

【DESCRIPTION】**【Invention Title】****ANTI-LILRB1 ANTIBODY AND USES THEREOF**5 **【Technical Field】**Cross-Reference to Related Applications

This application claims the benefits of KR 10-2019-0173414 filed on December 23, 2019 and KR 10-2020-0061907 filed on May 22, 2020 with the Korean Intellectual Property Office, the entire disclosure of which is herein
10 incorporated by reference.

The disclosure relates to an anti-LILRB1 antibody and uses thereof. More specifically, an anti-LILRB1 antibody or an antigen-binding fragment thereof, and a use thereof for cancer therapy are provided.

15 **【Background Art】**

Leukocyte immunoglobulin-like receptor subfamily B member 1 (LILRB1; also known as ILT2, CD85j, or LIR-1) is an inhibitory receptor, which is expressed in cells such as B cells, T cells, NK cells, dendritic cells, macrophages, and other immune cells. LILRB1 participates in a signal transduction mechanism of inhibiting activities of
20 immune cells by binding classical and non-classical MHC class I.

Meanwhile, it has been reported that various cancer cells overexpress MHC class I such as HLA-G for immune evasion. It has been expected that blocking the binding of LILRB1 to MHC Class I allows recovery of the inhibited activities of immune cells, thereby exhibiting anti-cancer effects.

25 Therefore, it is required to develop novel agent binding to LILRB1 and blocking the binding of LILRB1 to MHC Class I and/or the interaction between LILRB1 and MHC Class I.

【Disclosure】30 **【Technical Problem】**

This disclosure provides antibodies, which bind to LILRB1, act on LILRB1-

expressing immune cells, regulate activities of the immune cells, and exhibit anti-cancer effects, and uses thereof for cancer therapies.

An embodiment provides an anti-LILRB1 antibody, which binds to LILRB1, or an antigen-binding fragment thereof. The anti-LILRB1 antibody or an antigen-binding
5 fragment thereof may have an activity to block the binding of LILRB1 to MHC Class I and/or blocking the interaction between LILRB1 and MHC Class I. In addition, the anti-LILRB1 antibody or an antigen-binding fragment thereof may have an activity to inhibit immune evasion of cancer cells. Furthermore, the anti-LILRB1 antibody or an
10 antigen-binding fragment thereof may have an anti-cancer effect. The anti-cancer effect may be against a cancer cell expressing or overexpressing MHC Class I on its cell surface.

Another embodiment provides a pharmaceutical composition for treatment and/or prevention of a cancer, the composition comprising the anti-LILRB1 antibody or an antigen-binding fragment thereof as an active ingredient.

15 Another embodiment provides a pharmaceutical composition for inhibition of binding of LILRB1 to MHC Class I and/or blocking the interaction between LILRB1 and MHC Class I, the composition comprising the anti-LILRB1 antibody or an antigen-binding fragment thereof as an active ingredient.

Another embodiment provides a pharmaceutical composition for inhibiting
20 immune evasion of cancer cell, the composition comprising the anti-LILRB1 antibody or an antigen-binding fragment thereof as an active ingredient.

【Technical Solution】

An embodiment provides an anti-LILRB1 antibody, which binds to LILRB1, or an
25 antigen-binding fragment thereof. The anti-LILRB1 antibody or an antigen-binding fragment thereof may have an activity to block the binding of LILRB1 to MHC Class I and/or blocking the interaction between LILRB1 and MHC Class I. In addition, the anti-LILRB1 antibody or an antigen-binding fragment thereof may have an activity to inhibit immune evasion of cancer cells. In addition, the anti-LILRB1 antibody or an
30 antigen-binding fragment thereof may have an anti-cancer effect.

The anti-LILRB1 antibody or an antigen-binding fragment thereof may

comprise the following complementarity determining regions (CDRs):

(1) based on the CDR definition according to Kabat numbering (Kabat, E.A., Wu, T.T., Perry, H., Gottesman, K. and Foeller, C. (1991) Sequences of Proteins of Immunological Interest, Fifth Edition. NIH Publication No. 91-3242; <http://www.abysis.org/>),

a CDR-L1 comprising an amino acid sequence of SEQ ID NO: 1, 7, 13, 19, 25, 31, 37, 43, 49, 55, 61, 67, 73, 79, 85, 91, 97, 103, 109, or 115,

a CDR-L2 comprising an amino acid sequence of SEQ ID NO: 2, 8, 14, 20, 26, 32, 38, 44, 50, 56, 62, 68, 74, 80, 86, 92, 98, 104, 110, or 116,

10 a CDR-L3 comprising an amino acid sequence of SEQ ID NO: 3, 9, 15, 21, 27, 33, 39, 45, 51, 57, 63, 69, 75, 81, 87, 93, 99, 105, 111, or 117,

a CDR-H1 comprising an amino acid sequence of SEQ ID NO: 4, 10, 16, 22, 28, 34, 40, 46, 52, 58, 64, 70, 76, 82, 88, 94, 100, 106, 112, or 118,

15 a CDR-H2 comprising an amino acid sequence of SEQ ID NO: 5, 11, 17, 23, 29, 35, 41, 47, 53, 59, 65, 71, 77, 83, 89, 95, 101, 107, 113, or 119, and

a CDR-H3 comprising an amino acid sequence of SEQ ID NO: 6, 12, 18, 24, 30, 36, 42, 48, 54, 60, 66, 72, 78, 84, 90, 96, 102, 108, 114, or 120; or

(2) based on the CDR definition according to IMGT numbering (<http://www.imgt.org/>),

20 a CDR-L1 comprising an amino acid sequence of SEQ ID NO: 121, 126, 131, 136, 141, 146, 151, 156, 161, 166, 171, 176, 181, 186, 191, 196, 201, 206, 211, or 216,

a CDR-L2 comprising an amino acid sequence of SEQ ID NO: 122, 127, 132, 137, 142, 147, 152, 157, 162, 167, 172, 177, 182, 187, 192, 197, 202, 207, 212, or 217,

a CDR-L3 comprising an amino acid sequence of SEQ ID NO: 3, 9, 15, 21, 27, 33, 39, 45, 51, 57, 63, 69, 75, 81, 87, 93, 99, 105, 111, or 117,

30 a CDR-H1 comprising an amino acid sequence of SEQ ID NO: 123, 128, 133, 138, 143, 148, 153, 158, 163, 168, 173, 178, 183, 188, 193, 198, 203, 208, 213, or 218,

a CDR-H2 comprising an amino acid sequence of SEQ ID NO: 124, 129, 134,

139, 144, 149, 154, 159, 164, 169, 174, 179, 184, 189, 194, 199, 204, 209, 214, or 219, and

a CDR-H3 comprising an amino acid sequence of SEQ ID NO: 125, 130, 135, 140, 145, 150, 155, 160, 165, 170, 175, 180, 185, 190, 195, 200, 205, 210, 215, or 220.

In a specific embodiment, combinations of 6 CDRs (CDR-L1, CDR-L2, CDR-L3, CDR-H1, CDR-H2, and CDR-H3) that can be comprised in the anti-LILRB1 antibody or an antigen-binding fragment thereof provided in this disclosure are illustrated in Table 1:

【Table 1】

	CDR	Amino Acid Sequence (N→C) (Kabat)	SEQ ID NO	Amino Acid Sequence (N→C) (IMGT)	SEQ ID NO
E3/E 3.1	CDR-L1	QGDSLRNFIYAS	1	SLRNFIY	121
	CDR-L2	GKNNRPS	2	GKN	122
	CDR-L3	NSRDSSGSHLTGV	3	NSRDSSGSHLTGV	3
	CDR-H1	SYAMS	4	GFTFSSYA	123
	CDR-H2	AISGSGGSTYYADSVKG	5	ISGSGGST	124
	CDR-H3	DTYYYGSGRSNAFDI	6	ARDTYYYGSGRSNAFDI	125
B3	CDR-L1	QASQDISNYLN	7	QDISNY	126
	CDR-L2	DASNLET	8	DAS	127
	CDR-L3	QQYDNLP	9	QQYDNLP	9
	CDR-H1	DYAMH	10	GFTFDDYA	128
	CDR-H2	GISWNSGSIGYADSVKG	11	ISWNSGSI	129
	CDR-H3	VGDSSGWSDAFDI	12	ARVGDSSGWSDAFDI	130
A10	CDR-L1	RASQSVSSNLA	13	QSVSSN	131
	CDR-L2	GASTRAT	14	GAS	132
	CDR-L3	QQYGSSPRMYT	15	QQYGSSPRMYT	15
	CDR-H1	SYAIS	16	GGTFSSYA	133
	CDR-H2	GIPIFGTANYAQKFQG	17	IPIFGTA	134
	CDR-H3	GGLGELDNWFDP	18	ARGGLGELDNWFDP	135
G1	CDR-L1	SGYKLGDYVS	19	KLGDY	136
	CDR-L2	KDSQRPS	20	KDS	137
	CDR-L3	QAWDSGTGV	21	QAWDSGTGV	21
	CDR-H1	SYGIS	22	GGTFSSYG	138
	CDR-H2	WISAYNGNTNYAQELQ	23	ISAYNGNT	139

		G			
	CDR-H3	VGvagkldy	24	ARVGvagkldy	140
G9	CDR-L1	TGSSSDVGGYNYVS	25	SSDVGGYNY	141
	CDR-L2	DVSNRPS	26	DVS	142
	CDR-L3	SSYTGsSTLDVL	27	SSYTGsSTLDVL	27
	CDR-H1	SYWIG	28	GYSFTSYW	143
	CDR-H2	IIPGDSdTRYSPSFQG	29	IYPGDSdT	144
	CDR-H3	QYYDGGYYMDV	30	ASQYYDGGYYMDV	145
H2	CDR-L1	QGDSLrNYyAS	31	SLrNYy	146
	CDR-L2	GNNKRPS	32	GNN	147
	CDR-L3	NSLDSTYNHPI	33	NSLDSTYNHPI	33
	CDR-H1	SYDIH	34	GYTFTSYD	148
	CDR-H2	WISAYNGNTNYAQKLQ G	35	ISAYNGNT	149
	CDR-H3	DGGDAFDI	36	ARDGGDAFDI	150
H11	CDR-L1	QGDSLrSYyAS	37	SLrSYy	151
	CDR-L2	GRNNRPS	38	GRN	152
	CDR-L3	KSRDSSGNHYV	39	KSRDSSGNHYV	39
	CDR-H1	SYyMH	40	GYTFTSYy	153
	CDR-H2	IINPSGGSTSYAQKFQG	41	INPSGGST	154
	CDR-H3	DAGSSSDY	42	ARDAGSSSDY	155
F12	CDR-L1	AGTSSDIGDYDYVS	43	SSDIGDYDY	156
	CDR-L2	DVSRRPS	44	DVS	157
	CDR-L3	ASyTSSSVVV	45	ASyTSSSVVV	45
	CDR-H1	SYWIG	46	GYSFTSYW	158
	CDR-H2	IIPGDSdTRYSPSFQG	47	IYPGDSdT	159
	CDR-H3	QYYDGGYYMDV	48	ASQYYDGGYYMDV	160
B9	CDR-L1	RASQsISRYLN	49	QsISRY	161
	CDR-L2	GASSLQS	50	GAS	162
	CDR-L3	QQAYGFPLT	51	QQAYGFPLT	51
	CDR-H1	SYAIS	52	GGTFSSyA	163
	CDR-H2	GIIPiFGTANYAQKFQG	53	IIPiFGTA	164
	CDR-H3	GEIAVAQNWDYYGMDV	54	ARGEIAVAQNWDYYGMDV	165
G11	CDR-L1	TGTSSDVGGYNYVS	55	SSDVGGYNY	166
	CDR-L2	DVSKRPS	56	DVS	167
	CDR-L3	SSYSSSSTLVV	57	SSYSSSSTLVV	57
	CDR-H1	SYWIG	58	GYSFTSYW	168
	CDR-H2	IIPGDSdTRYSPSFQG	59	IYPGDSdT	169
	CDR-H3	QYYDGGYYMDV	60	ASQYYDGGYYMDV	170
G6	CDR-L1	QGDSLRRYYAT	61	SLRRYY	171
	CDR-L2	GQNYRPS	62	GQN	172

	CDR-L3	NSRDSSGNHVV	63	NSRDSSGNHVV	63
	CDR-H1	SYVMH	64	GYTFTSY	173
	CDR-H2	GIPIFGTANYAQKFQG	65	IPIFGTA	174
	CDR-H3	GWGYSSSFY	66	ARGWGYSSSFY	175
F11	CDR-L1	SGSSSNIGTNTVN	67	SSNIGTNT	176
	CDR-L2	SNDQRPS	68	SND	177
	CDR-L3	ETWDDSLKGPV	69	ETWDDSLKGPV	69
	CDR-H1	SYAMS	70	GFTFSSYA	178
	CDR-H2	TISGSGDSTYYADSVKG	71	ISGSGDST	179
	CDR-H3	EWELGDAFDI	72	AREWELGDAFDI	180
D3	CDR-L1	RASQSISSYLN	73	QSISSY	181
	CDR-L2	AASSLQS	74	AAS	182
	CDR-L3	QQSYSTRWT	75	QQSYSTRWT	75
	CDR-H1	SYAMS	76	GSTFSSYA	183
	CDR-H2	AISGSGGSTYYADSVKG	77	ISGSGGST	184
	CDR-H3	DRGSYGYYYGMDV	78	AKDRGSYGYYYGMDV	185
B12	CDR-L1	RASQSISSYLN	79	QSISSY	186
	CDR-L2	AASSLQS	80	AAS	187
	CDR-L3	QQSYSTLRT	81	QQSYSTLRT	81
	CDR-H1	GYVMH	82	GYTFTGY	188
	CDR-H2	WINPNSGGTNYAQKFQ G	83	INPNSGGT	189
	CDR-H3	AGASIVGATALDY	84	TRAGASIVGATALDY	190
E4	CDR-L1	TRSSGSIASNYVQ	85	SGSIASNY	191
	CDR-L2	EDNQRPS	86	EDN	192
	CDR-L3	QSYDTGNRNYV	87	QSYDTGNRNYV	87
	CDR-H1	SYTIS	88	GFTFSSYT	193
	CDR-H2	RIIPILGIANAYAQKFQG	89	IIPILGIA	194
	CDR-H3	GPSLNYAGYFDN	90	VRGPSLNYAGYFDN	195
E12	CDR-L1	QGDSLRSYYAS	91	SLRSYY	196
	CDR-L2	GKEKRPS	92	GKE	197
	CDR-L3	NSRGSTTDYMV	93	NSRGSTTDYMV	93
	CDR-H1	SYAMH	94	GFTFSSYA	198
	CDR-H2	VISYDGSNKYYADSVKG	95	ISYDGSNK	199
	CDR-H3	ERGSGMDV	96	ARERGSGMDV	200
D1	CDR-L1	KASQDIDDDMN	97	QDIDDD	201
	CDR-L2	EASTLVP	98	EAS	202
	CDR-L3	LQHDKFPYT	99	LQHDKFPYT	99
	CDR-H1	SYGIS	100	GYTFTSYG	203
	CDR-H2	WINPNSGGTNYAQKFQ G	101	INPNSGGT	204

	CDR-H3	RGVDEGDY	102	ASRGVDEGDY	205
E6	CDR-L1	TGSSGNIASNYVQ	103	SGNIASNY	206
	CDR-L2	RDDQRPS	104	RDD	207
	CDR-L3	QSYDSSSWV	105	QSYDSSSWV	105
	CDR-H1	TYDIT	106	GYTFTTYD	208
	CDR-H2	WMNPNSGNSRSAQKF QG	107	MNPNSGNS	209
	CDR-H3	GDYSGVVLATALDY	108	ATGDYSGVVLAT ALDY	210
E9	CDR-L1	SGSSSNIGNNYVY	109	SSNIGNNY	211
	CDR-L2	RNNQRPS	110	RNN	212
	CDR-L3	AAWDDSLSGWV	111	AAWDDSLSGWV	111
	CDR-H1	SYGMH	112	GFTFSSYG	213
	CDR-H2	NIKQDGSEKYYVDSVKG	113	IKQDGSEK	214
	CDR-H3	EDRIAAAGMRELDY	114	AREDRIAAAGMR ELDY	215
A11	CDR-L1	RSSQSLLHSNGYNYLD	115	QSLLHSNGYNY	216
	CDR-L2	LGSNRAS	116	LGS	217
	CDR-L3	MQGTHWPPYT	117	MQGTHWPPYT	117
	CDR-H1	SYAMT	118	GFSFTSYA	218
	CDR-H2	GISSDGTTTYADSVRG	119	ISSDGT	219
	CDR-H3	DQLLGWDALNV	120	ARDQLLGWDALN V	220

In an embodiment, the anti-LILRB1 antibody or an antigen-binding fragment thereof may comprise:

5 a light chain variable region comprising a CDR-L1, a CDR-L2, and CDR-L3,
and

a heavy chain variable region comprising a CDR-H1, a CDR-H2, and a CDR-H3, wherein the CDRs are as described above.

More specifically, the anti-LILRB1 antibody or an antigen-binding fragment thereof may comprise:

10 a light chain variable region comprising an amino acid sequence of SEQ ID NO: 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, or 345, and

a heavy chain variable region comprising an amino acid sequence of SEQ ID NO: 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252,
15 254, 256, 258, or 260.

In a specific embodiment, combinations of a light chain variable region and a heavy chain variable region that can be comprised in the anti-LILRB1 antibody or an antigen-binding fragment thereof provided in this disclosure are illustrated in Table 2:

【Table 2】

	variable region	Amino acid sequence(N→C)	SEQ ID NO
E3	light chain variable region	SYELTQDPAVSVALGQTVRITCQGDSLRNFYASWYQQKS GQAPVLVMYGKNNRPSGIPDRFSGSTSGNTASLTITGAQ AEDEADYYCNSRDSSSGSHLTGVFGGGTKVTVLGQPAAA	221
	heavy chain variable region	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVR QAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKN TLYLQMISLRAEDTAVYYCARDTYYYGSGRSNAFDIWGQ GTLVTVSS	222
B3	light chain variable region	DIQMTQSPSSLSASVGDRVITTCQASQDISNYLNWYQQK PGKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQ PEDIATYYCQQYDNLFPGGGTKVDIKRTAAA	223
	heavy chain variable region	EVQLLES GGGLVQPGRSLRLSCAASGFTFDDYAMHWVR QAPGKGLEWVSGISWNSG SIGYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCARVGDSSGWSDAFDIWGQG TMVTVSS	224
A10	light chain variable region	DIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQK PGQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISLQS EDFAVYYCQQYGSSPRMYTFGQGTKVDIKRTAAA	225
	heavy chain variable region	QMQLVQSGAEVKKPGSSVKV SCKASGGTFSSY AISWVR QAPGQGLEWMGGIIPFGTANYAQKFQGRVTITADKSIST AYMELSSLRSED TAVYYCARGGLGELDNWFDPWGQGT L VTVSS	226
G1	light chain variable region	SYELTQPPSLSVSPGQTASITCSGYKLGDYVSWYQQKT GQSPVVVIYKDSQRPSGVPERFSGSNSGNTATLTISGTQ AMDEADYYCQAWDSGTGVFGGGTKLTVLGQPAAA	227
	heavy chain variable region	EVQLVQSGAEVKKPGSSVKV SCKASGGTFSSYGISWVR QAPGQGLEWMGWISAYNGNTNYAQELQGRVTMTTDT S TSTAYMELRSLRSDDTAVYYCARVGVAGKLDYWGGGT L V TVSS	228
G9	light chain variable region	QSALTQPASVSGSPGQSITISCTGSSSDVGGYNYVSWYQ QH PGKAPKLMYDVS NRPSGVSDRFSGSKSGN MASLTIS GLQAEDEADYYCSSYTGSS TLDVLFGGGTKLTVLGQPAA A	233

	heavy chain variable region	QVQLVQPGAIEVKKPGESLKISCKGSGYSFTSYWIGWVR QMPGKGLEWMGIIYPGDS DTRYSPSFQGGQVTISADKSI TAYLQWSSLKASDTAMYYCASQYYDGGYYMDVWGQGT LTVSS	234
H2	light chain variable region	SYELTQDPAVSVALGQTVRITCQGDSLRLNYASWYQQKP GQAPILVISGNNKRPSGIPDRFSGSSSGDTASLTISGAQA EDEADYYCNSLDSTYNHPIFGGGTKVTVLGQPAAA	235
	heavy chain variable region	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYDIHWVR QATGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTST STAYMELRSLRSDDTAVYYCARDGGDAFDIWGQGT LTV SS	236
H11	light chain variable region	SYELTQDPAASVALGQTVRITCQGDSLRSYYASWYQQKP GQAPVVVIYGRNNRPSGIPDRFSGSSSGDTASLTITGAQ AEDEADYYCKSRDSSGNHYVFGTGKLTVLGQPAAA	231
	heavy chain variable region	QVQLVQSGAEVKKPGASVKVSCASGYTFTSYMHVVR QAPGQGLEWMGIIINPSGGSTSYAQKFQGRVTMTTRDTST STVYMELSSLRSED TAVYYCARDAGSSSDYWGRGTLVT VSS	232
F12	light chain variable region	QSVLTQPASVSGSPGQSITISCAGTSSDIGDYDYVSWYQ QHPGKTPKLMYDVSRRPSGVPDRFSGSKSGNTASLTIS GLQTEDEADYYCASYTSSSVVVFGGGKLTVLGQPAAA	237
	heavy chain variable region	QVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVR QMPGKGLEWMGIIYPGDS DTRYSPSFQGGQVTISADKSI TAYLQWSSLKASDTAMYYCASQYYDGGYYMDVWGQGT LTVSS	238
B9	light chain variable region	DIQMTQSPSSLSASVGDRVTITCRASQSI SRYLNWYQQK PGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISLQ PEDFATYHCQQAYGFPLTLGGGKVEIKRTAAA	229
	heavy chain variable region	QVQLVESGAIEVKKPGSSVKVSCASGGTFSSYAI SWVR QAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADESTST AYMELSSLRSED TAVYYCARGEI AQAQNDYYGMDVWG QGTLTVSS	230
G11	light chain variable region	QSALTQPRSVSGSPGQSVTISCTGTSSDVGGYNYVSWY QQHPGKAPKLMYDVS KRPSGVPDRFSGSKSGNTASLT SGLQAEDADYYCSSYSSSSTLVVFGGGKLTVLGQPAA A	239
	heavy chain variable region	QVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVR QMPGKGLEWMGIIYPGDS DTRYSPSFQGGQVTISADKSI TAYLQWSSLKASDTAMYYCASQYYDGGYYMDVWGQGT LTVSS	240
G6	light chain	SYELTQDPAVSVALGQTVTITCQGDSLRLRYATWYQQKP GQAPVLVIYGQNYRPSGIPDRFSGSNSGTASLTITGAQA	241

	variable region	EDEADYYCNSRDSSGNHVVFGGGTKLTVLGQPAAA	
	heavy chain variable region	EVQLVESGAIEVKKPGASVKVSCKASGYTFTSYMHVVR QAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADESTST AYMELSSLRSEDVAVYYCARGWGYSSSFYWGQGTTVT VSS	242
F11	light chain variable region	QSVLTQPPSTSGTPGQTFSIFCSGSSSNIGTNTVNWYQQ LPGTAPKLLIYSNDQRPSGVPDRFSGSKSGTSASLAISGL QSEDEADYYCETWDDSLKGPVFGGGTKVTVLGQPAAA	243
	heavy chain variable region	EVQLVESGGGLVQPGGSLKLSCAASGFTFSSYAMSWVR RPGKGLEWVSTISGSGDSTYYADSVKGRFTISRDN SKN TLYLQMNNLRAEDTAVYYCAREWELGDAFDIWGRGTLVT VSS	244
D3	light chain variable region	DIQMTQSPSSLSASVGDRVITICRASQSISSYLNWYQQK PGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQ PEDFATYYCQQSYSTRWTFGGGKVEIKRTAAA	245
	heavy chain variable region	EVQLLESGGGVVQPGRSLRLSCAASGFTFSSYAMSWVR QAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCAKDRGSYGYYYGMDVWGQ GTMVTVSS	246
B12	light chain variable region	DIQMTQSPSSLSASVGDRVITICRASQSISSYLNWYQQK PGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQ PEDFATYYCQQSYSTLRTFGGGKVEIKRTAAA	247
	heavy chain variable region	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYMHVVR RQAPGQGLEWMGWINPNSGGTNYAQKFQGRVTITADES TSTAYMELSSLRSEDVAVYYCTRAGASIVGATALDYWGQ GTLVTVSS	248
E4	light chain variable region	NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQ RPGSSPTTVIYEDNQRPSPGVDRFSGSIDSSSNSASLTIS GLKTEDEADYYCQSYDTGNRNYVFGTGTQLTVLGQPAA A	249
	heavy chain variable region	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYTISWVR QAPGQGLEWMGRIIPILGIANIYAQKFQGRVTMTRDMSTD TAYMELSSLTYYDDTAVYFCVRGPSLNYAGYFDNWGQGT LTVTVSS	250
E12	light chain variable region	SYELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKS GQAPVLVIYGKEKRPSGIPDRFSGSSSGNTASLTITGARA EDEADYYCNSRGSTTDYMFVGGGTQLTVLGQPAAA	251
	heavy chain variable region	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVR QAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKN TLYLQMNSLRAEDTAVYYCARERGSMDVWGQGTLVTV SS	252

D1	light chain variable region	ETTLTQSPAFMSATPGDKVNI SCKASQDIDDDMNWYQQK PGEAAISIIQEASTLVP GIPPRFSGSGYGTDFTLTINNIESE DAAYYFCLQHDKFPYTFGQGTKLEIKRTAAA	253
	heavy chain variable region	EVQLVQSGAEVKKPGASVKV SCKASGYTFTSYGISWVR QAPGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTS ISTAYMELSR LRSDDTAVYYCASRGVDEGDYWGQGTMV TVSS	254
E6	light chain variable region	NFMLTQPHSVSESPGKTVTL SCTGSSGNIASNYVQWYQ HRPGSAPTTVIYRDDQRPSGVPDRFSGSIDSSSNSASLTI SGLRPEDEADYYCQSYDSSSWVFGGGTKLTVLGQPAAA	255
	heavy chain variable region	QVQLVQSGAEVKKPGASVKV SCKASGYTFTTYDITWVR QAPGQGLEWMGWMNPNSGNSRSAQKFQGRVSMTSDS SISTAYMELSSLRSED TAVYYCATGDYSGVVL TATALDY WGQGTLVTVSS	256
E9	light chain variable region	QSELTQLPSASETPGQRTVISC GSSSNIGNNYVYWYQQ LPGTAPKLLIYRNNQRPSGVPDRFSGSKSGTSASLAISGL RSEDEADYYCAAWDDSLSGWVFGGGTKLTVLGQPAAA	257
	heavy chain variable region	QVQLVESGGGLVQPGRSLRL SCAASGFTFSSYGMHWV RQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDN A KNTLYLQMNSLRAEDTAVYYCAREDRIAAAGMRELDYW GQGTLVTVSS	258
A11	light chain variable region	DIVMTQSPLSLPVTGPGEPA SISRSSQSL LHSNGYNYLD WYLQKPGQSPQLLIYLG SNRASGVPDRFSGSGSGTDFT LKISRVEAEDVGVYYCMQ GTHWPPYTFGQGTKVEIKRTA AA	259
	heavy chain variable region	EVQLLESGGGLEQPGGFLRL SCAASGFSFTSYAMTWVR QAPGKGLEWVSGISSDGT TTTTYADSVRGRFTISRDN AKN TVYLQMNSLRDEDTAVYYCARDQLLGWDALNVWGQGT MTVSS	260
E3.1	light chain variable region	SYELTQDPAVSVALGQTVRIT CQGD SLRNFYASWYQQKS GQAPVLV MYGKNNRPSGIPDRFSGSTSGNTASLTITGAQ AEDEADYYCNSRDSSGSHLTGVFGGGTKVTVL	345
	heavy chain variable region	QVQLVESGGGLVQP GGSLRL SCAASGFTFSSYAMSWVR QAPGKGLEWVSAISGSGG STYYADSVKGRFTISRDN SKN TLYLQMISLRAEDTAVYYCARD TYYYGSGRSNAFDIWGQ GTLVTVSS	222

In this disclosure, the expression "an antibody or an antigen-binding fragment (for example, CDR, variable region, or heavy chain /light chain) comprising, consists of, or represented by a certain amino acid sequence" may refer to an antigen-binding

fragment that consists essentially of (1) the certain amino acid sequence or (2) an amino acid sequence wherein an insignificant mutation (for example, substitution, deletion, and/or addition of an amino acid residue(s); leading to no impact on the activity of the antibody) is introduced in the amino acid sequence (1).

5 The anti-LILRB1 antibody or an antigen-binding fragment thereof provided in this disclosure may have a binding affinity (K_D) to LILRB1 (for example, human LILRB1) of 10mM or less, 5 mM or less, 1mM or less, 0.5mM or less, 0.2mM, or 0.15mM or less, for example, 0.001nM to 10mM, 0.005nM to 10mM, 0.01nM to 10mM, 0.05nM to 10mM, 0.1nM to 10mM, 0.5nM to 10mM, 1nM to 10mM, 0.001nM
10 to 5mM, 0.005nM to 5mM, 0.01nM to 5mM, 0.05nM to 5mM, 0.1nM to 5mM, 0.5nM to 5mM, 1nM to 5mM, 0.001nM to 1mM, 0.005nM to 1mM, 0.01nM to 1mM, 0.05nM to 1mM, 0.1nM to 1mM, 0.5nM to 1mM, 1nM to 1mM, 0.001nM to 0.5mM, 0.005nM to 0.5mM, 0.01nM to 0.5mM, 0.05nM to 0.5mM, 0.1nM to 0.5mM, 0.5nM to 0.5mM, 1nM to 0.5mM, 0.001nM to 0.2mM, 0.005nM to 0.2mM, 0.01nM to 0.2mM, 0.05nM to
15 0.2mM, 0.1nM to 0.2mM, 0.5nM to 0.2mM, 1nM to 0.2mM, 0.001nM to 0.15mM, 0.005nM to 0.15mM, 0.01nM to 0.15mM, 0.05nM to 0.15mM, 0.1nM to 0.15mM, 0.5nM to 0.15mM, or 1nM to 0.15mM, when measured by surface plasmon resonance (SPR).

 Another embodiment provides a pharmaceutical composition comprising the
20 anti-LILRB1 antibody or an antigen-binding fragment thereof as an active ingredient. For example, the pharmaceutical composition may be a pharmaceutical composition for treating and/or preventing a cancer. The pharmaceutical composition may have an activity to inhibit the binding of LILRB1 to MHC Class I and/or the interaction between LILRB1 and MHC Class I. The cancer may be a cancer associated with the
25 interaction between LILRB1 and MHC Class I. In an embodiment, the pharmaceutical composition may have an activity to inhibit immune evasion of a cancer cell. The cancer cell may be a cell expressing or overexpressing MHC Class I on cell surface.

 Another embodiment provides a composition for blocking the binding of LILRB1 to MHC Class I and/or the interaction between LILRB1 and MHC Class I, the
30 composition comprising the anti-LILRB1 antibody or an antigen-binding fragment thereof as an active ingredient.

Another embodiment provides a composition for inhibiting immune evasion of a cancer cell, the composition comprising the anti-LILRB1 antibody or an antigen-binding fragment thereof as an active ingredient.

5 Another embodiment provides a method of treating and/or preventing a cancer, comprising administering (orally or parenterally) a pharmaceutically effective amount of the anti-LILRB1 antibody or an antigen-binding fragment thereof to a subject (e.g., a mammal including human) in need of treating and/or preventing the cancer.

10 Another embodiment provides a method of blocking the binding of LILRB1 to MHC Class I and/or a method of blocking the interaction between LILRB1 and MHC Class I, comprising administering (orally or parenterally) a pharmaceutically effective amount of the anti-LILRB1 antibody or an antigen-binding fragment thereof to a subject (e.g., a mammal including human) in need of inhibiting the binding of LILRB1 to MHC Class I and/or the interaction between LILRB1 and MHC Class I.

15 Another embodiment provides a method of inhibiting immune evasion of a cancer cell, comprising administering (orally or parenterally) a pharmaceutically effective amount of the anti-LILRB1 antibody or an antigen-binding fragment thereof to a subject (e.g., a mammal including human) in need of inhibiting immune evasion of the cancer cell.

20 The methods provided in this disclosure may further comprise a step of identifying the subject in need of treating and/or preventing the cancer, inhibiting the binding of LILRB1 to MHC Class I and/or the interaction between LILRB1 and MHC Class I, and/or inhibiting immune evasion of the cancer cell, prior to the step of administering.

25 Another embodiment provides a nucleic acid molecule (polynucleotide) encoding at least one polypeptide selected from the group consisting of CDR (CDR-L1, CDR-L2, CDR-L3, CDR-H1, CDR-H2, CDR-H3, a combination of CDR-L1, CDR-L2, and CDR-L3, or a combination of CDR-H1, CDR-H2, and CDR-H3), a light chain variable region comprising CDR-L1, CDR-L2, and CDR-L3, a heavy chain variable
30 region comprising CDR-H1, CDR-H2, and CDR-H3; a light chain comprising the light chain variable region, and a heavy chain comprising the heavy chain variable region,

of the anti-LILRB1 antibody described above.

Another embodiment provides a recombinant vector comprising the nucleic acid molecule. In an embodiment, the recombinant vector may comprise a nucleic acid molecule encoding the light chain variable region or light chain, and a nucleic acid molecule encoding the heavy chain variable region or heavy chain, respectively (e.g., in two separate vectors) or all together (e.g., in one vector). The recombinant vector may be used as an expression vector.

Another embodiment provides a recombinant cell comprising the nucleic acid molecule or the recombinant vector.

Another embodiment provides a method of preparing an anti-LILRB1 antibody or an antigen-binding fragment thereof, comprising expressing the nucleic acid molecule in a cell. The step of expressing the nucleic acid molecule may comprise culturing the recombinant cell.

As described herein, the antigen-binding fragment of an anti-LILRB1 antibody may refer to a fragment which is derived from an anti-LILRB1 antibody and retain antigen (LILRB1) binding affinity of the antibody. In an embodiment, the antigen-binding fragment may be a polypeptide comprising the 6 CDRs of an anti-LILRB1 antibody as described above, and, for example, may be scFv, scFv-Fc, scFv-Ck(kappa constant region), scFv-Cλ(lambda constant region), (scFv)₂, Fab, Fab', or a F(ab')₂, but not be limited thereto. In an embodiment, the antigen-binding fragment may be scFv, a fusion polypeptide (scFv-Fc) wherein scFv is fused with a Fc region of an immunoglobulin (e.g., IgA, IgD, IgE, IgG (IgG1, IgG2, IgG3, IgG4), IgM, etc.), or a fusion polypeptide (scFv-Ck or scFv-Cλ) wherein scFv is fused with a constant region (e.g., kappa or lambda) of a light chain.

The anti-LILRB1 antibody or an antigen-binding fragment thereof may have a regulatory activity, for example, an antagonistic or agonistic activity, on LILRB1 protein. In addition, the anti-LILRB1 antibody or an antigen-binding fragment thereof may have an activity of blocking the binding of LILRB1 to MHC Class I and/or the interaction between LILRB1 and MHC Class I. In addition, the anti-LILRB1 antibody or an antigen-binding fragment thereof may have an activity of inhibiting immune evasion of a cancer cell. Furthermore, the anti-LILRB1 antibody or an antigen-binding

fragment thereof may have an anti-cancer effect.

A protein LILRB1, which is an antigen of an anti-LILRB1 antibody or an antigen-binding fragment thereof provided in this disclosure, may be derived from mammal. For example, LILRB1 as an antigen may be a human LILRB1 (e.g.,
5 GenBank accession numbers AAH15731.1 (SEQ ID NO: 348), NP_001265328.2, NP_001265327.2, NP_001075108.2, NP_001075107.2, NP_001075106.2, NP_006660.4, NM_001081637.2, NM_001081638.3, NM_001081639.3, NM_001278398.2, NM_001278399.2, etc.), but not be limited thereto.

MHC Class I may be one of classes of major histocompatibility
10 complex (MHC) molecules. In an embodiment, the MHC Class I may be a human MHC Class I and may be at least one selected from the group consisting of HLA(human leukocyte antigen)-A, HLA-B, HLA-C, HLA-E, HLA-F, and HLA-G, but not be limited thereto.

As described herein, the term "antibody" may refer to a protein that
15 specifically binds to a specific antigen, and may be a protein produced by stimulation of an antigen in the immune system, or a protein produced by chemical synthesis or recombinant production, with no specific limitation. The antibody may be non-naturally occurring, for example, produced by recombinant or synthetic production. The antibody may be an animal antibody (e.g., a mouse antibody, etc.), a chimeric
20 antibody, a humanized antibody, or a human antibody. The antibody may be a monoclonal or polyclonal antibody.

In the anti-LILRB1 antibody or an antigen-binding fragment thereof provided herein, the portion, except for the heavy-chain CDR and light-chain CDR portions or the heavy-chain variable and light-chain variable regions as defined above, may be
25 derived from any subtype of immunoglobulin (e.g., IgA, IgD, IgE, IgG (IgG1, IgG2, IgG3, IgG4), IgM, and the like), and, for example, derived from the framework portions, and/or light-chain constant region and/or heavy-chain constant region. In an embodiment, the anti-LILRB1 antibody provided in this disclosure may be an antibody in a form of human IgG, for example, IgG1, IgG2, IgG3, or IgG4, but not be
30 limited thereto.

An intact antibody (e.g., IgG type) has a structure with two full-length light chains and two full-length heavy chains, in which each light chain is linked to a corresponding heavy chain via a disulfide bond. The constant region of an antibody is divided into a heavy-chain constant region and a light-chain constant region. The heavy-chain constant region is of a gamma (γ), mu (μ), alpha (α), delta (δ), or epsilon (ϵ) type, and has gamma1 (γ 1), gamma2 (γ 2), gamma3 (γ 3), gamma4 (γ 4), alpha1 (α 1) or alpha2 (α 2) as its subclass. The light chain constant region is of either a kappa (κ) or lambda (λ) type.

As used herein, the term "heavy chain" may be intended to encompass a full-length heavy chains and fragments thereof, wherein the full-length heavy chain may comprise a variable region VH including amino acid sequences sufficient to provide specificity to antigens, three constant regions CH1, CH2, and CH3, and a hinge. The term "light chain" may be intended to encompass full-length light chains and fragments thereof, wherein the full-length light chain may comprises a variable region VL including amino acid sequences sufficient to provide specificity to antigens, and a constant region CL.

The term "complementarity determining region (CDR)" may refer to a portion that confers antigen-binding specificity in a variable region of an antibody, and may refer to an amino acid sequence found in a hyper variable region of a heavy chain or a light chain of immunoglobulin. The heavy and light chains may respectively include three CDRs (CDRH1, CDRH2, and CDRH3; and CDRL1, CDRL2, and CDRL3). The CDR may provide contacting residues that play an important role in the binding of an antibody to its antigen or an epitope of the antigen. As used herein, the terms "specifically binding" and "specifically recognizing" may have the same general meaning as known to one of ordinary skill in the art, and indicate that an antibody and an antigen specifically interact with each other to lead to an immunological reaction.

In this disclosure, unless differently stated, the term "antibody" may encompass not only an intact antibody but also an antigen-binding fragment of the antibody possessing an antigen-binding capability.

The term “antigen-binding fragment” used herein may refer to a polypeptide in any type, which comprises a portion (e.g., 6 CDRs as described herein) capable of binding to an antigen, and, for example, may be scFv, (scFv)₂, scFv-Fc, Fab, Fab', or F(ab')₂, but is not limited thereto. In addition, as described above, the antigen-binding
5 fragment may be scFv, a fusion polypeptide wherein scFv is fused with a Fc region of an immunoglobulin (e.g., IgA, IgD, IgE, IgG (IgG1, IgG2, IgG3, IgG4), IgM, etc.) or a constant region (e.g., kappa or lambda).

Among the antigen-binding fragments, Fab includes light chain and heavy chain variable regions, a light chain constant region, and a first heavy chain constant
10 region CH1.

Fab' is different from Fab in that Fab' comprises a hinge region having at least one cysteine residue at the C-terminal of CH1.

F(ab')₂ antibody is formed through disulfide bridging of the cysteine residues in the hinge region of Fab'.

Fv is a minimal antibody fragment composed of only a heavy chain variable region and a light chain variable region. Recombination techniques of generating an
15 Fv fragment are widely known in the art.

Two-chain Fv comprises a heavy chain variable region and a light chain variable region which are linked to each other by a non-covalent bond. Single-chain
20 Fv generally comprises a heavy-chain variable region and a light-chain variable region which are linked to each other by a covalent bond via a peptide linker or directly linked at the C-terminals to have a dimer structure like two-chain Fv.

The antigen-binding fragments may be obtained using protease (for example, Fab may be obtained by restrictively cleaving a whole antibody with papain, and an
25 F(ab')₂ fragment may be obtained by cleaving with pepsin), or may be prepared by using a genetic recombination technique.

The term “hinge region” may refer to a region between CH1 and CH2 domains within heavy chain of an antibody, which functions to provide flexibility for the antigen-binding site in the antibody.

The anti-LILRB1 antibody may be a monoclonal or polyclonal antibody and, for example, a monoclonal antibody. A monoclonal antibody can be prepared using
30

a method widely known in the art, for example, using a phage display technique. Alternatively, the anti-LILRB1 antibody may be constructed in the form of a mouse-derived monoclonal antibody by a conventional method.

Meanwhile, individual monoclonal antibodies can be screened using a typical
5 ELISA (Enzyme-Linked ImmunoSorbent Assay) format, based on the binding potential against LILRB1. Inhibitory activities can be verified through functional analysis such as competitive ELISA for verifying the molecular interaction of binding assemblies or functional analysis such as a cell-based assay. Then, with regard to monoclonal antibody members selected on the basis of their strong inhibitory
10 activities, their affinities (K_d values) to LILRB1 may be each verified.

The pharmaceutical composition may further comprise a pharmaceutically acceptable carrier, in addition to the active ingredient (the anti-LILRB1 antibody or an antigen-binding fragment thereof). The pharmaceutically acceptable carrier may be anyone selected from those commonly used for the formulation of antibodies. For
15 example, the pharmaceutically acceptable carrier may be one or more selected from the group consisting of lactose, dextrose, sucrose, sorbitol, mannitol, starch, gum acacia, calcium phosphate, alginates, gelatin, calcium silicate, micro-crystalline cellulose, polyvinylpyrrolidone, cellulose, water, syrup, methyl cellulose, methylhydroxy benzoate, propylhydroxy benzoate, talc, magnesium stearate, mineral
20 oil, and the like, but are not limited thereto. The pharmaceutical composition may further comprise one or more selected from the group consisting of a diluent, an excipient, a lubricant, a wetting agent, a sweetener, a flavor enhancer, an emulsifying agent, a suspension agent, preservative, and the like, which can be commonly used for manufacturing pharmaceutical composition.

25 The pharmaceutical composition, or the antibody or an antigen-binding fragment thereof may be administered orally or parenterally in a pharmaceutically effective amount. The parenteral administration may be intravenous injection, subcutaneous injection, muscular injection, intraperitoneal injection, endothelial administration, intranasal administration, intrapulmonary administration, rectal
30 administration or intralesional local administration. Since proteins or peptides are digested when administered orally, the active ingredient in the compositions for oral

administration may be coated or formulated to prevent digestion in stomach. In addition, the antibody or the compositions may be administered using an optional device that enables the active ingredient to be delivered to target cells (e.g., cancer cells).

5 The anti-LILRB1 antibody or an antigen-binding fragment thereof may be comprised in the pharmaceutical composition or administered to a subject in a pharmaceutically effective amount. As used herein, the term “pharmaceutically effective amount” may refer to an amount of an active ingredient (the antibody or fragment thereof) at which the active ingredient can exert desired effects (e.g., anti-
10 cancer effect). The pharmaceutically effective amount may be prescribed in a variety of ways, depending on various factors, such as age, body weight, gender, pathologic conditions, diets, excretion speed, and/or reaction sensitivity of a subject, formulation types, administration time, administration interval, administration route, administration manner, and the like. For example, anti-LILRB1 antibody or an antigen-binding
15 fragment thereof may be administered at the amount of 0.005 ug/kg to 1000mg/kg, 0.005 ug/kg to 500mg/kg, 0.005 ug/kg to 250mg/kg, 0.005 ug/kg to 100mg/kg, 0.005 ug/kg to 75mg/kg, 0.005 ug/kg to 50mg/kg, 0.01 ug/kg to 1000mg/kg, 0.01 ug/kg to 500mg/kg, 0.01 ug/kg to 250mg/kg, 0.01 ug/kg to 100mg/kg, 0.01 ug/kg to 75mg/kg, 0.01 ug/kg to 50mg/kg, 0.05 ug/kg to 1000mg/kg, 0.05 ug/kg to 500mg/kg, 0.05 ug/kg
20 to 250mg/kg, 0.05 ug/kg to 100mg/kg, 0.05 ug/kg to 75mg/kg, or 0.05 ug/kg to 50mg/kg per day, but not be limited thereto. The daily dosage may be formulated into a single formulation in a unit dosage form or formulated in suitably divided dosage forms, or it may be manufactured to be contained in a multiple dosage container.

 The pharmaceutical compositions may be formulated into a form of a solution
25 in oil or an aqueous medium, a suspension, syrup, an emulsifying solution, an extract, powder, granules, a tablet, or a capsule, and may further comprise a dispersing or a stabilizing agent for the formulation.

 The subject, to whom the antibody, pharmaceutical composition, or method provided in this disclosure is applied, may be selected from mammals including a
30 mammal including primates such as humans and monkeys, rodents such as rats and mice, and the like.

The cancer may be a solid cancer or blood cancer. The cancer may be, but not limited to, one or more selected from the group consisting of lung cancer (e.g., squamous cell carcinoma of the lung, small-cell lung cancer, non-small-cell lung cancer, adenocarcinoma of the lung), peritoneal carcinoma, skin cancer, squamous cell carcinoma, melanoma in the skin or eyeball, rectal cancer, cancer near the anus, esophagus cancer, small intestinal tumor, endocrine gland cancer, parathyroid cancer, adrenal cancer, soft-tissue sarcoma, urethral cancer, leukemia (e.g., chronic or acute leukemia), lymphocytic lymphoma, hepatoma, gastric cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatocellular adenoma, breast cancer, colon cancer, large intestine cancer, endometrial carcinoma or uterine carcinoma, salivary gland tumor, renal cell carcinoma, kidney cancer, prostate cancer, vulvar cancer, thyroid cancer, head and neck cancer, brain cancer, biliary tract cancer, gallbladder cancer, bone osteosarcoma, and the like. The cancer may be a primary cancer or a metastatic cancer. The cancer may be a cancer characterized by expression or overexpression of MHC Class I on a surface of cancer cell, and, for example, may be colon adenocarcinoma, small cell lung carcinoma, breast cancer, pancreatic cancer, malignant melanoma, bone osteosarcoma, renal cell carcinoma, or gastric cancer. The overexpression of MHC Class I may refer to an overexpression compared to that of a normal cell or a cancer cell which is non-responsive or resistant to the immunotherapy, for example, T-cell (e.g., cytotoxic T-cell) mediated immunotherapy.

As used herein, the term “treatment of cancer” may refer to all anti-cancer actions that prevent, alleviate or ameliorate the symptoms of cancer, or partially or completely remove a cancer, such as, cancer cell death, inhibition of cancer cell proliferation, inhibition of cancer metastasis, and the like.

The anti-LILRB1 antibody or an antigen-binding fragment thereof provided in this disclosure may be co-administered with another drug, for example, at least one selected from the group consisting of conventionally used agents for immunotherapy, anti-cancer agents, cytotoxic agents, and the like. Accordingly, an embodiment provides a pharmaceutical composition of combined administration for treating and/or preventing a cancer, comprising (1) an anti-LILRB1 antibody or an antigen-binding

fragment thereof, and (2) at least one selected from the group consisting of agents for immunotherapy, anti-cancer agents, cytotoxic agents, and the like. Another embodiment provides a method of treating and/or preventing a cancer, comprising administering (1) an anti-LILRB1 antibody or an antigen-binding fragment thereof, and (2) at least one selected from the group consisting of agents for immunotherapy, anti-cancer agents, cytotoxic agents, and the like, to a subject in need of treating and/or preventing the cancer. The agents for immunotherapy, anti-cancer agents, and cytotoxic agents may include any drugs which are conventionally used for cancer therapy, and/or have cytotoxic activity, and for example, they may be at least one selected from the group consisting of proteins such as antibodies, nucleic acid molecules such as siRNA, and/or small molecular chemicals such as paclitaxel, docetaxel, and the like, but not limited thereto.

Another embodiment provides a polypeptide molecule comprising a heavy chain complementarity determining region (CDR-H1, CDR-H2, CDR-H3, or a combination thereof), a light chain complementarity determining region (CDR-L1, CDR-L2, CDR-L3, or a combination thereof), a combination thereof; or heavy chain variable region, light chain variable region, or a combination thereof, of the anti-LILRB1 antibody as described above. The polypeptide molecule may be used in preparing an antibody as a precursor of antibody, or comprised in a protein scaffold having an antibody-like structure (e.g., peptibody), a bispecific antibody, or a multispecific antibody, as a component thereof. In another embodiment, the polypeptide molecule may be used as a target (antigen) recognition domain or a secreted antibody, in cell therapeutics for target therapy, such as CAR-T. In another embodiment, the polypeptide molecule may be used for constructing anti-LILRB1 antibody-secreting cells as cell therapeutics.

Another embodiment provides a nucleic acid molecule encoding a heavy chain complementarity determining region (CDR-H1, CDR-H2, CDR-H3, or a combination thereof), a heavy chain variable region, or a heavy chain, of the anti-LILRB1 antibody.

Another embodiment provides a nucleic acid molecule encoding a light chain complementarity determining region (CDR-L1, CDR-L2, CDR-L3, or a combination thereof), a light chain variable region, or a light chain, of the anti-LILRB1 antibody.

Another embodiment provides a recombinant vector comprising a nucleic acid molecule encoding a heavy chain variable region or a heavy chain of the anti-LILRB1 antibody, and a light chain variable region or a light chain of the anti-LILRB1 antibody, respectively in two separate vectors or all together in one vector.

Another embodiment provides a recombinant cell comprising the nucleic acid molecule or the recombinant vector.

The term “vector” refers to a means for expressing a target gene in a host cell, as exemplified by a plasmid vector, a cosmid vector, and a viral vector such as a bacteriophage vector, a lentivirus vector, an adenovirus vector, a retrovirus vector, and an adeno-associated virus vector. The recombinant vector may be constructed from or by manipulating a plasmid (for example, pSC101, pGV1106, pACYC177, ColE1, pKT230, pME290, pBR322, pUC8/9, pUC6, pBD9, pHC79, pIJ61, pLAFR1, pHV14, pGEX series, pET series, pUC19, etc.), a phage (for example, λ gt4 λ B, λ -Charon, λ Δz1, M13, etc.), or a virus vector (for example, SV40, etc.), which is commonly used in the art.

In the recombinant vector, the nucleic acid molecule may be operatively linked to a promoter. The term “operatively linked” is intended to pertain to a functional linkage between a nucleotide sequence of interest and an expression regulatory sequence (for example, a promoter sequence). When being “operatively linked”, the regulatory element can control the transcription and/or translation of a polynucleotide of interest.

The recombinant vector may be constructed typically as a cloning vector or an expression vector. For recombinant expression vectors, a vector generally available in the relevant art for expressing a foreign protein in plant, animal, or microbial cells may be employed. Various methods well known in the art may be used for the construction of recombinant vectors.

For use in hosts, such as prokaryotic or eukaryotic cells, the recombinant vector may be constructed accordingly. For example, when a vector is constructed as

an expression vector for use in a prokaryotic host, the vector typically includes a strong promoter for transcription (e.g., a pL⁺ promoter, a CMV promoter, a *trp* promoter, a *lac* promoter, a *tac* promoter, a T7 promoter, etc.), a ribosomal binding site for initiating translation, and transcriptional/translational termination sequences.

5 On the other hand, an expression vector for use in a eukaryotic host includes an origin of replication operable in a eukaryotic cell, such as an f1 origin of replication, an SV40 origin of replication, a pMB1 origin of replication, an adeno origin of replication, an AAV origin of replication, and a BBV origin of replication, but is not limited thereto. In addition, the expression vector typically includes a promoter
10 derived from genomes of mammalian cells (for example, metallothionein promoter) or from mammalian viruses (for example, adenovirus late promoter, vaccinia virus 7.5K promoter, SV40 promoter, cytomegalovirus promoter, *tk* promoter of HSV, etc.), and a polyadenylation sequence as a transcription termination sequence.

The recombinant cell may be prepared by introducing the recombinant vector
15 into a suitable host cell. As long as it allows the sequential cloning and expression of the recombinant vector in a stable manner, any host cell known in the art may be employed in the present disclosure. Examples of the prokaryotic host cell available for the present disclosure may be selected from *E. coli* such as *E. coli* JM109, *E. coli* BL21, *E. coli* RR1, *E. coli* LE392, *E. coli* B, *E. coli* X 1776, *E. coli* W3110, *Bacillus*
20 spp. such as *Bacillus subtilis* and *Bacillus thuringiensis*, and enterobacteriaceae strains such as *Salmonella typhimurium*, *Serratia marcescens* and various *Pseudomonas* species. Eukaryotic host cells that may be used for transformation may selected from, but are not limited to, *Saccharomyces cerevisiae*, insect cells, and animal cells, such as Sp2/0, CHO (Chinese hamster ovary) K1, CHO DG44,
25 CHO S, CHO DXB11, CHO GS-KO, PER.C6, W138, BHK, COS-7, 293, HepG2, Huh7, 3T3, RIN, MDCK, etc.

The nucleic acid molecule or a recombinant vector carrying the same may be introduced (transfected) into a host cell using a method well known in the relevant art. For example, this transfection may be carried out using a CaCl₂ or electroporation
30 method when the host cell is prokaryotic. For eukaryotic host cells, the genetic introduction may be achieved using, but not limited to, microinjection, calcium

phosphate precipitation, electroporation, liposome-mediated transfection, or particle bombardment.

To select a transformed host cell, advantage may be taken of a phenotype associated with a selection marker according to methods well known in the art. For example, when the selection marker is a gene conferring resistance to a certain antibiotic, the host cells may be grown in the presence of the antibiotic in a medium to select a transformant of interest.

Another embodiment provides a method of preparing the anti-LILRB1 antibody or an antigen-binding fragment thereof, comprising expressing the nucleic acid molecule or a recombinant vector in a host cell. The step of expressing may be conducted by culturing the recombinant cell comprising the nucleic acid molecule (for example, in a recombinant vector) under a condition allowing the expression of the nucleic acid molecule. The method may further comprise isolating and/or purifying the antibody or its fragment from the cell culture, after the step of expressing or culturing.

【Advantageous Effects】

The anti-LILRB1 antibody or an antigen-binding fragment thereof provided in this disclosure can have high anti-cancer effect by inhibiting the immune evasion mechanism of cancer cells, allowing that the immune cells can exhibit their anti-cancer effect.

【Description of Drawings】

Fig. 1 is an electrophoresis image showing the results of SDS-PAGE gel analysis for anti-LILRB1 antibodies purified in an example.

Fig. 2 is a sensorgram showing the results of SPR (surface plasmon resonance) assay for anti-LILRB1 antibody B3 according to an example.

Fig. 3 is a sensorgram showing the results of SPR assay for anti-LILRB1 antibody E3 according to an example.

Fig. 4a is a graph showing binding ability of anti-LILRB1 antibody A10 according to an example to a human natural killer cell, KHYG-1; Fig. 4b is a graph

showing binding ability of anti-LILRB1 antibody E3 according to an example to a human natural killer cell, KHYG-1; and Fig. 4c is a graph showing binding ability of human IgG4 isotype control antibody to a human natural killer cell, KHYG-1.

Fig. 5 is a graph showing the level of binding of recombinant LILRB1-Fc proteins to HLA-G overexpressing cell surface measured by iQue screener, when treated with anti-LILRB1 antibodies according to an example and human IgG4 isotype control antibody, respectively.

Fig. 6 is a graph showing in vivo antitumor effects of anti-LILRB1 antibody E3 and B3 according to an example.

Figs. 7a to 7d are flow cytometry diagrams of binding of anti-LILRB1 antibody E3.1 according to an example to cells expressing various members of human LILR family.

Figs. 8a to 8d are flow cytometry diagrams of binding of anti-LILRB1 antibody H11 according to an example to cells expressing various members of human LILR family.

Fig. 9 is a graph showing release level of granzyme B in a human natural killer cell, KHYG-1, when treated with anti-LILRB1 antibody E3.1 or H11 according to an example, comparing with that in the cell treated with a control antibody (human IgG4 isotype).

Fig. 10 is a graph showing release level of perforin in a human natural killer cell, KHYG-1, when treated with anti-LILRB1 antibody E3.1 or H11 according to an example, comparing with that in the cell treated with a control antibody (human IgG4 isotype).

Fig. 11 is a graph showing results of luciferase reporter assay for evaluating ability of anti-LILRB1 antibody E3.1 or H11 according to an example to block LILRB1 signal pathway.

Fig. 12 is a graph showing in vivo anti-tumor effects of anti-LILRB1 antibody E3.1 and H11 according to an example.

【Mode for Invention】

Hereafter, the present invention will be described in detail by examples.

The following examples are intended merely to illustrate the invention and are not construed to restrict the invention.

Example 1: Preparation of human antibodies against LILRB1

1.1. Selection of human antibodies against LILRB1 using phage display

In order to select antibodies that specifically recognize human LILRB1, a phage display screening was performed using a library composed of human scFv antibodies. As an antigen, human LILRB1-His (Cat. No. 8989-T2) and human LILRB1-Fc (Cat. No. 2017-T2) (RnD systems) were used respectively. Each antigen was conjugated with biotin by EZ-Link Sulfo-NHS-Biotin kit (ThermoFisher Scientific) for use.

The phage display screening was performed using total 4-types of LILRB1 antigens (LILRB1-His, LILRB1-Fc, LILRB1-His-Biotin, and LILRB1-Fc-Biotin) through solid-phase screening and solution-phase screening. Additional screenings were performed by gradually decreasing the concentration of the used antigen, competitively eluting with control antibodies against LILRB1, conducting negative selection to Fc when LILRB1-Fc is used as an antigen, etc. The selected products were confirmed for their binding to the antigen through polyclonal phage ELISA.

1.2. Screening and analysis of monoclonal soluble scFvs

Genes encoding the scFvs, which were verified to bind the antigen in Example 1.1, were amplified by PCR to prepare expression vectors. For each selection, a certain number of transformants were transferred to a 96 well culture plate for screening. Antibodies in a scFv form were expressed using Autoinduction media (Studier, F.W. (2005) Protein Expression and Purification 41, 207-34) and then analyzed for their binding to the antigen by performing DELFIA immune assay (PerkinElmer). In addition, after allowing a certain amount of each scFv antibody to be captured on the surface, DELFIA for the antigen was performed to determine the ranking for antigen-antibody binding affinity.

1.3. Conversion of the screened scFvs into IgG antibodies

Among the clones which were confirmed to bind to the antigen in Example 1.2, a total of 376 clones were selected, and the DNA sequences of genes encoding the selected scFvs were analyzed by a general DNA sequencing to remove duplicate clones. In addition, a total of 93 clones were selected based on the ranking of the antigen-antibody binding affinity determined in Example 1.2. Genes encoding a heavy chain variable region(VH) and a light chain variable region(VL) were respectively amplified by PCR from each of the genes encoding the selected scFvs, and inserted into an expression vector (pTRIOZ-hIgG4, InvivoGen; alternatively, any one of vectors comprising CMV promoter or CMV/CHO beta-actin fusion promoter (KR10-1038126B1) and genes encoding human IgG4 heavy chain constant region and kappa or lambda light chain constant region can be used), wherein the expression vector was designed for encoding a human IgG4 antibody(IgG4 Fc: SEQ ID NO: 341, Kappa constant region: SEQ ID NO: 342, Lambda constant region: SEQ ID NO: 343). The DNA sequence of the expression vector was confirmed by sequencing.

1.4. Preparation of selected antibodies

The vectors constructed in Example 1.3 were purified using Plasmid Plus Maxi kit (Qiagen). The purified vectors were used for expressing antibodies in ExpiCHO-STM cells or Expi293TM cells.

In particular, the vectors constructed in Example 1.3 were transfected into ExpiCHO-STM cells(Gibco) (1.5×10^8 cells/Culture Volume 25 mL) by adding 80 μ L of ExpiFectamineTM CHO reagent (Thermo Fisher). One day post-transfection, 150 μ L of ExpiCHOTM Enhancer (Thermo Fisher) and 4 mL of ExpiCHOTM Feed (Thermo Fisher) were added to the culture. On day 5, 4 mL of ExpiCHOTM Feed was added to the culture. The transfected cells were cultured under the conditions of 32°C and 5% CO₂ for 7-11 days in total.

In addition, the vectors constructed in Example 1.3 were transfected into Expi293FTM cells (Gibco) (3×10^8 cells/Culture Volume 100 mL) by adding 320 μ L of ExpiFectamineTM 293 Reagent (Gibco) according to manufacturer's protocol. One day post-transfection, ExpiFectamineTM 293 Enhancer 1 (Thermo Fisher),

ExpiFectamine™ Enhancer 2 (Thermo Fisher), and glucose were added in the amount of 0.6 mL per Culture Volume 100 mL, 6 mL per Culture Volume 100 mL, and 3.6 g per 1 liter, respectively. The transfected cells were cultured under the conditions of 36.5°C and 5% CO₂ for 5 days in total. The cultured cells of two types were respectively centrifuged at 4000 rpm at 4°C for 20 minutes, and then, filtrated using 0.22 µm bottle-top filter system (Corning). The culture supernatant was harvested and purified using AKTA Pure L (GE healthcare). The culture supernatant was loaded into AKTA Pure L equipped with Hitrap MabSelectSure 1mL column (GE healthcare) at the flow rate of 1 mL/min,, and the column was washed with 20 column volumes (CV) of 1X PBS. Then, elutionbuffer (0.1 M sodium citrate pH 3.4 buffer) was loaded to the column, to elute a protein of interest. The eluate was concentrated using Amicon Ultra Filter Device (MWCO 10K, Merck),, centrifuged and subjected to buffer exchange with 1xPBS buffer.

The purified antibody samples were diluted with 1X PBS, to make the final concentration about 1 mg/mL. Ten (10) µL of Reducing Loading Buffer (3X) or Non-reducing Loading Buffer (3X) and 20 µL of the purified antibody sample were mixed and left in 95°C heating bath for 2 minutes, and then, brought out and cooled. The sample was injected into SDS-PAGE Gradient Gel (4-20% or 4-12%) equipped on an electrophoresis device at the amount of 10µg per well and developed on the gel. In order to analyze molecular weight of the sample, Precision Plus Protein™ Dual Color Standards (BIO-RAD) was injected to another separate well. The gel was stained with Coomassie staining solution and destained to obtain gel images.

Among 93 antibodies, gel electrophoresis images for antibodies A10, B3, E3, G1, G9 and H2 were representatively shown in Fig. 1. As shown in Fig. 1, the production of antibodies having disulfide bond was confirmed.

1.5. Analysis of binding affinity of the selected antibodies

The binding affinities of the 93 antibodies, which were selected in Example 1.3, to the antigen, LILRB1, were measured using Biacore T200 (GE healthcare). An anti-human IgG (Fc) antibody (GE healthcare, Cat. No. BR-1008-39, final concentration of 25 µg/mL) was flowed at the flow rate of 5 µL/min for 360 seconds to

be immobilized at 5000-7000 RU on Series S Sensor Chip CM5 (GE healthcare, Cat. No. BR-1005-30) using Amine Coupling Kit (GE healthcare, Cat. No. BR-1000-508). The antigen, human LILRB1 protein (LILRB1-His, RnD systems Cat. No. 8989-T2) was injected thereto in 4~9 different concentrations from 3.13 nM to 1600 nM at the flow rate of 30 μ L/min to determine k_a and k_d values as shown in Table 3 and calculate K_D value therefrom.

Among the 93 antibodies, 20 antibodies showing excellent binding affinities (K_D values) were selected and summarized in Table 3. Among them, SPR sensorgrams for antibody B3 showing the LILRB1 binding affinity (K_D) of about 99.8 nM and for antibody E3 showing the LILRB1 binding affinity (K_D) of about 101.2 nM are shown in Figs. 2 and 3, respectively (Fig. 2: SPR sensorgram for B3, Fig. 3: SPR sensorgram for E3):

【Table 3】

Antigen Binding Affinities (K_D) of Anti-LILRB1 antibodies to human LILRB1

Clone name	k_a ($\times 10^5$) (1/Ms)	k_d ($\times 10^{-4}$) (1/s)	K_D (nM)
A10	0.504	76.5	152
A11	0.001801	9.814	5448
B3	0.149	14.87	99.8
B9	0.09324	6.16	66.1
B12	1.84	14.42	7.84
D1	1.165	57.44	49.33
D3	0.0311	5.58	180
E3	0.3460	35.00	101.2
E4	0.1065	7.73	72.55
E6	0.2679	16.27	60.73
E9	0.105	10.48	99.86
E12	2.331	102.6	44.01
F11	2.72	6.15	2.26
F12	2.811	9.731	3.462
G1	4.33	14.19	3.28
G6	2.58	152.4	59.06
G9	1.43	4.36	3.05
G11	0.454	20.53	45.23
H2	5.865	95	16.20
H11	2.962	22.57	7.621

1.6. Sequence analysis of the selected antibodies

In the 20 antibodies which are analyzed for antigen binding affinity in Example 1.5, amino acid sequences of the CDRs defined according to Kabat numbering, light chain variable region, heavy chain variable region, light chain, and heavy chain, and nucleic acid sequence encoding the light chain variable region and the heavy chain variable region were analyzed by general amino acid sequencing and DNA sequencing methods and summarized in Tables 4-23:

【Table 4】

Antibody clone E3

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	QGDSLRFYAS	1
CDR-L2	GKNNRPS	2
CDR-L3	NSRDSSGSHLTGV	3
CDR-H1	SYAMS	4
CDR-H2	AISGSGGSTYYADSVKG	5
CDR-H3	DTYYYGSGRSNAFDI	6
light chain variable region	SYELTQDPAVSVALGQTVRITCQGDSLRFYASWYQQKSG QAPVLVMYGKNNRPSGIPDRFSGSTSGNTASLTITGAQAE DEADYYCNSRDSSGSHLTGVFGGGTKVTVLGQPAAA	221
light chain variable region coding gene	TCCTATGAGCTGACTCAGGACCCTGCTGTGTCTGTGGC CTTGGGACAGACAGTCAGGATCACATGCCAGGGAGACA GCCTCAGAACTTTTATGCAAGCTGGTACCAGCAGAAGT CAGGACAGGCCCCAGTTCTTGTCATGTATGGTAAAAACA ACCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCC ACCTCAGGAAACACAGCTTCCTTGACCATCACTGGGGC TCAGGCGGAAGATGAGGCTGACTATTACTGTAAC TCCCG GGACAGCAGTGGTAGCCATTTGACGGGCGTATTCGGCG GAGGGACCAAGGTCACCGTCCTAGGTCAGCCCGCGGC CGCA	261
heavy chain variable region	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVR QAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKN TLYLQMISLRAEDTAVYYCARDTYYYGSGRSNAFDI WGQG TLVTVSS	222
heavy chain variable region coding gene	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTAC AGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTC TGGATTACCTTTAGCAGCTATGCCATGAGCTGGGTCCG CCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCT ATTAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCC GTGAAGGGCCGGTTACCATCTCCAGAGACAATTCCAA GAATACGCTGTATCTGCAAATGATTAGCCTGAGAGCTGA	262

	GGACACGGCTGTGTATTACTGTGCGAGAGATACGTATTA CTATGGTTCGGGGAGAAGTAATGCTTTTGATATATGGGG CCAGGGAACCCTGGTCACCGTCTCGAGT	
light chain (Lambda)	SYELTQDPAVSVALGQTVRITCQGDSLRFYASWYQQKSG QAPVLVEMYGKNNRPSGIPDRFSGSTSGNTASLTITGAQAE DEADYYCNSRDSSGSHLTGVFGGGTKVTVLGQPAAAPSV TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQ VTHEGSTVEKTVAPTECS	301
heavy chain	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVR QAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKN TLYLQMISLR AEDTAVYYCARDTYYYGSGRSNAFDIWGGG TLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYF PEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPS SSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPCPAP EFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSDQEDPE VQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQ DWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTL PPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN YKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMH EALHNHYTQKSLSLGLK	302

【Table 5】

Antibody clone B3

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	QASQDISNYLN	7
CDR-L2	DASNLET	8
CDR-L3	QQYDNLP	9
CDR-H1	DYAMH	10
CDR-H2	GISWNSGSIGYADSVKG	11
CDR-H3	VGDSSGWSDAFDI	12
light chain variable region	DIQMTQSPSSLSASVGDRVITTCQASQDISNYLNWYQQKP GKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISLQPE DIATYYCQQYDNLPFGGGTKVDIKRTAAA	223
light chain variable region coding gene	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCA TCTGTAGGAGACAGAGTCACCATCACTTGCCAGGCGAGT CAGGACATTAGCAACTATTTGAATTGGTATCAGCAGAAAC CAGGGAAAGCCCCTAAGCTCCTGATCTACGATGCATCCA ATTTGGAAACAGGGGTCCCATCAAGGTTCAAGTGAAGTG GATCTGGGACAGATTTTACTTTACCATCAGCAGCCTGCA GCCTGAAGATATTGCAACATATTACTGTCAACAGTATGATA ATCTCCCTTTTCGGCGGAGGGACCAAAGTGGATATCAAAC GTACCGCGGCCGCA	263

heavy chain variable region	EVQLLESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSGISYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARVGDSSGWSDAFDIWGQGTMVT VSS	224
heavy chain variable region coding gene	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGCAGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTTGATGATTATGCCATGCACTGGGTCCGGCA AGCTCCAGGGAAGGGCCTGGAGTGGGTCTCAGGTATTA GTTGGGAATAGTGGTAGCATAGGCTACGCAGACTCCGTGA AGGGCCGATTACCATCTCCAGAGACAATTCCAAGAACA CGCTGTATCTTCAAATGAACAGTCTGAGAGCCGAGGACA CGGCCGTGTATTACTGTGCGAGAGTTGGGGATAGCAGTG GCTGGTCCGATGCTTTTGATATCTGGGGCCAAGGGACAA TGGTCACCGTCTCGAGT	264
light chain (Kappa)	DIQMTQSPSSLSASVGRVTITCQASQDISNYLNWYQQKP GKAPKLLIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPE DIATYYCQQYDNLPFGGGTKVDIKRTAAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPRKAVQWVKVDNALQSGNSQESVT EQDSKDYSLSSLTLSKADYEKHKLYACEVTHQGLSSPV TKSFNREGC	303
heavy chain	EVQLLESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSGISYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARVGDSSGWSDAFDIWGQGTMVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT KTYTCNVDPKPSNTKVDKRVEVKYGPCCPCPAPPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWY VDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTKAKGQPREPQVYTLPPSQEEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVL DSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYT QKSLSLSLGK	304

【Table 6】

Antibody clone A10

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	RASQSVSSNLA	13
CDR-L2	GASTRAT	14
CDR-L3	QQYGSSPRMYT	15
CDR-H1	SYAIS	16
CDR-H2	GIPIFGTANYAQKFQG	17
CDR-H3	GGLGELDNWFDP	18
light chain	DIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKP GQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISLQSED	225

variable region	FAVYYCQQYGSSPRMYTFGQGTKVDIKRTAAA	
light chain variable region coding gene	GATATTGTGATGACACAGTCTCCAGCCACCCTGTCTGTG TCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAG TCAGAGTGTTAGCAGCAACTTAGCCTGGTACCAGCAGAA ACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGCATC CACCAGGGCCACCGGTATCCCAGCCAGGTTCAAGTGGCA GTGGGTCTGGGACAGAGTTCACTCTCACCATCAGCAGC CTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGT ATGGTAGCTCACCTCGGATGTACACTTTTGGCCAGGGGA CCAAAGTGGATATCAAACGTACCGCGGCCGCA	265
heavy chain variable region	QMQLVQSGAEVKKPGSSVKVSCASGGTFSSYAISWVRQ APGQGLEWMGGIIPFGTANYAQKFQGRVTITADKSISTAYM ELSSLRSEDTAVYYCARGGLGELDNWFDWPWGQGTTLTVSS	226
heavy chain variable region coding gene	CAAATGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAA GCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCTG GAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGAC AGGCCCTGGACAAGGGCTTGAGTGGATGGGTGGGATC ATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTCC AGGGCAGAGTCACGATTACCGCGGACAAATCCATCAGCA CAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGAC ACGGCCGTGTATTACTGTGCGAGAGGCGGCCTCGGGGA GTTGGACAACTGGTTCGACCCCTGGGGCCAGGGAACCC TGGTCACCGTCTCGAGT	266
light chain (Kappa)	DIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKP GQAPRLLIYGASTRATGIPARFSGSGSGTEFTLTISLQSED FAVYYCQQYGSSPRMYTFGQGTKVDIKRTAAAPSVFIFPPS DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ ESVTEQDSKDYSLSSSTLTLSKADYEKHKLYACEVTHQGL SSPVTKSFNRGEC	305
heavy chain	QMQLVQSGAEVKKPGSSVKVSCASGGTFSSYAISWVRQ APGQGLEWMGGIIPFGTANYAQKFQGRVTITADKSISTAYM ELSSLRSEDTAVYYCARGGLGELDNWFDWPWGQGTTLTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKT YTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKS LSLSLGK	306

【Table 7】

Antibody clone G1

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	SGYKLGDYVS	19
CDR-L2	KDSQRPS	20
CDR-L3	QAWDSGTGV	21
CDR-H1	SYGIS	22
CDR-H2	WISAYNGNTNYAQELQG	23
CDR-H3	VGvagkldy	24
light chain variable region	SYELTQPPSLSVSPGQTASITCSGYKLGDYVSWYQQKTG QSPVVVIYKDSQRPSGVPERFSGSNSGNTATLTISGTQAMD EADYYCQAWDSGTGVFGGGTKLTVLGQAAA	227
light chain variable region coding gene	TCCTATGAGCTGACTCAGCCACCCTCACTGTCCGTGTCC CCAGGACAGACAGCCAGCATCACCTGCTCAGGATATAAA CTGGGAGATAGATATGTTTCCTGGTATCAGCAGAAGACAG GCCAGTCCCCTGTGGTGGTCATCTATAAAGATAGCCAGC GGCCCTCAGGGGTCCCTGAACGATTCTCTGGCTCCAAC TCTGGGAACACAGCCACTCTGACCATCAGCGGGACCCA GGCTATGGATGAGGCTGACTATTACTGTCAGGCGTGGGA CAGCGGCACTGGGGTATTCGGCGGAGGGACCAAGCTGA CCGTCCTAGGTCAGCCCGCGGCCGCA	267
heavy chain variable region	EVQLVQSGAEVKKPGSSVKVSCASGGTFSSYGISWVRQA PGQGLEWMGWISAYNGNTNYAQELQGRVTMTTDTSTSTA YMERLSLRSDDTAVYYCARVGVAGKLDYWGQGTLVTVSS	228
heavy chain variable region coding gene	GAAGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAA GCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCTG GAGGCACCTTCAGCAGCTATGGTATCAGCTGGGTGCGAC AGGCCCTGGACAAGGGCTTGAGTGGATGGGATGGATC AGCGCTTACAATGGTAACACAACTATGCACAGGAGCTC CAGGGCAGAGTCACCATGACCACAGACACATCCACGAG CACAGCCTATATGGAGCTGAGGAGCCTGAGATCTGACGA CACGGCCGTGTATTACTGTGCGAGAGTAGGGGTGGCTG GTAACTTGACTACTGGGGCCAAGGAACCCTGGTCACCG TCTCGAGT	268
light chain (Lambda)	SYELTQPPSLSVSPGQTASITCSGYKLGDYVSWYQQKTG QSPVVVIYKDSQRPSGVPERFSGSNSGNTATLTISGTQAMD EADYYCQAWDSGTGVFGGGTKLTVLGQAAAAPSVTLFPPS SEELQANKATLVCLISDFYPGAVTVAWKEDSSPVKAGVETT TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV EKTVAPECS	307
heavy chain	EVQLVQSGAEVKKPGSSVKVSCASGGTFSSYGISWVRQA PGQGLEWMGWISAYNGNTNYAQELQGRVTMTTDTSTSTA YMERLSLRSDDTAVYYCARVGVAGKLDYWGQGTLVTVSSA STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGKTYT	308

	CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSL SLGK	
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【Table 8】

Antibody clone G9

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	TGSSSDVGGYNYVS	25
CDR-L2	DVSNRPS	26
CDR-L3	SSYTGSSTLDVL	27
CDR-H1	SYWIG	28
CDR-H2	IYPGDS DTRYSPSFQG	29
CDR-H3	QYYDGGYYMDV	30
light chain variable region	QSALTQPASVSGSPGQSITISCTGSSSDVGGYNYVSWYQQ HPGKAPKLMYDVSNRPSGVSDRFSGSKSGNMASTISGL QAEDEADYYCSSYTGSSTLDVLFGGGTKLTVLGQAAA	233
light chain variable region coding gene	CAGTCTGCGCTGACTCAGCCTGCCTCCGTGTCTGGGTC TCCTGGACAGTCGATCACCATCTCCTGCACTGGAAGCAG CAGTGACGTTGGTGGTTATACTATGTCTCCTGGTACCAG CAACACCCAGGCAAAGCCCCCAAACATCATGATTTATGATG TCAGTAATCGGCCCTCAGGGGTTTCTGATCGCTTCTCTG GCTCCAAGTCTGGCAACATGGCCTCCCTGACCATCTCTG GGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCAGCT CATATACAGGAAGCAGCACTCTCGACGTGCTATTCGGCG GAGGGACCAAGCTGACCGTCCTAGGTCAGCCCGCGGCC GCA	269
heavy chain variable region	QVQLVQPGAIEVKKPGESLKISCKGSGYSFTSYWIGWVRQ MPGKGLEWMGIYYPGDS DTRYSPSFQGQVTISADKSISTAY LQWSSLKASDTAMYICASQYYDGGYYMDVWGQGT LTVTS S	234
heavy chain variable region coding gene	CAGGTGCAGCTGGTGCAGCCTGGAGCAGAGGTGAAAAA GCCGGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTCTG GATACAGCTTTACCAGCTACTGGATCGGCTGGGTGCGCC AGATGCCCGGGAAGGGCCTGGAGTGGATGGGGATCATC TATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCC AAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCA CCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGAC ACCGCCATGTATTACTGTGCGAGTCAATATTACGATGGGG GTTACTACATGGACGTCTGGGGCCAGGGAACCCTGGTC	270

	ACCGTCTCGAGT	
light chain (Lambd a)	QSALTQPASVSGSPGQSITISCTGSSSDVGGYNYVSWYQQ HPGKAPKLMYDVSNRPSGVSDRFSGSKSGNMASTISGL QAEDEADYYCSSYTGSSLDVLFGGGTKLTVLGQPAAAPS VTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPV KAGVETTTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQV THEGSTVEKTVAPTECS	309
heavy chain	QVQLVQPGAIEVKKPGESLKISCKGSGYSFTSYWIGWVRQ MPGKGLEWMGIIYPGDSSTRYSPSFQGGVTISADKSISTAY LQWSSLKASDTAMYCASQYYDGGYYMDVWGQGTLLTVS SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGKT YTCNVDPKPSNTKVDKRVEISKYGPCCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKS LSLSLGK	310

【Table 9】

Antibody clone H2

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	QGDSLRNYYAS	31
CDR-L2	GNNKRPS	32
CDR-L3	NSLDSTYNHPI	33
CDR-H1	SYDIH	34
CDR-H2	WISAYNGNTNYAQLQGG	35
CDR-H3	DGGDAFDI	36
light chain variable region	SYELTQDPAVSVALGQTVRITCQGDSLRNYYASWYQQKPG QAPILVISGNNKRPSGIPDRFSGSSSGDTASLTISGAQAEDE ADYYCNSLDSTYNHPIFGGGTKVTVLGQPAAA	235
light chain variable region coding gene	TCCTATGAGCTGACTCAGGACCCTGCTGTGTCTGGTGGCC TTGGGACAGACAGTCAGGATCACATGCCAAGGAGACAG CCTCAGAACTATTATGCAAGCTGGTACCAGCAGAAGCC AGGACAGGCCCTATTCTTGTCTCTCTGGTAACAACAAA CGGCCCTCGGGGATCCCAGACCGATTCTCTGGCTCCAG CTCAGGAGACACAGCTTCCTTGACCATCTCTGGGGCTCA GGCGGAAGATGAGGCTGACTATTACTGTAACCTCCCTAGA CAGCACTTATAACCATCCGATATTCTGGCGGAGGGACCAA GGTCACCGTCCTAGGTCAGCCCGCGGCCGCA	271
heavy chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQA TGQGLEWMGWISAYNGNTNYAQLQGRVTMTTDTSTSTA	236

variable region	YMELRSLRSDDTAVYYCARDGGDAFDIWGQGLTVTVSS	
heavy chain variable region coding gene	CAGGTCCAGCTTGTGCAGTCTGGGGCTGAGGTGAAGAA GCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTG GATACACCTTCACCAGTTATGATATCCACTGGGTGCGACA GGCCACTGGACAAGGGCTTGAGTGGATGGGATGGATCA GCGCTTACAATGGTAACACAACTATGCACAGAAGCTCCA GGGCAGAGTCACCATGACCACAGACACATCCACGAGCA CAGCCTACATGGAGCTGAGGAGCCTGAGATCTGACGAC ACGGCCGTGTATTACTGTGCGAGAGATGGGGGTGATGCT TTTGATATCTGGGGCCAAGGAACCCTGGTCACCGTCTCG AGT	272
light chain (Lambd a)	SYELTQDPAVSVALGQTVRITCQGDSLRNYYASWYQQKPG QAPILVISGNNKRPSGIPDRFSGSSSGDTASLTISGAQAEDE ADYYCNSLDSTYNHPIFGGGTKVTVLGQPAAAPSVTLFPPS SEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETT TPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTV EKTVAPTCS	311
heavy chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDIHWVRQA TGQGLEWMGWISAYNGNTNYAQKLQGRVTMTTDTSTSTA YMELRSLRSDDTAVYYCARDGGDAFDIWGQGLTVTVSSAS TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTC NVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLS LGK	312

【Table 10】

Antibody clone H11

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	QGDLSRSYYAS	37
CDR-L2	GRNNRPS	38
CDR-L3	KSRDSSGNHYV	39
CDR-H1	SYVMH	40
CDR-H2	IINPSGGSTSYAQKFQG	41
CDR-H3	DAGSSSDY	42
light chain variable region	SYELTQDPAASVALGQTVRITCQGDSLSRSYYASWYQQKPG QAPVVVIYGRNNRPSGIPDRFSGSSSGDTASLTITGAQAED EADYYCKSRDSSGNHYVFGTGTKLTVLGQPAAA	231

light chain variable region coding gene	TCCTATGAGCTGACTCAGGACCCTGCTGCGTCTGTGGCC TTGGGACAGACAGTCAGGATCACATGCCAAGGAGACAG CCTCAGAAGCTATTATGCAAGCTGGTACCAGCAGAAGCC AGGACAGGCCCTGTAGTTGTCATCTATGGTAGAAACAA CCGGCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCA GCTCAGGAGACACAGCTTCCTTGACCATCACTGGGGCT CAGGCGGAAGATGAGGCTGACTATTACTGTAAGTCCCGG GACAGCAGTGGTAACCATTATGTCTTCGGAACCTGGGACC AAGCTGACCGTCCTAGGTCAGCCCCGCGGCCGCA	273
heavy chain variable region	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVVRQ APGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTV YMESSLRSEDVAVYYCARDAGSSSDYWGRGTLVTVSS	232
heavy chain variable region coding gene	CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAA GCCTGGGGCCTCAGTGAAGGTTTCTGCAAGGCATCTG GATACACCTTCACCAGCTACTATATGCACTGGGTGCGACA GGCCCCTGGACAAGGGCTTGAGTGGATGGGAATAATCAA CCCTAGTGGTGGTAGCACAAAGCTACGCACAGAAGTTCCA GGGCAGAGTCACCATGACCAGGGACACGTCCACGAGCA CAGTCTACATGGAGCTGAGCAGCCTGAGATCTGAGGACA CGGCCGTGTATTACTGTGCGAGAGATGCCGGCAGCTCG TCCGATTACTGGGGCCGTGGCACCCCTGGTCACCGTCTC GAGT	274
light chain (Lambd a)	SYELTQDPAASVALGQTVRITCQGDSLRSYYASWYQQKPG QAPVVVIYGRNNRPSGIPDRFSGSSSGDTASLTITGAQAED EADYYCKSRDSSGNHYVFGTGTCLTVLGQPAAAPSVTLFP PSSEELQANKATLVCLISDFYPGAVTVAWKADSSSPVKAGVE TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGS TVEKTVAPTECS	313
heavy chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVVRQ APGQGLEWMGIINPSGGSTSYAQKFQGRVTMTRDTSTSTV YMESSLRSEDVAVYYCARDAGSSSDYWGRGTLVTVSSAS TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTC NVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF FLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLS LGK	314

【Table 11】

Antibody clone F12

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
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CDR-L1	AGTSSDIGDYDYVS	43
CDR-L2	DVSRRPS	44
CDR-L3	ASYTSSSVV	45
CDR-H1	SYWIG	46
CDR-H2	IYPGDS DTRYSPSFQG	47
CDR-H3	QYYDGGYYMDV	48
light chain variable region	QSVLTQPASVSGSPGQSITISCAGTSSDIGDYDYVSWYQQH PGKTPKLMYDVSRRPSGVPDRFSGSKSGNTASLTISGLQT EDEADYYCASYTSSSVVVFGGGTKLTVLGQPAAA	237
light chain variable region coding gene	CAGTCTGTGCTGACTCAGCCTGCCTCCGTGTCTGGGTCT CCTGGACAGTCGATCACCATCTCCTGCGCTGGAACCAGC AGTGACATTGGTGATTATGACTATGTCTCCTGGTACCAAC AGCACCCAGGCAAGACTCCCAAACATGATTTATGATGT CAGTAGGCGGCCCTCAGGGGTCCCTGATCGCTTCTCTG GCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTG GGCTCCAGACTGAGGACGAGGCTGATTATTACTGCGCCT CATATACAAGCAGCAGCGTCGTGGTCTTCGGCGGAGGG ACCAAGCTGACCGTCCTAGGTCAGCCCGCGGCCGCA	275
heavy chain variable region	QVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQ MPGKGLEWMGIIYPGDS DTRYSPSFQGGVTISADKSISTAY LQWSSLKASDTAMYCCASQYYDGGYYMDVWGQGLTVTS S	238
heavy chain variable region coding gene	CAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAA GCCCCGGGAGTCTCTGAAGATCTCCTGTAAGGGTTCTG GATACAGCTTTACCAGCTACTGGATCGGCTGGGTGCGCC AGATGCCCGGGAAAGGCCTGGAGTGGATGGGGATCATC TATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTTCC AAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCAGCA CCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGAC ACCGCCATGTATTACTGTGCGAGTCAATATTACGATGGGG GTTACTACATGGACGTCTGGGGCCAGGGCACCCCTGGTC ACCGTCTCGAGT	276
light chain (Lambd a)	QSVLTQPASVSGSPGQSITISCAGTSSDIGDYDYVSWYQQH PGKTPKLMYDVSRRPSGVPDRFSGSKSGNTASLTISGLQT EDEADYYCASYTSSSVVVFGGGTKLTVLGQPAAAPSVTLFP PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGS TVEKTVAPTECS	315
heavy chain	QVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQ MPGKGLEWMGIIYPGDS DTRYSPSFQGGVTISADKSISTAY LQWSSLKASDTAMYCCASQYYDGGYYMDVWGQGLTVTS SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKT YTCNVDHKPSNTKVDKRVESKYGPCCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD	316

	GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK	
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【Table 12】

Antibody clone B9

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	RASQISRYLN	49
CDR-L2	GASSLQS	50
CDR-L3	QQAYGFPLT	51
CDR-H1	SYAIS	52
CDR-H2	GIPIFGTANYAQKFQG	53
CDR-H3	GEIAVAQNWDYYGMDV	54
light chain variable region	DIQMTQSPSSLSASVGDRVITICRASQISRYLNWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYHCQQAYGFPLTLGGGTKVEIKRTAAA	229
light chain variable region coding gene	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCA TCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGT CAGAGCATTAGCAGGTATTTAAATTGGTATCAGCAGAAAC CAGGGAAAGCCCCCAAGCTCCTGATCTATGGTGCATCCA GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGTGGCAGT GGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTG CAGCCTGAAGATTTGCAACTTACCATTGTCAACAGGCTT ACGGTTTCCCCCTCACTCTCGGCGGAGGGACCAAGGTG GAGATCAAACGTACCGCGGCCGCA	277
heavy chain variable region	QVQLVESGAEVKKPGSSVKVSCASGGTFSSYAISWVRQAPGQGLEWMGGIPIFGTANYAQKFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCARGEIAVAQNWDYYGMDVWGQGTLV TVSS	230
heavy chain variable region coding gene	CAGGTGCAGCTGGTGGAGTCTGGGGCTGAGGTGAAGAA GCCTGGGTCTCGGTGAAGGTCTCCTGCAAGGCTTCTG GAGGCACCTTCAGCAGCTATGCTATCAGCTGGGTGCGAC AGGCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATC ATCCCTATCTTTGGTACAGCAAACTACGCACAGAAGTTCC AGGGCAGAGTCACGATTACCGCGGACGAATCCACGAGC ACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGA CACGGCCGTGTATTACTGTGCGAGAGGGGAAATAGCAGT GGCTCAAACTGGGACTACTACGGTATGGACGTCTGGGG CCAGGGCACCTGGTCACCGTCTCGAGT	278
light chain	DIQMTQSPSSLSASVGDRVITICRASQISRYLNWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISLQPE	317

(Kappa)	DFATYHCQQAYGFPLTLGGGTKVEIKRTAAAPSVFIFPPSDE QLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKLYACEVTHQGLSS PVTKSFNREGEC	
heavy chain	QVQLVESGAIEVKKPGSSVKVSCASGGTFSSYAISWVRQA PGQGLEWMGGIIPFGTANYAQKFQGRVTITADESTSTAYM ELSSLRSEDTAVYYCARGEIAVAQNWDYYGMDVWGQGTLV TVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLG TKTYTCNVDPKPSNTKVDKRVESESKYGPCCPPCPAPEFLGG PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNW YVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHY TQKSLSLSLGK	318

【Table 13】

Antibody clone G11

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	TGTSSDVGGYNYVS	55
CDR-L2	DVSKRPS	56
CDR-L3	SSYSSSSTLVV	57
CDR-H1	SYWIG	58
CDR-H2	IYPGDS DTRYSPSFQG	59
CDR-H3	QYYDGGYYMDV	60
light chain variable region	QSALTQPRSVSGSPGQSVTISCTGTSSDVGGYNYVSWYQ QHPPGKAPKLMIYDVSKRPSGVPDRFSGSKSGNTASLTISGL QAEDEADYYCSSYSSSSTLVVFGGGTKLTVLGQPAAA	239
light chain variable region coding gene	CAGTCTGCGCTGACTCAGCCTCGCTCAGTGTCCGGGTC TCCTGGACAGTCAGTCACCATCTCCTGCACTGGAACCAG CAGTGATGTTGGTGGTTATAACTATGTCTCCTGGTACCA ACAGCACCCAGGCAAAGCCCCCAAACATCATGATTTATGA TGTCAGTAAGCGGCCCTCAGGGGTCCCTGATCGCTTCT CTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACAATCT CTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGC AGCTCATATTCAAGCAGCAGCACTCTCGTGGTTTTTCGGC GGAGGGACCAAGCTGACCGTCCTAGGTCAGCCCGCGG CCGCA	279
heavy chain variable region	QVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQ MPGKGLEWMGIIYPGDS DTRYSPSFQGGVTISADKSISTAY LQWSSLKASDTAMYICASQYYDGGYYMDVWGQGTLVTVS S	240

heavy chain variable region coding gene	CAGGTCCAGCTGGTACAGTCTGGAGCAGAGGTGAAAAA GCCGGGGGAGTCTCTGAAGATCTCCTGTAAGGGTTCTG GATACAGCTTTACCAGCTACTGGATCGGCTGGGTGCGC CAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGATCAT CTATCCTGGTGACTCTGATACCAGATACAGCCCGTCCTT CCAAGGCCAGGTCACCATCTCAGCCGACAAGTCCATCA GCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCG GACACCGCCATGTATTACTGTGCGAGTCAATATTACGAT GGGGGTTACTACATGGACGTCTGGGGCCAGGGAACCTT GGTCACCGTCTCGAGT	280
light chain (Lambd a)	QSALTQPRSVSGSPGQSVTISCTGTSSDVGGYNYVSWYQ QHPGKAPKLMIYDVSKRPSGVPDRFSGSKSGNTASLTISGL QAEDEADYYCSSYSSSSTLVVFGGGTKLTVLGQPAAPSV TLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECS	319
heavy chain	QVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQ MPGKGLEWMGIIYPGDS TRYSPSFQGGQVTISADKSISTAY LQWSSLKASDTAMYCASQYYDGGYYMDVWGGQTLTVTS SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKT YTCNVDHKPSNTKVDKRVESKYGPCCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKS LSLSLGK	320

【Table 14】

Antibody clone G6

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	QGDSLRRYYAT	61
CDR-L2	GQNYRPS	62
CDR-L3	NSRDSSGNHV	63
CDR-H1	SYMH	64
CDR-H2	GIPIFGTANYAQKFQG	65
CDR-H3	GWGYSSSFY	66
light chain variable region	SYELTQDPAV/SVALGQTVTITCQGDSLRRYYATWYQQKPG QAPVLVIYGGNYRPSGIPDRFSGSNSGTTASLTITGAQAED EADYYCNSRDSSGNHVVFGGGKLTVLGQAAA	241
light chain	TCCTATGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCC TTGGGACAGACAGTCACGATCACATGCCAAGGAGACAG	281

variable region coding gene	CCTCAGAAGGTATTATGCAACCTGGTACCAGCAGAAGCC AGGACAGGCCCTGTCTTGTCTATGGTCAAACTA CCGGCCCTCGGGGATCCCAGACCGATTCTCTGGCTCCA ACTCAGGAACCAACAGCTTCCTTGACCATCACTGGGGCTC AGGCGGAAGATGAGGCTGACTATTACTGTAACCTCCCGGG ACAGCAGTGGTAACCATGTGGTATTCGGCGGAGGGACC AAGCTGACCGTCCTAGGTCAGCCCCGCGGCCGCA	
heavy chain variable region	EVQLVESGAIEVKKPGASVKVSCASGYTFTSYMHWRQ APGQGLEWMGGIIPFGTANYAQKFQGRVTITADESTSTAY MELSSLRSEDYAVYYCARGWGYSSSFYWGQGTTVTVSS	242
heavy chain variable region coding gene	GAGGTGCAGCTGGTGGAGTCTGGGGCTGAGGTGAAGAA GCCTGGGGCCTCAGTGAAGGTTTCTGCAAGGCATCTG GATACACCTTCACCAGCTACTATATGCACTGGGTGCGACA GGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGGATCA TCCCTATCTTTGGTACAGCAAACCTACGCACAGAAGTTCCA GGGCAGAGTCACGATTACCGCGGACGAATCCACGAGCA CAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGGAC ACGGCCGTGTACTACTGTGCGAGAGGGTGGGGGTATAG CAGCTCGTTTGACTACTGGGGGCAAGGGACCACGGTCA CCGTCTCGAGT	282
light chain (Lambd a)	SYELTQDPAV/SVALGQTVTITCQGDSLRRYYATWYQQKPG QAPVLVIYQQNYRPSGIPDRFSGSNSGTTASLTITGAQAED EADYYCNSRDSSGNHVFVGGGKLTVLGQPAAPSVTLFP PSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVE TTPPSKQSNKYAASSYLSLTPEQWKSQRSYSCQVTHEGS TVEKTVAPTECS	321
heavy chain	EVQLVESGAIEVKKPGASVKVSCASGYTFTSYMHWRQ APGQGLEWMGGIIPFGTANYAQKFQGRVTITADESTSTAY MELSSLRSEDYAVYYCARGWGYSSSFYWGQGTTVTVSS ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKT YTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKS LSLSLGK	322

【Table 15】

Antibody clone F11

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	SGSSSNIGTNTVN	67
CDR-L2	SNDQRPS	68

CDR-L3	ETWDDSLKGPV	69
CDR-H1	SYAMS	70
CDR-H2	TISGSGDSTYYADSVKG	71
CDR-H3	EWELGDAFDI	72
light chain variable region	QSVLTQPPSTSGTPGQTFSIFCSGSSSNIGTNTVNWYQQL PGTAPKLLIYSNDQRPSGVPDRFSGSKSGTSASLAISGLQS EDEADYYCETWDDSLKGPVFGGGTKVTVLGQPAAA	243
light chain variable region coding gene	CAGTCTGTGCTGACTCAGCCACCCTCAACGTCTGGGAC CCCCGGGCAGACGTTCTCCATTTTTTGTCTGGAAGCAG TTCGAACATCGGAATAATACTGTTAATTGGTACCAGCAG CTCCCAGGAACGGCCCCCAAACCTCCTCATCTATAGTAATG ATCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGC TCCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGG GCTCCAGTCTGAGGATGAGGCTGATTATTACTGTGAAACA TGGGATGACAGCCTGAAAGGCCCGGTGTTCCGGCGGGG GGACCAAGGTCACCGTCCTAGGTCAGCCCGCGGCCGCA	283
heavy chain variable region	EVQLVESGGGLVQPGGSLKLSCAASGFTFSSYAMSWVRR APGKGLEWVSTISGSGDSTYYADSVKGRFTISRDN SKNTLY LQMNNLRAEDTAVYYCAREWELGDAFDIWGRGTLTVSS	244
heavy chain variable region coding gene	GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCC AGCCTGGGGGGTCCCTGAAACTCTCCTGTGCAGCGTCT GGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC CGGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAACTAT TAGTGGTAGTGGTGATAGCACATACTACGCAGACTCCGT GAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAA CACGCTGTATCTGCAAATGAACAACCTGAGAGCCGAGGA CACGGCCGTATATTACTGTGCGAGAGAATGGGAACTAGG CGATGCTTTTGATATCTGGGGCCGTGGCACCCCTGGTCAC CGTCTCGAGT	284
light chain (Lambda)	QSVLTQPPSTSGTPGQTFSIFCSGSSSNIGTNTVNWYQQL PGTAPKLLIYSNDQRPSGVPDRFSGSKSGTSASLAISGLQS EDEADYYCETWDDSLKGPVFGGGTKVTVLGQPAAAPSVTL FPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG VETTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS	323
heavy chain	EVQLVESGGGLVQPGGSLKLSCAASGFTFSSYAMSWVRR APGKGLEWVSTISGSGDSTYYADSVKGRFTISRDN SKNTLY LQMNNLRAEDTAVYYCAREWELGDAFDIWGRGTLTVSSA STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV	324

	SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSL SLGK	
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【Table 16】

Antibody clone D3

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	RASQSISSYLN	73
CDR-L2	AASSLQS	74
CDR-L3	QQSYSTRWT	75
CDR-H1	SYAMS	76
CDR-H2	AISGSGGSTYYADSVKG	77
CDR-H3	DRGSYGYYYGMDV	78
light chain variable region	DIQMTQSPSSLSASVGDRVITICRASQSISSYLNWYQQKP GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED FATYYCQQSYSTRWTFGQGTKVEIKRTAAA	245
light chain variable region coding gene	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCA TCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGT CAGAGCATTAGCAGCTATTAAATTGGTATCAGCAGAAAC CAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCA GTTTGCAAAGTGGGGTCCCATCAAGGTTCAAGTGGCAGT GGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTG CAACCTGAAGATTTTGAACCTTACTACTGTCAACAGAGTT ACAGTACCCGGTGGACGTTTCGGCCAAGGGACCAAGGTG GAAATCAAACGTACCGCGGCCGCA	285
heavy chain variable region	EVQLLESGGGVVQPGRLRLSCAASGSTFSSYAMSWVRQ APGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCAKDRGSYGYYYGMDVWGQGTMTV TVSS	246
heavy chain variable region coding gene	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCGTGGTCC AGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCT GGATCCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGC CAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTAT TAGTGGTAGTGGTGGTAGCACATACTACGCAGACTCCGT GAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAA CACGCTGTATCTGCAAATGAACAGCCTGAGAGCCGAGGA CACGGCCGTATATTACTGTGCGAAAGACAGAGGCAGCTA TGGTTACTACTACGGTATGGACGTCTGGGGCCAAGGGAC AATGGTCACCGTCTCGAGT	286
light chain (Kappa)	DIQMTQSPSSLSASVGDRVITICRASQSISSYLNWYQQKP GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED FATYYCQQSYSTRWTFGQGTKVEIKRTAAAPSVTLFPSPSE ELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVETTP	325

	SKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVE KTVAPTECS	
heavy chain	EVQLLES GGGV VQPGRSLRLSCAASGSTFSSYAMSWVRQ APGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCAKDRGSYGYYYGMDVWGQGT MV TVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSSLG TKTYTCNV DHKPSNTKVDKR VESKYGPPCPPCPAPEFLGG PSVFLFPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNW YVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNG KEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEE MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHY TQKSLSLSLGK	326

【Table 17】

Antibody clone B12

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	RASQSISSYLN	79
CDR-L2	AASSLQS	80
CDR-L3	QQSYSTLRT	81
CDR-H1	GYYMH	82
CDR-H2	WINPNSGGTNYAQKFQG	83
CDR-H3	AGASIVGATALDY	84
light chain variable region	DIQMTQSPSSLSASV GDRVITICRASQSISSYLNWYQQKP GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTIS SLQPED FATYYCQQSYSTLRTFGQG TKVEIKRTAAA	247
light chain variable region coding gene	GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCA TCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGT CAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAAC CAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCA GTTTGCAAAGTGGGGTCCCATCAAGGTTTCAGTGGCAGT GGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTG CAACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTT ACAGTACCCTCCGGACGTTTCGGCCAAGGGACCAAGGTG GAGATCAAACGTACCGCGGCCGCA	287
heavy chain variable region	QVQLVQSGAEVKKPGASVKV SCKASGYTFTGYYMHWVRQ APGQGLEWMGWINPNSGGTNYAQKFQGRVTITADESTSTA YMESSLRSEDTAVYYCTRAGASIVGATALDYWGQGTLVTV SS	248
heavy chain variable	CAGGTCCAGCTGGTACAGTCTGGGGCTGAGGTGAAGAA GCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTG GATACACCTTCACCGGCTACTATATGCACTGGGTGCGAC	288

region coding gene	AGGCCCTGGACAAGGGCTTGAGTGGATGGGATGGATC AACCTAACAGTGGTGGCACAACTACGCACAGAAGTTC CAGGGCAGAGTCACGATTACCGCGGACGAATCCACGAG CACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGG ACACGGCCGTGTATTACTGTACGAGAGCCGGTGCTTCTA TAGTGGGAGCTACCGCGCTTGACTACTGGGGCCAGGGA ACCCTGGTCACCGTCTCGAGT	
light chain (Kappa)	DIQMTQSPSSLSASVGDRTITCRASQSISSYLNWYQQKP GKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPED FATYYCQQSYSTLRFTGQGTKVEIKRTAAAPSVFIFPPSDEQ LKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT EQDSKDSTYSLSSTLTLSKADYEKHKLYACEVTHQGLSSPV TKSFNRGEC	327
heavy chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQ APGQGLEWMGWINPNSGGTNYAQKFQGRVTITADESTSTA YMESSLRSEDTAVYYCTRAGASIVGATALDYWGQGTLLTV SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVT SWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGK TYTCNVDPKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPS VFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKE YKCKVSNKGLPSSIEKTKAKGQPREPQVYTLPPSQEEMT KNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD SDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQ KSLSLSLGK	328

【Table 18】

Antibody clone E4

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	TRSSGSIASNYVQ	85
CDR-L2	EDNQRPS	86
CDR-L3	QSYDTGNRNYV	87
CDR-H1	SYTIS	88
CDR-H2	RIIPILGIANYAQKFQG	89
CDR-H3	GPSLNYAGYFDN	90
light chain variable region	NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRP PGSSPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGL KTEDEADYYCQSYDTGNRNYVFGTGTQLTVLGQPAAA	249
light chain variable region coding	AATTTTATGCTGACTCAGCCCCACTCTGTGTCGGAGTCT CCGGGAAAGACGGTAACCATCTCCTGCACCCGCAGCAG TGGCAGCATTGCCAGCAACTATGTGCAGTGGTACCAGC AGCGCCCGGGCAGTTCCCCCACCCTGTGATCTATGAG GATAACCAAAGACCCTCTGGGGTCCCTGATCGGTTCTCT	289

gene	GGCTCCATCGACAGCTCCTCCAACCTCTGCCTCCCTCACC ATCTCTGGACTGAAGACTGAGGACGAGGCTGACTACTAC TGTCAGTCTTATGATACCGGCAATCGGAATTATGTCTTC GGAAGTGGGACCCAGCTCACCGTCCTAGGTCAGCCCCG GGCCGCA	
heavy chain variable region	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYTISWVRQA PGQGLEWMGRIIPILGIANYAQKFQGRVTMTRDMSTDY MELSSLTYDDTAVYFCVRGPSLNYAGYFDNWGQGLVTVS S	250
heavy chain variable region coding gene	CAGGTGCAGCTGGTGCAATCTGGGGCTGAGGTGAAGAA GCCTGGGTCCTCGGTGAAGGTCTCCTGCAAGGCTTCTG GAGGCACCTTCAGCAGCTATACTATCAGCTGGGTGCGAC AGGCCCTGGACAAGGGCTTGAGTGGATGGGAAGGATC ATCCCTATCCTTGGTATAGCAAACCTACGCACAGAAGTTCC AGGGCAGAGTCACCATGACCAGGGACATGTCCACAGAC ACAGCCTACATGGAGTTGAGCAGCCTGACATATGATGAC ACGGCCGTATATTTTTGTGTGAGAGGCCCTAGTCTTAATT ATGCCGGCTATTTTGACAACCTGGGGCCAGGGCACCCCTG GTCACCGTCTCGAGT	290
light chain (Lambd a)	NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQR PGSSPTTVIYEDNQRPSGVPDRFSGSIDSSSNSASLTISGL KTEDEADYYCQSYDTGNRNYVFGTGTQLTVLGQPAAAPSV TLFPPSSEEIQANKATLVCLISDFYPGAVTVAWKADSSPVK AGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVT HEGSTVEKTVAPTECS	329
heavy chain	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYTISWVRQA PGQGLEWMGRIIPILGIANYAQKFQGRVTMTRDMSTDY MELSSLTYDDTAVYFCVRGPSLNYAGYFDNWGQGLVTVS SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVTPSSSLGKT YTCNVDHKPSNTKVDKRVESKYGPCCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMHENHHTQKS LSLSLGK	330

【Table 19】

Antibody clone E12

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	QGDLSRSYYAS	91
CDR-L2	GKEKRPS	92
CDR-L3	NSRGSTTDYMV	93

CDR-H1	SYAMH	94
CDR-H2	VISYDGSNKYYADSVKG	95
CDR-H3	ERGSGMDV	96
light chain variable region	SYELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKSG QAPVLVIYGKEKRPSGIPDRFSGSSSGNTASLTITGARAED ADYYCNSRGSTTDYMFVGGGTQLTVLGQPAAA	251
light chain variable region coding gene	TCCTATGAGCTGACTCAGGACCCTGCTGTGTCTGTGGCC TTGGGACAGACAGTCAGGATCACATGCCAAGGAGACAG CCTCAGAAGCTATTATGCAAGCTGGTACCAGCAGAAGTC AGGACAGGCCCTGTACTTGTCTATCTATGGTAAAGAAAA GCGCCCCTCAGGGATCCCAGACCGATTCTCTGGCTCCA GCTCAGGAAACACAGCTTCCTTGACCATCACTGGGGCTC GGGCGGAAGATGAGGCTGACTATTACTGTAACCTCCGGG GCAGCACTACTGACTATATGGTGTTCGGCGGGGGGACCC AGCTCACCGTCCTAGGTCAGCCCGCGGCCGCA	291
heavy chain variable region	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQ APGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARERGSMDVWGQGT LTVTVSS	252
heavy chain variable region coding gene	CAGGTGCAGCTGGTGGAGTCCGGGGGAGGCTTAGTTCA GCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCCTCTG GATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCA GGCTCCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATAT CATATGATGGAAGCAATAAATACTACGCAGACTCCGTGAA GGGCCGATTACCATCTCCAGAGACAATTCCAAGAACAC GCTGTATCTGCAAATGAACAGCCTGAGAGCTGAGGACAC GGCTGTGTATTACTGTGCGAGAGAACGGGGAAAGTGGTAT GGACGTCTGGGGCCAAGGAACCCTGGTCACCGTCTCGA GT	292
light chain (Lambda)	SYELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKSG QAPVLVIYGKEKRPSGIPDRFSGSSSGNTASLTITGARAED ADYYCNSRGSTTDYMFVGGGTQLTVLGQPAAAPSVTLFPP SSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAGVET TTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHEGST VEKTVAPTECS	331
heavy chain	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQ APGKGLEWVAVISYDGSNKYYADSVKGRFTISRDN SKNTLY LQMNSLRAEDTAVYYCARERGSMDVWGQGT LTVTVSSAS TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWN SGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTYTC NVDHKPSNTKVDKRVESKYGPCCPPCAPEFLGGPSVFLF PPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVE VHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKV SNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQVS LTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF	332

	FLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLS LGK	
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【Table 20】

Antibody clone D1

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	KASQDIDDDMN	97
CDR-L2	EASTLVP	98
CDR-L3	LQHDKFPYT	99
CDR-H1	SYGIS	100
CDR-H2	WINPNSGGTNYAQKFQG	101
CDR-H3	RGVDEGDY	102
light chain variable region	ETTLTQSPAFMSATPGDKVNISCKASQDIDDDMNWYQQKP GEAAISIIQEASTLVP GIPPRFSGSGYGTDFLTINNIESEDAAYYFCLQHDKFPYTFGQGTKLEIKRTAAA	253
light chain variable region coding gene	GAAACGACACTCACGCAGTCTCCAGCATTTCATGTCAGCG ACTCCAGGAGACAAAGTCAACATCTCCTGCAAAGCCAGC CAAGACATTGATGATGATATGAACTGGTACCAACAGAAA CCAGGAGAAGCTGCTATTTCCATTATTCAAGAAGCTAGT ACTCTCGTTCCTGGAATCCCACCTCGATTTCAGTGGCAGC GGGTATGGAACAGATTTTACCCTCACAATTAATAACATAG AATCTGAGGATGCTGCATATTACTTCTGTCTACAACATGA TAAGTTCCCGTACACTTTTGGCCAGGGGACCAAGCTGGA GATCAAACGTACCGCGGCCGCA	293
heavy chain variable region	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQA PGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTA YMELSRRLRSDDTAVYYCASRGVDEGDYWGQGTMTVTVSS	254
heavy chain variable region coding gene	GAAGTGCAGCTGGTGCAGTCTGGAGCTGAGGTGAAGAA GCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTG GTTACACCTTTACCAGCTATGGTATCAGCTGGGTGCGAC AGGCCCTGGACAAGGGCTTGAGTGGATGGGATGGATC AACCCTAACAGTGGTGGCACAACCTATGCACAGAAGTTT CAGGGCAGGGTCACCATGACCAGGGACACGTCCATCAG CACAGCCTACATGGAGCTGAGCAGGCTGAGATCTGACG ACACGGCCGTGTATTACTGTGCGAGTCGGGGGGTTGAT GAGGGGGACTACTGGGGCCAAGGGACAATGGTCACCGT CTCGAGT	294
light chain (Kappa)	ETTLTQSPAFMSATPGDKVNISCKASQDIDDDMNWYQQKP GEAAISIIQEASTLVP GIPPRFSGSGYGTDFLTINNIESEDAAYYFCLQHDKFPYTFGQGTKLEIKRTAAAPSVFIFPPSDEQLK SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTE QDSKDSTYLSSTLTLSKADYEKHKLYACEVTHQGLSSPVT	333

	KSFNRGEC	
heavy chain	EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQA PGQGLEWMGWINPNSGGTNYAQKFQGRVTMTRDTSISTA YMELSRRLRSDDTAVYYCASRGVDEGDYWGQGTMTVSSA STKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSW NSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYT CNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSVFL FPPKPKDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGV EVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCK VSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEMTKNQV SLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGS FFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSL SLGK	334

【Table 21】

Antibody clone E6

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	TGSSGNIASNYVQ	103
CDR-L2	RDDQRPS	104
CDR-L3	QSYDSSSWV	105
CDR-H1	TYDIT	106
CDR-H2	WMNPNSGNSRSAQKFQG	107
CDR-H3	GDYSGVVLATALDY	108
light chain variable region	NFMLTQPHSVSESPGKTVTLCTGSSGNIASNYVQWYQHR PGSAPTTVIYRDDQRPSGVPDRFSGSIDSSSNSASLTISGL RPEDEADYYCQSYDSSSWVFGGGTKLTVLGQPAAA	255
light chain variable region coding gene	AATTTTATGCTGACTCAGCCCCACTCTGTGTCTCGGAGTCT CCGGGGAAGACGGTTACCCTCTCCTGCACCGGCAGCAG CGGCAACATTGCCAGTAACTATGTGCAGTGGTACCAGCA CCGCCCGGGCAGTGCCCCCACCCTGTGATCTACCGGG ATGACCAAAGACCCTCTGGAGTCCCTGATCGCTTCTCTG GCTCCATCGACAGTTCATCCAACCTCTGCCTCCCTCACGA TCTCTGGACTGAGGCCTGAGGACGAGGCTGACTATTACT GTCAGTCTTATGATAGCAGCTCTTGGGTGTTTCGGCGGAG GGACCAAGCTGACCGTCCTAGGTCAGCCCGCGGCCGCA	295
heavy chain variable region	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYDITWVRQA PGQGLEWMGWMNPNSGNSRSAQKFQGRVSMSTSDSSIST AYMELSSLRSEDTAVYYCATGDYSGVVLATALDYWGQGT LTVSS	256
heavy chain variable region	CAGGTCCAGCTTGTGCAGTCTGGAGCAGAGGTGAAGAA GCCTGGGGCCTCAGTGAAGGTCTCCTGCAAGGCTTCTG GATACACCTTCACCACTTATGATATCACCTGGGTGCGAC AGGCCCTGGACAAGGCCTTGAGTGGATGGGATGGATG	296

coding gene	AACCCGAACAGTGGTAACTCACGCTCTGCACAGAAGTTC CAGGGCAGAGTCAGCATGACCAGTGA CTCTCCATAAG CACAGCCTACATGGAGCTGAGCAGCCTGAGATCTGAGG ACACGGCCGTGTATTACTGTGCAACAGGAGACTACTCG GGTGTGGTACTAACTGCAACAGCACTTGACTACTGGGG CCAGGGAACCCTGGTCACCGTCTCGAGT	
light chain (Lambd a)	NFMLTQPHSVSESPGKTVTLCTGSSGNIASNYVQWYQHR PGSAPTTVIYRDDQRPSPGVDRFSGSIDSSSNSASLTISGL RPEDEADYYCQSYDSSSWVFGGGTKLTVLGQPAAAPSVTL FPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG VETTTTPSKQSNKYAASSYLSLTPEQWKSHRSYSCQVTHE GSTVEKTVAPTECS	335
heavy chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTTYDITWVRQA PGQGLEWMGWMNPNSGNSRSAQKFQGRVSM TSDSSIST AYMELSSLRSEDTAVYYCATGDYSGVVL TATALDYWGQGT LTVVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPE PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSS LGTKTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFL GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQF NWWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWL NGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQ EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK TTP PVLDSGDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHN HYTQKSLSLSLGK	336

【Table 22】

Antibody clone E9

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	SGSSSNIGNNYVY	109
CDR-L2	RNNQRPS	110
CDR-L3	AAWDDSLSGWV	111
CDR-H1	SYGMH	112
CDR-H2	NIKQDGSEKYYVDSVKG	113
CDR-H3	EDRIAAAGMRELDY	114
light chain variable region	QSELTQLPSASETPGQRV TISCSGSSSNIGNNYVYWYQQL PGTAPKLLIYRNNQRPSGVDRFSGSKSGTSASLAISGLRS EDEADYYCAAWDDSLSGWVFGGGTKLTVLGQPAAA	257
light chain variable region coding gene	CAGTCTGAGCTGACTCAGCTACCCTCAGCGTCTGAGACC CCCGGGCAGAGGGTCACCATCTCTTGTCTGGAAGCAG CTCCAACATCGGAAATAATTATGTATACTGGTACCAGCAAC TCCCCGGAACGGCCCCCAA CTCTCATCTATAGGAATAA TCAGCGGCCCTCAGGGGTCCCTGACCGATTCTCTGGCT CCAAGTCTGGCACCTCAGCCTCCCTGGCCATCAGTGGG	297

	CTCCGGTCCGAGGATGAGGCTGATTATTACTGTGCAGCA TGGGATGACAGCCTGAGTGGTTGGGTGTTCCGGCGGAGG GACCAAGCTGACCGTCCTAGGTCAGCCCGCGGCCGCA	
heavy chain variable region	QVQLVESGGGLVQPGRSLRLSCAASGFTFSSYGMHWVRQ APGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNKNTLY LQMNSLRAEDTAVYYCAREDRIAAAGMRELDYWGGGTLVT VSS	258
heavy chain variable region coding gene	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACA GCCTGGGAGGTCCTGAGACTCTCCTGTGCAGCGTCTG GATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTGGCCAAACATA AAGCAAGATGGAAGTGAGAAATACTATGTGGACTCTGTG AAGGGCCGATTACCCTCTCCAGAGACAACGCCAAGAAC ACGCTGTATCTCCAAATGAACAGCCTGAGAGCTGAGGAC ACGGCTGTGTATTACTGTGCGAGAGAGGACCGTATAGCA GCAGCTGGGATGCGGGAGTTGGACTACTGGGGCCAGG GCACCCTGGTCACCGTCTCGAGT	298
light chain (Lambd a)	QSELTQLPSASETPGQRVTISCSGSSSNIGNNYVYWYQQL PGTAPKLLIYRNNQRPSGVPDRFSGSKSGTSASLAISGLRS EDEADYYCAAWDDSLSGWVFGGGTKLTVLGQPAAAPSVT LFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKA GVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTH EGSTVEKTVAPTECS	337
heavy chain	QVQLVESGGGLVQPGRSLRLSCAASGFTFSSYGMHWVRQ APGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNKNTLY LQMNSLRAEDTAVYYCAREDRIAAAGMRELDYWGGGTLVT VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVT VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGT KTYTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGP SVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWY VDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGK EYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPSQEEM TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSGDSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYT QKSLSLSLGK	338

【Table 23】

Antibody clone A11

	Amino acid sequence (N→C) / Nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	RSSQSLLHSNGYNYLD	115
CDR-L2	LGSNRAS	116
CDR-L3	MQGTHWPPYT	117
CDR-H1	SYAMT	118
CDR-H2	GISSDGTTTTYADSVRG	119

CDR-H3	DQLLGWDALNV	120
light chain variable region	DIVMTQSPLSLPVTPGEPASISCRSSQSLLSNGYNYLDWY LQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISR VEAEDVGVYYCMQGTHWPPYTFGQGTKVEIKRTAAA	259
light chain variable region coding gene	GATATTGTGATGACCCAGTCTCCACTCTCCCTGCCCCGTC ACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAG TCAGAGCCTCCTGCATAGTAATGGATACAACTATTTGGA TTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCC TGATCTATTTGGGTTCTAACCGGGCCTCCGGGGTCCCTG ACAGGTTCACTGGCAGTGGATCAGGCACAGATTTTACAC TGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTT TATTACTGCATGCAAGGTACACACTGGCCTCCGTACACC TTTGCCAGGGGACCAAGGTGGAGATCAAACGTACCGC GGCCGCA	299
heavy chain variable region	EVQLLESQGGLEQPGGFLRLSCAASGFSFTSYAMTWVRQ APGKGLEWVSGISSDGTTTYADSVRGRFTISRDNKNTVY LQMNSLRDEDTAVYYCARDQLLGWDALNVWGQGTMTVS S	260
heavy chain variable region coding gene	GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGAACA GCCTGGGGGGTTCCTGAGACTCTCCTGTGCAGCCTCTG GATTCTCCTTTACCAGCTACGCCATGACCTGGGTCCGCC AGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGGTATT AGTAGTGATGGGACCACTACAACCTACGCGGACTCCGT GAGGGGCCGTTTACCATCTCCAGAGACAACGCCAAGA ACACGGTGTATCTCAAATGAACAGTCTGAGAGACGAGG ACACGGCTGTGTATTATTGTGCAAGAGATCAATTGTTGG GCTGGGATGCTCTGAATGTCTGGGGCCAAGGGACAATG GTCACCGTCTCGAGT	300
light chain (Kappa)	DIVMTQSPLSLPVTPGEPASISCRSSQSLLSNGYNYLDWY LQKPGQSPQLLIYLGSNRASGVDPDRFSGSGSGTDFTLKISR VEAEDVGVYYCMQGTHWPPYTFGQGTKVEIKRTAAAPS VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQS GNSQESVTEQDSKSTYSLSSLTTLKADYEKHKLYACEVT HQGLSSPVTKSFNRGEC	339
heavy chain	EVQLLESQGGLEQPGGFLRLSCAASGFSFTSYAMTWVRQ APGKGLEWVSGISSDGTTTYADSVRGRFTISRDNKNTVY LQMNSLRDEDTAVYYCARDQLLGWDALNVWGQGTMTVS SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS WNSGALTSGVHTFPAVLQSSGLYSLSSVTVPPSSSLGKT YTCNVDHKPSNTKVDKRVESKYGPPCPPCPAPEFLGGPSV FLFPPKPKDTLMISRTPEVTCVVVDVSDPEVQFNWYVD GVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYK CKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEEMTKN QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSD GSFFLYSRLTVDKSRWQEGNVFSCSVMEALHNHYTQKS	340

	LSLSLGK	
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Example 2: Assay of *in vitro* biological activities of the selected antibodies

2.1. Natural killer cell (NK cell) surface binding assay

5 In order to test whether or not 93 antibodies selected in Example 1.4 bind LILRB1 expressed on surface of immune cells, natural killer cell (NK cell) surface binding assay was performed. A human NK cell, KHYG-1 cell (JCRB) was cultured in RPMI 1640 medium (Gibco) supplemented with 10%(w/v) of FBS (Gibco) and 100 U/mL of interleukin-2 (Novartis). KHYG-1 cells were added to a U-bottom 96-well
10 tissue culture plate (BD Falcon) at the amount of 5×10^4 cells/well. Each of the selected antibodies was added to the well to the final concentration of 50 µg/mL per well and incubated at 4°C for 1 hour.

In order to see the level of LILRB1-specific binding of the selected antibodies, a human IgG4 isotype control antibody (Biolegend) was treated in the same manner.
15 After washing with FACS buffer, the cells were treated with an anti-human Fc-biotin antibody (life technologies) and incubated at 4°C for 1 hour. After washing with FACS buffer, the cells were treated with streptavidin PE (BD Pharmingen) and incubated at 4°C for 30 minutes. After washing with FACS buffer, the cells were resuspended and subjected to analysis using iQue screener (Sartorius).

20 Among the obtained results, the results for antibodies A10, E3, E4, F12, G1, G9, G11, H2 and H11 are representatively compared with that of human IgG4 isotype (control), which are shown in Table 24. The flow cytometry diagrams for A10, E3 and human IgG4 isotype (control) are shown in Figs. 4a (A10), 4b (E3), and 4c (isotype IgG4), respectively:

25 **【Table 24】**

	Mean Fluorescence Intensity	% of population 2
human IgG4 isotype control	142917.2	2.95
A10	222660.2	28.68

E3	268702.2	40.22
E4	272295.5	43.25
F12	262012.7	38.02
G1	321051.7	56.23
G9	263079.3	41.32
G11	262771.9	40.11
H2	238570.9	29.00
H11	244818.2	32.59

As shown in Table 24 and Figs. 4a~4c, the tested antibodies show higher level of binding to human NK cells (surface), compared to that of human IgG4 isotype control antibody.

5

2.2. Analysis of inhibition of LILRB1 binding to HLA-G by the selected antibodies

In order to test whether or not the antibodies selected in Example 1.5 exert an inhibitory effect on binding of LILRB1 to its ligand, HLA-G, the degree of blocking by the selected antibodies was analyzed.

10

For this purpose, JEG-3 cells (ATCC cat# HTB-36), which show high expression level of HLA-G, were used. JEG-3 cells were cultured in MEM medium (Gibco) supplemented with 10%(v/v) of FBS (Gibco) and 1%(v/v) of pen-strep (Gibco). The JEG-3 cells were added to U-bottom 96-well tissue culture plate (BD Falcon) at the amount of 5×10^4 cells/well. The well plate was washed with 1X PBS buffer. Each of the antibodies selected in Example 1.5 (A10, E3, F12, G1, G9, H2 and H11) and LILRB1-Fc (RnD systems) were mixed in FACS buffer (1X PBS + 1% BSA + 1 mM EDTA) to the final concentrations of 10 $\mu\text{g/mL}$ and 5 $\mu\text{g/mL}$, respectively. The cells were treated with 100 μL of the mixture solution per well and incubated on ice for 2 hours. An anti-LILRB1 antibody (clone HP-F1, Abcam) as a positive control and an anti-lysozyme IgG4 antibody (clone D1.3) as a negative control were treated in the same manner. After washing with FACS buffer twice, the cells were treated with PE-anti-hulgG-Fc antibody (Biolegend, 10 $\mu\text{g/mL}$) and incubated on ice for one hour.

15

20

After washing with FACS buffer twice, the cells were resuspended in 100 μ L of the same buffer and subjected to analysis using iQue screener (Sartorius).

The obtained results are shown in Fig. 5. As shown in Fig. 5, all the tested antibodies A10, E3, F12, G1, G9, H2 and H11 effectively inhibit the binding of LILRB1-Fc to HLA-G-overexpressing cell line.

2.3. Assay of cancer cell lysis by NK cells

In order to test whether or not the selected antibodies increase the degree of cancer cell lysis by NK cells, the cell death rate of HLA-G-overexpressing HEK293 cell by NK cell KHYG-1 was analyzed. KHYG-1 cells (JCRB) were added to 96-well tissue culture plate (BD Falcon) at the amount of 2×10^4 cells/well (4×10^4 cells/mL, total volume 50 μ L). The cells were treated with each antibody (Table 25) to the final concentration of 20 μ g/mL per well, and left at 37°C for one hour.

As a negative control, a human IgG4 isotype control antibody (Biolegend) was treated in the same manner.

HLA-G-overexpressing HEK293 cells (which were prepared by transduction of HEK293 cells (American Typo Culture Collection) with lentivirus constructed for expressing HLA-G) were stained with IncuCyte CytoLight Rapid Red Reagent (Sartorius) according to the manufacturer's protocol. After one hour, the HLA-G-overexpressing HEK293 cells were added to the plate at the amount of 1×10^4 cells/well (2×10^4 cells/mL, total volume 50 μ L). The plate was placed in IncuCyte S3(Sartorius) equipped in an incubator under the condition of 37°C and 5% CO₂, and images thereof were taken for 72 hours. Red area confluence indicating the density of live HLA-G-overexpressing HEK293 cells was measured, and cell viability was calculated. The obtained cell viabilities are shown in Table 25 (wherein the cell viabilities are shown as a relative value to that of control antibody (cell viability of IgG4 isotype-treated well = 1)):

$$\text{Relative cell viability (IgG4 Isotype = 1)} = \frac{\text{Normalized red area confluence value of antibody}}{\text{Normalized red area confluence value of IgG4 Isotype}}$$

【Table 25】

Antibody	Relative cell viability (IgG4 isotype=1)
human IgG4 Isotype control	1.00
A10	0.70
B9	0.81
D3	0.83
E1	0.82
E3	0.64
F12	0.81
G1	0.64
G6	0.78
G9	0.77
G11	0.82
H2	0.78
H11	0.60

As shown in Table 25, all the tested antibodies including A10, B9, D3, E1, E3, F12, G1, G6, G9, G11, H2 and H11 increase cell death of HLA-G-overexpressing HEK293 cells by KHYG-1, compared to that of human IgG4 isotype control antibody.

5

Example 3: Assay of *in vivo* biological activities of the selected antibodies

Among the antibodies selected in Example 1.5, two antibodies (E3 and B3) were tested for their *in vivo* anti-cancer efficacies. For this purpose, it was tested whether or not administration of the two antibodies reduces tumor size where the tumor was generated by engrafting human colorectal carcinoma cells (Bioware Brite Cell Line HCT116 Red-Fluc colorectal carcinoma cells (PerkinElmer)) and THP-1 derived macrophages to the mice. As a negative control, human colon cancer xenograft mice prepared as above were treated with a human IgG1 isotype control antibody (BioXcell, Cat. No. BP0297). Hereinafter, the processes are described in detail:

10

15

Preparation of THP-1 derived macrophages

The THP-1 derived macrophages used above were prepared by differentiating THP-1 cells (ATCC) with 150 nM phorbol 12-myristate 13-acetate

(PMA, Sigma), 20 ng/mL of interferon gamma (PeproTech) and 10 pg/mL of lipopolysaccharide (LPS, Sigma).

Measurement of anti-cancer efficacy in mouse model

5-week old female CIEA NOG mice [NOG immunodeficient mouse] (Central
 5 Institute for Experimental Animals, Japan) were subcutaneously injected with a
 mixture of 3×10^6 cells of HCT116 Red-Fluc colorectal carcinoma cells, 3×10^6 cells of
 THP-1 derived macrophages and each of two test antibodies (E3 or B3 antibody; 20
 µg per mouse). From the 4th day after tumor grafting, the antibody was administered
 to the mouse model at the dosage of 5 mg/kg by intraperitoneal injection twice a
 10 week. Then, the size (mm³) of the grafted tumor was measured and shown in Fig. 6.
 As shown in Fig. 6, all the tested antibodies, particularly antibody E3, exhibit
 statistically significant effect of inhibiting tumor growth in mouse models grafted with
 HCT116 colon cancer cells and THP-1 derived macrophages.

Example 4: Preparation of anti-LILRB1 antibody (E3.1)

The nucleic acid sequence encoding the full-length heavy chain (SEQ ID NO:
 302) of antibody E3, which was confirmed to have particularly significant effect in
 Example 3, was amplified by PCR. The nucleic acid sequence encoding the region
 from Ser1 to Leu110 of the light chain variable region (VL) (SEQ ID NO: 221) of
 20 antibody E3 was amplified by PCR and ligated to a nucleic acid sequence encoding
 the lambda constant region (Lambda CL.1, SEQ ID NO: 344) to amplify the nucleic
 acid sequence encoding lambda light chain by PCR. The amplified sequences were
 inserted into an expression vector (pTRIOZ-hIgG4, InvivoGen; alternatively, any one
 of vectors comprising CMV promoter or CMV/CHO beta-actin fusion promoter (KR10-
 25 1038126B1) and genes encoding human IgG4 heavy chain constant region and
 lambda light chain constant region, can be used), wherein the expression vector was
 designed for encoding a human IgG4 antibody. The DNA sequence of the expression
 vector was confirmed by sequencing.

An antibody (E3.1) was prepared using the constructed expression vector
 30 referring to Example 1.4, and the sequence of the antibody was analyzed referring to
 Example 1.6 and summarized in Table 26:

【Table 26】

Antibody clone E3.1

	amino acid sequence (N→C) / nucleic acid sequence (5'→3')	SEQ ID NO
CDR-L1	QGDSLRFYAS	1
CDR-L2	GKNNRPS	2
CDR-L3	NSRDSSGSHLTGV	3
CDR-H1	SYAMS	4
CDR-H2	AISGSGGSTYYADSVKG	5
CDR-H3	DTYYYGSGRSNAFDI	6
light chain variable region	SYELTQDPAVSVALGQTVRITCQGDSLRFYASWYQQKS GQAPVLV MYGKNNRPSGIPDRFSGSTSGNTASLTITGAQ AEDEADYYCNSRDSSGSHLTGVFGGGTKVTVL	345
light chain variable region coding gene	TCCTATGAGCTGACTCAGGACCCTGCTGTGTCTGTGG CCTTGGGACAGACAGTCAGGATCACATGCCAGGGAGA CAGCCTCAGAACTTTTATGCAAGCTGGTACCAGCAGA AGTCAGGACAGGCCCCAGTTCTTGTCATGTATGGTAAA AACAACCGGCCCTCAGGGATCCCAGACCGATTCTCTG GCTCCACCTCAGGAAACACAGCTTCCTTGACCATCACT GGGGCTCAGGCGGAAGATGAGGCTGACTATTACTGTA ACTCCCGGGACAGCAGTGGTAGCCATTTGACGGGCGT ATTCGGCGGAGGGACCAAGGTCACCGTCCTA	346
heavy chain variable region	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVR QAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKN TLYLQMISLRAEDTAVYYCARDTYYYGSGRSNAFDIWGQ GTLVTVSS	222
heavy chain variable region coding gene	CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTG GTA CAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCAGCC TCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGT CCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTC AGCTATTAGTGGTAGTGGTGGTAGCACATACTACGCAG ACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAA TTCCAAGAATACGCTGTATCTGCAAATGATTAGCCTGAG AGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATA CGTATTACTATGGTTCGGGGGAGAAGTAATGCTTTTGATA TATGGGGCCAGGGAACCCTGGTCACCGTCTCGAGT	262
light chain (Lambda)	SYELTQDPAVSVALGQTVRITCQGDSLRFYASWYQQKS GQAPVLV MYGKNNRPSGIPDRFSGSTSGNTASLTITGAQ AEDEADYYCNSRDSSGSHLTGVFGGGTKVTVLGQPKAN PTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADG SPVKAGVETTKPSKQSN NKYAASSYLSLTPEQWKSHRS YSCQVTHEGSTVEKTVAPTECS	347
heavy	QVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVR	302

chain	QAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDN SKN TLYLQMISLRAEDTAVYYCARDTYYYGSGRSNAFDIWGQ GTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDY FPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV PSSSLGTKTYTCNV DHKPSNTKVDKRVESKYGPPCPPC PAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQE DPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLT VLHQDWLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREP QVYTLPPSQQEEMTKNQVSLTCLVKGFYPSDIAVEWESNG QPENNYKTTTPVLDSDGSFFLYSRLTVDKSRWQEGNVF SCSVMHEALHNHYTQKSLSLGLK	
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Example 5: Generation of Human LILR-overexpressing cell lines

The nucleic acid sequences encoding the full-length human LILR family proteins (Table 27) were amplified by PCR, and each of the amplified sequences was inserted into an expression vector (pTRIOZ-hlgG4, InvivoGen; alternatively, any one of vectors comprising CMV promoter or CMV/CHO beta-actin fusion promoter (KR10-1038126B1) and genes encoding human IgG4 heavy chain constant region and lambda light chain constant region, can be used). The DNA sequence of the expression vector was confirmed by sequencing. The constructed vector was transfected into CHO cells, to generate 11 stable cell lines overexpressing each LILR protein on its surface.

【Table 27】

Protein	Genbank Accession No.	amino acid sequence (N→C)	SEQ ID NO	Antibody
LILRB1	AAH15731	MTPILTVLICLGLSLGPRTHVQAGHLPK PTLWAEPGSVITQGSPVTLRCQGGQE TQEYRLYREKKTAPWITRIPQELVKKG QFPIPSITWEHAGRYRCYYGSDTAGR SESSDPLELVVTGAYIKPTLSAQPSPVV NSGGNVTLQCDSQVAFDGFILCKEKE DEHPQCLNSQPHARGSSRAIFSVGPV SPSRWWYRCYAYDSNSPYEWSLPS DLLELLVLGVSKKPSLSVQPGPIVAPEE TLTLQCGSDAGYNRFVLYKDGERDFL QLAGAQPQAGLSQANFTLGPVSRSYG GQYRCYGAHNLSSEWSAPSDPLDILIA GQFYDRVSLSVQPGPTVASGENVTLL CQSQGWMQTFLLTKEGAADDPWRLR	348	Human LILRB1 antibody (ab185796, Abcam)

		STYQSQKYQAEFPMGPVTSAHAGTYR CYGSQSSKPYLLTHPSDPLELVVSGPS GGPSSPTTGPTSTSGPEDQPLTPTGS DPQSGLGRHLGVVIGILVAVILLLLLLLL LFLILRHRRQGKHWSTSTQRKADFQHP AGAVGPEPTDRGLQWRSSPAADAQE ENLYAAVKHTQPEDGVEMDTRSPHDE DPQAVTYAEVKHSRPRREMASPPSPL SGEFLDTKDRQAEEDRQMDTEAAASE APQDVTYAQLHSLTLRRKATEPPPSQE GPSPAVPSIYATLAIH		
LILRB2	AAH36827	MTPIVTVLICLGLSLGPRTHVQTGTIPK PTLWAEPDSVITQGSPVTLSCQGSLEA QEYRLYREKKSASWITRIRPELVKNGQ FHIPSITWEHTGRYGCQYYSRARWSE LSDPLVLVMTGAYPKPTLSAQPSPVVT SGGRVTLQCESQVAFGGFILCKEGED EHPQCLNSQPHARGSSRAIFSVGPVS PNRRWSHRCYGYDLNSPYVWSSPSD LLELLVPGVSKKPSLSVQPGPVVAPGE SLTLQCVSDVGYDRFVLYKEGERDLR QLPGRQPQAGLSQANFTLGPVSRSYG GQYRCYGAYNLSSEWSAPSDPLDILIT GQIHGTPFISVQPGPTVASGENVTLLC QSWRQFHTFLLTKAGAADAPLRLRSIH EYPKYQAEFPMSPVTSAHAGTYRCYG SLNSDPYLLSHPSEPLELVVSGPSMGS SPPPTGPISTPAGPEDQPLTPTGSDPQ SGLGRHLGVVIGILVAVVLLLLLLLLLLFLI LRHRRQGKHWSTSTQRKADFQHPAGA VGPEPTDRGLQWRSSPAADAQEENLY AAVKDTQPEDGVEMDTRAAASEAPQD VTYAQLHSLTLRRKATEPPPSQEGEPP AEPSIYATLAIH	349	Human LILRB2/ CD85d/I LT4 antibody (MAB20 78, R&D System s)
LILRB3	XP_00672 6377	MTPALTALLCLGLSLGPRTRVQAGPFP KPTLWAEPGSVISWGSPTIWCQGS EAQEYRLDKEGSPEPLDRNNPLEPKN KARFSIPSMTEHHAGRYRCHYYSSAG WSEPSDPLELVMTGFYNKPTLSALPSP VVASGGNMTLRCGSQKGYHHFVLMK EGEHQLPRTLDSQQQLHSGGFQALFPV GPVNPSHRWRFTCYYYMNTQPQVWS HPSDPLEILPSGVSRKPSLLTLQGVL PGQSLTLQCGSDVGYDRFVLYKEGER DFLQRPQGQPQAGLSQANFTLGPVSP SHGGQYRCYGAHNLSSEWSAPSDPL	350	Human LILRB3/ CD85a/I LT5 antibody (MAB18 06, R&D System s)

		NILMAGQIYDTVSLSAQPGPTVASGEN VTLLCQSWWQFDTFLLTKEGAHPPL RLRSMYGAHKYQAEFPMSPVTSAHA GTYRCYGSYSSNPHELLSFSEPLELM VSGHSGGSSLPPTGPPSTPGLGRYLE VLIGVSVAFVLLLFLLLFLLRRQRHSK HRTSDQRKTDQRPAGAAETEPKDRG LLRRSSPAADVQEENLYAAVKDTQSED RVELDSQSPHDEDPQAVTYAPVKHSS PRREMASPPSSLSGEFLDTKDRQVEE DRQMDTEAAASEASQDVTYAQLHSLT LRRKATEPPPSQEGEPPEPSIYATLAI H		
LILRB4	NP_00126 5355	MIPTFTALLCLGLSLGPRTHMQAGPLP KPTLWAEPSVISWGNSTIWCQGT EAREYRLDKEESPAPWDRQNP KARFSIPSMTEYAGRYRCYYRSPVG WSQPSDPLELVMGTGAYSKPTLSALPS PLVTSGKSVTLLCQSRSPMDTFLLIKE RAAHPLLHLRSEHGAQQHQA EFPMSPVTSVHGGTYRCFSSHGFSHYLLSHPS DPLELIVSGSLEGPRPSPTRSVSTAAG PEDQPLMPTGSVPHSGLRRHWEVLIG VLVVSILLLSLLLFLLLQHW RQGKHRTL AQRQADFQRPPGAAEPEPKDGG LQR RSSPAADVQGENFCAAVKNTQPEDGV EMDTRQSPHDEDPQAVTYAKVKHSRP RREMASPPSPLSGEFLDTKDRQAEED RQMDTEAAASEAPQDVTYARLHSFTL RQKATEPPPSQEGASPAEPSVYATLAI H	351	Human LILRB4/ CD85k/I LT3 antibody (MAB24 251, R&D System s)
LILRB5	NP_00683 1	MTLTLSVLICLGLSVGPRTCVQAGTLP KPTLWAEPASVIARGKPVTLWCQGP LE TEEYRLDKEGLPWARKRQNP LEPGAK AKFHIPSTVYDSAGRYRCYYET PAGW SEPSDPLELVATGFYAEPTLLALP SPVV ASGGNVTLCQDGLDGLTFVLVEE EQK LPRTLVSQKLKPGPSQALFPVGPVTPS CRWRFRCYYYRKNPQVWSNP SDLL EILVPGVSRKPSLLIPQGSV VARGGSLT LQCRSDVGYDIFVLYKEGEH DLVQGS GQQPQAGLSQANFTLGPVSR SHGGQ YRCYGAHNLSPRWSAPSDPLDIL IAGLI PDIPALSVQPGPKVASGENVTLLCQ SW HQIDTFFLTKEGAHPPLCLKSKYQSY RHQAEFMSMPVTSAQGGTYRCYSAIR	352	Human LILRB5/ CD85c/ LIR-8 antibody (MAB30 65, R&D System s)

		SYPYLLSSPSYPQELVSGPSGDPSLS PTGSTPTPGPEDQPLTPTGLDPQSGL GRHLGVVTGVSVAFVLLLFLLLFLLLRH RHQSKHRTSAHFYRPAGAAGPEPKDQ GLQKRASPVADIQEEILNAAVKDTQPK DGVEMDARAAASEAPQDVTYAQLHSL TLRREATEPPPSQEREPPAEPSIYAPL AIH		
LILRA1	NP_006854	MTPIVTVLICLRLSLGPRTHVQAGTLPK PTLWAEPGSVITQGSPVTLWCQGILET QEYRLYREKKTAPWITRIPQEIVKKGQF PIPSITWEHTGRYRCFYGSHTAGWSE PSDPLELVVTGAYIKPTLSALPSPVVT GGNVTLHCVSQVAFGSFILCKEGEDE HPQCLNSQPRTHGWSRAIFSVGPVSP SRRWSYRCYAYDSNSPHVWSLPSDLL ELLVLGVSKKPSLSVQPGPIVAPGESLT LQCVSDVSYDRFVLYKEGERDFLQLP GPQPQAGLSQANFTLGPVSRSYGGQ YRCSGAYNLSSEWSAPSDPLDILIAGQ FRGRPFISVHPGPTVASGENVTLLCQS WGPFTFLLTKAGAADAPLRLRSIHEY PKYQAEFPMSPVTSAHSGTYRCYGS SSNPYLLSHPSDSLELMVSGAAETLSP PQNKSDSKAGAANTLSPSQNKTAHP QDYTVENLIRMGIAGLVVLGILLFEA QHSQRSL	353	Human LILRA1/ LILRB1 antibody (MAB30 851, R&D System s)
LILRA2	AAH17412	MTPILTVLICLGLSLGPRTHVQAGHLPK PTLWAEPGSVIIQGSPVTLRCQGSLLQA EEYHLYRENKSASWVRRIQEPGKNGQ FPIPSITWEHAGRYHCQYYSHNHSSEY SDPLELVVTGAYSKPTLSALPSPVVT GGNVTLQCVSQVAFDGFILCKEGEDE HPQRLNSHSHARGWSWAIFSVGPVSP SRRWSYRCYAYDSNSPYVWSLPSDLL ELLVPGVSKKPSLSVQPGPMVAPGESL TLQCVSDVGYDRFVLYKEGERDFLQR PGWQPQAGLSQANFTLGPVSPSHGG QYRCYSAHNLSSEWSAPSDPLDILITG QFYDRPSLSVQPVPTVAPGKNVTLLC QSRGQFHTFLLTKEGAGHPPLHLRSE HQAQQNQAEFRMGPVTSAHVGTYRC YSSLSSNPYLLSLPSDPLELVVSASLG QHPQDYTVENLIRMGVAGLVVLGILL FEAQHSQRSLQDAAGR	354	Human LILRA2/ CD85h/I LT1 antibody (MAB63 64, R&D System s)
LILRA3	AAH28208	MTSILTVLICLGLSLDPRTHVQAGPLPK	355	Human

		PTLWAEPGSVITQGSPVTLRCQGSLET QEYHLYREKKTALWITRIPQELVKKGQF PILSITWEHAGRYCCYGSHTVGLSES SDPLELVVTGAYSKPTLSALPSPVVT GGNVTIQCDQSQVAFDGFILCKEGEDEH PQCLNSHSHARGSSRAIFSVGPVSPS RRWSYRCYGYDSRAPYVWSLPSDLL GLLVPGVSKKPSLSVQPGPVVAPGEKL TFQCGSDAGYDRFVLYKEWGRDFLQ RPGRQPQAGLSQANFTLGPVSRSYG GQYTCSGAYNLSSEWSAPSDPLDILIT GQIRARPFLSVRPGPTVASGENVTLLC QSQGGMHTFLLTKEGAADSPLRLKSK RQSHKYQAEFPMSPVTSAHAGTYRCY GSLSSNPYLLTHPSDPLELVVSGAAET LSPQNKSDSKAGE		LILRA3/ CD85e antibody (PA5- 47349, Invitro gen)
LILRA4	NP_03640 8	MTLILTSLLFFGLSLGPRTRVQAENLPK PILWAEPGPVITWHNPVTIWCQGTLEA QGYRLDKEGNSMSRHILKTLESENKV KLSIPSMWWEHAGRYHCYYQSPAGW SEPSDPLELVVTAYSRTLSALPSPVVT SGVNVTLRCASRLGLGRFTLIEEGDHR LSWTLNSHQHNHGKFQALFPMGPLTF SNRGTFRCYGYENNTPYVWSEPSDPL QLLVSGVSRKPSLLTLQGPVVTGENL TLQCGSDVGYIRYTYLYKEGADGLPQR PGRQPQAGLSQANFTLSPVSRSYGG QYRCYGAHNVSSEWSAPSDPLDILIAG QISDRPSLSVQPGPTVTSGEKVTLLCQ SWDPMFTFLLTKEGAAHPPLRLRSMY GAHKYQAEFPMSPVTSAHAGTYRCY GSRSSNPYLLSHPSEPLELVVSGATET LNPAQKKSDSKTAPHLQDYTVENLIRM GVAGLVLLFLGILLFEAQHSQRSPPRC SQEANSRKDNAPFRVVEPWEQI	356	CD85g (ILT7) antibody (16- 5179- 82, Invitro gen)
LILRA5	NP_06707 3	MAPWSHPSAQLQPVGGDAVSPALMV LLCLGLSLGPRTHVQAGNLSKATLWAE PGSVISRGNSVTIRCQGTLEAQEYRLV KEGSPEPWDTONPLEPKNKARFSIPS MTEHHAGRYRCYYSPAGWSEPSDP LELVVTGFYNKPTLSALPSPVVTSGEN VTLQCGSRLRFDRFILTEEGDHKLSWT LDSQLTPSGQFQALFPVGPVTPSHRW MLRCYGSRRHILQVWSEPSDLLEIPVS GAADNLSPSQNKSDSGTASHLQDYAV ENLIRMGMAGLILVVLGILIFQDWHWSQR	357	Human LILRA5/ CD85f antibody (MAB67 54, R&D System s)

		SPQAAAGR		
LILRA6	NP_001347096	MTPALTALLCLGLSLGPRTRVQAGPFP KPTLWAEPGSVISWGSPVTIWCQGSL EAQEYQLDKEGSPEPLDRNNPLEPKN KARFSIPSMTQHHAGRYRCHYYSSAG WSEPSDPLELVMTGfYNKPTLSALPSP VVASGGNMTLRCSQKGYHHFVLMK EGEHQLPRTLDSQQHLHSGGFQALFPV GPVTPSHRWRFTCYYYYTNTPRVWS HPSDPLEILPSGVSRKPSLLTLQGPVLA PGQSLTLQCGSDVGYDRFVLYKEGER DFLQRPQGQPQAGLSQANFTLGPVSP SHGGQYRCYGAHNLSSEWSAPSDPL NILMAGQIYDTVSLSAQPGPTVASGEN VTLLCQSRGYFDTFLLTKEGAHPPLR LRSMYGAHKYQAEFPMSPVTSAHAGT YRCYGSYSSNPHELLSFPSEPLELMVS GHSGGSSLPPTGPPSTPASHAKDYTV ENLIRMGMAGLVLVFLGILLFEAQHSQ RNPQDAAGR	358	Human LILRA6/CD85b antibody (MAB8656, R&D Systems)

Example 6: Determination of EC₅₀ for binding of the selected antibodies to LILRB1 overexpressing cell surface

In order to determine EC₅₀ values of the antibodies prepared in Examples 1 and 4 for binding to human LILRB1-overexpressing cell lines, a cell surface binding assay was performed. Representing the prepared antibodies, EC₅₀ values of E3.1 and H11 antibodies were measured. The CHO cells prepared in Example 5, which overexpress LILRB1 on surface, were added to U-bottom 96-well tissue culture plate (BD Falcon) at the amount of 1x10⁵ cells/well. Threefold serial dilutions of E3.1 and H11 antibodies were prepared starting from the final concentrations of 600 ug/mL and 27 ug/mL, respectively. The cells were treated with each of the diluted antibodies and incubated at 4°C for 60 minutes. After washing with FACS buffer, the cells were treated with anti-human Fc-biotin antibody (Invitrogen) and incubated at 4°C for 30 minutes. After washing with FACS buffer, the cells were treated with streptavidin (BD Pharmingen) labeled with PE fluorescence and incubated at 4°C for 30 minutes. After washing with FACS buffer, the cells were resuspended and subjected to analysis using iQue screener (Sartorius). EC₅₀ values were calculated using nonlinear regression formula of GraphPad Prism software, and the obtained results are shown

in Table 28:

【Table 28】

	E3.1	H11
EC ₅₀ (nM)	7.154	0.376

Example 7: Assessment of cross-reactivity of the selected antibodies to Human LILR family-overexpressing cell lines

In order to confirm whether or not the selected antibodies bind to human LILR family proteins other than LILRB1, a cell surface binding assay was performed. The CHO cells (prepared in Example 5) expressing each of various LILR family proteins on surface were added to U-bottom 96-well tissue culture plate (BD Falcon) at the amount of 1×10^5 cells/well. The cells in each well were treated with the selected antibody in the final concentration of 20 $\mu\text{g/mL}$ and incubated at 4°C for 60 minutes. After washing with FACS buffer, the cells were treated with anti-human Fc-biotin antibody (Invitrogen) and incubated at 4°C for 30 minutes. After washing with FACS buffer, the cells were treated with streptavidin (BD Pharmingen) labeled with PE or FITC fluorescence and incubated at 4°C for 30 minutes. After washing with FACS buffer, the cells were resuspended and subjected to analysis using iQue screener (Sartorius). The cells treated with each LILR protein specific antibody (Table 27) were used as a positive control, and the cells treated with human IgG4 isotype control antibody (Biolegend) were used as a negative control.

The results obtained for antibody E3.1 are shown in Figs. 7a to 7d (E3.1: red; LILR-specific antibody: blue; Isotype (hIgG4) control: gray), and the results obtained for antibody H11 are shown in Figs. 8a to 8d (H11: red; LILR-specific antibody: blue; Isotype (hIgG4) control: gray). As shown in Figs. 7a to 7d and Figs. 8a to 8d, the E3.1 and H11 antibodies do not bind at all or hardly bind to LILRs other than LILRB1. These results indicate that the antibodies provided by the examples have binding abilities specifically to LILRB1.

Example 8: Measurement of release of granzyme B and perforin by enzyme-linked immune absorbent spot (ELISPOT) assay

In order to confirm whether the E3.1 and H11 antibodies increase the level of cytotoxicity of NK cells, an enzyme-linked immune absorbent spot (ELISPOT) assay was performed. The level of cytotoxicity was determined by the release of cytotoxic granules, granzyme B and perforin, in NK cells.

5 5×10^3 cells of LILRB1-expressing KHYG-1 cell lines (JCRB) and 5×10^3 cells of HLA-G-overexpressing K562 cells (which were prepared by transduction of K562 cells (American Type Culture Collection) with lentivirus constructed for expressing HLA-G) were co-cultured in U-bottom 96-well tissue culture plate. Each antibody(E3.1, H11 or human IgG4 isotype control antibody) was added thereto with
10 final concentration of 50 ug/mL per each well and left incubated at 37°C for 30 minutes. The co-cultured cells were transferred onto 96 well plates (Immunospot, Cat. HGZBPFN-2M) (PVDF membrane) for ELISPOT, which were coated with anti-perforin antibody and anti-granzyme B antibody, respectively, and further incubated at 37°C for 8 hours. The PVDF membranes were washed with a washing solution
15 (0.05% tween 20 in PBS), then treated with anti-granzyme B-HRP and anti-perforin-biotin antibodies. Then, detection processes were performed according to the manufacturer's protocol. The PVDF membranes were dried at room temperature for 24 hours, and the number of spots for granzyme B and perforin were counted by ELISPOT analyzer (Immunospot).

20 The results are shown in Fig 9 (granzyme b; Gzmb) and Fig. 10 (perforin; Prf), respectively (Y-axis indicates the total number of spots). As shown in Fig. 9 and Fig. 10, the release levels of both of granzyme B and perforin are significantly increased in E3.1 or H11 antibody-treated group, as compared with the human IgG4 isotype control antibody-treated group. Unpaired T-test was performed, and all experiments
25 were performed three times under the same conditions for the reliability of the experiment, and the results are shown as average values.

Example 9: preparation of Chimeric GHI/75 antibody

30 In order to see if antibodies provided by the examples show higher efficacy compared to pre-existing antibodies, a chimeric GHI/75 antibody comprising a variable region of GHI/75 antibody (Biolegend, cat# 333721), which is a mouse-

derived anti-human LILRB1 antibody, and a constant region of human antibody was prepared.

More specifically, the amino acid sequence of the GHI/75 antibody was analyzed through peptide mapping, and a vector, in which the nucleic acid sequence corresponding to the variable region (VH and VL domain) of a human IgG4 antibody was replaced by the nucleic acid sequence corresponding to the variable region (VH and VL domain) of mouse GHI/75 antibody, was prepared. In the vector, the region corresponding to upper hinge of human IgG4 was substituted with the nucleic acid sequence corresponding to the amino acid sequence (EPKSCDKTHT; SEQ ID NO: 359) of human IgG1 upper hinge. The vector was expressed as described in Example 1.4, and the obtained antibody was purified and used as a comparative antibody in examples below.

Example 10: Measurement of inhibitory effect of the selected antibodies on LILRB1 signaling using IL-2 promoter luciferase assay

In order to confirm whether the antibodies prepared in Examples 1 and 4 inhibit signaling by LILRB1, a luciferase reporter assay was performed. Among the antibodies prepared in Examples 1 and 4, the assay was performed representatively for E3.1 and H11 antibodies, and the chimeric GHI/75 antibody prepared in Example 9 was used for comparison. Jurkat cells expressing LILRB1 and interleukin 2 (IL-2) promoter luciferase (which were prepared by inserting IL-2 promoter luciferase vector (Promega) into Jurkat cell line (American Type Culture Collection) followed by transduction with lentivirus constructed for expressing LILRB1) and HLA-G-overexpressing K562 cells were used. Ninety six-well plates were coated with anti-CD3 antibody (Biolegend) by incubating with the antibody overnight at 4°C. On the next day, Jurkat cells expressing LILRB1 and IL-2 promoter luciferase were added to U-bottom 96-well plates at the amount of 1×10^5 cells/well, and the plates were treated with each antibody (E3.1, H11, chimeric GHI/75 or human IgG4 isotype (control)) to the final concentration of 20 ug/mL and incubated at 37°C for one hour. HLA-G-overexpressing K562 cells (1×10^5 cells/well) were added to the plates and incubated at 37°C for 30 minutes. The obtained suspension was transferred to the plate coated

with anti-CD3 antibody, and anti-CD28 antibody (Biolegend) was added thereto to the final concentration of 10 ug/mL. The plate was incubated at 37°C for 6 hours. Steady-Glo® solution (Promega) was added to each well, and the luminescence intensity was recorded using a luminometer (Envision, PerkinElmer).

5 The results are shown in Fig. 11. As shown in Fig. 11, E3.1 and H11 antibodies provided in examples exhibit considerably increased LILRB1 signaling inhibitory activity compared to human IgG4 isotype control antibody and the chimeric GHI/75 control antibody.

10 **Example 11: Analysis of anti-cancer effect of selected antibodies in mouse model**

For analysis of anti-cancer effects of selected antibodies, referring to Example 3, a mixture of 3×10^6 cells of HCT116 Red-Fluc colorectal carcinoma cells, 3×10^6 cells of THP-1 derived macrophages and an antibody (20 µg/mouse) was
15 subcutaneously injected to 5-week old female CIEA NOG mice (NOG immunodeficient mouse; Central Institute for Experimental Animals, Japan). The antibody used was E3.1 or H11 antibody, and human IgG4 isotype was used as a control antibody for comparison. From the 4th day after grafting tumor cells, the antibody was administered to the mouse model at the dosage of 5 mg/kg by
20 intraperitoneal injection twice a week, and the tumor volume was measured and shown in Fig. 12. As shown in Fig. 12, E3.1 and H11 antibodies exhibit significant effect of inhibiting tumor growth in mouse models grafted with HCT116 colon cancer cells and THP-1 derived macrophages compared to the control antibody.

【CLAIMS】**【Claim 1】**

An anti-LILRB1 antibody or an antigen-binding fragment thereof, comprising complementarity determining regions (CDRs) as follows:

- 5 a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1, 7, 13, 19, 25, 31, 37, 43, 49, 55, 61, 67, 73, 79, 85, 91, 97, 103, 109, or 115,
- a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2, 8, 14, 20, 26, 32, 38, 44, 50, 56, 62, 68, 74, 80, 86, 92, 98, 104, 110, or 116,
- a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3, 9, 15, 21,
- 10 27, 33, 39, 45, 51, 57, 63, 69, 75, 81, 87, 93, 99, 105, 111, or 117,
- a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4, 10, 16, 22, 28, 34, 40, 46, 52, 58, 64, 70, 76, 82, 88, 94, 100, 106, 112, or 118,
- a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 5, 11, 17, 23, 29, 35, 41, 47, 53, 59, 65, 71, 77, 83, 89, 95, 101, 107, 113, or 119, and
- 15 a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6, 12, 18, 24, 30, 36, 42, 48, 54, 60, 66, 72, 78, 84, 90, 96, 102, 108, 114, or 120,
- wherein the CDRs are defined based on Kabat numbering.

【Claim 2】

20 The anti-LILRB1 antibody or an antigen-binding fragment thereof of claim 1, comprising:

- (1) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 1, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 2, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 3, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 4, a CDR-H2 comprising the amino acid sequence of SEQ
- 25 ID NO: 5, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 6;

- (2) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 7, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 8, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 9, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 10, a CDR-H2 comprising the amino acid sequence of SEQ
- 30 ID NO: 11, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 12;

- (3) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 13, a

CDR-L2 comprising the amino acid sequence of SEQ ID NO: 14, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 15, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 16, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 17, and a CDR-H3 comprising the amino acid sequence of
5 SEQ ID NO: 18;

(4) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 19, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 20, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 21, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 22, a CDR-H2 comprising the amino acid
10 sequence of SEQ ID NO: 23, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 24;

(5) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 25, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 26, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 27, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 28, a CDR-H2 comprising the amino acid
15 sequence of SEQ ID NO: 29, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 30;

(6) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 31, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 32, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 33, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 34, a CDR-H2 comprising the amino acid
20 sequence of SEQ ID NO: 35, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 36;

(7) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 37, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 38, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 39, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 40, a CDR-H2 comprising the amino acid
25 sequence of SEQ ID NO: 41, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 42;

(8) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 43, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 44, a CDR-L3
30

comprising the amino acid sequence of SEQ ID NO: 45, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 46, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 47, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 48;

5 (9) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 49, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 50, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 51, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 52, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 53, and a CDR-H3 comprising the amino acid sequence of
10 SEQ ID NO: 54;

(10) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 55, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 56, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 57, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 58, a CDR-H2 comprising the amino acid
15 sequence of SEQ ID NO: 59, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 60;

(11) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 61, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 62, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 63, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 64, a CDR-H2 comprising the amino acid
20 sequence of SEQ ID NO: 65, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 66;

(12) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 67, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 68, a CDR-L3
25 comprising the amino acid sequence of SEQ ID NO: 69, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 70, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 71, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 72;

(13) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 73, a
30 CDR-L2 comprising the amino acid sequence of SEQ ID NO: 74, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 75, a CDR-H1 comprising the

amino acid sequence of SEQ ID NO: 76, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 77, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 78;

5 (14) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 79, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 80, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 81, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 82, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 83, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 84;

10 (15) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 85, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 86, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 87, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 88, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 89, and a CDR-H3 comprising the amino acid sequence of
15 SEQ ID NO: 90;

(16) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 91, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 92, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 93, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 94, a CDR-H2 comprising the amino acid
20 sequence of SEQ ID NO: 95, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 96;

(17) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 97, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 98, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 99, a CDR-H1 comprising the
25 amino acid sequence of SEQ ID NO: 100, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 101, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 102;

(18) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 103, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 104, a CDR-L3
30 comprising the amino acid sequence of SEQ ID NO: 105, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 106, a CDR-H2 comprising the amino acid

sequence of SEQ ID NO: 107, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 108;

(19) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 109, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 110, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 111, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 112, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 113, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 114; or

(20) a CDR-L1 comprising the amino acid sequence of SEQ ID NO: 115, a CDR-L2 comprising the amino acid sequence of SEQ ID NO: 116, a CDR-L3 comprising the amino acid sequence of SEQ ID NO: 117, a CDR-H1 comprising the amino acid sequence of SEQ ID NO: 118, a CDR-H2 comprising the amino acid sequence of SEQ ID NO: 119, and a CDR-H3 comprising the amino acid sequence of SEQ ID NO: 120.

【Claim 3】

The anti-LILRB1 antibody or an antigen-binding fragment thereof of claim 1, comprising:

a light chain variable region comprising the amino acid sequence of SEQ ID NO: 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, or 345, and

a heavy chain variable region comprising the amino acid sequence of SEQ ID NO: 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, or 260.

【Claim 4】

The anti-LILRB1 antibody or an antigen-binding fragment thereof of claim 1, wherein the antibody is a human IgG1 or IgG4 antibody.

【Claim 5】

The anti-LILRB1 antibody or an antigen-binding fragment thereof of claim 1, wherein the antigen-binding fragment is scFv, (scFv)₂, Fab, Fab', F(ab')₂, a fusion polypeptide comprising scFv fused with an immunoglobulin Fc, or a fusion polypeptide comprising scFv fused with a constant region of a light chain.

【Claim 6】

A pharmaceutical composition for treating or preventing a cancer, comprising the anti-LILRB1 antibody or an antigen-binding fragment thereof of any one of claims 1 to 5, and a pharmaceutically acceptable carrier.

5 **【Claim 7】**

The pharmaceutical composition of claim 6, wherein the cancer is characterized by overexpression of MHC Class I.

【Claim 8】

10 A nucleic acid molecule encoding the antibody or an antigen-binding fragment thereof of any one of claims 1 to 5.

【Claim 9】

A recombinant vector comprising the nucleic acid molecule of claim 8.

【Claim 10】

15 A recombinant cell comprising the nucleic acid molecule of claim 8 or a recombinant vector comprising the nucleic acid molecule.

【Claim 11】

A method of preparing an anti-LILRB1 antibody or an antigen-binding fragment thereof, comprising culturing the recombinant cell of claim 10.