	Ig	HEAVY						LIGHT				REACTIVITY				
#	m-SLE100CR	VH	D	RF	JH	CDR3 (aa)	Length	Vκ	Jκ	CDR3 (aa)	Length	ssDNA	dsDNA	Insulin	LPS	HEp-2
1	m-SLE100CR-10	4-4	2-15	1	4	RGVRGYCSGGSCYSQDY	17	3-11	3	QQRSNWPLT	9	X	X	X	X	X
2	m-SLE100CR-14	1-18	6-13	3	4	DRIAAAGTLDY	11	3-20	4	QQYGSWLT	8	/	/	/	/	/
3	m-SLE100CR-20	3-74	5-24	2	5	DPSRRDGYK	9	2-30	5	MQGTHWPPSIT	11	/	/	/	/	/
4	m-SLE100CR-21	5-51	4-11	1	3	PRHMTTVTTDAFDI	14	3-11	1	QQRSNWPWT	9	/	/	/	/	/
5	m-SLE100CR-27#	3-30	3-16	3	4	EGDYVWGSYRPPLAY	15	1-5	4	QQYNSYST	8					
6	m-SLE100CR-29#	3-21	3-10	1	4	TPFPTGSPFDY	11	3-20	3	QQYGSFFT	8					
7	m-SLE100CR-31#	3-23	6-13	1	5	GIAAAWLSDW	10	2D-40	5	MQRIEFPIT	9					
8	m-SLE100CR-34#	4-39	3-10	2	4	LWFGELLPLPD	11	3-20	1	QQYGSSSWT	9					
9	m-SLE100CR-38#	4-31	4-17	3	4	DPRNYGDSTGDY	12	3-20	1	QQYGSSLWT	9					
10	m-SLE100CR-40	3-15	4-17	1	3	DYGDYLDAFDI	11	3-15	1	QQYNNWPPWT	10	/	/	/	/	/
11	m-SLE100CR-42	4-39	6-19	3	4	RIAVAGTPYYFDY	13	3-15	1	QQYNNWPPGGT	11	/	/	/	/	X
12	m-SLE100CR-44#	4-4	6-19	3	6	ALIAVADNYYGMDV	14	3-20	3	QQYGSSPFT	9					
13	m-SLE100CR-45	1-18	1-20	3	4	ESFETGNHPNDY	12	1-5	2	QQYNSYIGMCS	11	/	/	/	/	/
14	m-SLE100CR-52	4-39	6-19	2	2	PVITPLYSSGANWYFDL	17	3-20	2	QQYGSSMCS	9	/	/	/	/	/
15	m-SLE100CR-55	4-59	3-22	1	4	HGSSGYYYY	9	1D-39	1	QQSYSTPPT	9	/	/	/	/	/
16	m-SLE100CR-57	3-30	3-10	2	6	DMSHGSGNYYYYGMDV	16	3-20	5	QQYGSSPPIT	10	/	/	/	/	/
17	m-SLE100CR-58	3-33	3-22	2	4	DDYYDSSGWD	10	1D-39	1	QQSYSTTWT	9	/	/	/	/	/
18	m-SLE100CR-59κ	4-34	3-22	2	3	AQDSSGNRAFDI	12	1-5	1	QQYNSYSRT	9	X	X	X	X	X
19	m-SLE100CR-62	3-21	3-10	2	4	VGDYYGSGSYPFDY	14	3-20	2	QQYGSSPPCS	10	/	/	/	/	/
20	m-SLE100CR-76	1-8	3-10	2	4	RLPDLWVGEGGFDY	14	1-9	3	QQLNSYPGFT	10	/	/	/	/	X
21	m-SLE100CR-83	4-34	6-13	3	4	GQQQADY	7	3-20	4	QQYGSSPGLT	10	/	/	/	/	/
22	m-SLE100CR-84	4-4	3-22	2	3	YDSSGEDAFDI	11	3-11	3	QQRSNWPPG	9	/	/	/	/	/
23	m-SLE100CR-115	1-46	5-24	3	3	DRRRRDGYNYKSYAFDI	17	3-20	2	QQYGSSPRS	9	X	X	X	X	X
24	m-SLE100CR-122#	1-18	3-9	3	6	DPTSEGYFDHSDGMDV	16	1-8	1	QQYYSYPRT	9					
25	m-SLE100CR-146	4-39	3-16	3	4	HGFTFGGVLDY	11	1-39	2	QQSYSTPYT	9	/	/	/	/	/
26	m-SLE100CR-168#	4-59	3-22	2	4	AGRSGYYFDY	10	1-8	1	QQYYSYPPGT	10					
27	m-SLE100CR-192	3-7	3-22	1	4	CANYYDSSGYYYFDY	15	3-15	3	QQYNNWPPF	9	/	/	/	/	/
28	m-SLE100CR-196	3-53	2-21	3	4	DPYCGGDCYTNY	12	1D-39	1	QQSYSTPRT	9	/	/	/	/	/
#	m-SLE100CR	VH	D	RF	JH	CDR3 (aa)	Length	Vλ	Jλ	CDR3 (aa)	Length	ssDNA	dsDNA	Insulin	LPS	HEp-2
29	m-SLE100CR-9	3-33	5-18	2	4	LGSSYGDGFDY	11	1-47	2	AAWDDSLSGLVV	12	/	/	/	/	/
30	m-SLE100CR-22	3-30	5-24	1	4	TDGYNFHFDY	10	3-21	1	QVWDSSSDRSYV	12	/	/	/	/	/
31	m-SLE100CR-26	4-59	6-13	2	4	AESPHPAAGTHFDY	14	1-51	2	GTWDSSLSAHVV	12	/	/	/	/	/
32	m-SLE100CR-37#	3-15	1-26	3	4	DDSGSFSFDY	10	6-57	2	QSYDSSNHVV	10					
33	m-SLE100CR-41#	4-39	6-19	3	4	HVGIAVEGPYYFDY	14	2-14	3	SSYTSSSTFV	10					
34	m-SLE100CR-47	3-73	1-26	1	5	TSGSYTT	7	1-51	2	GTWDSSLSAVV	11	/	/	/	/	/
35	m-SLE100CR-51	5-51	6-19	2	4	RSESSGWYFDY	11	3-25	3	QSADSSGTYPV	11	/	/	/	/	/
36	m-SLE100CR-53	3-53	5-24	3	6	DGGTFGDQPYYGMDV	15	1-51	2	GTWDSSLSAGV	11	/	/	/	/	/
37	m-SLE100CR-59λ							2-8	1	SSYAGSNNYV	10	X	X	X	X	X
38	m-SLE100CR-64	3-48	1-26	3	4	AGGYSGSYCLGY	12	3-1	2	QAWDSSTYVV	10	/	/	/	/	X
39	m-SLE100CR-68#	4-39	3-10	2	4	LRAPIVPY	8	7-46	7	LLSYSGAAV	9					
40	m-SLE100CR-70	4-39	3-10	2	5	QPPRPYGSGSYRGVWFDP	18	6-57	2	QSYDSSRVV	9	/	/	/	/	X
41	m-SLE100CR-74	1-18	3-10	1	3	TGGYRITMVRGVIIEGDDAFDI	22	1-40	3	QSYDSSLSVWV	11	/	/	/	/	/
42	m-SLE100CR-90	4-34	3-10	3	6	GRTRPNYYGSGSSEDV	16	2-8	1	SSYAGSNNYV	10	/	/	/	/	X
43	m-SLE100CR-134	5-51	3-10	1	5	GGDPSGWFDP	10	1-40	3	QSYDSSLSGWV	11	/	/	/	/	/
44	m-SLE100CR-159	4-39	/	/	3	HWETTQTIPAGAFDI	15	2-8	2	SSYAGSNNVV	10	X	X	X	X	X
45	m-SLE100CR-169	4-39	4-23	3	4	HRAVVTRYYFDY	12	1-40	1	QSYDSSLSGTV	11	/	/	/	/	/
46	m-SLE100CR-170	4-39	3-10	3	5	QPPRPYGSGSYRGVWLDP	18	2-8	1	SSYAGSNNYV	10	/	X	X	X	X
47	m-SLE100CR-188	1-18	3-10	3	6	DRGGTMVRGVINYYYGMDV	19	2-8	1	SSYAGSNNYV	10	/	/	/	/	/

- not expressed

	Ig	HEAVY						LIGHT				REACTIVITY				
#	m-SLE101CR	VH	D	RF	JH	CDR3 (aa)	Length	Vκ	Jκ	CDR3 (aa)	Length	ssDNA	dsDNA	Insulin	LPS	HEp-2
1	m-SLE101CR-4	3-7	6-19	2	4	DRPLSGWPPPADFDY	15	3-11	1	QQRSNWPT	8	/	/	/	/	/
2	m-SLE101CR-5	3-23	4-17	3	4	DQAPTVTTLDY	11	3-11	2	QQRSNWPYT	9	/	/	/	/	/
3	m-SLE101CR-6κ	4-4	6-13	1	4	FQQLVWFDY	9	4-1	1	QQYYSTPRT	9	/	/	/	/	/
4	m-SLE101CR-7	4-59	3-3	2	5	ASPYYDFWSGYYPNWFDP	18	1-12	4	QQANSFPLT	9	/	/	/	/	X
5	m-SLE101CR-13	4-39	6-19	2	2	QGDFPSSGWYWYFDL	15	1-5	1	QQYNSYPCT	9	/	/	/	/	/
6	m-SLE101CR-18#κ	1-3	3-22	2	4	PQYYDSYYFDY	11	1-5	2	QQYNSYSYT	9					
7	m-SLE101CR-19	5-51	3-22	2	1	YNYYDSSGYSRAEYFQH	17	4-1	1	QQYYSTPPT	9	/	/	/	/	/
8	m-SLE101CR-24	4-34	1-26	3	5	GGSMGATQRRSNWFDP	16	4-1	1	QQYYSTPPWT	10	/	/	/	/	/
9	m-SLE101CR-26	4-34	2-2	3	6	IGVVPAASYGMDV	13	3-20	2	QQYGSSPYT	9	/	/	/	/	/
10	m-SLE101CR-27	4-39	/	/	6	LYHHPSLRGMDV	12	3-11	2	QQRSNWGMST	10	X	X	/	X	X
11	m-SLE101CR-30	3-33	6-25	3	4	TPGIAAYYFDY	11	3-15	5	QQYNNWPPIT	10	/	/	/	/	/
12	m-SLE101CR-31	3-15	6-13	2	4	VKYSSSWPSDY	11	1-39	2	QQSYSTPYT	9	/	/	/	/	/
13	m-SLE101CR-33	1-18	6-13	3	6	VLDQTIAAAATGGMDV	16	4-1	1	QQYYSTPWT	9	/	/	/	/	/
14	m-SLE101CR-39	4-34	4-17	2	4	GINYGDPSIQPDY	13	3-15	1	QQYNNWPRT	9	/	/	/	/	/
15	m-SLE101CR-40	4-31	6-19	3	3	DCSYGGIAVAGTPVSAFDI	19	3-15	2	QQYNNWPLT	9	/	/	/	/	/
16	m-SLE101CR-46	1-2	3-10	2	4	GPGSYYGSGRRDLGY	15	1-33	2	QQYDNPLWT	9	/	/	/	/	/
17	m-SLE101CR-47	4-39	6-13	3	4	SLPIGYGIAAADPYYFDY	18	1-5	1	QQYNSYSPT	9	/	/	/	/	/
18	m-SLE101CR-50	4-34	6-19	3	4	SSPLYIAVAGTIDYFDY	17	1-39	1	QQSYSTPPPT	10	/	/	/	/	/
19	m-SLE101CR-53	4-39	6-13	2	5	QGRRSSSPLQWFDP	14	1-5	4	QQYNSYPLT	9	/	/	/	/	/
20	m-SLE101CR-54	3-74	/	/	6	KVGATPHYGMDV	12	1-5	4	QQYNSYSWT	9	/	/	/	/	/
21	m-SLE101CR-55	4-39	/	/	3	QLTDMGAFDI	10	3-20	1	QQYGSSLWT	9	/	/	/	/	/
22	m-SLE101CR-57	1-18	1-7	2	6	ESPYNWNYEDYYYYYGMDV	19	3-20	2	QQYGSSPKT	9	/	/	/	/	/
23	m-SLE101CR-58	4-34	3-22	2	4	PYYYDSSGDY	10	3-20	1	QQYGSSPRT	9	/	/	/	/	/
24	m-SLE101CR-65	4-39	6-19	3	4	LRLAVAGTVGDY	12	1-5	4	QQYNSYLRLT	10	/	/	/	/	/
25	m-SLE101CR-66	3-7	2-2	1	5	DLAQYQLSGW	10	1D-17	1	LQHNSYPRT	9	/	/	/	/	/
26	m-SLE101CR-69	5-51	6-6	3	6	SIAARIQTYYGMDV	14	2-28	2	MQALQTPGT	9	/	/	/	/	/
27	m-SLE101CR-71#	3-53	6-13	1	6	QQLAPYYYYGMDV	13	1-27	1	QKYNSAPWT	9					
28	m-SLE101CR-73	1-69	5-5/5-18	2	4	SFSGTRPRYSLGVQPRFDY	19	1D-16	4	QQYNSYPLT	9	/	/	/	/	/
29	m-SLE101CR-76	4-34	/	/	5	GLGFPQRMQNENFDP	15	3-11	4	QQRSNWPPT	9	/	/	/	/	/
30	m-SLE101CR-80	3-53	3-22	2	5	VGDYDSSGYYGV	12	1-39	4	QQSYSTPLT	9	/	/	/	/	/
31	m-SLE101CR-86	1-69	6-19	3	1	CIAVAGTIGYFQH	13	1-5	1	QQYNSYSGT	9	/	/	/	/	X
32	m-SLE101CR-89	4-31	7-27	1	3	ELGMGAFDI	9	3-20	2	QQYGSSPRMYT	11	/	/	/	/	/
33	m-SLE101CR-91	4-31	3-10	2	4	GAYYGSGSYGY	11	1-33	4	QQYDNLPLT	9	/	/	/	/	/
34	m-SLE101CR-94	3-15	3-22	2	3	EPYYYDSSGWDI	12	3-20	3	QQYGSSPPRFT	11	/	/	/	/	/
35	m-SLE101CR-103	3-48	2-2	3	6	GRVVVPAALDYYGMDV	16	3-20	1	QQYGSSGGWT	10	/	/	/	/	/
36	m-SLE101CR-104	5-51	/	/	1	PKAGP	5?	1-5	3	QQYNSYSVT	9	/	/	/	/	X
37	m-SLE101CR-120#	4-59	3-22	2	4	SDSSGYYFDY	10	3-11	5	QQRSNWPPRIT	11					
38	m-SLE101CR-129	3-30	3-3	3	6	ERSLGFFGGNYYYGMDV	17	1-39	4	QQSYSTPPLT	10	/	/	/	/	X
39	m-SLE101CR-136	3-11	6-13	3	4	GERAAAGTGRLGAIDY	16	1-39	2	QQSYSTPYT	9	/	/	/	/	/
40	m-SLE101CR-153#	3-33	/	/	5	DRWEQHRDMNAFDI	14	3-15	1	QQYNNWPPWT	10					
41	m-SLE101CR-155	4-59	/	/	5	LNSLGWFDP	9	3-11	5	QQRSNWPPP	9	/	/	/	/	/
42	m-SLE101CR-166	4-34	4-17	2	4	GPPYGDYTGEDFDY	14	3-11	2	QQRSNWPPYT	10	/	/	/	/	/
43	m-SLE101CR-169	3-30	3-22	2	6	DRRGSSYSRDAFDI	15	1-5	3	QQYNSYSRT	9	/	/	/	/	X
44	m-SLE101CR-174	4-39	3-10	2	5	SYGSGSYYSVMDWFDP	16	1-27	3	QKYNSALIT	9	/	/	/	/	X
45	m-SLE101CR-175	3-30	3-16	1	4	DLTSGTRLGEFCYYFDY	17	3-11	4	QQRSNWPPLT	10	/	/	/	/	/
46	m-SLE101CR-177	4-34	2-2	3	6	GLLLRPSIVVVPAATLSPFHYYYYGMDV	28	2-28	1	MQALQTPT	8	/	/	/	/	X
47	m-SLE101CR-179	3-33	2-15	2	4	GGAGYCSGGSSYSGDY	16	3-20	4	QQYGSSPPLT	10	/	/	/	/	/
48	m-SLE101CR-180	3-30	4-17	3	3	ISSILLNPTTVTTEGDAFDI	20	3-11	3	QQRSNSFT	8	/	/	/	/	X
49	m-SLE101CR-187	4-34	5-5/5-18	3	4	GGVDTAMVSSPVRYYFDY	18	3-15	1	QQYNNWPET	9	/	/	/	/	/
50	m-SLE101CR-188	4-39	/	/	1	WIVSYEYFQH	10	1-39	2	QQSYSTPYT	9	/	/	/	/	/
51	m-SLE101CR-192#	3-48	3-22	2	5	GPRYYYDSSGYEGYNWFDP	19	1-27	3	QKYNSALFT	9					
52	m-SLE101CR-193#	4-34	4-17	2	4	GSGAYGDYDPPYFDY	15	3-20	2	QQYGSSPMYT	10					
53	m-SLE101CR-195	4-4	/	/	4	DTAGTDY	7	3-20	5	QQYGSSST	8	/	/	/	/	/
#	m-SLE101CR	VH	D	RF	JH	CDR3 (aa)	Length	Vλ	Jλ	CDR3 (aa)	Length	ssDNA	dsDNA	Insulin	LPS	HEp-2
54	m-SLE101CR-2	5-51	4-17	2	4	LHDYGDQTNFDY	12	2-23	3	CSYAGSWV	8	/	/	/	/	/
55	m-SLE101CR-3	1-46	3-22	2	6	DLVDDSSGYYYTHIYYYYGMDV	22	1-51	1	GTWDSSLSAYV	11	/	/	/	/	/
56	m-SLE101CR-6λ							2-23	2	CSYAGSSTWVV	11	/	/	/	/	/
57	m-SLE101CR-14	3-48	3-22	2	4	VRYYDSSGREAVVDY	15	3-1	2	QAWDSSPL	8	/	/	/	/	/
58	m-SLE101CR-18λ							3-1	2	QAWDSSTVV	9	X	X	X	X	X
59	m-SLE101CR-43	3-30	6-19	3	5	PDRAVAGPTMFDP	13	1-40	3	QSYDSSLSGHWV	12	/	/	/	/	/
60	m-SLE101CR-67	1-46	2-15	2	3	SGYCSGGACYIGSDAFDI	18	1-51	3	GTWDSSLSAGWV	12	/	/	/	/	X
61	m-SLE101CR-68	3-30	3-22	2	5	GVEGYYYDSSGYYGNNWFDP	20	1-40	1	QSYDSSLSGYV	11	/	/	/	/	/
62	m-SLE101CR-72#	4-31	3-3	2	6	ATDFWSGPLYAFDI	14	1-40	2	RSYDSSLSAYVV	12					
63	m-SLE101CR-81#	4-59	3-9	2	2	DLTYYDILTGYSAAYFDL	18	1-47	2	AAWDDSLSGVV	11					
64	m-SLE101CR-88#	4-31	1-26	3	3	DLPSAVGATHLGAFDI	16	3-1	1	QAWDSSTGGV	10					
65	m-SLE101CR-102	3-9	3-22	2	4	DIRYYDSSGNFDY	13	2-23	2	CPYAGSSTFVV	11	/	/	/	/	/
66	m-SLE101CR-106#	4-34	3-10	2	5	CPFGSGNDDGRGWFDP	16	1-40	3	QSYDSSLSGSV	11					
67	m-SLE101CR-114	3-9	3-22	2	3	REKRDYYDRNTKGDFDI	17	2-14	3	SSYTSSSTLWV	11	/	/	/	/	/
68	m-SLE101CR-121	3-9	3-22	2	6	DYYDSSGYFGYYGMDV	16	2-11	2	CSYAGSYTLV	10	/	/	/	/	/
69	m-SLE101CR-122	4-39	3-3	2	4	DPYYDFWSGYYTGTDY	16	2-8	1	SSYAGSNKRRV	11	/	/	/	/	X
70	m-SLE101CR-126	1-18	1-26	2	5	VGGSYYNWFDP	11	1-51	2	GTWDSSLSAGV	11	/	/	/	/	/
71	m-SLE101CR-131#	4-59	2-2	1	5	SVVVPAAIMRNWFDP	15	1-51	2	GTWDSSLSAVV	11					
72	m-SLE101CR-141	4-31	3-3	2	2	DAVRDFWSGHNWYFDL	16	2-14	1	SSYTSSSTYV	10	/	/	/	/	X
73	m-SLE101CR-142	4-61	3-3	3	4	GLGTIFGVVILRFDY	15	1-44	3	AAWDDSLNALV	11	/	/	/	/	X
74	m-SLE101CR-145	4-31	2-15	2	5	GHCSGGSSSRNNWFDP	16	1-40	3	QSYDSSLSGSV	11	/	/	/	/	X
75	m-SLE101CR-151	3-9	3-22	2	3	DFSNYYDSRGDAFDI	15	1-44	3	AAWDDSLNGWV	11	/	/	/	/	/
76	m-SLE101CR-156	3-30	3-10	3	6	GDGITMVRGVTAPYYYYGMDV	21	1-51	2	GTWDSSLSAFVV	12	/	/	/	/	/
77	m-SLE101CR-162	3-11	6-19	2	6	DSESSGWSLYYYYGMDV	17	9-49	3	GADHGSGSNFVPRV	14	/	/	/	/	/
78	m-SLE101CR-182#	4-4	2-15	2	4	DLLGYCSGGSCYYFDY	16	1-51	1	GTWDSSLSAYV	11					
79	m-SLE101CR-194	1-18	6-13/6-19	2	6	VPSTGYSRHYYYGMDV	16	3-25	2	QSADSSGTYVV	11	/	/	/	/	/

- not expressed

	Ig	HEAVY						LIGHT				REACTIVITY				
#	m-SLE122CR	VH	D	RF	JH	CDR3 (aa)	Length	Vκ	Jκ	CDR3 (aa)	Length	ssDNA	dsDNA	LPS	insulin	ANA
1	m-SLE122CR-2	3-23	4-17	2	3	DPNDYGDYVGAFDI	14	3-20	1	QQYGSSPGT	9	/	/	/	/	X
2	m-SLE122CR-6#	1-46	2-2	3	6	GVVVPDARGGMDV	13	1-16	5	QQYNSYPLT	9					
3	m-SLE122CR-15	3-30	3-10	1	2	DRFEGFGADWYFDL	14	1-5	2	QQYNSYSQACS	11	/	/	/	/	/
4	m-SLE122CR-22	3-33	2-15	2	6	GSKSGGSCDV	10	1D-33	4	QQYDNLFT	8	/	/	/	/	/
5	m-SLE122CR-25	3-7	4-17	2	6	QGVFDYYGMDV	11	1D-39	5	QQSYSTPIT	9	/	/	/	/	/
6	m-SLE122CR-28	1-69	3-16	1	6	GKGLGERYYYYGMDV	15	1D-39	4	QQSYSTLLT	9	/	/	/	/	X
7	m-SLE122CR-33	4-34	3-3	3	4	GPPRITIFGVAHIRGYFDY	19	3-20	4	QQYGSSHT	8	X	X	X	X	X
8	m-SLE122CR-35#	3-74	3-3	2	5	GVHGFWSGYYN	11	3-11	4	QQRSNWP	7					
9	m-SLE122CR-43	3-15	3-3	2	4	GTDYDFWSGYSY	12	1D-33	4	QQYDNLPLT	9	/	/	/	/	/
10	m-SLE122CR-44	1-3	3-16	1	3	DWRSGEAFDI	10	2D-29	5	MQSIQLPIT	9	/	/	/	/	/
11	m-SLE122CR-50	1-18	/	/	6	DSQGGMDV	8	1D-33	2	QQYDNLPPYT	10	/	/	/	/	/
12	m-SLE122CR-53#	1-46	6-19	2	4	VGFSSGWTNYFDY	13	1-16	4	QQYNSYPLT	9					
13	m-SLE122CR-54	3-23	6-13	2	4	SSSSSPY	7	1-5	2	QQYNSIRGT	9	/	/	/	/	/
14	m-SLE122CR-57#	4-39	3-3	2	1	TNYDFWSGYGAEYFQH	16	3-20	2	QQYGSSSCS	9					
15	m-SLE122CR-60#κ	4-34	/	/	6	GRGVPFYYYYYGMDV	15	3-11	3	QQRSNWLT	8					
16	m-SLE122CR-63	3-30	/	/	5	DSGLQPNWFDP	11	3-11	4	QQRSNWPLT	9	/	/	/	/	/
17	m-SLE122CR-64	3-11	5-24	3	5	DLGMATCG	8	2D-28	2	MQALQTPYT	9	/	/	/	/	X
18	m-SLE122CR-73#	3-7	2-2	2	6	PYCSSTRVCFDYGMDV	16	4-1	4	QQYYSTPLT	9					
19	m-SLE122CR-74	3-23	1-1	3	3	APTGAFDI	8	1-5	1	QQYNSYSGT	9	/	/	/	/	/
20	m-SLE122CR-75	3-15	/	/	4	DGAAAY	6	1-5	1	QQYNSYSPWT	10	X	X	X	X	X
21	m-SLE122CR-83	3-72	2-2	3	3	HSIVVGTFDI	10	3-15	1	QQYNNWPPWT	10	/	/	/	/	/
22	m-SLE122CR-84	3-11	6-19	2	4	GSSGWPY	7	3-11	4	QQRSNWPPLT	10	/	/	/	/	/
23	m-SLE122CR-86	3-21	6-25	2	5	GVGPMDFSG	9	2D-29	1	MQSIQLPWT	9	/	/	/	/	/
24	m-SLE122CR-90	3-23	2-2	2	3	GYCSSTSCYGAFDI	14	1-5	1	QQYNSYWT	8	/	/	/	/	/
25	m-SLE122CR-91	1-69	/	/	4	FLTSRSY	7	3-20	5	QQYGSSLIT	9	X	X	X	X	X
26	m-SLE122CR-102#	1-69	6-19	3	1	ELAVAGTEHFQH	12	1D-39	1	QQSYSTPRT	9					
27	m-SLE122CR-103	1-69	3-22	2	2	DHYYDSSGYYLYWYFDL	17	3-20	1	QQYGSSPGT	9	X	/	/	/	X
28	m-SLE122CR-109	3-11	2-2	3	5	NGDIVVVPAAPGDNWFDP	18	1-16	5	QQYNSYPPT	9	/	/	/	/	X
29	m-SLE122CR-111	3-23	3-3	3	6	VITIFDV	7	1-27	1	QKYNSAPWT	9	X	X	X	X	X
30	m-SLE122CR-114	4-34	3-16	1	3	GRIHLGELSLPAFDI	15	2D-28	1	MQALQTPRT	9	/	/	/	/	X
31	m-SLE122CR-116	3-53	6-19	3	4	GTHIAVAGTLDY	12	1-9	4	QQLNSYLLT	9	X	X	X	X	X
32	m-SLE122CR-117#	1-69	6-19	2	5	DRIAAAEGWFDP	11	2D-30	4	MQGTHWPLT	9					
33	m-SLE122CR-119#	1-8	6-19	3	6	GTVALGV	7	2-29	1	MQGIHLPPGT	10					
34	m-SLE122CR-121#	3-7	2-2	3	6	EGIVVVPAALPLDV	14	3-15	2	QQYNNWPSYT	10					
35	m-SLE122CR-125	3-53	5-12	3	5	GIVGAGVGWFDP	12	1-5	1	QQYNSYPWT	9	/	/	/	/	/
36	m-SLE122CR-126	3-23	3-22	2	4	GASSGYHANY	10	1D-33	3	QQYDNLPPT	9	/	/	/	/	/
37	m-SLE122CR-134	3-48	/	/	5	PKGPG	5	1D-33	4	QQYDNLPLT	9	/	/	/	/	/
38	m-SLE122CR-136κ	3-9	3-16	3	6	DIGGVVDYGMDV	12	3D-7	4	QQDYNLLG	8	/	/	/	/	/
39	m-SLE122CR-143	3-15	6-13	2	4	VGYSSSWKYFDY	12	3-11	2	QQRSS	5	/	/	/	/	/
40	m-SLE122CR-145	4-31	3-22	2	4	GAYYYDSSGYGGIGDY	16	2D-28	2	MQALQTPYT	9	/	/	/	/	X
41	m-SLE122CR-152	3-23	3-22	3	6	DPDTMIVVEDV	11	1D-39	5	QQSYSTPSIT	10	/	/	X	/	/
42	m-SLE122CR-155	3-23	4-23	3	4	KGWGLTVVTPLDY	13	2D-28	3	MQALQTPFT	9	/	X	X	/	/
43	m-SLE122CR-156	4-61	1-7	2	4	DSNWNYGVDP	10	1-16	4	QQYNSYPLT	9	/	/	/	/	/
44	m-SLE122CR-158	3-30	1-20	3	4	DITSGSLDY	9	1D-39	5	QQSYSTPIT	9	/	/	/	/	/
45	m-SLE122CR-159	4-34	4-23	2	4	CGNCYSGRFDY	11	3-15	5	QQYNNWPPIT	10	/	/	/	/	/
46	m-SLE122CR-161#	3-33	4-17	2	4	GDYGDH	6	4-1	1	QQYWGTLWT	9					
47	m-SLE122CR-164	3-21	1-20	2	3	GDWNHDAFDI	10	1-5	2	QQYNSYLYT	9	/	/	/	/	/
48	m-SLE122CR-166#	3-49	6-6	3	4	ARATSEY	7	3-15	4	QQYNNWPLT	9					
49	m-SLE122CR-167	5-51	2-2	2	1	DVGYCSSTSCDRYFQH	16	3-20	4	QQYGSSLT	8	/	/	/	/	X
50	m-SLE122CR-170	4-31	6-6	2	6	SSSSRNYYGMDV	12	1-17	5	LQHNSYPIT	9	/	X	/	/	X
51	m-SLE122CR-178	4-34	/	/	4	PFLPGAKGPFDY	12	1D-39	4	QQSYSTLALT	10	/	/	X	/	X
52	m-SLE122CR-182#	1-18	2-2	3	5	GGIVVVPALNWFDP	14	2D-28	4	MQALQTPLT	9					
53	m-SLE122CR-183#	3-53	5-12	3	3	HRVDVDIVATGAFDI	15	1D-33	5	QQYDNLPPIT	10					
54	m-SLE122CR-185#	5-51	3-22	2	3	PPGYYDSSGYVAFDI	15	3-20	1	QQYGSSPGT	9					
55	m-SLE122CR-187#	5-51	1-7	3	4	HITGTTPPHFDY	12	3-20	2	QQYGSSPPLCS	11					
56	m-SLE122CR-190#	3-53	6-13	3	1	VGAAAGTVEYFQH	13	2-29	5	MQGIHLLIT	9					
#	m-SLE122CR	VH	D	RF	JH	CDR3 (aa)	Length	Vλ	Jλ	CDR3 (aa)	Length	ssDNA	dsDNA	LPS	insulin	ANA
57	m-SLE122CR-1	3-15	3-3	3	5	DPTIFGVVP	9	1-44	2	AAWDDSLNVV	10	X	X	X	X	X
58	m-SLE122CR-14#	3-23	2-2	2	4	SPRGCSTSCYPDY	13	2-23	2	CSYAGSSPL	9					
59	m-SLE122CR-17	4-4	3-3	3	4	DRITIFGVVIIYFDY	15	1-44	1	AAWDDSLNGYV	11	/	/	/	/	X
60	m-SLE122CR-29#	3-15	/	/	2	FGLAASYWYFDL	12	3-21	3	QVWDSSSDHPV	11					
61	m-SLE122CR-37	1-2	2-2	2	6	DCSSTSCYYGMDV	13	2-8	1	SSYAGSNGNV	10	/	/	/	/	/
62	m-SLE122CR-52	3-30	3-22	2	4	DRPRDYYGSGSHFDY	15	2-11	2	CSYAGREDVV	10	/	/	/	/	/
63	m-SLE122CR-60λ							2-8	1	SSYAGSNNPYV	11					
64	m-SLE122CR-112#	4-31	3-16	2	4	ASGEIYDYIWGTYYFDY	17	2-23	1	CSYAGSYV	8					
65	m-SLE122CR-136λ							2-11	1	CSYAGSLYV	9	/	/	/	/	X
66	m-SLE122CR-142#	3-49	2-2	3	6	VVIVLVPAAPYYYGMDV	17	2-28	2	SSYAGSNNSGV	11					
67	m-SLE122CR-150	1-18	2-21	2	1	AYCGGDCYWDFQH	13	6-57	2	QSYDSSNKVV	10	/	/	/	/	/
68	m-SLE122CR-162	3-11	/	/	4	DRDYFDY	7	1-44	2	AAWDDSLNGPV	11	/	/	/	/	/
69	m-SLE122CR-163	1-69	2-2	3	6	DIAKRYYYYGMDV	13	2-11	3	CSYAGSYTP	9	X	X	X	X	X
70	m-SLE122CR-169#	4-39	2-2	3	5	SHIVVVPARFDP	12	2-23	1	CSYAGSSTPFV	11					
71	m-SLE122CR-175#	1-2	2-2	1	4	HQLLSEGTLDY	11	2-8	2	SSYAGSNNSV	10					
72	m-SLE122CR-189	3-49	1-26	3	4	EGIVGATCFDY	11	3-21	2	QVWDSSSDHVV	11	/	/	/	/	/

- not expressed

	Ig	HEAVY						LIGHT				REACTIVITY				
#	m-SLE14CR	VH	D	RF	JH	CDR3 (aa)	Length	Vκ	Jκ	CDR3 (aa)	Length	ssDNA	dsDNA	Insulin	LPS	HEp-2
1	m-SLE14CR-1	1-69	5-18	3	5	DLSGYSYGPNWFDP	14	1D-39	1	QQSYSTPRT	9	X	X	X	X	X
2	m-SLE14CR-8	3-23	1-26	3	4	EEGVGALFDY	10	3-15	2	QQYNNWPPYT	10	/	/	/	/	/
3	m-SLE14CR-20	4-4	5-24	3	4	DPGDGYNWRGPFDY	14	3-20	1	QQYGSSPWT	9	/	/	/	/	X
4	m-SLE14CR-26	3-21	1-26	3	6	DAGSYSNPGYYYGMDV	16	1-27	1	QKYNSAPRT	9	/	/	/	/	X
5	m-SLE14CR-27	3-23	3-16	2	4	RDPFGVD	7	1-17	4	LQHNSYPLT	9	X	X	X	X	X
6	m-SLE14CR-32	1-18	3-3	2	4	GRESDFWSGIYYFDY	15	1D-39	1	QQSYSTPQT	9	/	/	/	/	/
7	m-SLE14CR-36	3-23	/	/	4	VHY	3	3-20	1	QQYGSSLWT	9	X	X	X	X	/
8	m-SLE14CR-49	4-4	3-9	3	5	DGPPGKNYEKRNWFDP	16	1D-39	3	QQSYSTLFT	9	/	/	/	/	/
9	m-SLE14CR-51	1-46	1-26	3	3	DVGSGSKDAFDI	12	1D-39	1	QQSYSTPRT	9	/	/	/	/	/
10	m-SLE14CR-55	3-7	3-3	1	4	YYDFWSGYRYFDY	13	1D-39	4	QQSYSTSLT	9	/	/	/	/	/
11	m-SLE14CR-59	4-34	2-15	1	4	YGARGAGSGGSCYDY	15	3-20	1	QQYGSSPRT	9	X	X	X	X	X
12	m-SLE14CR-62#	3-30	6-19	2	4	AVGAHYSSADY	11	1-16	4	QQYNSYPLT	9					
13	m-SLE14CR-64	1-69	6-19	2	4	VYYSSGWYGADY	12	2D-28	4	MQALQTPLT	9	/	/	/	/	/
14	m-SLE14CR-65#	1-69	3-10	3	6	WYYYGSGSYYDGDSYYYGMDV	21	3-20	3	QQRSNWPPRG	10					
15	m-SLE14CR-69	3-53	/	/	5	EAR	3	1D-33	2	QQYDNLPNT	9	/	/	/	/	/
16	m-SLE14CR-70	1-69	3-22	3	4	ERSNYYDSSGYYELGY	16	1D-39	2	QQSYSTPLYT	10	/	/	/	/	X
17	m-SLE14CR-74#	4-31	3-3	2	6	AVDWSRKYYYYGMDV	15	3-11	5	QQRSNWPVIT	10					
18	m-SLE14CR-78	3-21	5-12	3	6	DRGGGGYLSGYYGMDV	16	1D-39	3	QQSYSTIFT	9	X	X	X	X	X
19	m-SLE14CR-82	4-39	4-17	3	4	PYGYSAD	7	1-27	5	QKYNSAVIT	9	/	/	/	/	/
20	m-SLE14CR-85	1-18	/	/	4	DRGDGYYFDY	10	3-20	1	QQYGSSPRT	9	/	/	/	/	/
21	m-SLE14CR-87#	1-24	4-11	2	5	VDYSPRNWFDP	11	3-20	1	QQYGSSPPT	9					
22	m-SLE14CR-89	3-23	6-13	2	3	VALLRTSSSWFNDAFDI	17	3-20	1	QQYGSSPPWT	10	X	/	X	/	/
23	m-SLE14CR-91	3-23	2-15	2	4	GGVCDGSCYSYYFDY	15	1-27	3	QKYNSAPLFT	10	/	/	/	/	/
24	m-SLE14CR-101	3-30	3-10	3	4	GRFGELLGYAYYFDY	15	3-15	2	QQYNNWPPYT	10	X	X	X	X	X
25	m-SLE14CR-113	1-2	3-10	2	4	KDYGSGSYFFDY	12	2D-28	1	MQALQTPWT	9	/	/	/	/	/
26	m-SLE14CR-121	4-61	1-26	3	4	DLVGAILFDY	10	3-15	2	QQYNNWPP	9	/	/	/	/	/
27	m-SLE14CR-144#	3-15	6-19	3	4	DKRVGAVAGIRFFDY	15	1D-39	1	QQSYSTPWT	9					
28	m-SLE14CR-145	3-7	4-23	2	5	GTHYGGNWFDP	11	1D-39	1	QQSYSTQWT	9	/	/	/	/	/
29	m-SLE14CR-151#	1-18	5-18	1	6	QGQLWLLYYGMDV	13	1D-39	5	QQSYSTPIT	9					
30	m-SLE14CR-153#	3-23	3-22	3	4	DGDNYYDSSGYYY	13	3-11	4	QQRSNWPPLT	10					
31	m-SLE14CR-154	1-18	3-22	3	4	DWFSYYDSSGYIPYFDY	17	1D-39	3	QQSYSTPR	8	/	/	/	/	X
32	m-SLE14CR-162	3-23	/	/	4	GSQLAPRSCDY	11	2D-28	2	MQALQTPRT	9	/	/	/	/	X
33	m-SLE14CR-165	1-2	3-22	2	4	APYYYDSSGYYY	12	1-27	1	QKYNSAPWT	9	/	/	/	/	/
34	m-SLE14CR-166	3-53	3-9	2	5	ADFDWLLSS	9	3-15	2	QQYNNWPPYT	10	/	/	/	/	/
35	m-SLE14CR-171	4-34	6-19	3	4	GGRQWLVPYSPFDY	14	1-17	5	LQHNSYPIT	9	X	X	X	X	X
36	m-SLE14CR-172	3-15	/	/	4	DGDYNSAVGDY	11	1D-39	3	QQSYSTPFT	9	X	X	X	X	X
37	m-SLE14CR-176	3-53	/	/	6	DSDPTGYYYYYGMDV	15	1D-39	1	QQSYSTPPT	9	/	/	/	/	X
38	m-SLE14CR-179	3-30	2-8	3	6	GLGMVYATTYGMDV	14	2D-28	3	MQALQTPFT	9	/	/	/	/	/
39	m-SLE14CR-182#	3-11	6-13	1	4	YIDIAAARGGFDY	13	1D-39	4	QQSYSTPT	8					
40	m-SLE14CR-188	3-23	3-3	3	4	GTFYYDFWTGPFDY	14	3-20	3	QQYGSSPPT	9	/	/	/	/	/
41	m-SLE14CR-191	3-23	5-18	1	4	TPPIGTAMARAYFDY	15	3-15	2	QQYNNWPYT	9	/	/	/	/	/
#	m-SLE14CR	VH	D	RF	JH	CDR3 (aa)	Length	Vλ	Jλ	CDR3 (aa)	Length	ssDNA	dsDNA	Insulin	LPS	HEp-2
42	m-SLE14CR-15	3-21	6-19	3	4	VGGEGYSSGWYTLDY	15	2-11	3	CSYAGSYTVWV	11	/	/	/	/	/
43	m-SLE14CR-18#	1-69	2-2	1	6	EPYCSSTSCYTTGYYGARYYYYGMDV	26	2-8	3	SSYAGSNNWV	10					
44	m-SLE14CR-30	4-34	/	3	4	GHYFDY	6	2-14	3	SSYTSSSTWV	10	/	/	/	/	/
45	m-SLE14CR-40#	1-24	6-6	1	5	VRPDFHSSPYSARFDP	16	2-23	1	CSYAGSSTYV	10					
46	m-SLE14CR-41#	3-23	2-15	1	4	VDFIVVVVAAQFDY	14	1-40	1	QSYDSSLSGYV	11					
47	m-SLE14CR-42	4-34	6-19	2	5	IPTPGIAVAGKGGHNNWFDP	20	1-40	2	QSYDSSLSGSV	11	/	/	/	/	/
48	m-SLE14CR-73	3-48	5-18	1	4	DRGYSYKGDY	10	1-44	3	AAWDDSLSNWV	11	/	/	/	/	/
49	m-SLE14CR-92#	3-48	6-19	1	5	DGTSGWSVH	9	1-47	2	AAWDDRRVV	9					
50	m-SLE14CR-106	3-73	2-21	3	4	PVVTGPDY	8	1-47	3	AAWDDSLSAWV	11	X	X	X	X	X
51	m-SLE14CR-137	4-4	3-22	3	5	DGDYDSSGYYSSNWFDP	17	2-14	2	SSYTSSSTRV	10	/	/	/	/	/
52	m-SLE14CR-167	3-23	3-22	1	2	AYYYDSSGYYLATPKKADWYFDL	23	1-40	1	QSYDSSLSGYV	11	/	/	/	/	/

- not expressed

	Ig	HEAVY						LIGHT				REACTIVITY				
#	m-SLE21CR	VH	D	RF	JH	CDR3 (aa)	Length	Vκ	Jκ	CDR3 (aa)	Length	ssDNA	dsDNA	Insulin	LPS	HEp-2
1	m-SLE21CR-8	4-39	2-2	3	5	GRDIVVVPAAPSNWFDP	17	1D-39	2	QQSYSTLYT	9	/	/	/	/	/
2	m-SLE21CR-19	4-34	/	/	3	LLEDAFDI	8	3-20	4	QQYGSSLFT	9	/	/	/	/	/
3	m-SLE21CR-34	3-21	5-18	2	4	VSNTAMVFDY	10	3-15	2	QQYNNWRGT	9	/	/	/	/	/
4	m-SLE21CR-41	3-48	3-10	3	6	DQLLWFGESPYYYGMDV	17	3-20	4	QQYGSSPPLT	10	/	/	/	/	/
5	m-SLE21CR-43	3-15	1-26	3	3	KWELLRDAFDI	11	3-20	4	QQYGSSLT	8	/	/	/	/	/
6	m-SLE21CR-47	4-59	7-27	2	4	GGNWGFYDY	9	1-39	1	QQSYSTPPET	10	/	/	/	/	/
7	m-SLE21CR-50	4-4	3-3	3	4	GFLGARKKGAYFDY	14	3-20	3	QQYGSSLFT	9	X	X	X	X	X
8	m-SLE21CR-58	4-39	3-10	2	4	PMVRGVRGGDDY	12	1-17	1	LQHNSYPWT	9	/	/	/	/	X
9	m-SLE21CR-63	3-49	3-22	3	6	GYYDSSGYYLDYYYYGMDV	19	1-39	2	QQSYSTPHT	9	/	/	/	/	/
10	m-SLE21CR-68	4-4	/	/	2	ASQGYFDL	8	1-5	1	QQYNSYWT	8	X	X	X	X	X
11	m-SLE21CR-70	4-34	2-2	3	3	GWYCSSTSCYEDAFDI	16	4-1	1	QQYYSTPPT	9	/	/	/	/	/
12	m-SLE21CR-76	4-34	3-22	3	4	RTYYYDSSGYSFNY	14	1-9	3	QQLNSYPLT	9	/	/	/	/	/
13	m-SLE21CR-79	3-15	3-22	3	4	EDSKSHYYDSSGYQDY	16	3-11	2	QQRSNWPPYT	10	/	/	/	/	/
14	m-SLE21CR-89	4-34	2-8	3	4	DSGTMVYADFDY	12	1-39	2	QQSYSTLLYT	10	/	/	/	/	/
15	m-SLE21CR-94	3-48	/	/	3	LSRDDAFDI	9	3-11	4	QQRSNWLT	8	/	/	/	/	/
16	m-SLE21CR-102	3-30	/	/	4	ASFRSFDY	8	3-20	1	QQYGSSPWT	9	X	X	X	X	X
17	m-SLE21CR-105#	3-20	/	/	6	VLGGSGYGMDV	11	1-39	1	QQSYSTLRT	9					
18	m-SLE21CR-111	3-48	/	/	6	VRGYYGMDV	9	1-16	3	QQYNSYPLT	9	/	/	/	/	/
19	m-SLE21CR-131	3-30	1-26	2	6	GPLVGATLYSGYYGMDV	17	1-39	2	QQSYSTPYT	9	/	/	/	/	/
20	m-SLE21CR-140	1-69	5-18	1	6	SRIPRKTDRGYSYGEYYYYYYMDV	24	3-20	4	QQYGSSPPVT	10	X	X	X	X	X
21	m-SLE21CR-141	4-39	6-19	2	1	QKPGYSSGWVRRVAEYFQH	19	3-15	1	QQYNNWPPLGT	11	X	X	X	X	X
22	m-SLE21CR-144	4-31	2-2	2	3	FVVVAAFDI	9	2-40	2	MQRPESRVLRRT	12	/	/	/	/	/
23	m-SLE21CR-153	3-33	/	/	6	DELHQGIYYYGMDV	14	3-20	4	QQYGSSLT	8	/	/	/	/	/
24	m-SLE21CR-155	4-59	1-26	3	2	SVGATSRYFDL	11	4-1	4	QQYYSTLLT	9	X	X	X	X	X
25	m-SLE21CR-160	4-34	5-24	3	6	GVEEMATIEAVYMDV	15	1-39	3	QQSYSTPS	8	/	/	/	/	/
26	m-SLE21CR-162	4-59	5-18	1	3	DTVDTAMAPDAFDI	14	3-11	3	QQRSNWPPV	9	/	/	/	/	/
27	m-SLE21CR-173#	3-11	6-13	1	5	GDFIAAAGSKGLFDP	15	3-15	4	QQYNNWPLT	9					
28	m-SLE21CR-186#	1-18	/	/	4	DPQLGDFDY	9	1-5	2	QQYNSYT	7					
29	m-SLE21CR-188	3-7	2-2	1	6	VFEYCSSTSCFDYYYGMDV	19	1-39	1	QQSYSTPWT	9	/	/	/	/	/
30	m-SLE21CR-193	4-34	1-26	1	3	SWELLSPDAFDI	12	4-1	2	QQYYSTLYT	9	/	/	/	/	/
#	m-SLE21CR	VH	D	RF	JH	CDR3 (aa)	Length	Vλ	Jλ	CDR3 (aa)	Length	ssDNA	dsDNA	Insulin	LPS	HEp-2
31	m-SLE21CR-59	1-69	/	/	6	GLTKRPHYYYYMDV	14	2-14	2	SSYTSSSTLVV	11	X	X	X	X	/
32	m-SLE21CR-64	3-15	4-17	3	4	DRIGRGPELAATVTYKVDY	19	3-22	3	LSGDEDNPRV	10	/	/	/	/	/
33	m-SLE21CR-78	5-51	1-26	3	4	HSEGVGATPYFDFDY	15	1-40	3	QSYDSSLSGV	10	/	/	/	/	/
34	m-SLE21CR-82#	4-34	/	/	4	RRRAKIIDY	9	1-51	3	GTWDSSLSVWV	11					
35	m-SLE21CR-86	3-23	6-13	2	1	DRNPIIAAAGTAEYFQH	17	1-51	3	GTWDSSLSAGV	11	/	/	/	/	X
36	m-SLE21CR-107	1-2	1-26	3	5	GGSYLYNWFDP	11	2-11	1	CSYAGSYTSYV	11	/	/	/	/	/
37	m-SLE21CR-125	4-59	/	/	6	ERSSYRSCYMDV	12	1-51	3	GTWDSSLSAEV	11	X	X	X	X	X
38	m-SLE21CR-128	3-49	6-19	3	4	GGDSGWYVVPDY	13	2-8	3	SSYAGSNNSGV	11	/	/	/	/	/
39	m-SLE21CR-136	1-18	6-19	2	5	VEAVAGSNWFDP	12	1-44	2	AAWDDSLNGLV	11	/	/	/	/	/
40	m-SLE21CR-138	1-69	6-13	2	4	GSLQQPSDYDY	11	1-40	2	QSYDSSLSGWDVV	13	/	/	/	/	/
41	m-SLE21CR-142	3-66	3-16	3	4	DQLLGGVADDY	11	1-47	3	AAWDDSLSGRV	11	/	/	/	/	/
42	m-SLE21CR-149	3-48	/	/	6	VDYYYYYGMDV	11	2-11	2	CSYAGSYTLV	10	/	/	/	/	X
43	m-SLE21CR-154	4-31	6-13	2	5	GAEQQLDANWFDP	13	2-14	3	SSYTSSSSWV	10	/	/	/	/	/
44	m-SLE21CR-168	4-28	/	/	4	ANPPVDY	7	2-14	3	SSYTSSSTWV	10	/	/	/	/	/
45	m-SLE21CR-174	1-2	2-2	2	5	GGARQLLWTLANWFDP	16	2-14	1	SSYTSSSTLNYV	12	X	X	X	X	X
46	m-SLE21CR-181	3-73	1-26	3	4	HGVVGATTNFDY	12	1-40	3	QSYDSSLSGSV	11	/	/	/	/	/
47	m-SLE21CR-183	3-48	/	/	3	APRFGSWFASDAFDI	15	1-47	2	AAWDDSLSGPCVV	13	/	/	/	/	/
48	m-SLE21CR-190#	4-34	6-6	1	4	RIAARPGNFDY	11	2-14	2	SSYTSSSTLVV	11					
49	m-SLE21CR-192	3-23	3-3	2	5	DLNHAYYDFWSGYHA	15	2-23	1	CSYAGYWNV	9	/	/	/	/	/
50	m-SLE21CR-194	1-24	3-10	3	5	EGLLLWFLGGFDP	13	2-23	3	CSYAGSSSRV	10	/	/	/	/	/

- not expressed

	Ig	HEAVY						LIGHT				REACTIVITY				
#	m-SLE33CR	VH	D	RF	JH	CDR3 (aa)	Length	V_K	J_K	CDR3 (aa)	Length	ssDNA	dsDNA	Insulin	LPS	HEp-2
1	m-SLE33CR-3#	1-18	3-3	3	4	DPGITIFGVVIIPVLYFDY	19	3-20	1	QQYGSSRGT	9					
2	m-SLE33CR-4	4-59	6-6	3	2	DAGIAARNYYYYYMDV	16	1D-39	1	QQSYSTPRT	9	/	/	/	/	X
3	m-SLE33CR-5#	3-53	6-19	3	4	PPGYSSGWDYLDY	13	3-11	1	QQRSNWPWT	9					
4	m-SLE33CR-6	4-4	6-25	3	6	VLRVGRSGWSPGFEDYYYYMDV	22	1-5	1	QQYNSYSWT	9	X	X	X	X	X
5	m-SLE33CR-7#	3-53	2-2	3	5	GLGYCSSTSCVNWFDP	16	1D-33	5	QQYDNLPLT	9					
6	m-SLE33CR-9	3-9	3-9	1	4	DEGYDILTGYFDY	13	1D-39	2	QQSYSTMYT	9	/	/	/	/	/
7	m-SLE33CR-11	5-51	6-25	1	3	GQVAGSAFDI	10	1D-39	1	QQSYSTLWT	9	/	/	/	/	/
8	m-SLE33CR-13	3-11	3-10	2	5	DEGMVRGVHP	10	1-9	4	QQLNSYPRIT	10	/	/	/	/	X
9	m-SLE33CR-17#	3-7	3-3	3	6	DRVLEWPRNGYYYYMDV	17	3-11	5	QQRSNWPPIT	10					
10	m-SLE33CR-18	1-18	3-22	3	4	GDSSGYYASDY	11	4-1	4	QQYYSTPLT	9	/	/	/	/	/
11	m-SLE33CR-21	3-48	4-17	1	4	WHGDPYFDY	9	1-6	1	LQDYNYPWT	9	/	/	/	/	/
12	m-SLE33CR-22	4-59	2-2	1	6	RGVVPAANSYYYYYYMDV	18	1D-39	1	QQSYSTPQT	9	/	/	/	/	/
13	m-SLE33CR-25#	3-53	/	/	4	EKSTVRIVGGGESDY	15	4-1	2	QQYYSTPGYT	10					
14	m-SLE33CR-26	3-30	3-16	2	4	DQGWDYVWGSYRYTAFDY	18	4-1	2	QQYYSTSYT	9	/	/	/	/	/
15	m-SLE33CR-31	4-59	2-2	2	6	EGPIVVVPADNL	12	4-1	4	QQYYSTPLT	9	/	/	/	/	/
16	m-SLE33CR-32	3-30	3-10	2	4	DGSRYGSGSYYSNY	14	1-5	1	QQYGT	5	X	X	X	X	X
17	m-SLE33CR-34	4-59	2-2	3	4	IVRPRYCSSTSCYIMDY	17	1D-39	4	QQSYSTPLT	9	/	/	/	/	/
18	m-SLE33CR-35	3-7	3-10	2	4	DGRPAVGRSPRASGEFDY	18	2-30	2	MQGTHWPPYT	10	X	X	X	X	X
19	m-SLE33CR-40	4-59	6-13	3	6	VSSIAAAGTFDYYYYYMDV	19	1D-39	4	QQSYSTLLT	9	/	/	/	/	X
20	m-SLE33CR-43	3-53	4-17	2	4	ADYGDFFDY	9	3-15	2	QQYNNWPPYT	10	/	/	/	/	/
21	m-SLE33CR-48	3-23	4-17	3	3	DRSTVTTRNAFDI	13	1-27	3	QKYNSAPFT	9	/	/	/	/	/
22	m-SLE33CR-53	4-34	3-10	2	5	GIKDYYGSGSYYMMSRAASGRFDP	24	1D-39	4	QQSYSTRGLT	10	X	X	X	X	X
23	m-SLE33CR-57	1-2	1-1	3	4	GANWNDKSDY	10	1D-39	1	QQSYSTPHT	9	/	/	/	/	/
24	m-SLE33CR-73#	3-23	6-13	2	4	DGDSSSWYGGN	11	2-29	4	MQGIHLPLT	9					
25	m-SLE33CR-75#	3-13	/	/	3	MRGGAFDI	8	1D-33	2	QQYDNLPYT	9					
26	m-SLE33CR-76	4-59	6-6	1	6	LGGGYSSSSWVGYYYYYYMDV	21	3-20	4	QQYGSSLT	8	/	/	/	/	X
27	m-SLE33CR-79	3-21	1-26	2	4	DQEGVGATIDY	11	4-1	2	QQYYSTLYT	9	/	/	/	/	/
28	m-SLE33CR-85	3-7	5-12	2	6	EAHSGYETYYYYYYYMDV	18	3-20	2	QQYGSSPRMYT	11	/	/	/	/	/
29	m-SLE33CR-94	3-21	2-2	1	5	SPSHHIVVVPAASFYVGNWFDP	22	3-15	2	QQYNNWPYT	9	/	/	/	/	X
30	m-SLE33CR-96	1-8	3-3	2	5	GTVYYDFWSGSQGGLGWFDP	20	1D-39	2	QQSYSTPLYT	10	/	/	/	/	X
31	m-SLE33CR-101#	3-66	/	/	4	DRYYLDY	7	1D-39	2	QQSYSTRMYT	10					
32	m-SLE33CR-103	3-23	4-11	2	4	PRRVTTFAY	9	3-20	2	QQYGSSPSMYT	11	/	/	/	X	X
33	m-SLE33CR-105#	3-21	3-10	2	4	DRDGYYGSGSYYLDY	15	1-8	4	QQYYSYPLT	9					
34	m-SLE33CR-108	3-13	6-6	2	6	YSSSGHYMDV	10	1D-39	1	QQSYSTPWT	9	/	/	/	/	/
35	m-SLE33CR-114#	3-23	3-10	1	4	SLEMGYYGSGSPSDY	15	1-27	1	QKYNSAPRT	9					
36	m-SLE33CR-125#	3-23	6-19	3	4	KESSGWRSSVDY	12	1-17	2	LQHNSYPYT	9					
37	m-SLE33CR-129#	3-21	2-2	3	4	PGQLLYAGFDY	11	1D-39	2	QQSYSTRRYT	10					
38	m-SLE33CR-139	1-18	3-3	2	6	DTDDYDFWSDHYYYYMDV	18	2-28	1	MQALQTPRT	9	/	/	/	/	/
39	m-SLE33CR-141	4-34	6-19	1	2	SEGWYPEDWYFDL	13	1-5	4	QQYNSYSRT	9	/	/	/	/	/
40	m-SLE33CR-149#	4'54	5-18	1	6	SPGVRSGYSYGYYYYYMDV	19	3-11	4	QQRSNWLT	8					
41	m-SLE33CR-151	3-49	3-10	2	4	APTVLLWFGDFFDY	14	1D-39	1	QQSYSTAWT	9	X	X	X	X	X
42	m-SLE33CR-161	4-39	3-3	3	4	RFGWSGYPFDY	11	1D-39	1	QQSYSTPWT	9	/	/	/	/	X
43	m-SLE33CR-177	3-48	/	/	4	DREDPVGETVVY	12	2D-29	1	MQSIQLPWT	9	/	/	/	/	/
44	m-SLE33CR-208#	3-21	3-3	2	4	DARSWSGYPRGDFDY	15	1D-39	2	QQSYSTPQT	9					
45	m-SLE33CR-214	3-64	/	/	3	RGGTTLGSAFDI	12	1-9	2	QQLNSYPPYT	10	/	/	/	/	X
46	m-SLE33CR-220	3-23	5-12	2	6	DIVATVDYYYMDV	13	3-20	1	QQYGSSPWT	9	/	/	/	/	/
47	m-SLE33CR-228	3-53	5-12	2	3	DLLYPGYSWFYAFDI	15	3-20	2	QQYGSSPPYT	10	/	/	/	/	/
48	m-SLE33CR-232#	4-34	/	/	6	GRVLYYYYMDV	11	3-20	2	QQYGSSLYT	9					
49	m-SLE33CR-244	3-23	3-9	3	4	DAPFDLTGYPFDY	13	1-17	2	LQHNSYLYT	9	/	/	/	/	/
50	m-SLE33CR-254#	4-4	6-19	2	3	EIYSSGWSTDDAFDI	15	1-27	1	QKYNSAPCT	9					
51	m-SLE33CR-255	4-34	4-23	3	4	VGYGGNSGGLDY	12	1D-33	4	QQYDNLPLT	9	/	/	/	/	/
52	m-SLE33CR-263	3-48	2-2	1	4	NGYCSSTSCYTGMGY	15	1-8	1	QQYYSYPWT	9	X	X	X	X	X
53	m-SLE33CR-266#	1-24	6-13	1	4	KVHSSSWYFPFSDY	14	4-1	5	QQYYSTPPT	9					
54	m-SLE33CR-281	4-4	/	/	5	GLPFDP	6	2-28	2	MQALQTPPYT	10	/	/	/	/	/

#	m-SLE33CR	VH	D	RF	JH	CDR3 (aa)	Length	Vλ	Jλ	CDR3 (aa)	Length	ssDNA	dsDNA	Insulin	LPS	HEp-2
55	m-SLE33CR-14#	1-8	2-2	1	6	RDCSSTSCHEGHGYYYYYYMDV	22	2-8	3	SSYAGSNNWV	10					
56	m-SLE33CR-42#	4-34	5-12	1	6	ARGYSGYGSVYLDV	14	1-51	2	GTWDSSLSAVV	11					
57	m-SLE33CR-93#	3-11	5-18	2	6	DLRRSEQLWVYYYYMDV	17	8-61	1	VLYMGSGLYV	10					
58	m-SLE33CR-109	1-18	4-17	2	4	DRSRGLLLDY	10	6-57	2	QSYDSSNVV	9	/	/	/	/	/
59	m-SLE33CR-157	4-34	/	/	6	RGEKSRAPKRSHYYYYYMDV	20	2-14	3	SSYTSSSTV	9	X	X	X	X	X
60	m-SLE33CR-203#	4-34	1-26	2	4	GRGGSYYFN	9	1-47	2	AAWDDSLSGVV	11					
61	m-SLE33CR-206	1-2	3-10	1	4	DPASYGSGSPTVDY	14	2-14	3	SSYTSSSTWV	10	/	/	/	/	X
62	m-SLE33CR-217	3-21	3-10	3	4	HTLKTYYYGSGDGY	14	4-69	3	QTWGTGIRV	9	X	X	X	X	X
63	m-SLE33CR-221	3-74	6-13	2	5	GGSSSWEAWFDP	12	1-47	1	AAWDDSLSGYV	11	/	/	/	/	X