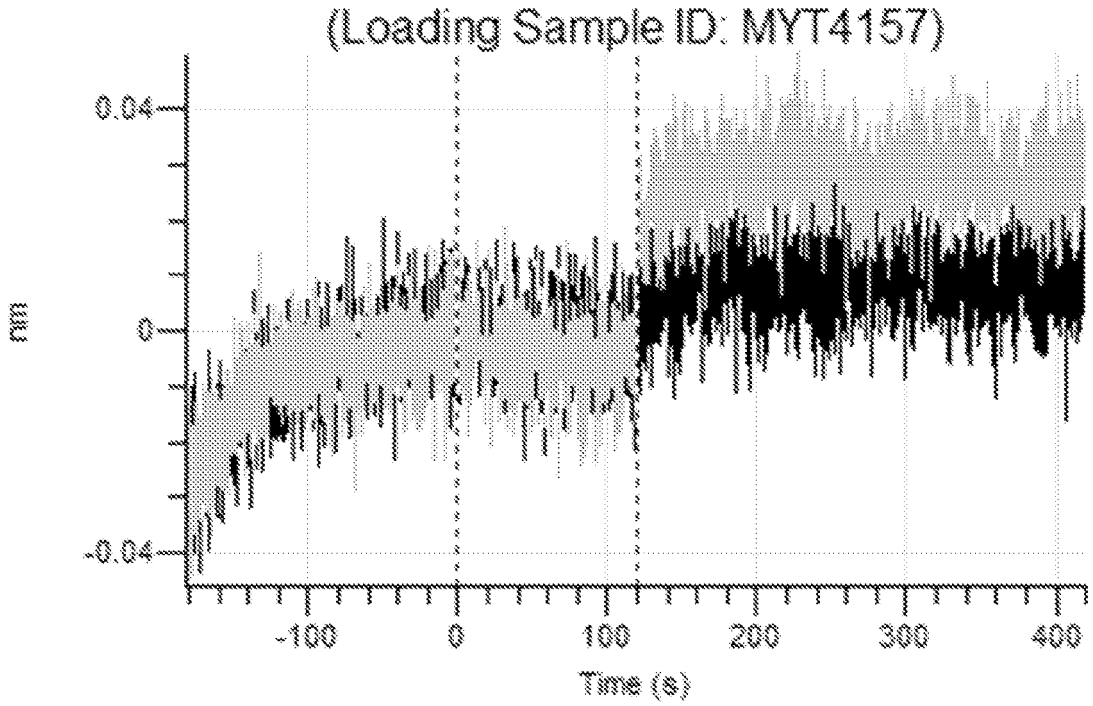

(Loading Sample ID: MYT4157)
0.04
0
-0.04
nm
-100
0
100
200
300
400
Time (s)

FIG. 38X

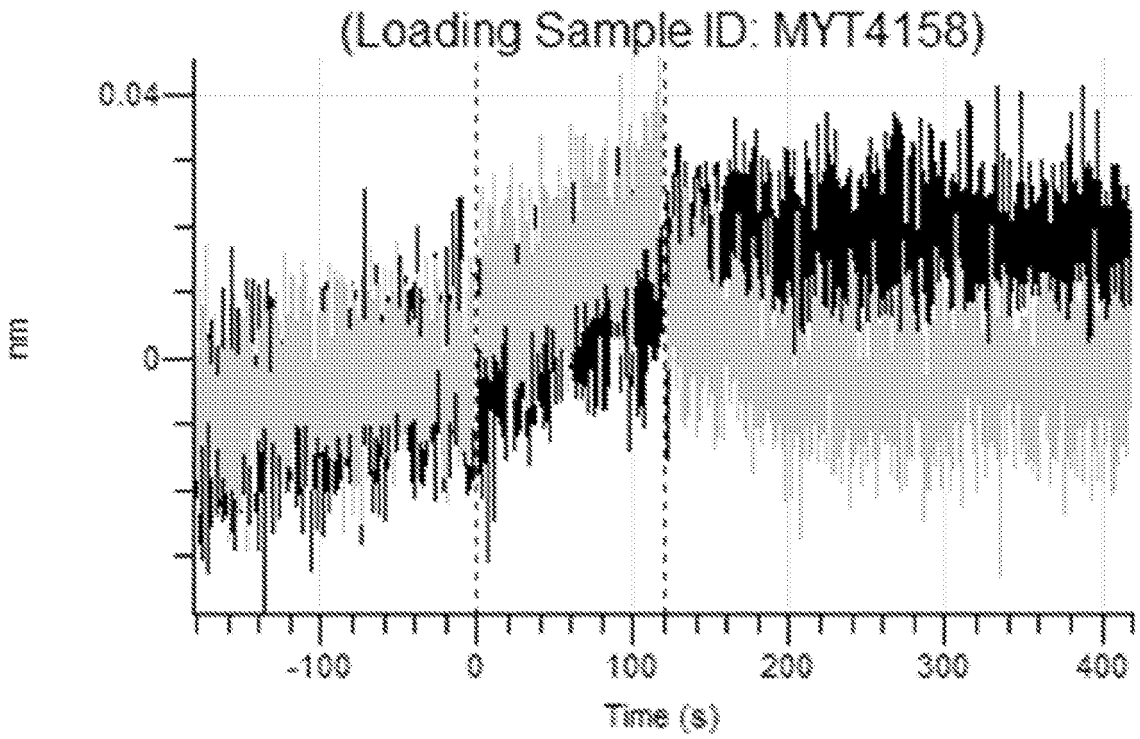


FIG. 38Y

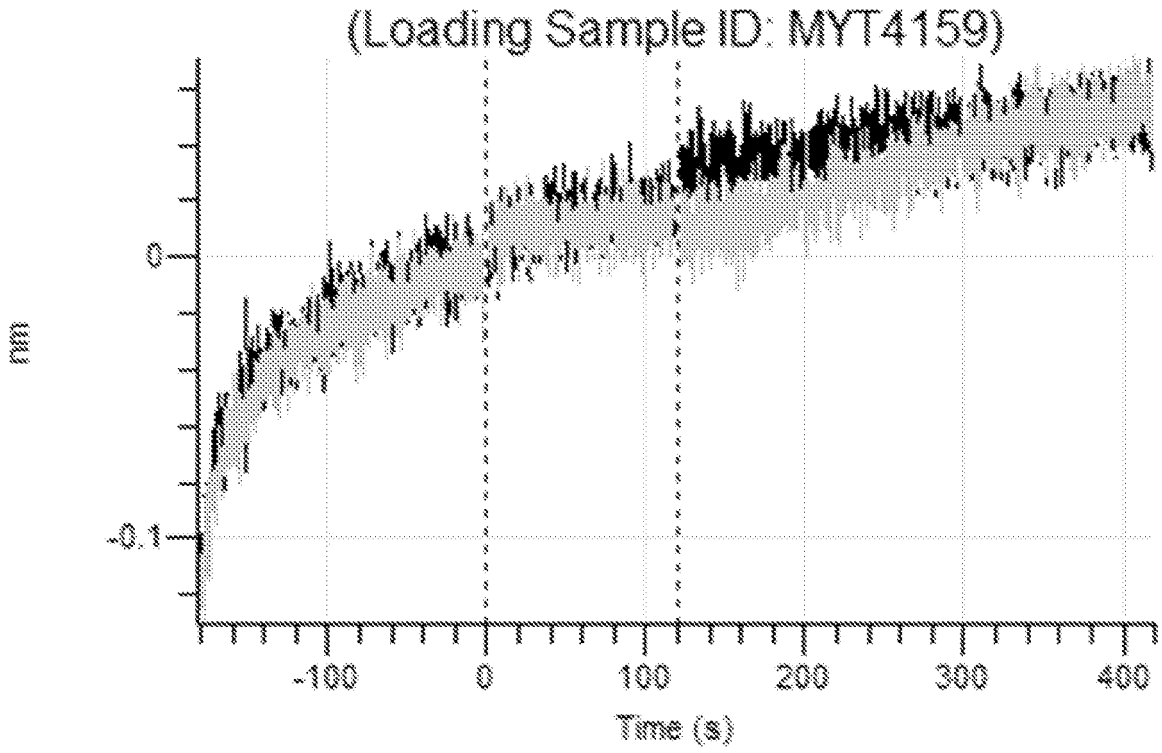


FIG. 38Z

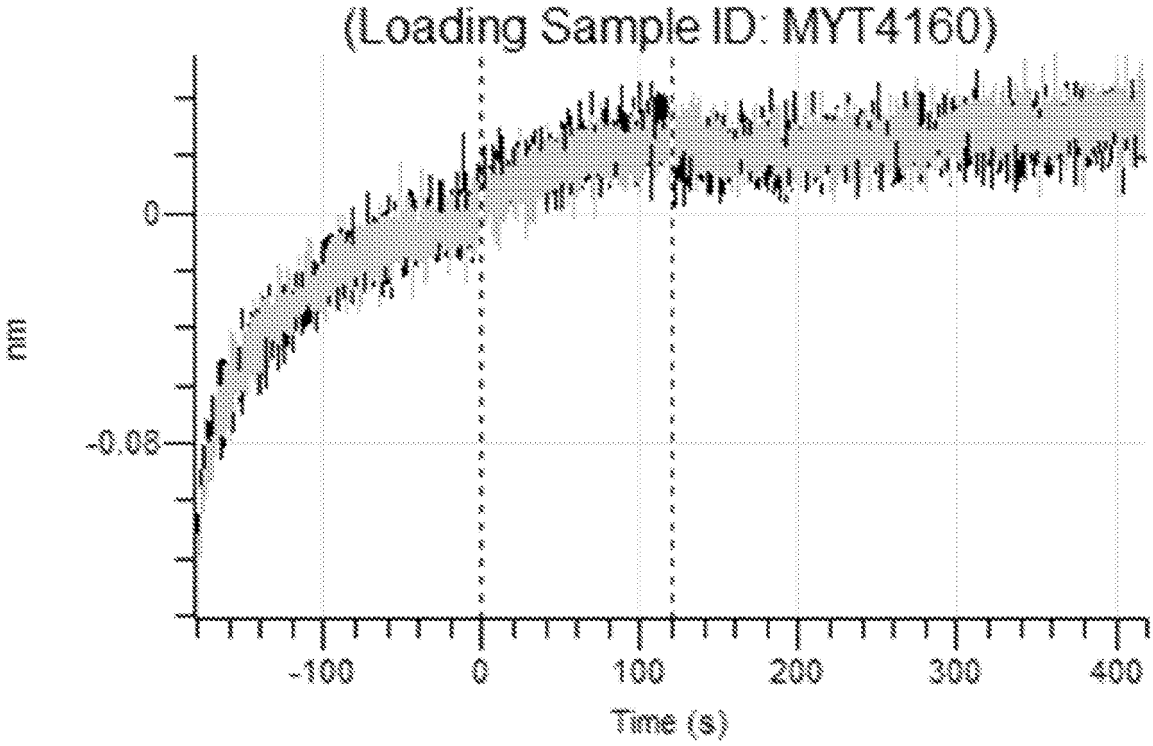


FIG. 38AA

	Heavy	Light	CDRH1	CDRH2	CDRH3	CDRL1	CDRL2	CDRL3
MYT3179 (huAD208.12.1)	272	273	274	275	276	277	278	279
MYT4134	272	324						
MYT4135	272	325						
MYT4136	272	326						
MYT4137	272	327						
MYT4138	272	328						
MYT4139	272	329						
MYT4140	272	330						
MYT4141	272	331						
MYT4142	272	332						
MYT4143	272	333						
MYT4144	272	334						
MYT4145	272	335						
MYT4146	272	336						
MYT4147	272	337						
MYT4148	272	338						
MYT4149	272	339						
MYT4150	272	340						
MYT4151	272	341						
MYT4152	272	342						
MYT4153	272	343						
MYT4154	272	344						
MYT4155	272	345						
MYT4156	272	346						
MYT4157	272	347						
MYT4158	272	348						
MYT4159	272	349						
MYT4160	272	350						

FIG. 39

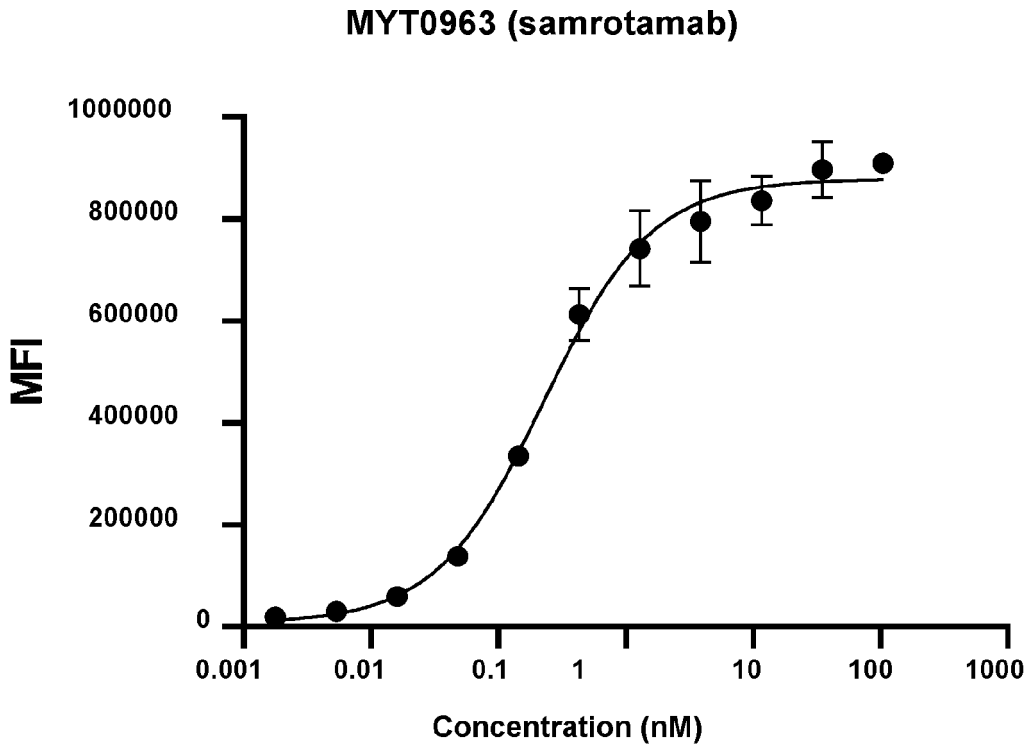

MYT0963 (samrotamab)
1000000
800000
600000
400000
200000
0
MFI
0.001
0.01
0.1
1
10
100
1000
Concentration (nM)

FIG. 40A

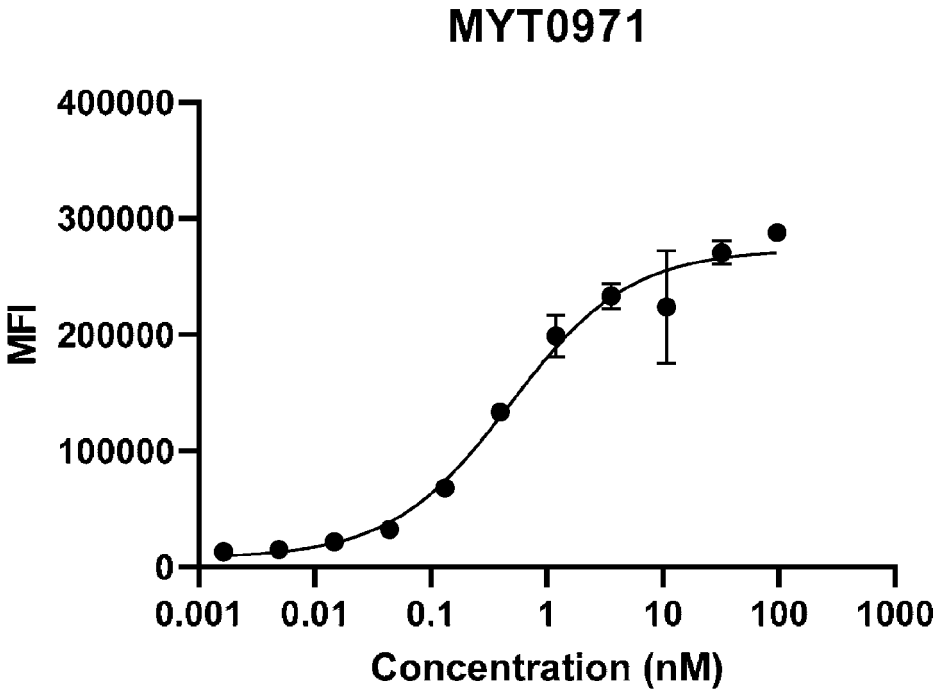

MYT0971
400000
300000
200000
100000
0
MFI
0.001
0.01
0.1
1
10
100
1000
Concentration (nM)

FIG. 40B

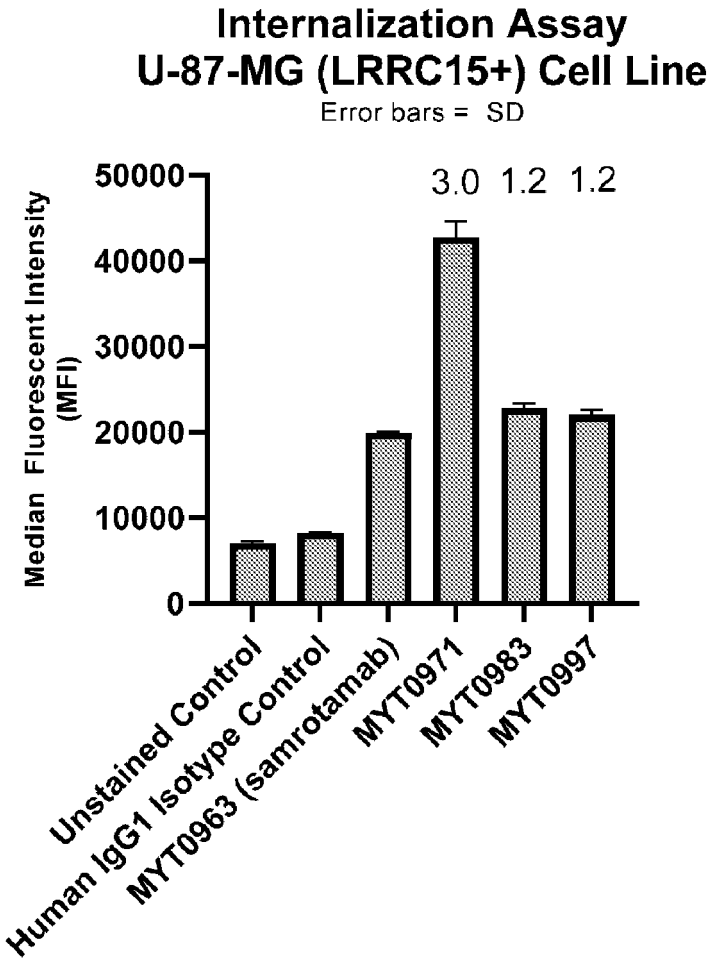

Internalization Assay
U-87-MG (LRRC15+) Cell Line
Error bars = SD
Median Fluorescent Intensity (MFI)
50000
40000
30000
20000
10000
0
3.0
1.2
1.2
Unstained Control
Human IgG1 Isotype Control
MYT0963 (samrotamab)
MYT0971
MYT0983
MYT0997

FIG. 41A

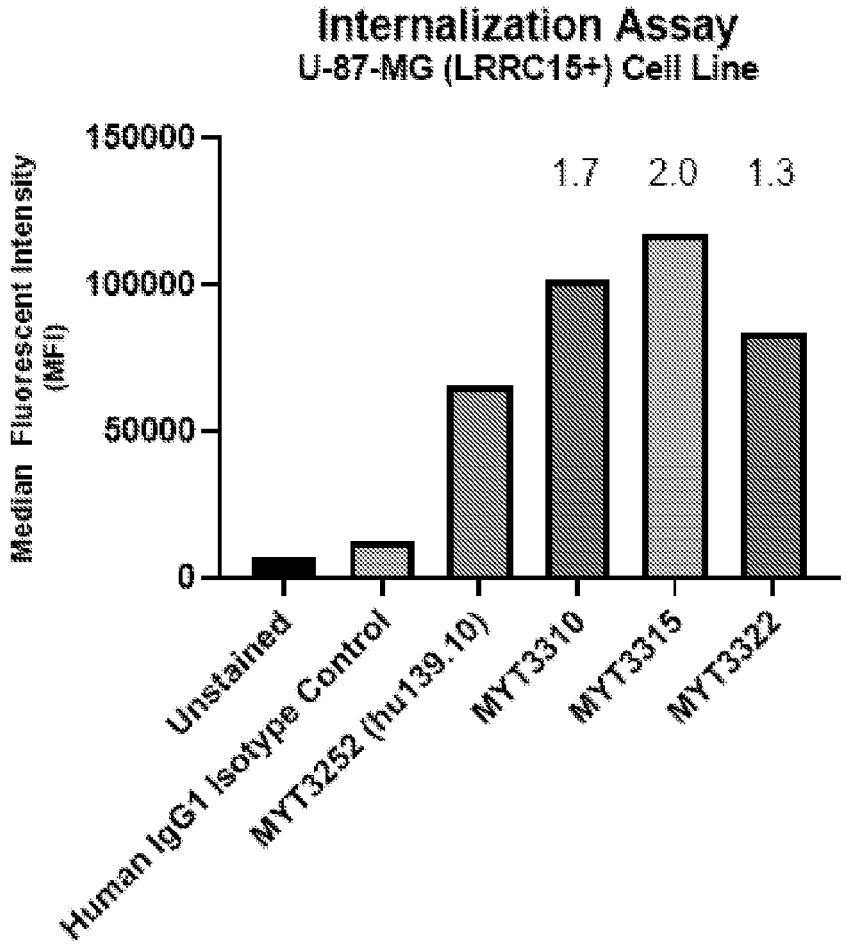

Internalization Assay
U-87-MG (LRRC15+) Cell Line
Median Fluorescent Intensity (MFI)
150000
100000
50000
0
1.7
2.0
1.3
Unstained
Human IgG1 Isotype Control
MYT3252 (hu139.10)
MYT3310
MYT3315
MYT3322

FIG. 41B

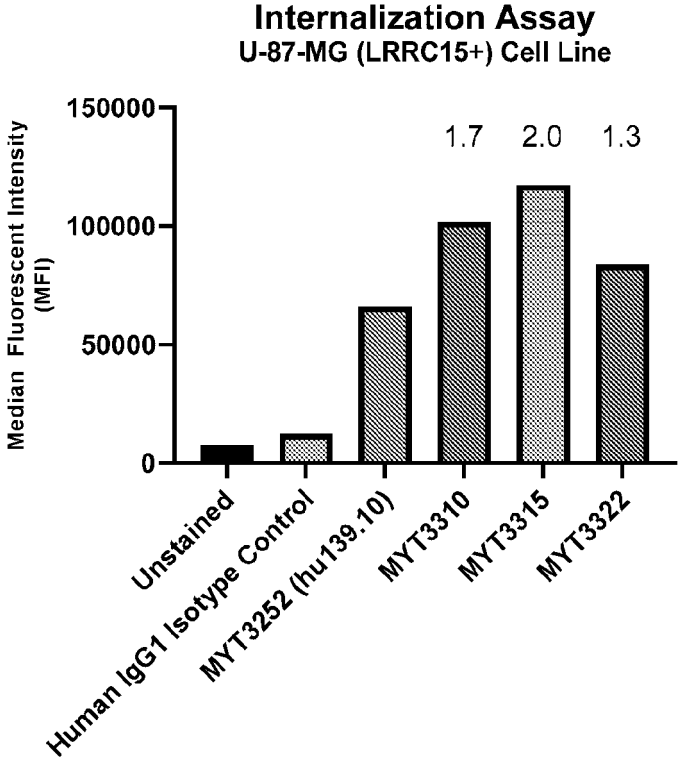

Internalization Assay
U-87-MG (LRRC15+) Cell Line
Median Fluorescent Intensity (MFI)
150000
100000
50000
0
1.7
2.0
1.3
Unstained
Human IgG1 Isotype Control
MYT3252 (hu139.10)
MYT3310
MYT3315
MYT3322

FIG. 41C

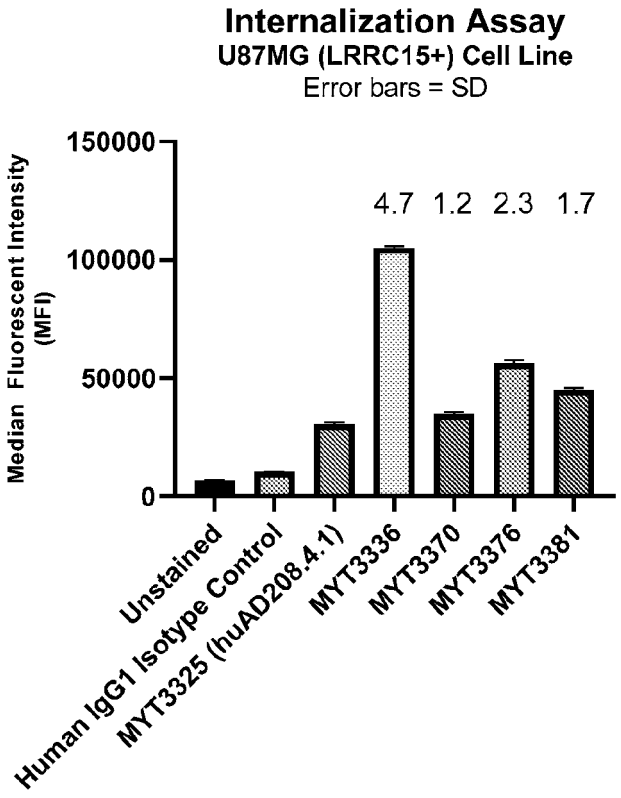

Internalization Assay
U87MG (LRRC15+) Cell Line
Error bars = SD
Median Fluorescent Intensity (MFI)
150000
100000
50000
0
4.7
1.2
2.3
1.7
Unstained
Human IgG1 Isotype Control
MYT3325 (huAD208.4.1)
MYT3336
MYT3370
MYT3376
MYT3381

FIG. 41D

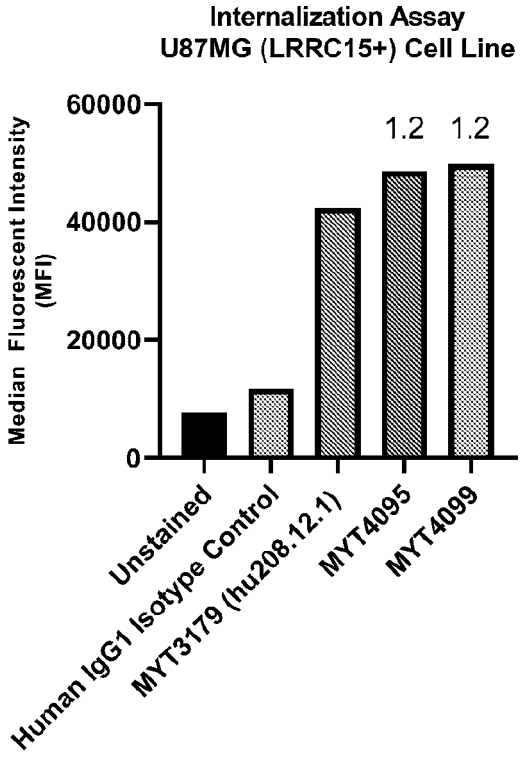

Internalization Assay
U87MG (LRRC15+) Cell Line
Median Fluorescent Intensity (MFI)
60000
40000
20000
0
1.2
1.2
Unstained
Human IgG1 Isotype Control
MYT3179 (hu208.12.1)
MYT4095
MYT4099

FIG. 41E

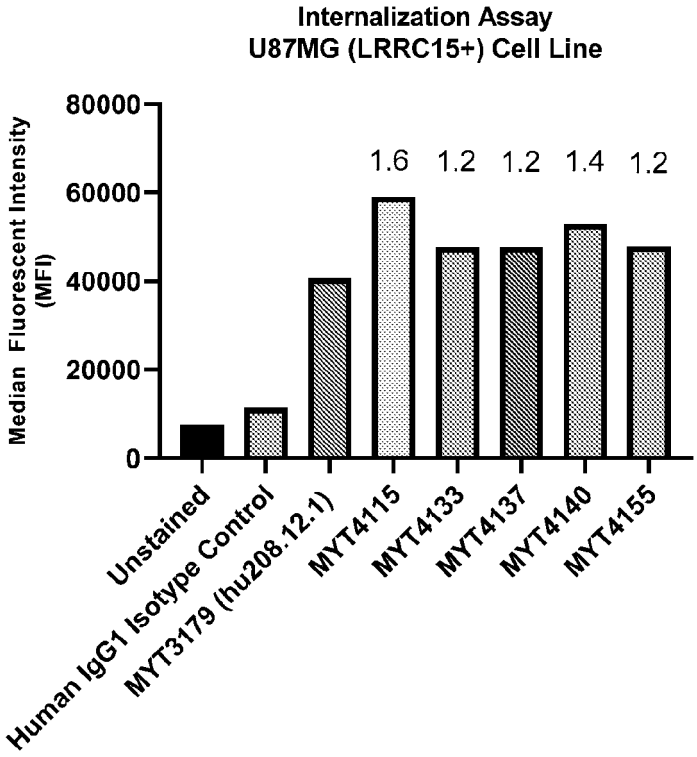

Internalization Assay
U87MG (LRRC15+) Cell Line
Median Fluorescent Intensity (MFI)
80000
60000
40000
20000
0
1.6
1.2
1.2
1.4
1.2
Unstained
Human IgG1 Isotype Control
MYT3179 (hu208.12.1)
MYT4115
MYT4133
MYT4137
MYT4140
MYT4155

FIG. 41F

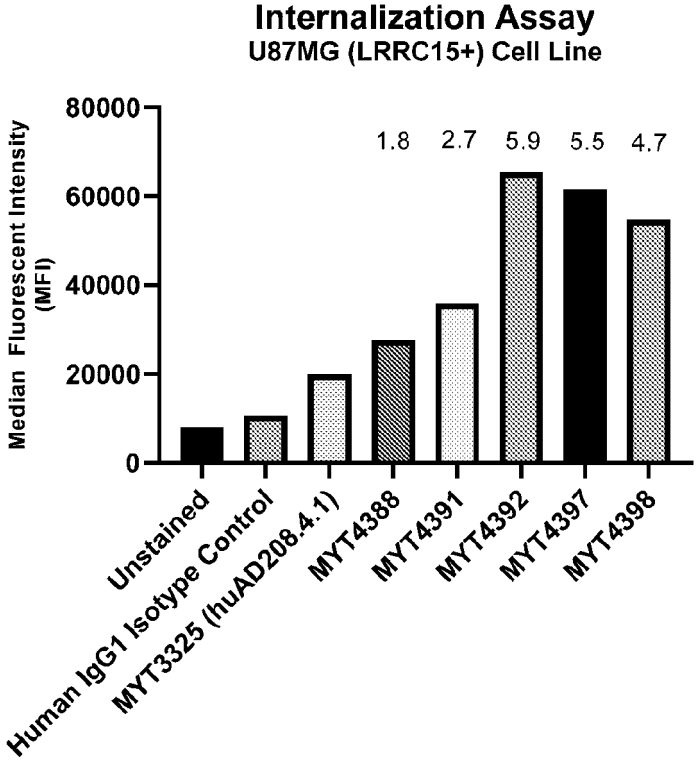

Internalization Assay
U87MG (LRRC15+) Cell Line
Median Fluorescent Intensity (MFI)
80000
60000
40000
20000
0
1.8
2.7
5.9
5.5
4.7
Unstained
Human IgG1 Isotype Control
MYT3325 (huAD208.4.1)
MYT4388
MYT4391
MYT4392
MYT4397
MYT4398

FIG. 41G

	Tm 1 (°C)	Tm 2 (°C)
MYT0963 (samrotamab)	70.4	77.8
MYT0971	70.6	76.2

FIG. 42

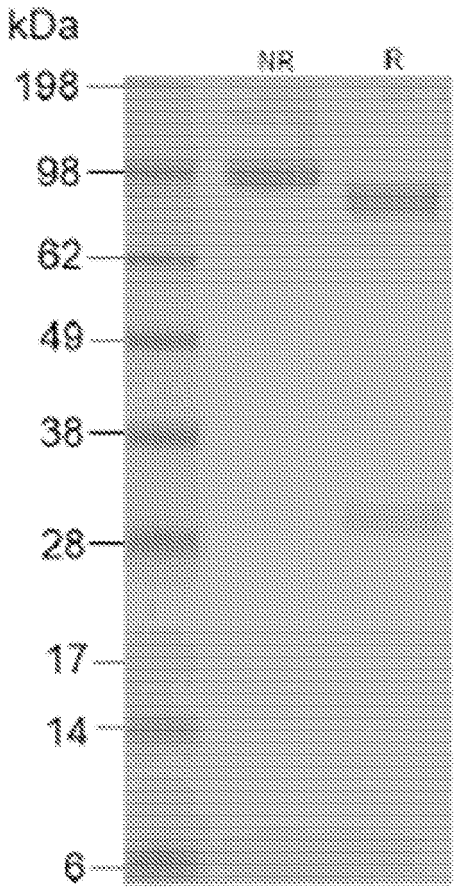


FIG. 43

SEQUENCE LISTING

<110> MYTHIC THERAPEUTICS, INC.

<120> ANTIGEN-BINDING PROTEIN CONSTRUCTS AND ANTIBODIES AND USES THEREOF

<130> 45395-0045WO1

<140>
<141>

<150> 63/171,705
<151> 2021-04-07

<160> 377

<170> PatentIn version 3.5

<210> 1
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG"

<400> 1
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr

65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 2
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG"

<400> 2
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 Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 3
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="Heavy Chain CDR1 of samrotamab"

<400> 3
Gly Tyr Lys Phe Ser Ser Tyr Trp Ile Glu
1 5 10

<210> 4
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic peptide"

<220>
<221> source
<223> /note="Heavy Chain CDR2 of samrotamab"

<400> 4
Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Asp

<210> 5
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> source
<223> /note="Heavy Chain CDR3 of samrotamab"

<400> 5
Ala Arg Asp Arg Gly Asn Tyr Arg Ala Trp Phe Gly Tyr
1 5 10

<210> 6
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> source
<223> /note="Light Chain CDR1 of samrotamab"

<400> 6
Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 7
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> source

<223> /note="Light Chain CDR2 of samrotamab"

<400> 7
Tyr Thr Ser Arg Leu His Ser
1   5

<210> 8
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<220>
<221> source
<223> /note="Light Chain CDR3 of samrotamab"

<400> 8
Gln Gln Gly Glu Ala Leu Pro Trp Thr
1   5

<210> 9
<211> 581
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Mature Human LRRC15"

<400> 9
Met Pro Leu Lys His Tyr Leu Leu Leu Leu Val Gly Cys Gln Ala Trp
1   5   10   15

Gly Ala Gly Leu Ala Tyr His Gly Cys Pro Ser Glu Cys Thr Cys Ser
            20   25   30

Arg Ala Ser Gln Val Glu Cys Thr Gly Ala Arg Ile Val Ala Val Pro
        35   40   45

Thr Pro Leu Pro Trp Asn Ala Met Ser Leu Gln Ile Leu Asn Thr His
    50   55   60

```
Ile Thr Glu Leu Asn Glu Ser Pro Phe Leu Asn Ile Ser Ala Leu Ile
65                  70                  75                  80

Ala Leu Arg Ile Glu Lys Asn Glu Leu Ser Arg Ile Thr Pro Gly Ala
                85                  90                  95

Phe Arg Asn Leu Gly Ser Leu Arg Tyr Leu Ser Leu Ala Asn Asn Lys
            100                 105                 110

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

Ser Leu Leu Leu Ser Ser Asn Gln Leu Leu Gln Ile Gln Pro Ala His
    130                 135                 140

Phe Ser Gln Cys Ser Asn Leu Lys Glu Leu Gln Leu His Gly Asn His
145                 150                 155                 160

Leu Glu Tyr Ile Pro Asp Gly Ala Phe Asp His Leu Val Gly Leu Thr
                165                 170                 175

Lys Leu Asn Leu Gly Lys Asn Ser Leu Thr His Ile Ser Pro Arg Val
            180                 185                 190

Phe Gln His Leu Gly Asn Leu Gln Val Leu Arg Leu Tyr Glu Asn Arg
        195                 200                 205

Leu Thr Asp Ile Pro Met Gly Thr Phe Asp Gly Leu Val Asn Leu Gln
    210                 215                 220

Glu Leu Ala Leu Gln Gln Asn Gln Ile Gly Leu Leu Ser Pro Gly Leu
225                 230                 235                 240

Phe His Asn Asn His Asn Leu Gln Arg Leu Tyr Leu Ser Asn Asn His
                245                 250                 255
```

```
Ile Ser Gln Leu Pro Pro Ser Val Phe Met Gln Leu Pro Gln Leu Asn
            260                 265                 270

Arg Leu Thr Leu Phe Gly Asn Ser Leu Lys Glu Leu Ser Pro Gly Ile
        275                 280                 285

Phe Gly Pro Met Pro Asn Leu Arg Glu Leu Trp Leu Tyr Asp Asn His
    290                 295                 300

Ile Ser Ser Leu Pro Asp Asn Val Phe Ser Asn Leu Arg Gln Leu Gln
305                 310                 315                 320

Val Leu Ile Leu Ser Arg Asn Gln Ile Ser Phe Ile Ser Pro Gly Ala
                325                 330                 335

Phe Asn Gly Leu Thr Glu Leu Arg Glu Leu Ser Leu His Thr Asn Ala
            340                 345                 350

Leu Gln Asp Leu Asp Gly Asn Val Phe Arg Met Leu Ala Asn Leu Gln
        355                 360                 365

Asn Ile Ser Leu Gln Asn Asn Arg Leu Arg Gln Leu Pro Gly Asn Ile
    370                 375                 380

Phe Ala Asn Val Asn Gly Leu Met Ala Ile Gln Leu Gln Asn Asn Gln
385                 390                 395                 400

Leu Glu Asn Leu Pro Leu Gly Ile Phe Asp His Leu Gly Lys Leu Cys
                405                 410                 415

Glu Leu Arg Leu Tyr Asp Asn Pro Trp Arg Cys Asp Ser Asp Ile Leu
            420                 425                 430

Pro Leu Arg Asn Trp Leu Leu Leu Asn Gln Pro Arg Leu Gly Thr Asp
        435                 440                 445

Thr Val Pro Val Cys Phe Ser Pro Ala Asn Val Arg Gly Gln Ser Leu
    450                 455                 460
```

```
Ile Ile Ile Asn Val Asn Val Ala Val Pro Ser Val His Val Pro Glu
465                 470                 475                 480


Val Pro Ser Tyr Pro Glu Thr Pro Trp Tyr Pro Asp Thr Pro Ser Tyr
                485                 490                 495


Pro Asp Thr Thr Ser Val Ser Ser Thr Thr Glu Leu Thr Ser Pro Val
            500                 505                 510


Glu Asp Tyr Thr Asp Leu Thr Thr Ile Gln Val Thr Asp Asp Arg Ser
        515                 520                 525


Val Trp Gly Met Thr Gln Ala Gln Ser Gly Leu Ala Ile Ala Ala Ile
    530                 535                 540


Val Ile Gly Ile Val Ala Leu Ala Cys Ser Leu Ala Ala Cys Val Gly
545                 550                 555                 560


Cys Cys Cys Cys Lys Lys Arg Ser Gln Ala Val Leu Met Gln Met Lys
                565                 570                 575


Ala Pro Asn Glu Cys
            580
```

<210> 10
<211> 1743
<212> DNA
<213> Homo sapiens

<220>
<221> source
<223> /note="cDNA Encoding Mature Human LRRC15"

<400> 10
atgccactga agcattatct ccttttgctg gtgggctgcc aagcctgggg tgcagggttg 60

gcctaccatg gctgccctag cgagtgtacc tgctccaggg cctcccaggt ggagtgcacc 120

ggggcacgca ttgtggcagt gcccaccct ctgccctgga acgccatgag cctgcagatc 180

ctcaacacgc acatcactga actcaatgag tccccgttcc tcaatatctc agccctcatc 240

gccctgagga ttgagaagaa tgagctgtcg cgcatcacgc ctggggcctt ccgaaacctg 300

ggctcgctgc gctatctcag cctcgccaac aacaagctgc aggttctgcc catcggcctc 360

ttccagggcc tggacagcct cgagtctctc cttctgtcca gtaaccagct gttgcagatc 420

cagccggccc acttctccca gtgcagcaac ctcaaggagc tgcagttgca cggcaaccac 480

ctggaataca tccctgacgg agccttcgac cacctggtag gactcacgaa gctcaatctg 540

ggcaagaata gcctcaccca catctcaccc agggtcttcc agcacctggg caacctccag 600

gtcctccggc tgtatgagaa caggctcacg gatatcccca tgggcacttt tgatgggctt 660

gttaacctgc aggaactggc tctgcagcag aaccagattg gactgctctc ccctggtctc 720

ttccacaaca accacaacct ccagagactc tacctgtcca acaaccacat ctcccagctg 780

ccacccagcg tcttcatgca gctgccccag ctcaaccgtc ttactctctt tgggaattcc 840

ctgaaggagc tctctccggg gatcttcggg cccatgccca acctgcggga gctttggctc 900

tatgacaacc acatctcttc tctacccgac aatgtcttca gcaacctccg ccagttgcag 960

gtcctgattc ttagccgcaa tcagatcagc ttcatctccc cgggtgcctt caacgggcta 1020

acggagcttc gggagctgtc cctccacacc aacgcactgc aggacctgga cgggaacgtc 1080

ttccgcatgt tggccaacct gcagaacatc tccctgcaga acaaccgcct cagacagctc 1140

ccagggaata tcttcgccaa cgtcaatggc ctcatggcca tccagctgca gaacaaccag 1200

ctggagaact tgcccctcgg catcttcgat cacctgggga aactgtgtga gctgcggctg 1260

tatgacaatc cctggaggtg tgactcagac atccttccgc tccgcaactg gctcctgctc 1320

aaccagccta ggttagggac ggacactgta cctgtgtgtt tcagcccagc caatgtccga 1380

ggccagtccc tcattatcat caatgtcaac gttgctgttc caagcgtcca tgtccccgag 1440

gtgcctagtt acccagaaac accatggtac ccagacacac ccagttaccc tgacaccaca 1500

tccgtctctt ctaccactga gctaaccagc cctgtggaag actacactga tctgactacc 1560

attcaggtca ctgatgaccg cagcgtttgg ggcatgaccc aggcccagag cgggctggcc 1620

attgccgcca ttgtaattgg cattgtcgcc ctggcctgct ccctggctgc ctgcgtcggc 1680

tgttgctgct gcaagaagag gagccaagct gtcctgatgc agatgaaggc acccaatgag 1740

tgt 1743

<210> 11
<211> 517
<212> PRT
<213> Homo sapiens

<220>
<221> source
<223> /note="Extracellular Domain of LRRC15"

<400> 11
Tyr His Gly Cys Pro Ser Glu Cys Thr Cys Ser Arg Ala Ser Gln Val
1 5 10 15

Glu Cys Thr Gly Ala Arg Ile Val Ala Val Pro Thr Pro Leu Pro Trp
20 25 30

Asn Ala Met Ser Leu Gln Ile Leu Asn Thr His Ile Thr Glu Leu Asn
35 40 45

Glu Ser Pro Phe Leu Asn Ile Ser Ala Leu Ile Ala Leu Arg Ile Glu
50 55 60

Lys Asn Glu Leu Ser Arg Ile Thr Pro Gly Ala Phe Arg Asn Leu Gly
65 70 75 80

Ser Leu Arg Tyr Leu Ser Leu Ala Asn Asn Lys Leu Gln Val Leu Pro
85 90 95

Ile Gly Leu Phe Gln Gly Leu Asp Ser Leu Glu Ser Leu Leu Leu Ser
100 105 110

Ser Asn Gln Leu Leu Gln Ile Gln Pro Ala His Phe Ser Gln Cys Ser
115 120 125

Asn Leu Lys Glu Leu Gln Leu His Gly Asn His Leu Glu Tyr Ile Pro
130 135 140

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Asp Gly Ala Phe Asp His Leu Val Gly Leu Thr Lys Leu Asn Leu Gly
145                 150                 155                 160

Lys Asn Ser Leu Thr His Ile Ser Pro Arg Val Phe Gln His Leu Gly
                165                 170                 175

Asn Leu Gln Val Leu Arg Leu Tyr Glu Asn Arg Leu Thr Asp Ile Pro
            180                 185                 190

Met Gly Thr Phe Asp Gly Leu Val Asn Leu Gln Glu Leu Ala Leu Gln
        195                 200                 205

Gln Asn Gln Ile Gly Leu Leu Ser Pro Gly Leu Phe His Asn Asn His
    210                 215                 220

Asn Leu Gln Arg Leu Tyr Leu Ser Asn Asn His Ile Ser Gln Leu Pro
225                 230                 235                 240

Pro Ser Val Phe Met Gln Leu Pro Gln Leu Asn Arg Leu Thr Leu Phe
                245                 250                 255

Gly Asn Ser Leu Lys Glu Leu Ser Pro Gly Ile Phe Gly Pro Met Pro
            260                 265                 270

Asn Leu Arg Glu Leu Trp Leu Tyr Asp Asn His Ile Ser Ser Leu Pro
        275                 280                 285

Asp Asn Val Phe Ser Asn Leu Arg Gln Leu Gln Val Leu Ile Leu Ser
    290                 295                 300

Arg Asn Gln Ile Ser Phe Ile Ser Pro Gly Ala Phe Asn Gly Leu Thr
305                 310                 315                 320

Glu Leu Arg Glu Leu Ser Leu His Thr Asn Ala Leu Gln Asp Leu Asp
                325                 330                 335

Gly Asn Val Phe Arg Met Leu Ala Asn Leu Gln Asn Ile Ser Leu Gln
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            340                 345                 350

Asn Asn Arg Leu Arg Gln Leu Pro Gly Asn Ile Phe Ala Asn Val Asn
        355                 360                 365

Gly Leu Met Ala Ile Gln Leu Gln Asn Asn Gln Leu Glu Asn Leu Pro
    370                 375                 380

Leu Gly Ile Phe Asp His Leu Gly Lys Leu Cys Glu Leu Arg Leu Tyr
385                 390                 395                 400

Asp Asn Pro Trp Arg Cys Asp Ser Asp Ile Leu Pro Leu Arg Asn Trp
                405                 410                 415

Leu Leu Leu Asn Gln Pro Arg Leu Gly Thr Asp Thr Val Pro Val Cys
            420                 425                 430

Phe Ser Pro Ala Asn Val Arg Gly Gln Ser Leu Ile Ile Ile Asn Val
        435                 440                 445

Asn Val Ala Val Pro Ser Val His Val Pro Glu Val Pro Ser Tyr Pro
    450                 455                 460

Glu Thr Pro Trp Tyr Pro Asp Thr Pro Ser Tyr Pro Asp Thr Thr Ser
465                 470                 475                 480

Val Ser Ser Thr Thr Glu Leu Thr Ser Pro Val Glu Asp Tyr Thr Asp
                485                 490                 495

Leu Thr Thr Ile Gln Val Thr Asp Asp Arg Ser Val Trp Gly Met Thr
            500                 505                 510

Gln Ala Gln Ser Gly
        515
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<210> 12
<211> 1551
<212> DNA

<213> Homo sapiens

<220>
<221> source
<223> /note="cDNA Encoding Extracellular Domain of LRRC15"

<400> 12
taccatggct gccctagcga gtgtacctgc tccagggcct cccaggtgga gtgcaccggg 60

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aacacgcaca tcactgaact caatgagtcc ccgttcctca atatctcagc cctcatcgcc 180

ctgaggattg agaagaatga gctgtcgcgc atcacgcctg gggccttccg aaacctgggc 240

tcgctgcgct atctcagcct cgccaacaac aagctgcagg ttctgcccat cggcctcttc 300

cagggcctgg acagcctcga gtctctcctt ctgtccagta accagctgtt gcagatccag 360

ccggcccact tctcccagtg cagcaacctc aaggagctgc agttgcacgg caaccacctg 420

gaatacatcc ctgacggagc cttcgaccac ctggtaggac tcacgaagct caatctgggc 480

aagaatagcc tcacccacat ctcacccagg gtcttccagc acctgggcaa cctccaggtc 540

ctccggctgt atgagaacag gctcacggat atccccatgg gcacttttga tgggcttgtt 600

aacctgcagg aactggctct gcagcagaac cagattggac tgctctcccc tggtctcttc 660

cacaacaacc acaacctcca gagactctac ctgtccaaca accacatctc ccagctgcca 720

cccagcgtct tcatgcagct gccccagctc aaccgtctta ctctctttgg gaattccctg 780

aaggagctct ctccggggat cttcgggccc atgcccaacc tgcgggagct ttggctctat 840

gacaaccaca tctcttctct acccgacaat gtcttcagca acctccgcca gttgcaggtc 900

ctgattctta gccgcaatca gatcagcttc atctccccgg gtgccttcaa cgggctaacg 960

gagcttcggg agctgtccct ccacaccaac gcactgcagg acctggacgg gaacgtcttc 1020

cgcatgttgg ccaacctgca gaacatctcc ctgcagaaca accgcctcag acagctccca 1080

gggaatatct tcgccaacgt caatggcctc atggccatcc agctgcagaa caaccagctg 1140

gagaacttgc ccctcggcat cttcgatcac ctggggaaac tgtgtgagct gcggctgtat 1200

gacaatccct ggaggtgtga ctcagacatc cttccgctcc gcaactggct cctgctcaac 1260

cagcctaggt tagggacgga cactgtacct gtgtgtttca gcccagccaa tgtccgaggc 1320

cagtccctca ttatcatcaa tgtcaacgtt gctgttccaa gcgtccatgt ccccgaggtg 1380

cctagttacc cagaaacacc atggtaccca gacacaccca gttaccctga caccacatcc 1440

gtctcttcta ccactgagct aaccagccct gtggaagact acactgatct gactaccatt 1500

caggtcactg atgaccgcag cgtttggggc atgacccagg cccagagcgg g 1551

<210> 13
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #1"

<400> 13
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser His Tyr Lys Phe Ser Ser Tyr
20 25 30

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 14
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine scanning variant #2"

<400> 14
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 15
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #3"

<400> 15
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 16
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #4"

<400> 16
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Lys His Ser Ser Tyr
            20   25   30

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 17
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #5"

<400> 17
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 18
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #6"

<400> 18
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 19
<211> 120

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #7"

<400> 19
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 20
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #8"

<400> 20
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 21
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #9"

<400> 21
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

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

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 22
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #10"

<400> 22
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

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

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 23
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #11"

<400> 23
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly His Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 24
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source

<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #12"

<400> 24
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu His Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 25
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #13"

<400> 25
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile His Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 26
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #14"

<400> 26

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


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


Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Glu Ile Leu His Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80


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


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


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 27
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #15"

<400> 27
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Lys Phe Ser Ser Tyr
            20                  25                  30


Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Glu Ile Leu Pro His Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80


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


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


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 28
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #16"

<400> 28
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Lys Phe Ser Ser Tyr
            20   25   30

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Leu Pro Gly His Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 29
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #17"

<400> 29
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

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Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Glu Ile Leu Pro Gly Ser His Thr Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80


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


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


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 30
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #18"

<400> 30
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


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

```
Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Glu Ile Leu Pro Gly Ser Asp His Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80


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


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


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 31
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #19"

<400> 31
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


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


Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
```

```
Gly Glu Ile Leu Pro Gly Ser Asp Thr His Asn Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80


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


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


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 32
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #20"

<400> 32
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


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


Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
```

```
Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr His Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80


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


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


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 33
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #21"

<400> 33
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


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


Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn His Asn Glu Lys Phe
    50                  55                  60
```

```
Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80


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


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


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 34
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #22"

<400> 34
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


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


Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr His Glu Lys Phe
    50                  55                  60
```

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 35
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine scanning variant #23"

<400> 35
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn His Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 36
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine scanning variant #24"

<400> 36
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu His Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 37
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine scanning variant #25"

<400> 37
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys His
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 38
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine scanning variant #26"

<400> 38
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

His Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 39
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine scanning variant #27"

<400> 39
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys His Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 40
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #28"

<400> 40
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

His Arg Asp Arg Gly Asn Tyr Arg Ala Trp Phe Gly Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 41
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #29"

<400> 41
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

Ala His Asp Arg Gly Asn Tyr Arg Ala Trp Phe Gly Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 42
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #30"

<400> 42
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg His Arg Gly Asn Tyr Arg Ala Trp Phe Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 43
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #31"

<400> 43
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Asp His Gly Asn Tyr Arg Ala Trp Phe Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 44
<211> 120

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #32"

<400> 44
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Asp Arg His Asn Tyr Arg Ala Trp Phe Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 45
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #33"

<400> 45
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

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

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 46
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #34"

<400> 46
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

Ala Arg Asp Arg Gly Asn His Arg Ala Trp Phe Gly Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 47
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #35"

<400> 47
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

Ala Arg Asp Arg Gly Asn Tyr His Ala Trp Phe Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 48
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #36"

<400> 48
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

Ala Arg Asp Arg Gly Asn Tyr Arg His Trp Phe Gly Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 49
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source

<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #37"

<400> 49
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

Ala Arg Asp Arg Gly Asn Tyr Arg Ala His Phe Gly Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 50
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
scanning variant #38"

<400> 50
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

Ala Arg Asp Arg Gly Asn Tyr Arg Ala Trp His Gly Tyr Trp Gly Gln
            100   105   110

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 51
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #39"

<400> 51

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


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


Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Asp Arg Gly Asn Tyr Arg Ala Trp Phe His Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 52
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG histidine
      scanning variant #40"

<400> 52
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15
```

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


Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Asp Arg Gly Asn Tyr Arg Ala Trp Phe Gly His Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 53
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine
      scanning variant #1"

<400> 53
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 His Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35                  40                  45


Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 54
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine
      scanning variant #2"

<400> 54
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 His Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35                  40                  45
```

```
Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 55
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine
      scanning variant #3"

<400> 55
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 His Gln Asp Ile Ser Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35                  40                  45


Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 56
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine scanning variant #4"

<400> 56
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 His Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 57
<211> 107
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine scanning variant #5"

<400> 57
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 His Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 58
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine
scanning variant #6"

<400> 58
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 Asp His Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 59
<211> 107
<212> PRT
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<220>

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine
scanning variant #7"

<400> 59
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 Asp Ile His Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 60
<211> 107
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine
scanning variant #8"

<400> 60
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 Asp Ile Ser His Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 61
<211> 107
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine
scanning variant #9"

<400> 61
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

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Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Ser Asn His
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35                  40                  45


Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 62
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine
      scanning variant #10"

<400> 62
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 Asp Ile Ser Asn Tyr
            20                  25                  30
```

```
His Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35                  40                  45


Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 63
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine
      scanning variant #11"

<400> 63
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 Asp Ile Ser Asn Tyr
            20                  25                  30


Leu His Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35                  40                  45


Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 64
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine scanning variant #12"

<400> 64
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 Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr His Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 65
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine scanning variant #13"

<400> 65
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 Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr His Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 66
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine
scanning variant #14"

<400> 66
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 Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr Thr His Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 67
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine
scanning variant #15"

<400> 67
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 Asp Ile Ser Asn Tyr
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35   40   45

Tyr Tyr Thr Ser His Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 68
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine
scanning variant #16"

<400> 68
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 Asp Ile Ser Asn Tyr
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35   40   45

Tyr Tyr Thr Ser Arg His His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 69
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine
scanning variant #17"

<400> 69

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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 Asp Ile Ser Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35                  40                  45


Tyr Tyr Thr Ser Arg Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 70
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Light Chain of samrotamab IgG histidine
      scanning variant #18"

<400> 70
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 Asp Ile Ser Asn Tyr
            20                  25                  30
```

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His His Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 71
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine
scanning variant #19"

<400> 71
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 Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

```
Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Phe Cys His Gln Gly Glu Ala Leu Pro Trp
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 72
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine
      scanning variant #20"

<400> 72
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 Asp Ile Ser Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35                  40                  45


Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
```

Glu Asp Phe Ala Thr Tyr Phe Cys Gln His Gly Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 73
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine scanning variant #21"

<400> 73
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 Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln His Glu Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 74
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine scanning variant #22"

<400> 74
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 Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly His Ala Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 75
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine
scanning variant #23"

<400> 75
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 Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu His Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 76
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine
scanning variant #24"

<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 Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
35 40 45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala His Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105

<210> 77
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine
scanning variant #25"

<400> 77
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 Asp Ile Ser Asn Tyr
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35   40   45

Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu His Trp
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105

<210> 78
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine
      scanning variant #26"

<400> 78
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 Asp Ile Ser Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35                  40                  45


Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro His
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 79
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG histidine
      scanning variant #27"

<400> 79
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 Asp Ile Ser Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35                  40                  45
```

```
Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
                85                  90                  95


His Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105


<210> 80
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain Combinations of samrotamab IgG histidine
      scanning variant #1"

<400> 80
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


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


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


Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr His Tyr Asn Glu Lys Phe
    50                  55                  60
```

```
Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80


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


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


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 81
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain Combinations of samrotamab IgG histidine
      scanning variant #2"

<400> 81
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


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


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


Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80
```

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


Ala Arg Asp Arg Gly Asn His Arg Ala Trp Phe Gly Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 82
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain Combinations of samrotamab IgG histidine
      scanning variant #3"

<400> 82
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


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


Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr His Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80
```

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

Ala Arg Asp Arg Gly Asn His Arg Ala Trp Phe Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 83
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Heavy Chain Combinations of samrotamab IgG histidine scanning variant #4"

<400> 83
Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

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

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

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr His Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

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Ala Arg Asp Arg Gly Asn His Arg Ala Trp Phe Gly Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210> 84
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Heavy Chain of hu139.10 IgG"

<400> 84
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
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100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 85
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Light Chain of hu139.10 IgG"

<400> 85
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 Leu Leu Asn Ser
20 25 30

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

Ser 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 86
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> source
<223> /note="Heavy Chain CDR1 of hu139.10"

<400> 86
Gly Phe Ser Leu Thr Ser Tyr Gly Val His
1 5 10

<210> 87
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> source
<223> /note="Heavy Chain CDR2 of hu139.10"

<400> 87
Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met Ser
1 5 10 15

<210> 88
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> source

<223> /note="Heavy Chain CDR3 of hu139.10"

<400> 88
Ala Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr
1   5   10

<210> 89
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<220>
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<223> /note="Light Chain CDR1 of hu139.10"

<400> 89
Lys Ser Ser Gln Ser Leu Leu Asn Ser Arg Thr Arg Lys Asn Tyr Leu
1   5   10   15

Ala

<210> 90
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
<221> source
<223> /note="Light Chain CDR2 of hu139.10"

<400> 90
Trp Ala Ser Thr Arg Glu Ser
1   5

<210> 91

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> source
<223> /note="Light Chain CDR3 of hu139.10"

<400> 91
Lys Gln Ser Tyr Asn Leu Pro Thr
1 5

<210> 92
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #1"

<400> 92
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 Val Ser His Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

```
Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 93
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #2"

<400> 93
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 Val Ser Gly His Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80
```

```
Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 94
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #3"

<400> 94
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 Val Ser Gly Phe His Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80
```

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 95
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine scanning variant #4"

<400> 95
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 Val Ser Gly Phe Ser His Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 96
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine scanning variant #5"

<400> 96
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 Val Ser Gly Phe Ser Leu His Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 97
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine scanning variant #6"

<400> 97
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 Val Ser Gly Phe Ser Leu Thr His Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 98
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #7"

<400> 98
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 Val Ser Gly Phe Ser Leu Thr Ser His
            20   25   30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35   40   45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50   55   60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85   90   95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 99
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #8"

<400> 99
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20   25   30

His Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35   40   45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50   55   60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85   90   95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 100
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #9"

<400> 100
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly His His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 101
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #10"

<400> 101
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val Ala Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 102
<211> 120

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #11"

<400> 102
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly His Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 103
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #12"

<400> 103
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val His Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 104
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #13"

<400> 104
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile His Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 105
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #14"

<400> 105
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp His Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 106
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #15"

<400> 106
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala His Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 107
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source

<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #16"

<400> 107
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly His Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 108
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #17"

<400> 108
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20   25   30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35   40   45

Gly Val Ile Trp Ala Gly Gly His Thr Asn Tyr Asn Ser Ala Leu Met
    50   55   60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85   90   95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 109
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #18"

<400> 109

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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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser His Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 110
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #19"

<400> 110
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr His Tyr Asn Ser Ala Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 111
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #20"

<400> 111
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr Asn His Asn Ser Ala Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 112
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #21"

<400> 112
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30
```

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr His Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 113
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #22"

<400> 113
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

```
Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn His Ala Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 114
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #23"

<400> 114
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
```

```
Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser His Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 115
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #24"

<400> 115
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45
```

```
Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala His Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 116
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #25"

<400> 116
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu His
    50                  55                  60
```

```
Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 117
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #26"

<400> 117
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60
```

```
His Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 118
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #27"

<400> 118
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80
```

```
Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys His
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 119
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #28"

<400> 119
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80
```

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

His His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 120
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine scanning variant #29"

<400> 120
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

```
Thr Ala Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 121
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #30"

<400> 121
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95
```

Thr His His Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 122
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine scanning variant #31"

<400> 122
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met His Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 123
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #32"

<400> 123
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20   25   30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35   40   45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50   55   60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85   90   95

Thr His Met Ile His Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 124
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
      scanning variant #33"

<400> 124
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20   25   30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35   40   45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50   55   60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85   90   95

Thr His Met Ile Thr His Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 125
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #34"

<400> 125
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu His Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 126
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #35"

<400> 126
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp His Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 127
<211> 120

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #36"

<400> 127
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr His Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 128
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #37"

<400> 128
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr His Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 129
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #38"

<400> 129
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly His Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 130
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #39"

<400> 130
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met His Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 131
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG histidine
scanning variant #40"

<400> 131
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp His Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 132
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source

<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #1"

<400> 132
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 His Ser Ser Gln Ser Leu Leu Asn Ser
20 25 30

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

Ser 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 133
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #2"

<400> 133
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 His Ser Gln Ser Leu Leu Asn Ser
            20                  25                  30


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


Ser 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 Lys Gln
                85                  90                  95


Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 134
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #3"

<400> 134
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 His Gln Ser Leu Leu Asn Ser
            20                  25                  30
```

```
Arg Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 Lys Gln
                85                  90                  95


Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 135
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #4"

<400> 135
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 His Ser Leu Leu Asn Ser
            20                  25                  30


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


Ser 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 Lys Gln
                85                  90                  95


Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 136
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #5"

<400> 136
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 His Leu Leu Asn Ser
            20                  25                  30


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


Ser 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 137
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Light Chain of hu139.10 IgG histidine scanning variant #6"

<400> 137
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 His Leu Asn Ser
20 25 30

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

Ser 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 138
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #7"

<400> 138
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 Leu His Asn Ser
20 25 30

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

Ser 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 139
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #8"

<400> 139
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 Leu Leu His Ser
20 25 30

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

Ser 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 140
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #9"

<400> 140
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 Leu Leu Asn His
            20   25   30

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

Ser 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 Lys Gln
                85   90   95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 141
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #10"

<400> 141

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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 Leu Leu Asn Ser
            20                  25                  30


His Thr Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 Lys Gln
                85                  90                  95


Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 142
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #11"

<400> 142
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 Leu Leu Asn Ser
            20                  25                  30
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Arg His Arg Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser 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 Lys Gln
                85                  90                  95


Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 143
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #12"

<400> 143
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 Leu Leu Asn Ser
            20                  25                  30


Arg Thr His Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45
```

Ser 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 Lys Gln
                85   90   95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 144
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #13"

<400> 144
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 Leu Leu Asn Ser
            20   25   30

Arg Thr Arg His Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Ser 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 145
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine scanning variant #14"

<400> 145
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 Leu Leu Asn Ser
20 25 30

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

Ser 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 146
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine scanning variant #15"

<400> 146
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 Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn His Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 147
<211> 112

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #16"

<400> 147
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 Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr His Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 148
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #17"

<400> 148
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 Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 149
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #18"

<400> 149
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 Leu Leu Asn Ser
            20   25   30

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

Ser Pro Lys Leu Leu Ile Tyr His 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 Lys Gln
                85   90   95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 150
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #19"

<400> 150
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 Leu Leu Asn Ser
            20   25   30

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

Ser Pro Lys Leu Leu Ile Tyr Trp His 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 Lys Gln
                85   90   95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 151
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #20"

<400> 151
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 Leu Leu Asn Ser
            20   25   30

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

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Ser Pro Lys Leu Leu Ile Tyr Trp Ala His 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 Lys Gln
                85                  90                  95


Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 152
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #21"

<400> 152
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 Leu Leu Asn Ser
            20                  25                  30


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


Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser His Arg Glu Ser Gly Val
    50                  55                  60
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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 Lys Gln
                85                  90                  95


Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 153
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #22"

<400> 153
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 Leu Leu Asn Ser
            20                  25                  30


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


Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr His 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 Lys Gln
                85                  90                  95
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Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 154
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine scanning variant #23"

<400> 154
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 Leu Leu Asn Ser
20 25 30

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

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 155
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #24"

<400> 155
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 Leu Leu Asn Ser
20 25 30

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

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu His 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 156
<211> 112
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #25"

<400> 156
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 Leu Leu Asn Ser
20 25 30

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

Ser 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 His Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 157
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source

<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #26"

<400> 157
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 Leu Leu Asn Ser
20 25 30

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

Ser 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 Lys His
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 158
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #27"

<400> 158
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 Leu Leu Asn Ser
            20                  25                  30


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


Ser 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 Lys Gln
                85                  90                  95


His Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 159
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #28"

<400> 159
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 Leu Leu Asn Ser
            20                  25                  30
```

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

Ser 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 Lys Gln
                85   90   95

Ser His Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 160
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #29"

<400> 160
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 Leu Leu Asn Ser
            20   25   30

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

Ser 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 Lys Gln
85 90 95

Ser Tyr His Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 161
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #30"

<400> 161
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 Leu Leu Asn Ser
20 25 30

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

Ser 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 Lys Gln
                85                  90                  95


Ser Tyr Asn His Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 162
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
      scanning variant #31"

<400> 162
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 Leu Leu Asn Ser
            20                  25                  30


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


Ser 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 Lys Gln
                85                  90                  95


Ser Tyr Asn Leu His Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
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<210> 163
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of hu139.10 IgG histidine
scanning variant #32"

<400> 163
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 Leu Leu Asn Ser
20 25 30

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

Ser 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro His Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 164
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain Combinations of hu139.10 IgG histidine
scanning variant #1"

<400> 164
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly His Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

Thr Ala Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 165
<211> 120
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain Combinations of hu139.10 IgG histidine
scanning variant #2"

<400> 165
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20   25   30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35   40   45

Gly Val Ile Trp Ala Gly Gly His Thr Asn Tyr Asn Ser Ala Leu Met
    50   55   60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85   90   95

Thr His Met Ile Thr Glu Asp His Tyr Gly Met Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 166
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="Heavy Chain Combinations of hu139.10 IgG histidine scanning variant #3"

<400> 166
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20   25   30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35   40   45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50   55   60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85   90   95

Thr Ala Met Ile Thr Glu Asp His Tyr Gly Met Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 167
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain Combinations of hu139.10 IgG histidine
scanning variant #4"

<400> 167
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20   25   30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35   40   45

Gly Val Ile Trp Ala Gly Gly His Thr Asn Tyr Asn Ser Ala Leu Met
    50   55   60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85   90   95

Thr Ala Met Ile Thr Glu Asp His Tyr Gly Met Asp Tyr Trp Gly Gln
            100   105   110

Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 168
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source

<223> /note="Light Chain Combinations of hu139.10 IgG histidine scanning variant #1"

<400> 168
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 Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr His 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 169
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of hu139.10 IgG histidine scanning variant #2"

<400> 169
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 Leu Leu Asn Ser
            20                  25                  30


Arg Thr Arg Lys Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln
        35                  40                  45


Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His 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 Lys Gln
                85                  90                  95


Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 170
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of hu139.10 IgG histidine
      scanning variant #3"

<400> 170
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 Leu Leu Asn Ser
            20                  25                  30
```

Arg Thr Arg Lys Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Ser 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 Lys Gln
                85   90   95

Ser Tyr Asn His Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 171
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of hu139.10 IgG histidine
      scanning variant #4"

<400> 171
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 Leu Leu Asn Ser
            20   25   30

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

Ser Pro Lys Leu Leu Ile Tyr His Ala Ser Thr Arg His 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 Lys Gln
                85                  90                  95


Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 172
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of hu139.10 IgG histidine
      scanning variant #5"

<400> 172
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 Leu Leu Asn Ser
            20                  25                  30


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


Ser Pro Lys Leu Leu Ile Tyr His 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 Lys Gln
                85                  90                  95


Ser Tyr Asn His Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 173
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of hu139.10 IgG histidine
      scanning variant #6"

<400> 173
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 Leu Leu Asn Ser
            20                  25                  30


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


Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His 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 Lys Gln
                85                  90                  95


Ser Tyr Asn His Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110
```

<210> 174
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of hu139.10 IgG histidine
scanning variant #7"

<400> 174
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 Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr His Ala Ser Thr Arg His 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 Lys Gln
85 90 95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 175
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of hu139.10 IgG histidine
scanning variant #8"

<400> 175
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 Leu Leu Asn Ser
20 25 30

Arg Thr Arg Lys Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Ser Pro Lys Leu Leu Ile Tyr His 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 Lys Gln
85 90 95

Ser Tyr Asn His Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 176
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of hu139.10 IgG histidine
scanning variant #9"

<400> 176
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 Leu Leu Asn Ser
            20   25   30

Arg Thr Arg Lys Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Gln
        35   40   45

Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg His 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 Lys Gln
                85   90   95

Ser Tyr Asn His Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 177
<211> 112
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of hu139.10 IgG histidine
scanning variant #10"

<400> 177

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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 Leu Leu Asn Ser
            20                  25                  30


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


Ser Pro Lys Leu Leu Ile Tyr His Ala Ser Thr Arg His 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 Lys Gln
                85                  90                  95


Ser Tyr Asn His Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 178
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG"

<400> 178
Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30
```

```
Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 179
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG"

<400> 179
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20                  25                  30


Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
```

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85   90   95

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

<210> 180
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<220>
<221> source
<223> /note="Heavy Chain CDR1 of huAD208.4.1"

<400> 180
Lys Ala Ser Gly Phe Thr Phe Thr Asp Tyr Tyr Ile His
1   5   10

<210> 181
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<220>
<221> source
<223> /note="Heavy Chain CDR2 of huAD208.4.1"

<400> 181
Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe Lys
1   5   10   15

Gly

<210> 182
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<220>
<221> source
<223> /note="Heavy Chain CDR3 of huAD208.4.1"

<400> 182
Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr
1   5   10

<210> 183
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<220>
<221> source
<223> /note="Light Chain CDR1 of huAD208.4.1"

<400> 183
Arg Ala Ser Gln Ser Val Ser Thr Ser Ser Tyr Ser Tyr Met His
1   5   10   15

<210> 184
<211> 7

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> source
<223> /note="Light Chain CDR2 of huAD208.4.1"

<400> 184
Tyr Ala Ser Ser Leu Glu Ser
1 5

<210> 185
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> source
<223> /note="Light Chain CDR3 of huAD208.4.1"

<400> 185
Glu Gln Ser Trp Glu Ile Arg Thr
1 5

<210> 186
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
scanning variant #1"

<400> 186
Glu 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 His Ala Ser Gly Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 187
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #2"

<400> 187

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Glu 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 His Ser Gly Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 188
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #3"

<400> 188
Glu 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 His Gly Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 189
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #4"

<400> 189
Glu 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 His Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 190
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #5"

<400> 190
Glu 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 His Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 191
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #6"

<400> 191
Glu 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 Phe His Phe Thr Asp Tyr
            20   25   30

```
Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 192
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #7"

<400> 192
Glu 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 Phe Thr His Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
```

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 193
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #8"

<400> 193
Glu 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 Phe Thr Phe His Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 194
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #9"

<400> 194
Glu 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 Phe Thr Phe Thr His Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

```
Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 195
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #10"

<400> 195
Glu 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 Phe Thr Phe Thr Asp His
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
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```
Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 196
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #11"

<400> 196
Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30


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


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80
```

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


Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 197
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #12"

<400> 197
Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr His His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80
```

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 198
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine scanning variant #13"

<400> 198
Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

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

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 199
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine scanning variant #14"

<400> 199
Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly His Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 200
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine scanning variant #15"

<400> 200
Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Leu His Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
        115

<210> 201
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #16"

<400> 201
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val His Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 202
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #17"

<400> 202
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr His Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 203
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
scanning variant #18"

<400> 203
Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Leu Val Tyr Pro His Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 204
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
scanning variant #19"

<400> 204
Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Leu Val Tyr Pro Tyr His Gly Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 205
<211> 119

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
scanning variant #20"

<400> 205
Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Leu Val Tyr Pro Tyr Ile His Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 206
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
scanning variant #21"

<400> 206
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly His Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 207
<211> 119
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
scanning variant #22"

<400> 207
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly His Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 208
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
scanning variant #23"

<400> 208
Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr His Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 209
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
scanning variant #24"

<400> 209
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn His Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 210
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source

<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
scanning variant #25"

<400> 210
Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr His Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 211
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
scanning variant #26"

<400> 211
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn His Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 212
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #27"

<400> 212

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Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln His Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 213
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #28"

<400> 213
Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys His
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 214
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #29"

<400> 214
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

His Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 215
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #30"

<400> 215
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys His Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 216
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #31"

<400> 216
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

```
Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


His Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 217
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #32"

<400> 217
Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
```

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala His Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 218
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #33"

<400> 218
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg His Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 219
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #34"

<400> 219
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

```
Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly His Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 220
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #35"

<400> 220
Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
```

```
Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly Asp His Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 221
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #36"

<400> 221
Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80
```

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


Ala Arg Gly Asp Asn His Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 222
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #37"

<400> 222
Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80
```

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

Ala Arg Gly Asp Asn Lys His Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 223
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine scanning variant #38"

<400> 223
Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr His Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 224
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine scanning variant #39"

<400> 224
Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr Asp His Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 225
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.4.1 IgG histidine scanning variant #40"

<400> 225
Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala His Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
        115

<210> 226
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #41"

<400> 226
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met His Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 227
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG histidine
      scanning variant #42"

<400> 227
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp His Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 228
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #1"

<400> 228
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys His Ala Ser Gln Ser Val Ser Thr Ser
            20   25   30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85   90   95

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

<210> 229
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #2"

<400> 229
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg His Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 230
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #3"

<400> 230
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys Arg Ala His Gln Ser Val Ser Thr Ser
            20   25   30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85   90   95

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

<210> 231
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #4"

<400> 231

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Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser His Ser Val Ser Thr Ser
            20                  25                  30


Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85                  90                  95


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


<210> 232
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
      scanning variant #5"

<400> 232
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln His Val Ser Thr Ser
            20                  25                  30
```

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 233
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine scanning variant #6"

<400> 233
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser His Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85   90   95

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

<210> 234
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
      scanning variant #7"

<400> 234
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val His Thr Ser
            20   25   30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

```
Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85                  90                  95


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


<210> 235
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
      scanning variant #8"

<400> 235
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser His Ser
            20                  25                  30


Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85                  90                  95
```

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

<210> 236
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine scanning variant #9"

<400> 236
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr His
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 237
<211> 110

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #10"

<400> 237
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

His Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 238
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #11"

<400> 238
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser His Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 239
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #12"

<400> 239
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20   25   30

Ser Tyr His Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85   90   95

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

<210> 240
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
      scanning variant #13"

<400> 240
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

```
Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20                  25                  30


Ser Tyr Ser His Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85                  90                  95


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


<210> 241
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
      scanning variant #14"

<400> 241
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20                  25                  30


Ser Tyr Ser Tyr His His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
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Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85                  90                  95


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


<210> 242
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
      scanning variant #15"

<400> 242
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20                  25                  30


Ser Tyr Ser Tyr Met Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50                  55                  60
```

```
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85                  90                  95


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


<210> 243
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
      scanning variant #16"

<400> 243
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20                  25                  30


Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Lys His Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85                  90                  95
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Glu Ile Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

<210> 244
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Light Chain of huAD208.4.1 IgG histidine scanning variant #17"

<400> 244
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr His Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 245
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #18"

<400> 245
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala His Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 246
<211> 110
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #19"

<400> 246
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser His Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 247
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #20"

<400> 247
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser His Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 248
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #21"

<400> 248
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

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Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20                  25                  30


Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu His Ser Gly Val Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85                  90                  95


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


<210> 249
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
      scanning variant #22"

<400> 249
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20                  25                  30
```

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu His Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85   90   95

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

<210> 250
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
      scanning variant #23"

<400> 250
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20   25   30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys His Gln Ser Trp
85 90 95

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

<210> 251
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine scanning variant #24"

<400> 251
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu His Ser Trp
85 90 95

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

<210> 252
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine scanning variant #25"

<400> 252
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln His Trp
85 90 95

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

<210> 253
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #26"

<400> 253
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser His
85 90 95

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

<210> 254
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #27"

<400> 254
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20   25   30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85   90   95

His Ile Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 255
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #28"

<400> 255
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20   25   30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85   90   95

Glu His Arg Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 256
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
scanning variant #29"

<400> 256

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Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20                  25                  30


Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85                  90                  95


Glu Ile His Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110


<210> 257
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG histidine
      scanning variant #30"

<400> 257
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20                  25                  30
```

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85   90   95

Glu Ile Arg His Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100   105   110

<210> 258
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain Combinations of huAD208.4.1 IgG histidine
      scanning variant #1"

<400> 258
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

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

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65   70   75   80

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

Ala Arg Gly Asp Asn Lys His Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 259
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain Combinations of huAD208.4.1 IgG histidine
      scanning variant #2"

<400> 259
Glu 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 Phe Thr Phe Thr Asp Tyr
            20   25   30

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

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50   55   60

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Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly Asp Asn Lys Tyr Asp Ala His Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 260
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain Combinations of huAD208.4.1 IgG histidine
      scanning variant #3"

<400> 260
Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60
```

```
Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly Asp Asn Lys His Asp Ala His Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Thr Val Thr Val Ser Ser
        115


<210> 261
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain Combinations of huAD208.4.1 IgG histidine
      scanning variant #4"

<400> 261
Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30


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


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80
```

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

Ala Arg Gly Asp Asn Lys His Asp Ala His Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser
115

<210> 262
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #1"

<400> 262
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg His His Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 263
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #2"

<400> 263
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg His Ser Gln Ser Val Ser His Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 264
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of huAD208.4.1 IgG histidine
scanning variant #3"

<400> 264
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg His Ser Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser His Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 265
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of huAD208.4.1 IgG histidine
scanning variant #4"

<400> 265
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala His Gln Ser Val Ser His Ser
20 25 30

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 266
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of huAD208.4.1 IgG histidine
scanning variant #5"

<400> 266
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys Arg Ala His Gln Ser Val Ser Thr Ser
            20   25   30

Ser Tyr Ser His Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85   90   95

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

<210> 267
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of huAD208.4.1 IgG histidine
scanning variant #6"

<400> 267

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Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser His Ser
            20                  25                  30


Ser Tyr Ser His Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85                  90                  95


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


<210> 268
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of huAD208.4.1 IgG histidine
      scanning variant #7"

<400> 268
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15


Glu Arg Ala Thr Ile Asn Cys Arg His His Gln Ser Val Ser His Ser
            20                  25                  30
```

Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 269
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain Combinations of huAD208.4.1 IgG histidine
scanning variant #8"

<400> 269
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg His His Gln Ser Val Ser Thr Ser
20 25 30

Ser Tyr Ser His Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85   90   95

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

<210> 270
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Light Chain Combinations of huAD208.4.1 IgG histidine
      scanning variant #9"

<400> 270
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys Arg His Ser Gln Ser Val Ser His Ser
            20   25   30

Ser Tyr Ser His Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35   40   45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50   55   60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65   70   75   80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 271
<211> 110
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Light Chain Combinations of huAD208.4.1 IgG histidine scanning variant #10"

<400> 271
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Arg Ala His Gln Ser Val Ser His Ser
20 25 30

Ser Tyr Ser His Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
35 40 45

Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
50 55 60

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65 70 75 80

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
85 90 95

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

<210> 272
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.12.1 IgG"

<400> 272
Glu 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 Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 273
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of huAD208.12.1 IgG"

<400> 273
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 Ser Ser Asn Asn
20 25 30

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

Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 274
<211> 13
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> source
<223> /note="Heavy Chain CDR1 of huAD208.12.1"

<400> 274
Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Trp Met His
1 5 10

<210> 275
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
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<223> /note="Heavy Chain CDR2 of huAD208.12.1"

<400> 275
Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe Arg
1 5 10 15

Gly

<210> 276
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> source
<223> /note="Heavy Chain CDR3 of huAD208.12.1"

<400> 276
Ala Arg Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val
1   5   10

<210> 277
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      peptide"

<220>
<221> source
<223> /note="Light Chain CDR1 of huAD208.12.1"

<400> 277
Arg Ala Ser Gln Ser Ser Ser Asn Asn Leu His
1   5   10

<210> 278
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
<221> source
<223> /note="Light Chain CDR2 of huAD208.12.1"

<400> 278
Tyr Val Ser Gln Ser Ile Ser
1   5

<210> 279
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
peptide"

<220>
<221> source
<223> /note="Light Chain CDR3 of huAD208.12.1"

<400> 279
Gln Gln Ser Asn Ser Trp Pro Phe Thr
1 5

<210> 280
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #1"

<400> 280
Glu 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 His Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 281
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine scanning variant #2"

<400> 281
Glu 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 His Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 282
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine scanning variant #3"

<400> 282
Glu 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 His Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 283
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #4"

<400> 283
Glu 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 His Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 284
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #5"

<400> 284
Glu 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 His Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 285
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #6"

<400> 285
Glu 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 Tyr His Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 286
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #7"

<400> 286
Glu 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 Tyr Thr His Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 287
<211> 121

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #8"

<400> 287
Glu 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 Tyr Thr Phe His Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 288
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #9"

<400> 288
Glu 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 Tyr Thr Phe Thr His Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 289
<211> 121
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #10"

<400> 289
Glu 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 Tyr Thr Phe Thr Asn His
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 290
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #11"

<400> 290
Glu 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 Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 291
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #12"

<400> 291
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 292
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source

<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #13"

<400> 292
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 293
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #14"

<400> 293
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly His Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 294
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #15"

<400> 294

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Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30


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


Gly Met His His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 295
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #16"

<400> 295
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30


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


Gly Met Ile Ala Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 296
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #17"

<400> 296
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30


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


Gly Met Ile His His Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 297
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #18"

<400> 297
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30
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Trp Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Met Ile His Pro His Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 298
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #19"

<400> 298
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30
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Trp Met His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Met Ile His Pro Asn His Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 299
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #20"

<400> 299
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30


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

Gly Met Ile His Pro Asn Ser His Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 300
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #21"

<400> 300
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly His Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 301
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.12.1 IgG histidine scanning variant #22"

<400> 301
Glu 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 Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser His Lys His Asn Glu Lys Phe
50 55 60

```
Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 302
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #23"

<400> 302
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30


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


Gly Met Ile His Pro Asn Ser Gly Ser Thr His His Asn Glu Lys Phe
    50                  55                  60
```

```
Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 303
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #24"

<400> 303
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30


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


Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys Ala Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 304
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
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<220>
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<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #25"

<400> 304
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30


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


Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His His Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 305
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.12.1 IgG histidine scanning variant #26"

<400> 305
Glu 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 Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn His Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 306
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine scanning variant #27"

<400> 306
Glu 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 Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu His Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 307
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.12.1 IgG histidine scanning variant #28"

<400> 307
Glu 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 Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys His
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 308
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #29"

<400> 308
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

His Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 309
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #30"

<400> 309
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg His Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 310
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #31"

<400> 310
Glu 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 Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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

His Arg Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 311
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #32"

<400> 311
Glu 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 Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 His Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 312
<211> 121

<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #33"

<400> 312
Glu 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 Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 His Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 313
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #34"

<400> 313
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser His Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 314
<211> 121
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #35"

<400> 314
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp His Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 315
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #36"

<400> 315
Glu 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 Tyr Thr Phe Thr Asn Tyr
20 25 30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
50 55 60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe His Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
100 105 110

Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 316
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #37"

<400> 316
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly His Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 317
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source

<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #38"

<400> 317
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn His Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 318
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
scanning variant #39"

<400> 318
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr His Trp Tyr Phe Asp Val Trp Gly
            100   105   110

Gln Gly Thr Thr Val Thr Val Ser Ser
        115   120

<210> 319
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #40"

<400> 319

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Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30


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


Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg His Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 320
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #41"

<400> 320
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30


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


Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp His Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 321
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #42"

<400> 321
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30


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


Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr His Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 322
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #43"

<400> 322
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30
```

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


Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe His Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 323
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG histidine
      scanning variant #44"

<400> 323
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30
```

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


Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp His Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210> 324
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Light Chain of huAD208.12.1 IgG histidine
      scanning variant #1"

<400> 324
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 His Ala Ser Gln Ser Ser Ser Asn Asn
            20                  25                  30


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

```
Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 325
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Light Chain of huAD208.12.1 IgG histidine
      scanning variant #2"

<400> 325
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 His Ser Gln Ser Ser Ser Asn Asn
            20                  25                  30


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


Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 326
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine scanning variant #3"

<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 His Gln Ser Ser Ser Asn Asn
20 25 30

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

Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 327
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine scanning variant #4"

<400> 327
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 His Ser Ser Ser Asn Asn
20 25 30

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

Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 328
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of huAD208.12.1 IgG histidine
scanning variant #5"

<400> 328
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 His Ser Ser Asn Asn
20 25 30

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

Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 329
<211> 107
<212> PRT
<213> Artificial Sequence

<220>

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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
scanning variant #6"

<400> 329
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 His Ser Asn Asn
20 25 30

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

Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 330
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source

<223> /note="Light Chain of huAD208.12.1 IgG histidine
scanning variant #7"

<400> 330
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 Ser His Asn Asn
20 25 30

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

Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 331
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
scanning variant #8"

<400> 331
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 Ser Ser His Asn
            20                  25                  30


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


Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 332
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
      scanning variant #9"

<400> 332
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 Ser Ser Asn His
            20                  25                  30
```

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


Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 333
<211> 107
<212> PRT
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<220>
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<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Light Chain of huAD208.12.1 IgG histidine
      scanning variant #10"

<400> 333
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 Ser Ser Asn Asn
            20                  25                  30


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


Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 334
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine scanning variant #11"

<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 Ser Ser Asn Asn
20 25 30

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

Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 335
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
      scanning variant #12"

<400> 335
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 Ser Ser Asn Asn
            20                  25                  30


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


Lys His Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105
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<210> 336
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
scanning variant #13"

<400> 336
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 Ser Ser Asn Asn
20 25 30

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

Lys Tyr His Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 337
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
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<223> /note="Light Chain of huAD208.12.1 IgG histidine
scanning variant #14"

<400> 337
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 Ser Ser Asn Asn
20 25 30

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

Lys Tyr Val His Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 338
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
scanning variant #15"

<400> 338
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 Ser Ser Asn Asn
            20   25   30

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

Lys Tyr Val Ser His Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 339
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
scanning variant #16"

<400> 339

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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 Ser Ser Asn Asn
            20                  25                  30


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


Lys Tyr Val Ser Gln His Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 340
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
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<223> /note="Light Chain of huAD208.12.1 IgG histidine
      scanning variant #17"

<400> 340
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 Ser Ser Asn Asn
            20                  25                  30
```

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


Lys Tyr Val Ser Gln Ser His Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 341
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
      scanning variant #18"

<400> 341
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 Ser Ser Asn Asn
            20                  25                  30


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

```
Lys Tyr Val Ser Gln Ser Ile His 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 342
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
      scanning variant #19"

<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 Ser Ser Asn Asn
            20                  25                  30


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


Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys His Gln Ser Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 343
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine scanning variant #20"

<400> 343
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 Ser Ser Asn Asn
20 25 30

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

Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln His Ser Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 344
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine scanning variant #21"

<400> 344
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 Ser Ser Asn Asn
20 25 30

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

Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln His Asn Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 345
<211> 107

<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
scanning variant #22"

<400> 345
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 Ser Ser Asn Asn
20 25 30

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

Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser His Ser Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 346
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic

polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
scanning variant #23"

<400> 346
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 Ser Ser Asn Asn
20 25 30

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

Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn His Trp Pro Phe
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 347
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
scanning variant #24"

<400> 347
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 Ser Ser Asn Asn
            20   25   30

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

Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser His Pro Phe
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100   105

<210> 348
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
      scanning variant #25"

<400> 348
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 Ser Ser Asn Asn
            20                  25                  30


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


Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp His Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 349
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
      scanning variant #26"

<400> 349
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 Ser Ser Asn Asn
            20                  25                  30


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

```
Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro His
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105


<210> 350
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG histidine
      scanning variant #27"

<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 Ser Ser Asn Asn
            20                  25                  30


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


Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
85 90 95

His Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 351
<211> 329
<212> PRT
<213> Homo sapiens

<400> 351

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

```
Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
    130                 135                 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145                 150                 155                 160

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
225                 230                 235                 240

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly
```

325

<210> 352
<211> 329
<212> PRT
<213> Homo sapiens

<400> 352

Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys
1 5 10 15

Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
20 25 30

Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
35 40 45

Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
50 55 60

Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
65 70 75 80

Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
85 90 95

Arg Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
100 105 110

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
115 120 125

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
130 135 140

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
145 150 155 160

```
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
                165                 170                 175

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
            180                 185                 190

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
        195                 200                 205

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
    210                 215                 220

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
225                 230                 235                 240

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
                245                 250                 255

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
            260                 265                 270

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
        275                 280                 285

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
    290                 295                 300

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
305                 310                 315                 320

Gln Lys Ser Leu Ser Leu Ser Pro Gly
                325
```

<210> 353
<211> 107
<212> PRT
<213> Homo sapiens

<400> 353

```
Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
1               5                   10                  15


Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
            20                  25                  30


Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
        35                  40                  45


Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
    50                  55                  60


Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
65                  70                  75                  80


Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
                85                  90                  95


Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
            100                 105


<210>  354
<211>  449
<212>  PRT
<213>  Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG + LS mutation"

<400> 354

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


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Lys Phe Ser Ser Tyr
```

```
            20                  25                  30

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80

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

Ala Arg Asp Arg Gly Asn Tyr Arg Ala Trp Phe Gly 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 Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220
```

```
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 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 His Glu
            260                 265                 270


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


Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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                 395                 400


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


Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Leu His
```

420 425 430

Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
435 440 445

Gly

<210> 355
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG + YTE mutation"

<400> 355

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

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
50 55 60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65 70 75 80

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

```
Ala Arg Asp Arg Gly Asn Tyr Arg Ala Trp Phe Gly 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 Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

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

Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg 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                 395                 400

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

Lys Ser Arg Trp Gln Gln 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 Pro
        435                 440                 445

Gly
```

<210> 356
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<221> source

<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG + A118C"

<400> 356

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


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


Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60


Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80


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


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


Gly Thr Leu Val Thr Val Ser Ser Cys 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 Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 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 His Glu
            260                 265                 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg 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                 395                 400

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

Lys Ser Arg Trp Gln Gln 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 Pro
        435                 440                 445

Gly
```

<210> 357
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG + A118C + LS mutation"

<400> 357

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

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

```
Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50                  55                  60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65                  70                  75                  80

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

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

Gly Thr Leu Val Thr Val Ser Ser Cys 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 Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 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 His Glu
            260                 265                 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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                 395                 400

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Leu His
            420                 425                 430
```

Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435   440   445

Gly

<210> 358
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of samrotamab IgG + A118C + YTE"

<400> 358

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

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

Trp Ile Glu Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35   40   45

Gly Glu Ile Leu Pro Gly Ser Asp Thr Thr Asn Tyr Asn Glu Lys Phe
    50   55   60

Lys Asp Arg Ala Thr Phe Thr Ser Asp Thr Ser Ile Asn Thr Ala Tyr
65   70   75   80

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

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

```
Gly Thr Leu Val Thr Val Ser Ser Cys 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 Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

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

Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg 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                 395                 400


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


Lys Ser Arg Trp Gln Gln 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 Pro
        435                 440                 445


Gly
```

<210> 359
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Light Chain of samrotamab IgG + V205C"

<400> 359

```
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 Asp Ile Ser Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ala Val Lys Phe Leu Ile
        35                  40                  45


Tyr Tyr Thr Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Glu Ala Leu Pro Trp
                85                  90                  95


Thr Phe Gly Gly 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 Cys Thr Lys Ser
195 200 205

Phe Asn Arg Gly Glu Cys
210

<210> 360
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG + LS Mutation"

<400> 360

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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
35 40 45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
50 55 60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65 70 75 80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
85 90 95

```
Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 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 His Glu
            260                 265                 270

Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
        275                 280                 285
```

```
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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                 395                 400

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Leu His
            420                 425                 430

Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly
```

<210> 361
<211> 449
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG + YTE Mutation"

<400> 361

```
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

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

Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg 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                 395                 400

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

Lys Ser Arg Trp Gln Gln 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 Pro
        435                 440                 445

Gly
```

<210> 362
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG + A118C Mutation"

<400> 362

```
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30
```

```
Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110

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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 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 His Glu
            260                 265                 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg 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                 395                 400

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

Lys Ser Arg Trp Gln Gln 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 Pro
        435   440   445

Gly

<210> 363
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG + A118C + LS Mutation"

<400> 363

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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20   25   30

Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35   40   45

Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50   55   60

Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65   70   75   80

Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85   90   95

Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100   105   110

```
Gly Thr Thr Val Thr Val Ser Ser Cys 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 Arg Val Glu Pro Lys Ser Cys Asp
    210                 215                 220

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 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 His Glu
            260                 265                 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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                 395                 400

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

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Leu His
            420                 425                 430

Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
        435                 440                 445

Gly
```

<210> 364
<211> 449
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of hu139.10 IgG + A118C + YTE Mutation"

<400> 364

```
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 Val Ser Gly Phe Ser Leu Thr Ser Tyr
            20                  25                  30


Gly Val His Trp Val Arg Gln Ala Thr Gly Lys Gly Leu Glu Trp Leu
        35                  40                  45


Gly Val Ile Trp Ala Gly Gly Ser Thr Asn Tyr Asn Ser Ala Leu Met
    50                  55                  60


Ser Arg Leu Thr Ile Ser Lys Glu Asn Ala Lys Ser Ser Val Tyr Leu
65                  70                  75                  80


Gln Met Asn Ser Leu Arg Ala Gly Asp Thr Ala Met Tyr Tyr Cys Ala
                85                  90                  95


Thr His Met Ile Thr Glu Asp Tyr Tyr Gly Met Asp Tyr Trp Gly Gln
            100                 105                 110


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

Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
225                 230                 235                 240

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

Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
            260                 265                 270

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

Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg 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
385 390 395 400

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

Lys Ser Arg Trp Gln Gln 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 Pro
435 440 445

Gly

<210> 365
<211> 219
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Light Chain of hy139.10 IgG + V205"

<400> 365

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 Leu Leu Asn Ser
20 25 30

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

```
Ser 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 Lys Gln
                85                  90                  95

Ser Tyr Asn Leu Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
        115                 120                 125

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
    130                 135                 140

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
145                 150                 155                 160

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
                165                 170                 175

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
            180                 185                 190

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
        195                 200                 205

Pro Cys Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210                 215
```

<210> 366
<211> 448
<212> PRT
<213> Artificial Sequence

<220>

<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG + LS Mutation"

<400> 366

```
Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45


Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60


Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80


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


Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110


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


Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 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 His Glu Asp
            260                 265                 270

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys
                405                 410                 415

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

Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
        435                 440                 445
```

<210> 367
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG + YTE Mutation"

<400> 367

```
Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45
```

```
Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110

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

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Tyr Ile Thr
                245                 250                 255
```

```
Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg 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 Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln 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 Pro Gly
        435                 440                 445
```

<210> 368
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG + A118C
Mutation"

<400> 368

Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Cys Ser Thr Lys Gly Pro Ser Val Phe
115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 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 His Glu Asp
            260                 265                 270

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg 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 Lys Leu Thr Val Asp Lys
                405                 410                 415

Ser Arg Trp Gln Gln 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 Pro Gly
        435                 440                 445


<210> 369
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG + A118C + LS
      Mutation"

<400> 369

Glu 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 Phe Thr Phe Thr Asp Tyr
            20                  25                  30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
        35                  40                  45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
    50                  55                  60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65                  70                  75                  80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly
            100                 105                 110

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

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
    210                 215                 220
```

```
Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu 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 His Glu Asp
            260                 265                 270

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg Asp Glu Leu 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 Lys Leu Thr Val Asp Lys
                405                 410                 415
```

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

Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly
435 440 445

<210> 370
<211> 448
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.4.1 IgG + A118C + YTE Mutation"

<400> 370

Glu 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 Phe Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Leu Val Tyr Pro Tyr Ile Gly Gly Thr Asn Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Thr Ser Thr Thr Thr Ala Tyr
65 70 75 80

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

Ala Arg Gly Asp Asn Lys Tyr Asp Ala Met Asp Tyr Trp Gly Gln Gly

```
            100                 105                 110

Thr Thr Val Thr Val Ser Ser Cys Ser Thr Lys Gly Pro Ser Val Phe
        115                 120                 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly 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 Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
        195                 200                 205

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

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
225                 230                 235                 240

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

Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
            260                 265                 270

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

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 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 Ala Leu Pro Ala Pro 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 Arg 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 Lys Leu Thr Val Asp Lys
                405                 410                 415


Ser Arg Trp Gln Gln 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 Pro Gly
        435                 440                 445


<210> 371
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.4.1 IgG + V205C"
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<400> 371

```
Asp Ile Val Leu Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                  10                  15


Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Gln Ser Val Ser Thr Ser
            20                  25                  30


Ser Tyr Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45


Lys Leu Leu Ile Lys Tyr Ala Ser Ser Leu Glu Ser Gly Val Pro Asp
    50                  55                  60


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
65                  70                  75                  80


Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Glu Gln Ser Trp
                85                  90                  95


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


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


Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro
    130                 135                 140


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


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


Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His
            180                 185                 190
```

Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Cys
        195   200   205

Thr Lys Ser Phe Asn Arg Gly Glu Cys
    210   215

<210> 372
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG + LS Mutation"

<400> 372

Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly

```
            100                 105                 110

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

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

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 Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300
```

```
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320


Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335


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


Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365


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


Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


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


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Leu
            420                 425                 430


His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly
    450


<210> 373
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"
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<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG + YTE Mutation"

<400> 373

```
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30


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


Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110


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


Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140


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 Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Tyr
                245                 250                 255

Ile Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
```

370 375 380

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385 390 395 400

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
420 425 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
435 440 445

Pro Gly
450

<210> 374
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source
<223> /note="Heavy Chain of huAD208.12.1 IgG + A118C Mutation"

<400> 374

Glu 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 Tyr Thr Phe Thr Asn Tyr
20 25 30

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

```
Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110

Gln Gly Thr Thr Val Thr Val Ser Ser Cys Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

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 Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
```

```
                245                 250                 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

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

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

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445
```

Pro Gly
    450

<210> 375
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Heavy Chain variable domain of huAD208.12.1 IgG +
      A118C Mutation + LS Mutation"

<400> 375

Glu 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 Tyr Thr Phe Thr Asn Tyr
            20   25   30

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

Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50   55   60

Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100   105   110

```
Gln Gly Thr Thr Val Thr Val Ser Ser Cys Ser Thr Lys Gly Pro Ser
        115                 120                 125

Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140

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 Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

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

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320
```

```
Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

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

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
        355                 360                 365

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

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400

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

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Leu
            420                 425                 430

His Glu Ala Leu His Ser His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445

Pro Gly
    450
```

<210> 376
<211> 450
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic polypeptide"

<220>
<221> source

<223> /note="Heavy Chain variable domain of huAD208.12.1 IgG + A118C Mutation + YTE Mutation"

<400> 376

```
Glu 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 Tyr Thr Phe Thr Asn Tyr
            20                  25                  30


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


Gly Met Ile His Pro Asn Ser Gly Ser Thr Lys His Asn Glu Lys Phe
    50                  55                  60


Arg Gly Lys Ala Thr Leu Thr Val Asp Glu Ser Thr Thr 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 Ser Asp Phe Gly Asn Tyr Arg Trp Tyr Phe Asp Val Trp Gly
            100                 105                 110


Gln Gly Thr Thr Val Thr Val Ser Ser Cys Ser Thr Lys Gly Pro Ser
        115                 120                 125


Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
    130                 135                 140


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 Gln Thr Tyr Ile Cys Asn Val Asn His
        195                 200                 205

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

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly
225                 230                 235                 240

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Tyr
                245                 250                 255

Ile Thr Arg Glu Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
            260                 265                 270

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
        275                 280                 285

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
    290                 295                 300

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
305                 310                 315                 320

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile
                325                 330                 335

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

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

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
    370                 375                 380
```

```
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
385                 390                 395                 400


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


Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
            420                 425                 430


His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
        435                 440                 445


Pro Gly
    450


<210> 377
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<221> source
<223> /note="Description of Artificial Sequence: Synthetic
      polypeptide"

<220>
<221> source
<223> /note="Light Chain of huAD208.12.1 IgG + V205C"

<400> 377

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 Ser Ser Asn Asn
            20                  25                  30


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


Lys Tyr Val Ser Gln Ser Ile Ser 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 Phe Cys Gln Gln Ser Asn Ser Trp Pro Phe
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Leu 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 Cys Thr Lys Ser
        195                 200                 205

Phe Asn Arg Gly Glu Cys
    210
```