Figure 1

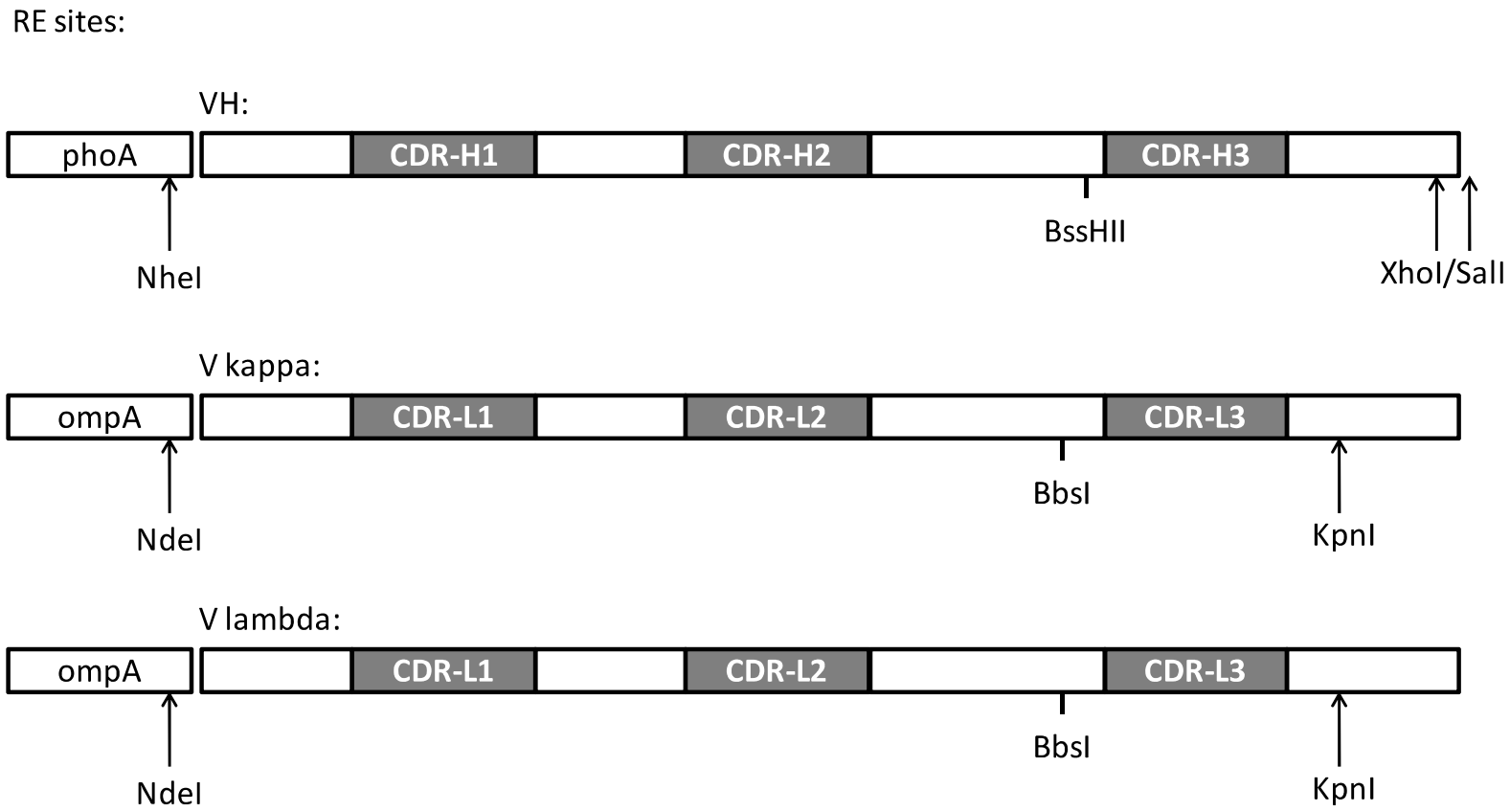

RE sites:
VH:
phoA
CDR-H1
CDR-H2
CDR-H3
NheI
BssHII
XhoI/SalI
V kappa:
ompA
CDR-L1
CDR-L2
CDR-L3
NdeI
BbsI
KpnI
V lambda:
ompA
CDR-L1
CDR-L2
CDR-L3
NdeI
BbsI
KpnI

Figure 2

Summary 20 VH region genes

		CDR lengths									Epibase check			Aggresolve
	Heavy chain germline genes	**Kabat CDR-H1**	**Kabat CDR2-H2**	**VNTI pI**	**Ranking pos**	**PTMs** (w/o NxS/T)	**NxS/T**	**Met in CDRs**	**Cysteine** (to be removed)		**Deviations from germline**	**Strong T-cell epitope**		**Theoretical aggregation propensity**
1	hVH_1_2	**5**	**17**	**9.4**	**14**	**2**	**0**	**1**	**0**		**0**	**0**		intermediate
2	hVH_1_18	**5**	**17**	**9.2**	**9**	**2**	**0**	**0**	**0**		**0**	**0**		**high**
3	hVH_1_69	**5**	**17**	**9.3**	**7**	**0**	**0**	**0**	**0**		**0**	**0**		intermediate
4	hVH_1_46	**5**	**17**	**9.2**	**21**	**0**	**0**	**1**	**0**		**0**	**0**		n.d.
5	hVH_3_7	**5**	**17**	**8.6**	**8**	**4**	**0**	**1**	**0**		**0**	**0**		low
6	hVH_3_11	**5**	**17**	**9.0**	**17**	**2**	**0**	**1**	**0**		**0**	**0**		n.d.
7	hVH_3_15	**5**	**19**	**9.0**	**12**	**3**	**0**	**1**	**0**		**0**	**0**		low
8	hVH_3_21	**5**	**17**	**9.0**	**11**	**3**	**0**	**1**	**0**		**0**	**0**		intermediate
9	hVH_3_23	**5**	**17**	**8.7**	**1**	**3**	**0**	**1**	**0**		**0**	**0**		intermediate
10	hVH_3_30	**5**	**17**	**9.3**	**2**	**4**	**0**	**1**	**0**		**0**	**0**		intermediate
11	hVH_3_33	**5**	**17**	**9.3**	**15**	**4**	**0**	**1**	**0**		**0**	**0**		n.d.
12	hVH_3_48	**5**	**17**	**8.0**	**10**	**3**	**0**	**1**	**0**		**0**	**0**		intermediate
13	hVH_3_53	**5**	**16**	**8.7**	**16**	**3**	**0**	**1**	**0**		**0**	**0**		intermediate
14	hVH_3_73	**5**	**19**	**9.5**	**33**	**3**	**0**	**1**	**0**		**0**	**0**		n.d.
15	hVH_3_74	**5**	**17**	**9.1**	**19**	**4**	**0**	**1**	**0**		**0**	**0**		n.d.
16	hVH_4_4	**6**	**16**	**9.3**	**20**	**0**	**0**	**0**	**1**		**0**	**0**		n.d.
17	hVH_4_31	**7**	**16**	**9.2**	**13**	**0**	**0**	**0**	**0**		**0**	**0**		n.d.
18	hVH_4_39	**7**	**16**	**9.0**	**3**	**0**	**0**	**0**	**0**		**0**	**0**		n.d.
19	hVH_5_51	**5**	**17**	**8.6**	**6**	**1**	**0**	**0**	**0**		**0**	**0**		intermediate
20	hVH_6_1	**7**	**18**	**9.3**	**39**	**3**	**0**	**1**	**0**		**0**	**0**		n.d.

Figure 3

Summary 20 VL region genes

	Light chain germline genes	Kabat CDR-L1	Kabat CDR-L2	VNTI pI	Ranking pos	PTMs (w/o NxS/T)	NxS/T	Met in CDRs	Cysteine (to be removed)		Deviations from germline	Strong T-cell epitope		Theoretical aggregation propensity
1	hVL_1-40	14	7	4.9	2	1	0	0	0		0	0		intermediate
2	hVL_1-47	13	7	5.0	5	0	0	0	0		0	0		intermediate
3	hVL_1-51	13	7	6.2	4	0	0	0	0		1	0		intermediate
4	hVL_2-11	14	7	6.7	8	0	0	0	0		0	0		n.d.
5	hVL_2-23	14	7	6.7	6	0	0	0	0		0	0		n.d.
6	hVL_2-14	14	7	5.6	1	0	0	0	0		0	0		high
7	hVL_3-1	11	7	4.5	9	2	0	0	1		2	1*		n.d.
8	hVL_3-21	11	7	4.8	7	2	0	0	0		1	1*		n.d.
9	hVK_1_5	11	7	5.0	3	1	0	0	0		0	0		high
10	hVK_1_6	11	7	8.0	16	0	0	0	0		0	0		n.d.
11	hVK_1_9	11	7	8.0	9	0	0	0	0		0	0		n.d.
12	hVK_1_12	11	7	8.0	15	0	0	0	0		0	0		n.d.
13	hVK_1_16	11	7	8.0	14	0	0	0	0		0	0		n.d.
14	hVK_1_17	11	7	8.7	11	0	0	0	0		0	0		n.d.
15	hVK_1_27	11	7	8.7	12	0	0	0	0		0	0		n.d.
16	hVK_1_39	11	7	8.0	2	0	0	0	0		0	0		high
17	hVK_2_30	16	7	8.0	10	2	0	0	0		0	0		n.d.
18	hVK_3_11	11	7	6.3	6	0	0	0	0		0	0		intermediate
19	hVK_3_15	11	7	8.0	4	0	0	0	0		0	0		intermediate
20	hVK_3_20	12	7	6.3	1	0	0	0	0		0	0		low
alt.	hVK_1_8	11	7	8.9	13	0	0	0	1		n.d.	n.d.		n.d.

Figure 4

1358.0	IGKV3-20	IGKV1-39/1D-39	IGKV1-5	IGKV3-15	IGKV4-1	IGKV3-11	IGKV2-28/2D-28	IGKV1-33/1D-33	IGKV1-9	IGKV2-30	IGKV1-17	IGKV1-27	IGKV1-8	IGKV1-16	IGKV1-12	IGKV1-6	IGKV2D-29	IGKV1-13	IGKV2-24	IGKV1D-8	IGKV2-29	IGKV5-2	IGKV3D-20	IGKV1D-12	IGKV2-40/2D-40	IGKV1D-43	IGKV2D-30	IGKV1D-16	IGKV3D-15	IGKV1D-13	IGKV1D-17
>VH3-23	24	12	27	20	13	9	7	6	3	1	5	4	4	3	1	0	2	0	0	0	2	0	1	1	2	0	0	0	0	1	0
>VH3-30	14	12	9	9	11	12	4	2	7	2	1	1	2	1	0	2	1	1	2	2	0	1	0	0	0	0	1	0	0	0	0
>VH4-39	13	18	14	22	5	6	5	4	0	2	1	4	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
>VH4-59	15	19	3	8	10	4	0	2	0	1	1	3	1	1	2	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	1
>VH4-34	25	18	9	8	7	6	6	3	2	0	2	1	1	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH5-51	10	7	4	7	8	6	4	3	1	2	1	1	0	0	1	0	0	6	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH1-69	12	14	5	7	8	8	3	3	0	1	0	2	2	1	0	1	1	0	0	0	0	0	0	0	0	0	1	1	2	0	0
>VH3-7	6	10	10	8	5	4	3	0	2	4	2	2	3	0	0	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	1
>VH1-18	15	8	5	4	2	4	5	7	0	2	1	0	1	1	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0
>VH3-48	12	8	1	6	6	7	3	6	2	0	2	1	3	2	0	1	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0
>VH3-21	5	7	9	9	4	2	2	0	0	0	0	2	2	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-15	10	6	6	4	4	3	3	4	3	1	0	1	0	0	0	0	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0
>VH4-31	7	4	4	4	2	7	4	3	0	0	2	2	0	0	0	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
>VH1-2	12	6	3	2	3	0	2	1	0	1	0	2	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-33	6	6	5	8	6	2	4	2	2	0	1	0	1	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-53	2	5	8	6	4	4	1	5	1	0	1	2	2	0	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0
>VH3-11	3	5	6	5	2	3	3	1	1	0	1	0	0	0	1	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
>VH3-9	1	3	3	2	3	2	1	0	0	0	1	1	1	2	1	0	3	0	0	1	0	0	0	0	0	0	0	0	0	0	0
>VH3-74	4	3	3	3	3	2	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH4-4	6	5	4	3	3	3	2	0	0	0	1	1	0	0	0	1	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0
>VH1-46	6	5	3	3	1	2	0	1	4	0	0	2	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH4-61	0	3	0	2	5	1	1	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH1-8	2	1	1	4	2	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
>VH1-24	1	3	0	3	1	4	2	1	0	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0
>VH1-3	2	4	1	3	0	0	0	1	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-49	2	4	2	1	0	1	1	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH4-28	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-43	0	0	3	1	1	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-64	0	0	2	1	0	2	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH7-81	3	2	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-13	0	3	1	0	2	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-72	1	0	2	2	0	0	0	0	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-73	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH1-58	2	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-66	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH4-30.2	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH7-4.1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH2-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH6-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH4-30.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-20	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Figure 5

779.0	IGLV 2-14	IGLV 1-40	IGLV 1-44	IGLV 1-51	IGLV 1-47	IGLV 2-23	IGLV 3-21	IGLV 2-11	IGLV 3-1	IGLV 2-8	IGLV 6-57	IGLV 1-36	IGLV 3-25	IGLV 4-69	IGLV 7-43	IGLV 7-46	IGLV 2-18	IGLV 3-27	IGLV 9-49	IGLV 3-10	IGLV 3-9	IGLV 8-61	IGLV 3-12	IGLV 3-19	IGLV 3-22	IGLV 4-60
>VH3-23	13	6	5	3	1	4	6	5	5	1	0	2	0	0	1	0	1	0	0	0	0	0	0	1	0	0
>VH3-30	7	5	4	9	1	2	3	2	3	1	1	0	0	0	0	0	0	1	2	2	0	0	0	0	0	0
>VH4-39	10	6	7	5	3	5	13	0	2	10	2	0	0	0	0	1	3	0	0	0	1	0	0	0	0	0
>VH4-59	4	8	4	4	3	2	2	2	5	1	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
>VH4-34	10	6	2	9	6	2	2	1	0	4	0	1	2	0	1	0	0	0	1	0	0	0	0	0	0	0
>VH5-51	11	14	5	0	4	3	3	0	0	0	0	2	2	0	1	0	0	0	0	0	0	0	0	0	0	0
>VH1-69	8	7	8	5	2	3	2	5	2	4	1	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0
>VH3-7	2	4	3	3	3	1	3	0	1	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0
>VH1-18	5	5	3	3	0	1	0	1	0	2	2	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0
>VH3-48	6	1	1	1	6	1	1	2	3	0	0	0	1	0	0	1	0	0	1	0	0	0	0	0	0	0
>VH3-21	5	2	2	9	3	1	2	2	1	1	1	0	1	2	0	1	0	0	0	0	0	0	0	0	0	0
>VH3-15	1	2	4	2	1	1	1	0	2	2	1	0	1	0	2	3	1	0	0	0	0	0	0	0	1	0
>VH4-31	8	3	1	3	3	4	2	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0
>VH1-2	8	6	5	3	0	3	1	1	3	2	0	0	0	0	0	2	0	1	0	0	0	0	0	0	0	0
>VH3-33	4	1	1	1	4	4	4	1	1	0	2	0	0	1	0	0	0	1	1	0	1	0	0	0	0	0
>VH3-53	2	0	9	1	1	1	0	1	1	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
>VH3-11	3	1	3	1	1	2	2	3	3	1	0	0	1	2	0	1	0	0	1	0	0	1	0	0	0	0
>VH3-9	6	1	4	1	3	7	2	3	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1
>VH3-74	2	0	0	0	1	3	3	1	1	1	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0
>VH4-4	4	3	6	2	0	2	0	1	1	2	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0
>VH1-46	3	1	3	4	1	1	1	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH4-61	3	0	4	0	0	1	1	2	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
>VH1-8	4	0	0	1	2	0	0	1	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
>VH1-24	1	1	1	0	0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH1-3	2	1	0	0	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-49	1	1	0	0	0	1	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH4-28	1	0	2	2	0	4	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-43	1	0	0	2	0	0	0	1	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0
>VH3-64	1	0	0	0	0	0	2	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
>VH7-81	2	1	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-13	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-72	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-73	0	1	0	1	1	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH1-58	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-66	0	0	1	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH4-30.2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH7-4.1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH2-5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH6-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH4-30.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
>VH3-20	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Figure 6A

	Matsuda et al	Tomlinson et al	Protein sequence
IGHV1-2	VH 1-2	DP-75	QVQLVQSGAEVKKPGASVKVSCKASGYTFTGYYMHWVRQAPGQGLEWMG WINPNSGGTNYAQKFQGRVTMTRDTSISTAYMELSRLRSDDTAVYYCAR
IGHV1-3	VH 1-3	DP-25	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYAMHWVRQAPGQRLEWMG WSNAGNGNTKYSQEFQGRVTITRDTSASTAYMELSSLRSEDMAVYYCAR
IGHV1-8	VH 1-8	DP-15	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYDINWVRQATGQGLEWMGW MNPNSGNTGYAQKFQGRVTMTRNTSISTAYMELSSLRSEDTAVYYCARG
IGHV1-18	VH 1-18	DP-14	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGW ISAYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCAR
IGHV1-24	VH 1-24	DP-5	QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMG GFDPEDGETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCAT
IGHV1-45	VH 1-45	--	QMQLVQSGAEVKKTGSSVKVSCKASGYTFTYRYLHWVRQAPGQALEWMG WITPFNGNTNYAQKFQDRVTITRDRSMSTAYMELSSLRSEDTAMYYCAR
IGHV1-46	VH 1-46	DP-7	QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYYMHWVRQAPGQGLEWMGI INPSGGSTSYAQKFQGRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
IGHV1-58	VH 1-58	DP-2	QMQLVQSGPEVKKPGTSVKVSCKASGFTFTSSAMQWVRQARGQRLEWIGW IVVGSGNTNYAQKFQERVTITRDMSTSTAYMELSSLRSEDTAVYYCAA
IGHV1-69*01	VH 1-69	DP-10	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGG IIPIFGTANYAQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCAR
IGHV1-69*06, IGHV1-e	VH 1-69	DP-88	QVQLVQSGAEVKKPGSSVKVSCKASGGTFSSYAISWVRQAPGQGLEWMGG IIPIFGTANYAQKFQGRVTITADKSTSTAYMELSSLRSEDTAVYYCAR
IGHV1-c	--	--	KSGASVKVSCSFSGFTITSYGIHWVQQSPGQGLEWMGWINPGNGSPSYAKK FQGRFTMTRDMSTTTAYTDLSSLTSEDMAVYYYAR
IGHV1-f	--	DP-3	EVQLVQSGAEVKKPGATVKISCKVSGYTFTDYYMHWVQQAPGKGLEWMGL VDPEDGETIYAEKFQGRVTITADTSTDTAYMELSSLRSEDTAVYYCAT
IGHV2-5	VH 2-5	DP-76	QITLKESGPTLVKPTQTLTLTCTFSGFSLSTSGVGVGWIRQPPGKALEWLALI YWNDDKRYSPSLKSRLTITKDTSKNQVVLTMTNMDPVDTATYYCAHR
IGHV2-26	VH 2-26	DP-26	QVTLKESGPVLVKPTETLTLTCTVSGFSLSNARMGVSWIRQPPGKALEWLAH IFSNDEKSYSTSLKSRLTISKDTSKSQVVLTMTNMDPVDTATYYCARI
IGHV2-70	VH 2-70	DP-27	QVTLRESGPALVKPTQTLTLTCTFSGFSLSTSGMCVSWIRQPPGKALEWLALI DWDDDKYYSTSLKTRLTISKDTSKNQVVLTMTNMDPVDTATYYCARI
IGHV3-7	VH 3-7	DP-54	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVA NIKQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-9	VH 3-9	DP-31	EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSG ISWNSGSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKD

Figure 6B

IGHV3-11	VH 3-11	DP-35	QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYI SSSGSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-13	VH 3-13	DP-48	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYDMHWVRQATGKGLEWVSA IGTAGDTYYPGSVKGRFTISRENAKNSLYLQMNSLRAGDTAVYYCAR
IGHV3-15	VH 3-15	DP-38	EVQLVESGGGLVKPGGSLRLSCAASGFTFSNAWMSWVRQAPGKGLEWVG RIKSKTDGGTTDYAAPVKGRFTISRDDSKNTLYLQMNSLKTEDTAVYYCTT
IGHV3-16	VH 3-16		EVQLVESGGGLVQPGGSLRLSCAASGFTFSNSDMNWARKAPGKGLEWVSG VSWNGSRTHYVDSVK.RRFIISRDNSRNSLYLQKNRRRAEDMAVYYCVR
IGHV3-20	VH 3-20	DP-32	EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVS GINWNGGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYHCAR
IGHV3-21	VH 3-21	DP-77	EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSI SSSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-23	VH 3-23	DP-47	EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAI SGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK
IGHV3-30	VH 3-30	DP-49	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-30-3	--	DP-46	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAV ISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-30-5	--	–	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVA VISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK
IGHV3-33	VH 3-33	DP-50	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVA VIWYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-35	VH 3-35	DP-59	EVQLVESGGGLVQPGGSLRLSCAASGFTFSNSDMNWVHQAPGKGLEWVSG VSWNGSRTHYADSVKGRFIISRDNSRNTLYLQTNSLRAEDTAVYYCVR
IGHV3-38	VH 3-38P	–	EVQLVESGGGLVQPRGSLRLSCAASGFTVSSNEMSWIRQAPGKGLEWVSSI SGGSTYYADSRKGRFTISRDNSKNTLYLQMNNLRAEGTAAYYCARY
IGHV3-43	VH 3-43	DP-33	EVQLVESGGVVVQPGGSLRLSCAASGFTFDDYTMHWVRQAPGKGLEWVSLI SWDGGSTYYADSVKGRFTISRDNSKNSLYLQMNSLRTEDTALYYCAKD
IGHV3-48	VH 3-48	DP-51	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSY ISSSSSTIYYADSVKGRFTISRDNAKNSLYLQMNSLRDEDTAVYYCAR
IGHV3-49	VH 3-49	3-49RB	EVQLVESGGGLVQPGRSLRLSCTASGFTFGDYAMSWFRQAPGKGLEWVGF IRSKAYGGTTEYAASVKGRFTISRDDSKSIAYLQMNSLKTEDTAVYYCTR
IGHV3-53	VH 3-53	DP-42	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI YSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-64	VH 3-64	DP-61	EVQLVESGEGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEYVSAI SSNGGSTYYADSVKGRFTISRDNSKNTLYLQMGSLRAEDMAVYYCAR
IGHV3-66	VH 3-66	DP-86	EVQLVESGGGLIQPGGSLRLSCAASGFTVSSNYMSWVRQAPGKGLEWVSVI YSCGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-72	VH 3-72	DP-29	EVQLVESGGGLVQPGGSLRLSCAASGFTFSDHYMDWVRQAPGKGLEWVG RTRNKANSYTTEYAASVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCAR
IGHV3-73	VH 3-73	DA-11	EVQLVESGGGLVQPGGSLKLSCAASGFTFSGSAMHWVRQASGKGLEWVGR IRSKANSYATAYAASVKGRFTISRDDSKNTAYLQMNSLKTEDTAVYYCTR
IGHV3-74	VH 3-74	DP-53	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQAPGKGLVWVS RINSDGSSTSYADSVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCAR

Figure 6C

IGHV3-d	--	--	EVQLVESRGVLVQPGGSLRLSCAASGFTVSSNEMSWVRQAPGKGLEWVSSI SGGSTYYADSRKGRFTISRDNSKNTLHLQMNSLRAEDTAVYYCKK
IGHV4-4	VH 4-4	DP-70	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPAGKGLEWIGRIY TSGSTNYNPSLKSRVTMSVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-28	VH 4-28	DP-68	QVQLQESGPGLVKPSDTLSLTCAVSGYSISSSNWWGWIRQPPGKGLEWIGYI YYSGSTYYNPSLKSRVTMSVDTSKNQFSLKLSSVTAVDTAVYYCAR
IGHV4-30-1	--	--	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIG YIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-30-2	--	DP-64	QLQLQESGSGLVKPSQTLSLTCAVSGGSISSGGYSWSWIRQPPGKGLEWIG YIYHSGSTYYNPSLKSRVTISVDRSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-30-4	--	DP-78	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGDYYWSWIRQPPGKGLEWIG YIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-31	VH 4-31	DP-65	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGGYYWSWIRQHPGKGLEWIG YIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-34	VH 4-34	DP-63	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEI NHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARG
IGHV4-39	VH 4-39	DP-79	QLQLQESGPGLVKPSETLSLTCTVSGGSISSSSYYWGWIRQPPGKGLEWIGS IYYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-59	VH 4-59	DP-71	QVQLQESGPGLVKPSETLSLTCTVSGGSISSYYWSWIRQPPGKGLEWIGYIY YSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-61	VH 4-61	DP-66	QVQLQESGPGLVKPSETLSLTCTVSGGSVSSGGYYWSWIRQPPGKGLEWIG YIYYSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV4-b	--	DP-67	QVQLQESGPGLVKPSETLSLTCAVSGYSISSGYYWGWIRQPPGKGLEWIGSI YHSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR
IGHV5-51	VH 5-51	DP-73	EVQLVQSGAEVKKPGESLKISCKGSGYSFTSYWIGWVRQMPGKGLEWMGII YPGDSDTRYSPSFQGQVTISADKSISTAYLQWSSLKASDTAMYYCAR
IGHV5-a	--	--	EVQLVQSGAEVKKPGESLRISCKGSGYSFTSYWISWVRQMPGKGLEWMGRI DPSDSYTNYSPSFQGHVTISADKSISTAYLQWSSLKASDTAMYYCAR
IGHV6-1	VH 6-1	DP-74	QVQLQQSGPGLVKPSQTLSLTCAISGDSVSSNSAAWNWIRQSPSRGLEWLG RTYYRSKWYNDYAVSVKSRITINPDTSKNQFSLQLNSVTPEDTAVYYCAR
IGHV7-4-1	--	DP-21	QVQLVQSGSELKKPGASVKVSCKASGYTFTSYAMNWVRQAPGQGLEWMG WINTNTGNPTYAQGFTGRFVFSLDTSVSTAYLQICSLKAEDTAVYYCAR
IGHV7-81	VH 7-81	--	QVQLVQSGHEVKQPGASVKVSCKASGYSFTTYGMNWVPQAPGQGLEWMG WFNTYTGNPTYAQGFTGRFVFSMDTSASTAYLQISSLKAEDMAMYYCAR

51 functional

5 open reading frames

Figure 7A

	Zachau	Protein sequence
IGKV1-5	L12	DIQMTQSPSTLSASVGDRVTITCRASQSISSWLAWYQQKPGKAPKLLIYDASS LESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYS
IGKV1-6	L11	AIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQDYNYP
IGKV1-8	L9	AIRMTQSPSSFSASTGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTL QSGVPSRFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSYP
IGKV1-9	L8	DIQLTQSPSFLSASVGDRVTITCRASQGISSYLAWYQQKPGKAPKLLIYAASTL QSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCQQLNSYP
IGKV1-12	L5	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFP
IGKV1-13	L4/18a	AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSL ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNSYP
IGKV1-16	L1	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWFQQKPGKAPKSLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYP
IGKV1-17	A30	DIQMTQSPSSLSASVGDRVTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASS LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP
IGKV1-27	A20	DIQMTQSPSSLSASVGDRVTITCRASQGISNYLAWYQQKPGKVPKLLIYAASTL QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAP
IGKV1-33	O18	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASN LETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLP
IGKV1-37	O14	DIQLTQSPSSLSASVGDRVTITCRVSQGISSYLNWYRQKPGKVPKLLIYSASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYGQRTYNAPP
IGKV1-39	O12	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP
IGKV1D-08	L24	VIWMTQSPSLLSASTGDRVTISCRMSQGISSYLAWYQQKPGKAPELLIYAAST LQSGVPSRFSGSGSGTDFTLTISCLQSEDFATYYCQQYYSFP
IGKV1D-12	L19	DIQMTQSPSSVSASVGDRVTITCRASQGISSWLAWYQQKPGKAPKLLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQANSFP
IGKV1D-13	L18	AIQLTQSPSSLSASVGDRVTITCRASQGISSALAWYQQKPGKAPKLLIYDASSL ESGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQFNNYP
IGKV1D-16	L15	DIQMTQSPSSLSASVGDRVTITCRASQGISSWLAWYQQKPEKAPKSLIYAASS LQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYNSYP
IGKV1D-17	L14	NIQMTQSPSAMSASVGDRVTITCRARQGISNYLAWFQQKPGKVPKHLIYAASS LQSGVPSRFSGSGSGTEFTLTISSLQPEDFATYYCLQHNSYP
IGKV1D-33	O8	DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQQKPGKAPKLLIYDASN LETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDNLP
IGKV1D-37	O4	DIQLTQSPSSLSASVGDRVTITCRVSQGISSYLNWYRQKPGKVPKLLIYSASNL QSGVPSRFSGSGSGTDFTLTISSLQPEDVATYYGQRTYNAPP

Figure 7B

IGKV1D-39	O2	DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAPKLLIYAASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTP
IGKV1D-42	L22	DIQMIQSPSFLSASVGDRVSIICWASEGISSNLAWYLQKPGKSPKLFLYDAKDL HPGVSSRFSGRGSGTDFTLTIISLKPEDFAAYYCKQDFSYPP
IGKV1D-43	L23	AIRMTQSPFSLSASVGDRVTITCWASQGISSYLAWYQQKPAKAPKLFIYYASSL QSGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQYYSTP
IGKV2-24	A23	DIVMTQTPLSSPVTLGQPASISCRSSQSLVHSDGNTYLSWLQQRPGQPPRLLI YKISNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCMQATQFP
IGKV2-28	A19	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLI YLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
IGKV2-29	A18b	DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQSPQLLI YEVSSRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGIHLP
IGKV2-30	A17	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRR LIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP
IGKV2-40	O11	DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSDDGNTYLDWYLQKPGQSPQLL IYTLSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQRIEFP
IGKV2D-24	A7	DIVMTQTPLSSPVTLGQPASISFRSSQSLVHSDGNTYLSWLQQRPGQPPRLLI YKVSNRFSGVPDRFSGSGAGTDFTLKISRVEAEDVGVYYCTQATQFP
IGKV2D-26	A5	EIVMTQTPLSLSITPGEQASISCRSSQSLLHSDGYTYLYWFLQKARPVSTLLIYE VSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDFGVYYCMQDAQDPP
IGKV2D-28	A3	DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLI YLGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQTP
IGKV2D-29	A2	DIVMTQTPLSLSVTPGQPASISCKSSQSLLHSDGKTYLYWYLQKPGQPPQLLI YEVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQSIQLP
IGKV2D-30	A1	DVVMTQSPLSLPVTLGQPASISCRSSQSLVYSDGNTYLNWFQQRPGQSPRR LIYKVSNWDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWP
IGKV2D-40	O1	DIVMTQTPLSLPVTPGEPASISCRSSQSLLDSDDGNTYLDWYLQKPGQSPQLL IYTLSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQRIEFP
IGKV3-7	L10	EIVMTQSPPTLSLSPGERVTLSCRASQSVSSSYLTWYQQKPGQAPRLLIYGAS TRATSIPARFSGSGSGTDFTLTISSLQPEDFAVYYCQQDHNLPP
IGKV3-11	L6	EIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWP
IGKV3-15	L2	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP

Figure 7C

IGKV3-20	A27	EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGAS SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP
IGKV3D-07	L25	EIVMTQSPATLSLSPGERATLSCRASQSVSSSYLSWYQQKPGQAPRLLIYGAS TRATGIPARFSGSGSGTDFTLTISSLQPEDFAVYYCQQDYNLP
IGKV3D-11	L20	EIVLTQSPATLSLSPGERATLSCRASQGVSSYLAWYQQKPGQAPRLLIYDASN RATGIPARFSGSGPGTDFTLTISSLEPEDFAVYYCQQRSNWH
IGKV3D-15	L16	EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGAS TRATGIPARFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP
IGKV3D-20	A11	EIVLTQSPATLSLSPGERATLSCGASQSVSSSYLAWYQQKPGLAPRLLIYDAS SRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSP
IGKV4-1	B3	DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKL LIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTP
IGKV5-2	B2	ETTLTQSPAFMSATPGDKVNISCKASQDIDDDMNWYQQKPGEAAIFIIQEATTL VPGIPPRFSGSGYGTDFTLTINNIESEDAAYYFCLQHDNFP
IGKV6-21	A26	EIVLTQSPDFQSVTPKEKVTITCRASQSIGSSLHWYQQKPDQSPKLLIKYASQS FSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSLP
IGKV6D-21	A10	EIVLTQSPDFQSVTPKEKVTITCRASQSIGSSLHWYQQKPDQSPKLLIKYASQS FSGVPSRFSGSGSGTDFTLTINSLEAEDAATYYCHQSSSLP
IGKV6D-41	A14	DVVMTQSPAFLSVTPGEKVTITCQASEGIGNYLYWYQQKPDQAPKLLIKYASQ SISGVPSRFSGSGSGTDFTFTISSLEAEDAATYYCQQGNKHP

38 functional

8 open reading frames

Figure 8A

	Kawasaki et al	Frippiat et al	Protein sequence
IGLV1-36	VL 1-11	1a	QSVLTQPPSVSEAPRQRVTISCSGSSSNIGNNAVNWYQQLPGKAPKLLIYYDD LLPSGVSDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGP
IGLV1-40	VL 1-13	1e	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPGTAPKLLIYG NSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSGS
IGLV1-44	VL 1-16	1c	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNTVNWYQQLPGTAPKLLIYSNN QRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGP
IGLV1-47	VL 1-17	1g	QSVLTQPPSASGTPGQRVTISCSGSSSNIGSNYVYWYQQLPGTAPKLLIYSNN QRPSGVPDRFSGSKSGTSASLAISGLRSEDEADYYCAAWDDSLSGP
IGLV1-50	VL 1-18	1f	QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYVVHWYQQLPGTAPKLLIYG NSNRPSGVPDQFSGSKSGTSASLAITGLQSEDEADYYCKAWDNSLNA
IGLV1-51	VL 1-19	1b	QSVLTQPPSVSAAPGQKVTISCSGSSSNIGNNYVSWYQQLPGTAPKLLIYDNN KRPSGIPDRFSGSKSGTSATLGITGLQTGDEADYYCGTWDSSLSAG
IGLV2-08	VL 1-2	2c	QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIY EVSKRPSGVPDRFSGSKSGNTASLTVSGLQAEDEADYYCSSYAGSNNF
IGLV2-11	VL 1-3	2e	QSALTQPRSVSGSPGQSVTISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIY DVSKRPSGVPDRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSYTF
IGLV2-14	VL 1-4	2a2	QSALTQPASVSGSPGQSITISCTGTSSDVGGYNYVSWYQQHPGKAPKLMIYE VSNRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCSSYTSSSTL
IGLV2-18	VL 1-5	2d	QSALTQPPSVSGSPGQSVTISCTGTSSDVGSYNRVSWYQQPPGTAPKLMIYE VSNRPSGVPDRFSGSKSGNTASLTISGLQAEDEADYYCSLYTSSSTF
IGLV2-23	VL 1-7	2b2	QSALTQPASVSGSPGQSITISCTGTSSDVGSYNLVSWYQQHPGKAPKLMIYE GSKRPSGVSNRFSGSKSGNTASLTISGLQAEDEADYYCCSYAGSSTF
IGLV2-33	VL 1-9	2f	QSALTQPPFVSGAPGQSVTISCTGTSSDVGDYDHVFWYQKRLSTTSRLLIYN VNTRPSGISDLFSGSKSGNMASLTISGLKSEVEANYHCSLYSSSYTF
IGLV3-1	VL 2-1	3r	SYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQQKPGQSPVLVIYQDSK RPSGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTA
IGLV3-9	VL 2-6	3j	SYELTQPLSVSVALGQTARITCGGNNIGSKNVHWYQQKPGQAPVLVIYRDSN RPSGIPERFSGSNSGNTATLTISRAQAGDEADYYCQVWDSSTA
IGLV3-10	VL 2-7	3p	SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQQKSGQAPVLVIYEDSK RPSGIPERFSGSSSGTMATLTISGAQVEDEADYYCYSTDSSGNH
IGLV3-12	VL 2-8	3i	SYELTQPHSVSVATAQMARITCGGNNIGSKAVHWYQQKPGQDPVLVIYSDSN RPSGIPERFSGSNPGNTATLTISRIEAGDEADYYCQVWDSSSDHP
IGLV3-16	VL 2-11	3a	SYELTQPPSVSVSLGQMARITCSGEALPKKYAYWYQQKPGQFPVLVIYKDSE RPSGIPERFSGSSSGTIVTLTISGVQAEDEADYYCLSADSSGTYP
IGLV3-19	VL 2-13	3l	SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNN RPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHL
IGLV3-21	VL 2-14	3h	SYVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDS DRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHP
IGLV3-22	VL 2-15	3e	SYELTQLPSVSVSPGQTARITCSGDVLGENYADWYQQKPGQAPELVIYEDSE RYPGIPERFSGSTSGNTTTLTISRVLTEDEADYYCLSGDEDNP
IGLV3-25	VL 2-17	3m	SYELTQPPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQAPVLVIYKDSE RPSGIPERFSGSSSGTTVTLTISGVQAEDEADYYCQSADSSGTYP
IGLV3-27	VL 2-19	--	SYELTQPSSVSVSPGQTARITCSGDVLAKKYARWFQQKPGQAPVLVIYKDSE RPSGIPERFSGSSSGTTVTLTISGAQVEDEADYYCYSAADNNL

Figure 8B

IGLV3-32	VL 2-23P	3i1	SSGPTQVPAVSVALGQMARITCQGDSMEGSYEHWYQQKPGQAPVLVIYDSS DRPSRIPERFSGSKSGNTTTLTITGAQAEDEADYYYQLIDNHA
IGLV4-3	VL 5-1	4c	LPVLTQPPSASALLGASIKLTCTLSSEHSTYTIEWYQQRPGRSPQYIMKVKSD GSHSKGDGIPDRFMGSSSGADRYLTFSNLQSDDEAEYHCGESHTIDGQVG
IGLV4-60	VL 5-4	4a	QPVLTQSSSASASLGSSVKLTCTLSSGHSSYIIAWHQQQPGKAPRYLMKLEG SGSYNKGSGVPDRFSGSSSGADRYLTISNLQFEDEADYYCETWDSNT
IGLV4-69	VL 5-6	4b	QLVLTQSPSASASLGASVKLTCTLSSGHSSYAIAWHQQQPEKGPRYLMKLNS DGSHSKGDGIPDRFSGSSSGAERYLTISSLQSEDEADYYCQTWGTG
IGLV5-37	VL 4-1	5e	QPVLTQPPSSSASPGESARLTCTLPSDINVGSYNIYWYQQKPGSPPRYLLYYY SDSDKGQGSGVPSRFSGSKDASANTGILLISGLQSEDEADYYCMIWPSNAS
IGLV5-39	--	5a	QPVLTQPTSLSASPGASARFTCTLRSGINVGTYRIYWYQQKPGSLPRYLLRYK SDSDKQQGSGVPSRFSGSKDASTNAGLLLISGLQSEDEADYYCAIWYSSTS
IGLV5-45	VL 4-2	5c	QAVLTQPSSLSASPGASASLTCTLRSGINVGTYRIYWYQQKPGSPPQYLLRYK SDSDKQQGSGVPSRFSGSKDASANAGILLISGLQSEDEADYYCMIWHSSAS
IGLV5-48	VL 4-3	5d	QPVLTQPTSLSASPGASARLTCTLRSGINLGSYRIFWYQQKPESPPRYLLSYY SDSSKHQGSGVPSRFSGSKDASSNAGILVISGLQSEDEADYYCMIWHSSAS
IGLV5-52	VL 4-4	5b	QPVLTQPSSHSASSGASVRLTCMLSSGFSVGDFWIRWYQQKPGNPPRYLLY YHSDSNKGQGSGVPSRFSGSNDASANAGILRISGLQPEDEADYYCGTWHSN SKT
IGLV6-57	VL 1-22	6a	NFMLTQPHSVSESPGKTVTISCTRSSGSIASNYVQWYQQRPGSSPTTVIYED NQRPSGVPDRFSGSIDSSSNSASLTISGLKTEDEADYYCQSYDSSN
IGLV7-43	VL 3-2	7a	QTVVTQEPSLTVSPGGTVTLTCASSTGAVTSGYYPNWFQQKPGQAPRALIYS TSNKHSWTPARFSGSLLGGKAALTLSGVQPEDEAEYYCLLYYGGAQ
IGLV7-46	VL 3-3	7b	QAVVTQEPSLTVSPGGTVTLTCGSSTGAVTSGHYPYWFQQKPGQAPRTLIYD TSNKHSWTPARFSGSLLGGKAALTLLGAQPEDEAEYYCLLSYSGAR
IGLV8-61	VL 3-4	8a	QTVVTQEPSFSVSPGGTVTLTCGLSSGSVSTSYYPSWYQQTPGQAPRTLIYS TNTRSSGVPDRFSGSILGNKAALTITGAQADDESDYYCVLYMGSGIS
IGLV9-49	VL 5-2	9a	QPVLTQPPSASASLGASVTLTCTLSSGYSNYKVDWYQQRPGKGPRFVMRVG TGGIVGSKGDGIPDRFSVLGSGLNRYLTIKNIQEEDESDYHCGADHGSGSNFV
IGLV10-54	VL 1-20	10a	QAGLTQPPSVSKGLRQTATLTCTGNSNIVGNQGAAWLQQHQGHPPKLLSYR NNNRPSGISERFSASRSGNTASLTITGLQPEDEADYYCSALDSSLSA
IGLV11-55	VL 4-6	--	RPVLTQPPSLSASPGATARLPCTLSSDLSVGGKNMFWYQQKPGSSPRLFLY HYSDSDKQLGPGVPSRVSGSKETSSNTAFLLISGLQPEDEADYYCQVYESSA N

Figure 9

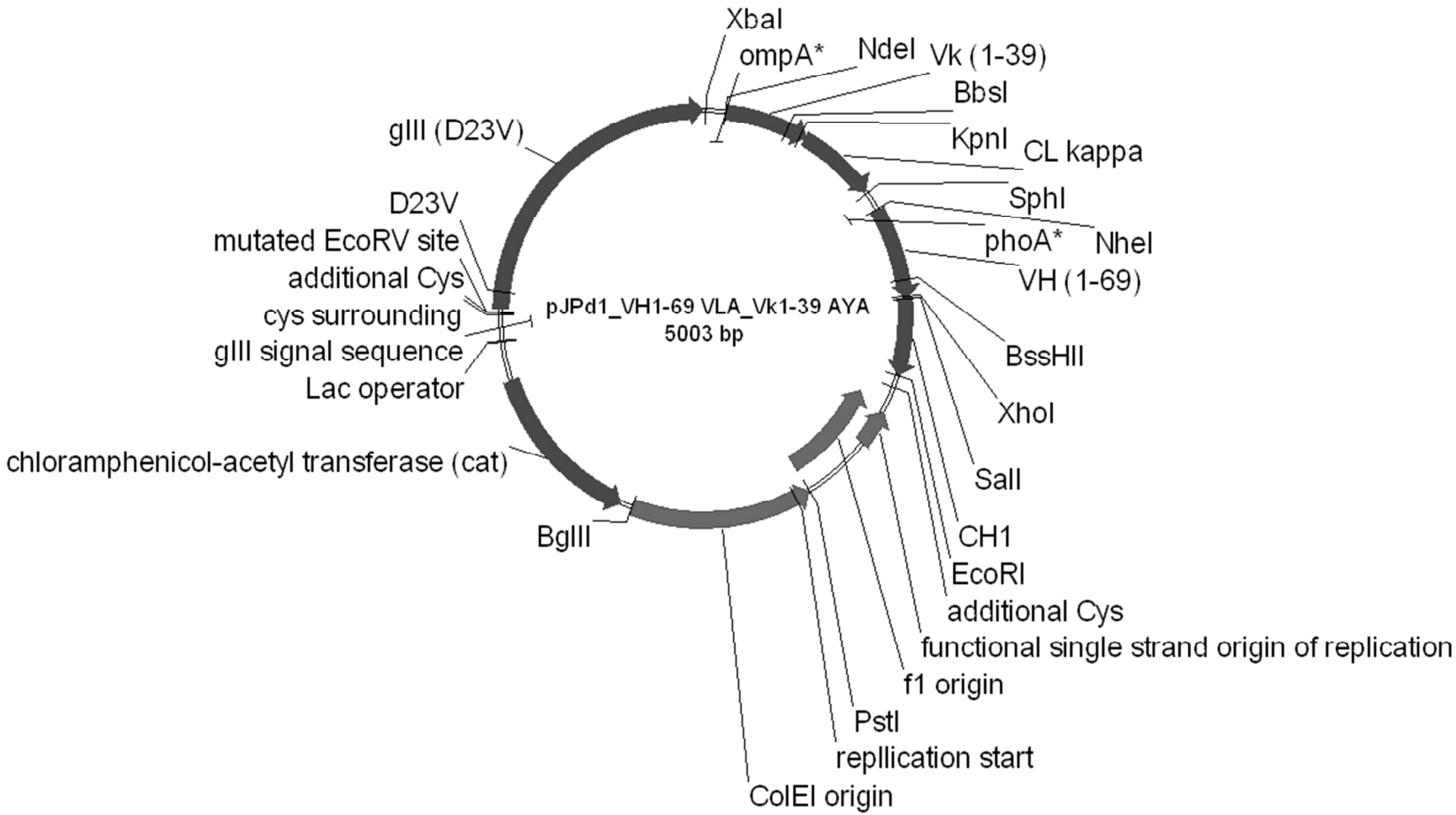

XbaI
ompA*
NdeI
Vk (1-39)
BbsI
KpnI
CL kappa
SphI
NheI
phoA*
VH (1-69)
BssHII
XhoI
SalI
CH1
EcoRI
additional Cys
functional single strand origin of replication
f1 origin
PstI
repllication start
ColEI origin
BglII
chloramphenicol-acetyl transferase (cat)
Lac operator
gIII signal sequence
cys surrounding
additional Cys
mutated EcoRV site
D23V
gIII (D23V)
pJPd1_VH1-69 VLA_Vk1-39 AYA
5003 bp

Figure 10

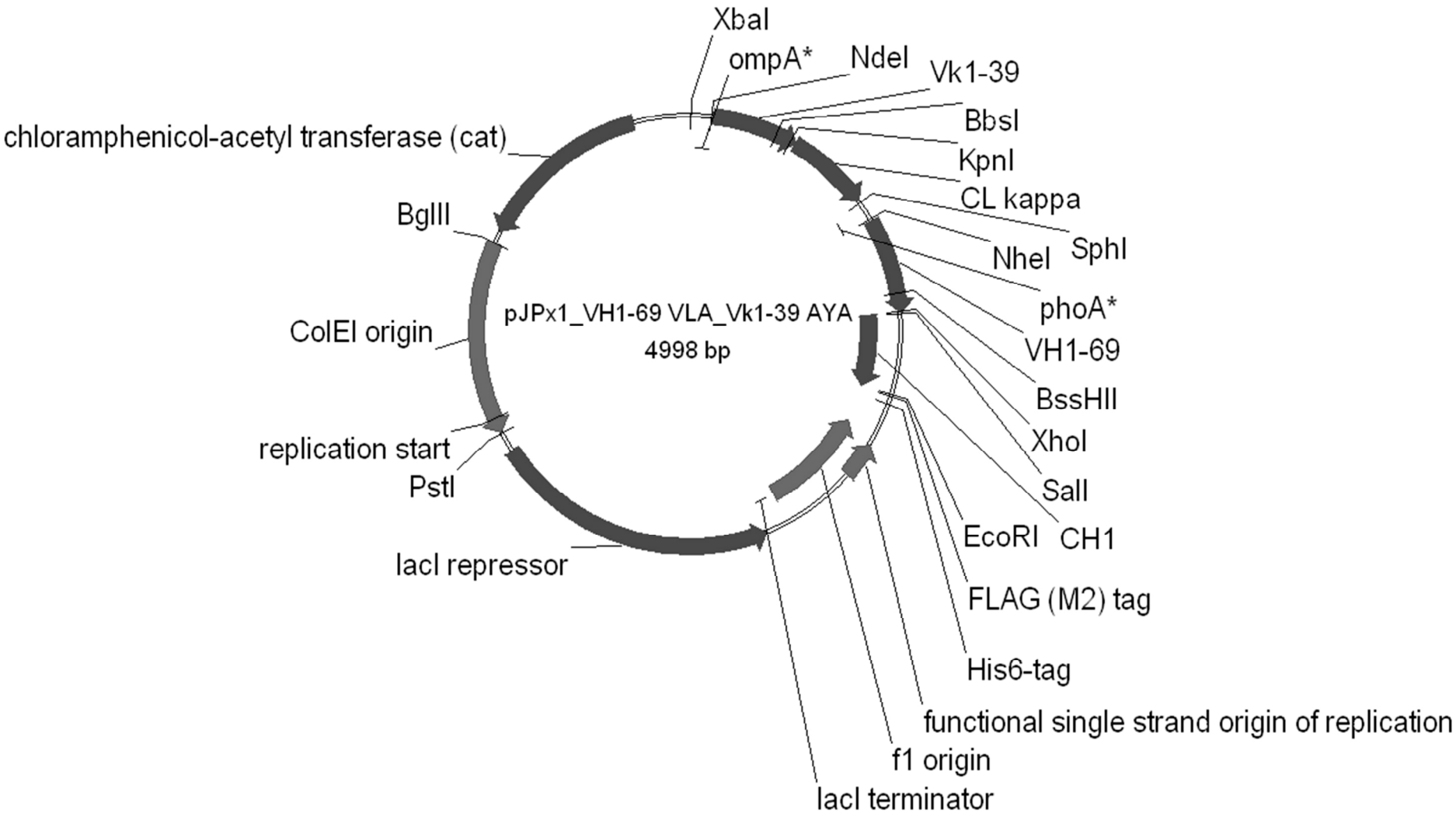

XbaI
ompA*
NdeI
Vk1-39
BbsI
KpnI
CL kappa
SphI
NheI
phoA*
VH1-69
BssHII
XhoI
SalI
CH1
EcoRI
FLAG (M2) tag
His6-tag
functional single strand origin of replication
f1 origin
lacI terminator
lacI repressor
PstI
replication start
ColEI origin
BglII
chloramphenicol-acetyl transferase (cat)
pJPx1_VH1-69 VLA_Vk1-39 AYA
4998 bp

Figure 11

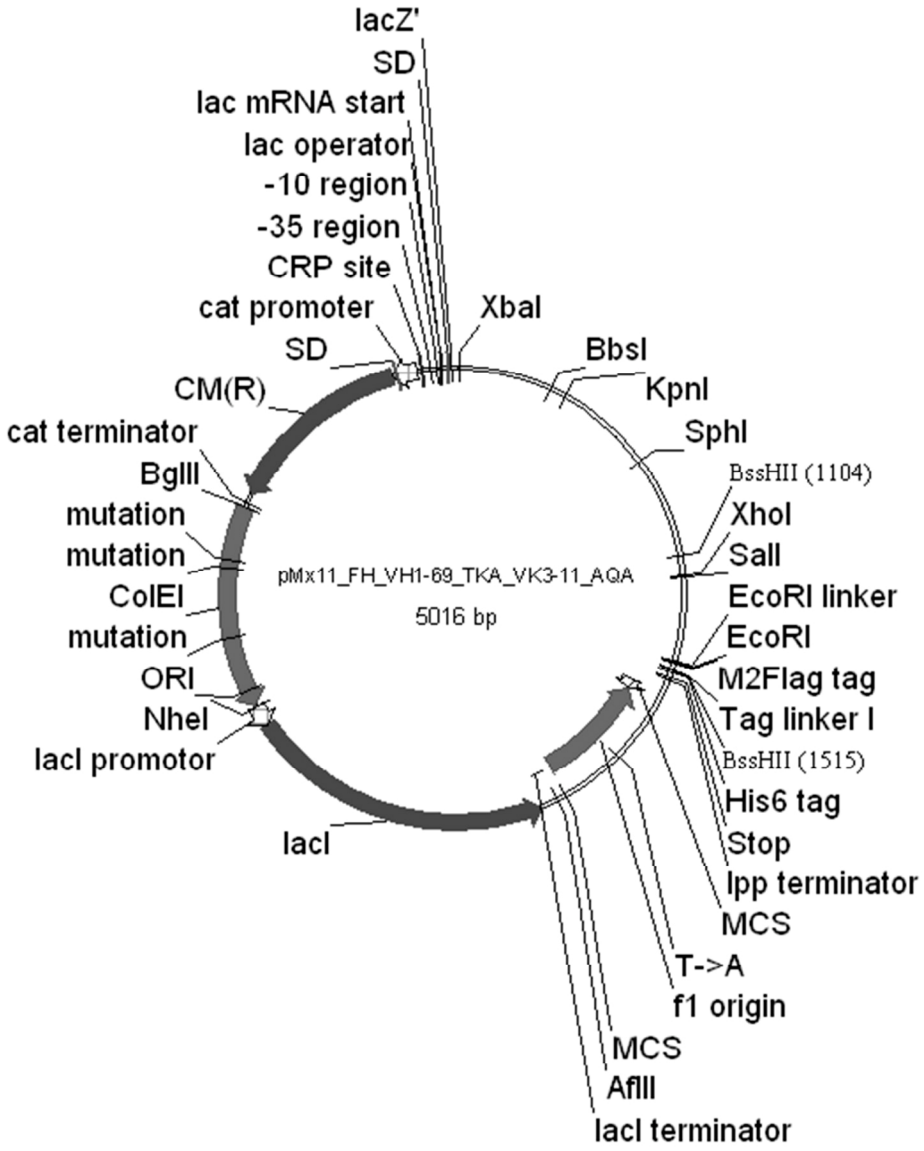

lacZ'
SD
lac mRNA start
lac operator
-10 region
-35 region
CRP site
cat promoter
SD
CM(R)
cat terminator
BglII
mutation
mutation
ColEI
mutation
ORI
NheI
lacI promotor
lacI
XbaI
BbsI
KpnI
SphI
BssHII (1104)
XhoI
SalI
EcoRI linker
EcoRI
M2Flag tag
Tag linker I
BssHII (1515)
His6 tag
Stop
lpp terminator
MCS
T->A
f1 origin
MCS
AflII
lacI terminator
pMx11_FH_VH1-69_TKA_VK3-11_AQA
5016 bp

Figure 12

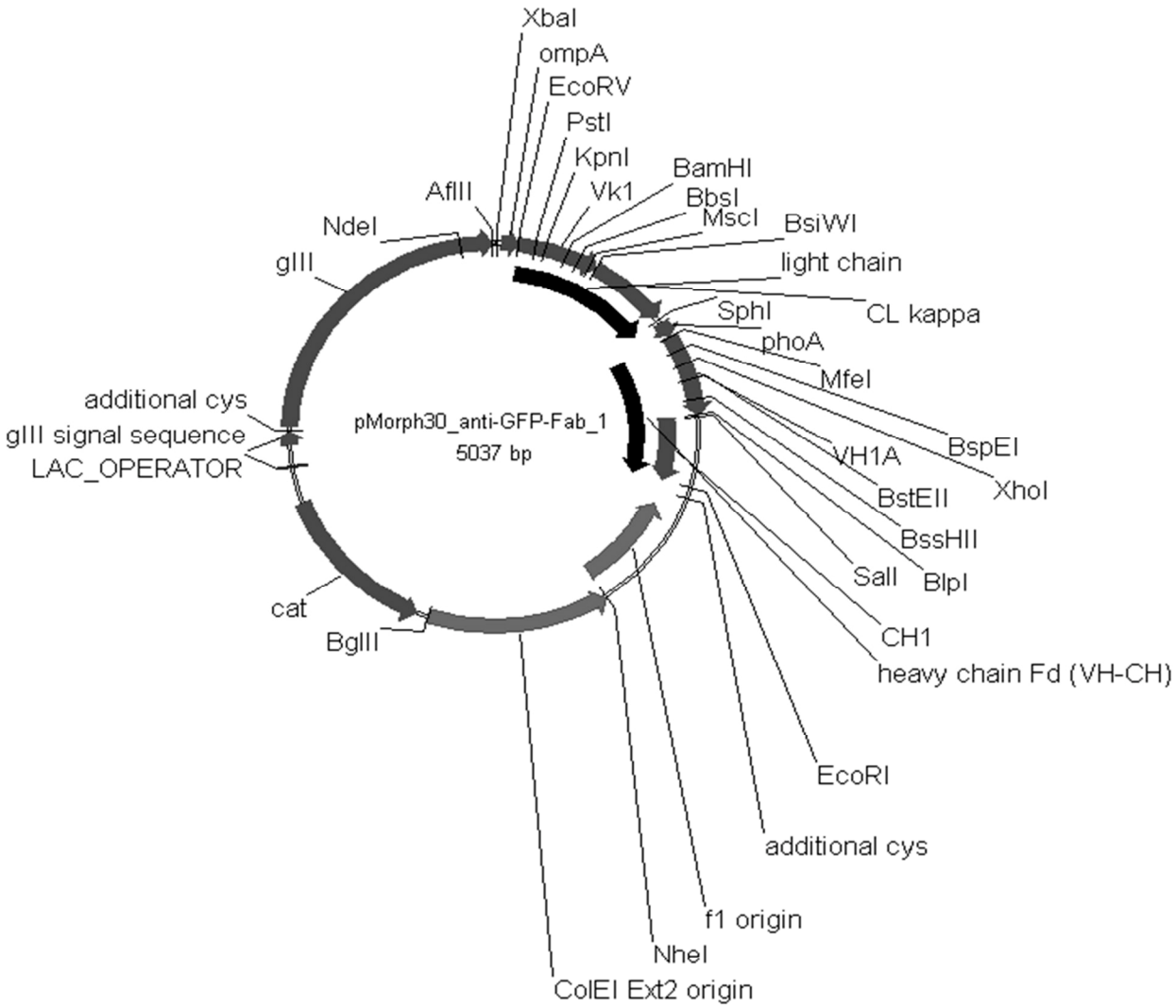

XbaI
ompA
EcoRV
PstI
KpnI
BamHI
AflII
Vk1
BbsI
NdeI
MscI
BsiWI
gIII
light chain
CL kappa
SphI
phoA
MfeI
additional cys
gIII signal sequence
LAC_OPERATOR
pMorph30_anti-GFP-Fab_1
5037 bp
BspEI
VH1A
XhoI
BstEII
BssHII
SalI
BlpI
cat
CH1
BglII
heavy chain Fd (VH-CH)
EcoRI
additional cys
f1 origin
NheI
ColEI Ext2 origin

Figure 13

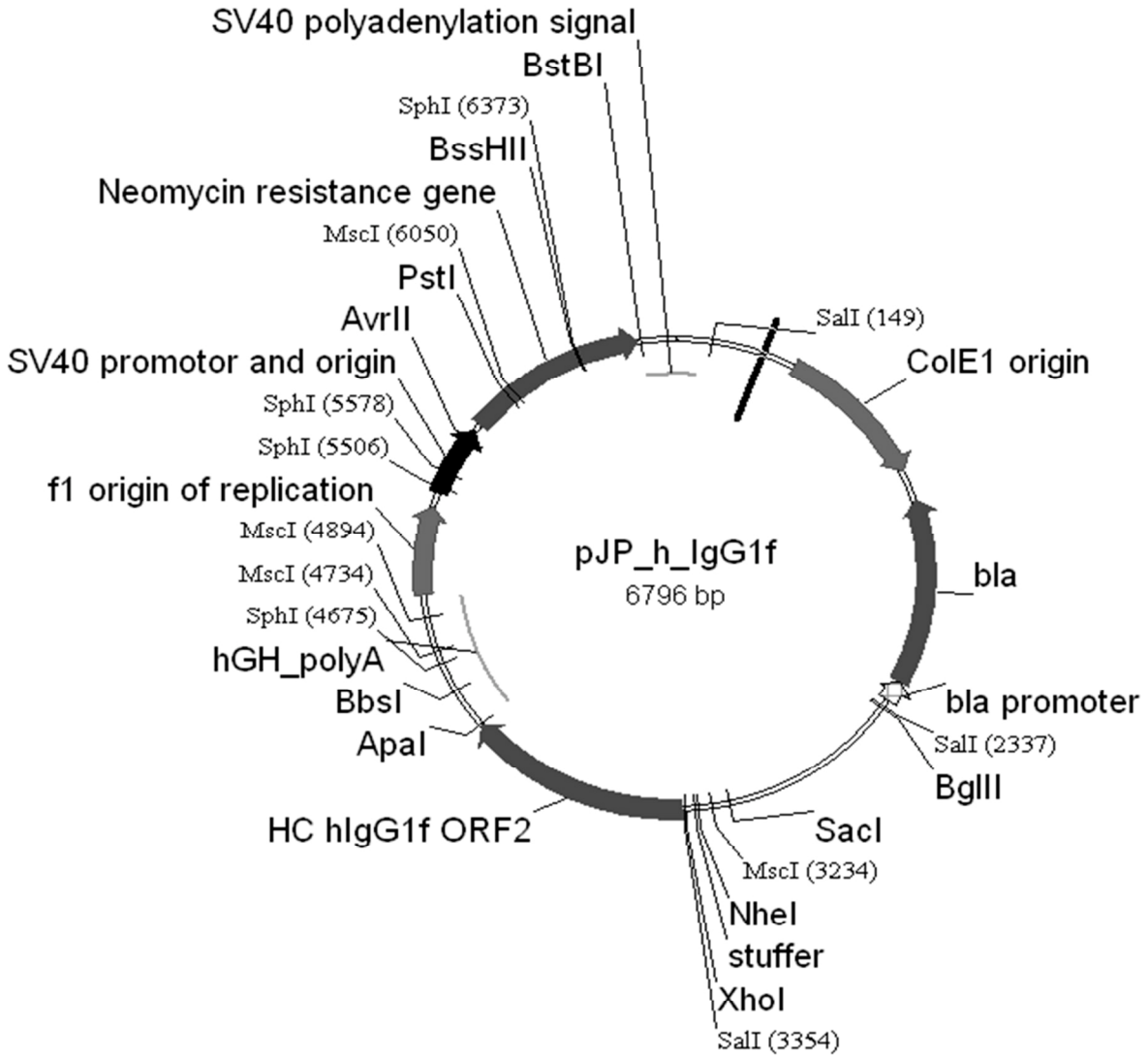

SV40 polyadenylation signal
BstBI
SphI (6373)
BssHII
Neomycin resistance gene
MscI (6050)
PstI
AvrII
SV40 promotor and origin
SphI (5578)
SphI (5506)
f1 origin of replication
MscI (4894)
MscI (4734)
SphI (4675)
hGH_polyA
BbsI
ApaI
HC hIgG1f ORF2
SalI (149)
ColE1 origin
bla
bla promoter
SalI (2337)
BglII
SacI
MscI (3234)
NheI
stuffer
XhoI
SalI (3354)
pJP_h_IgG1f
6796 bp

Figure 14

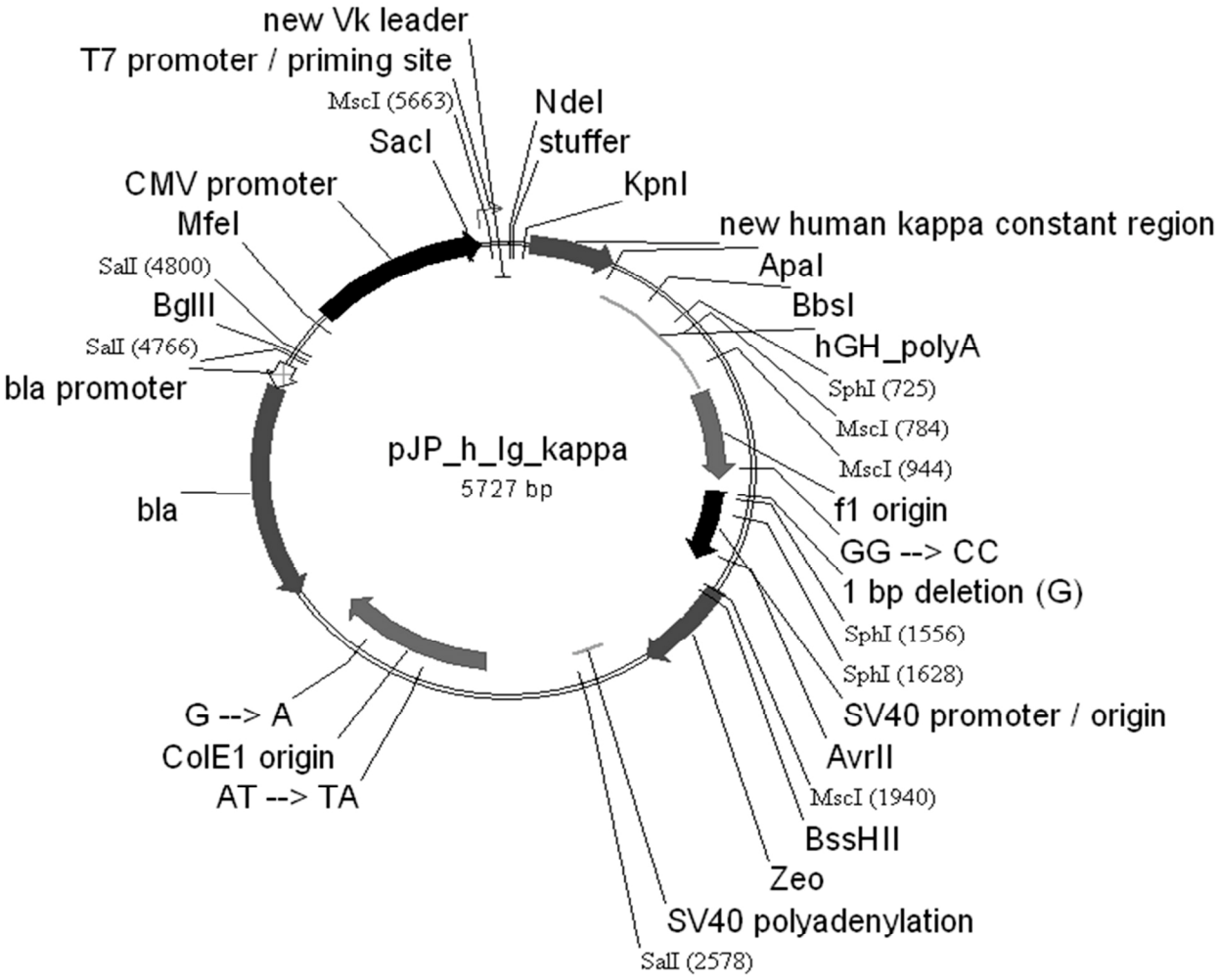

new Vk leader
T7 promoter / priming site
MscI (5663)
NdeI
stuffer
SacI
KpnI
CMV promoter
MfeI
new human kappa constant region
SalI (4800)
ApaI
BglII
BbsI
SalI (4766)
hGH_polyA
bla promoter
SphI (725)
MscI (784)
MscI (944)
pJP_h_lg_kappa
5727 bp
f1 origin
bla
GG --> CC
1 bp deletion (G)
SphI (1556)
SphI (1628)
SV40 promoter / origin
G --> A
AvrII
ColE1 origin
MscI (1940)
AT --> TA
BssHII
Zeo
SV40 polyadenylation
SalI (2578)

Figure 15

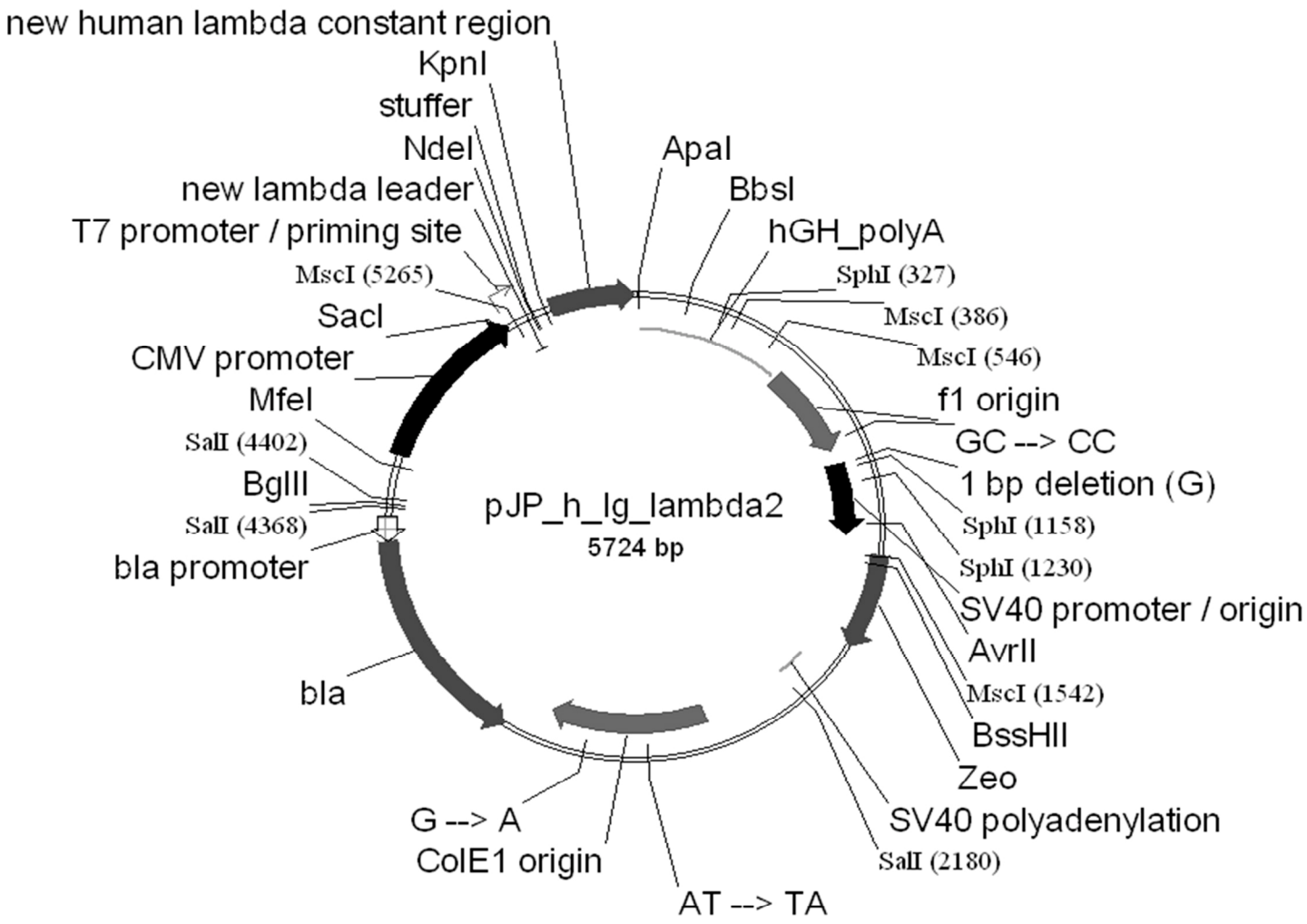

new human lambda constant region
KpnI
stuffer
NdeI
new lambda leader
T7 promoter / priming site
MscI (5265)
SacI
CMV promoter
MfeI
SalI (4402)
BglII
SalI (4368)
bla promoter
bla
G --> A
ColE1 origin
AT --> TA
SalI (2180)
SV40 polyadenylation
Zeo
BssHII
MscI (1542)
AvrII
SV40 promoter / origin
SphI (1230)
SphI (1158)
1 bp deletion (G)
GC --> CC
f1 origin
MscI (546)
MscI (386)
SphI (327)
hGH_polyA
BbsI
ApaI
pJP_h_lg_lambda2
5724 bp

Figure 16

No.	VH	VL	Purified fab expression mg/L	Purified Fab % monomer	Purified Fab Thermo-fluor	Purified IgG1 Expression mg/L	Purified IgG1 % monomer	Purified IgG1 Thermafluor	IgG1 Isoelectric point
1	VH_1_18	VK_1_39	2,5	100	75.2 / 75.4	36	100	78,4	9,2
2	VH_1_18	VK_3_11	3	97	75,2				
3	VH_1_18	VK_3_15	5	99	76,39	36,1	99	81,9	9,2
4	VH_1_18	VK_3_20	5	100	73.8 / 73.6	44	100	77	9
5	*VH_1_18*	*VL_1-40*				59,1	90	83,6	8,9
6	VH_1_18	VL_1-47	6,5	98	74.1 / 74.3	52,9	98	83,9	9,3
7	*VH_1_18*	*VL_2-23*	4.0 / 5.0 / 4.5	98.0 / 99.0 / 97.0	73.8 / 71.0	45,9	93	80,4	9
8	*VH_1_18*	*VL_3-1*	2,5	97	75	60,8	96	84,5	8,2
9	VH_1_46	VK_1_09	2,5	95	73,1	42,8	100	77,6	8,9
10	VH_1_46	VK_3_15	3	100	74.5 / 74.3	60,9	100	76,5	8,9
11	*VH_1_46*	*VL_1-40*	6,5	99	73.9 / 73.4	50,7	93	80,5	8,2
12	VH_1_46	VL_1-51	4,5	100	73,56	65	100	79,5	8,6
13	VH_1_46	VL_2-23	7	100	72.9 / 72.7	49,6	98	78,5	8,6
14	VH_1_46	VL_3-1				78,8	98	75,8	8,2
15	VH_1_46	VL_3-21	3	98		50,4	100	74,5	8,2
16	VH_1_69*01	VK_1_27	3,5	98	74,8				
17	VH_1_69*01	VK_3_11	2,5	97	72,9	22,6	100	77,8	8,2
18	*VH_1_69*01*	*VL_1-40*	4.5 / 6.5	90.0 / 99.0	73.8 / 72.7	34,7	95	81,7	8,2
19	VH_1_69*01	VL_1-51	7,5	99	73.3 / 72.9	53,9	99	77,9	8,6
20	VH_1_69*01	VL_3-1	2.0 / 3.0	99.0 / 96.0	74,4	36,4	99	79,6	7,4
21	VH_1_69*01	VL_3-21	4	98	73.3 / 73.1	34,5	98	76	8,2
22	VH_3_07	VK_1_12	6,5	100	74.0 / 74.1	57	100	77,6	8,9
23	VH_3_07	VK_1_16	7	98		50	100	74	8,9
24	VH_3_07	VK_1_27	6	99	76.0 / 76.0	64	100	80	8,9
25	VH_3_07	VK_1_39	7	98	74.2 / 74.3	53,3	100	80	8,9
26	VH_3_07	VK_3_15	6	100	74.8 / 75.3	65,5	100	79	8,9
27	VH_3_07	VK_3_20				32,7	100	78,4	8,7
28	VH_3_07	VL_1-47	9,5	99	72.0 / 71.3	56,7	99	79,4	9,1
29	VH_3_07	VL_1-51	8,5	99	72.0 / 71.3	63,3	100	79,9	8,7
30	*VH_3_07*	*VL_2-23*	3	97	72.5 / 72.2	43,3	90	81,4	8,7
31	*VH_3_07*	*VL_3-1*	1,5	94	n.a.	43,5	97	n.a.	7,6
32	VH_3_11	VK_1_05	4,5	98	70.0 / 70.1	56,4	100	74,3	8,6

Figure 17

No.	VH	VL	Purified fab expression mg/L	Purified Fab % monomer	Purified Fab Thermo-fluor	Purified IgG1 expression mg/L	Purified IgG1 % monomer	Purified IgG1 Thermafluor	IgG1 Isoelectric point
33	VH_3_11	VK_1_39	3,5	100		55,7	99	79	9
34	VH_3_11	VK_3_15	6,5	99	74.1 / 73.8	57,4	100	78,6	9,1
35	VH_3_11	VL_1-40	7	99	72	30	99	79,2	8,6
36	VH_3_11	VL_1-47	7,5	99	71.8 / 71.5	52,7	99	77,2	9,2
37	VH_3_11	VL_1-51	13	100	71.7 / 72.2	59,1	100	77	8,9
38	VH_3_11	VL_2-23	7	99	70.2 / 70.5	50	99	74,5	8,9
39	VH_3_15	VK_1_05	8,5	100	72.3 / 72.7	59,1	100	76	8,9
40	VH_3_15	VK_1_06	5	100	72,3	38	100	74,5	9,3
41	VH_3_15	VK_1_09	9,5	100	75.8 / 76.7	20	99	82	9,2
42	VH_3_15	VK_1_12	9	99	75.6 / 75.3	54,5	100	79,2	9,2
43	*VH_3_15*	*VK_1_16*	8,5	99	73.3 / 73.1	52,7	100	76,5	9,2
44	VH_3_15	VK_1_27	4,5	100	76,24	32	100	78,5	9,2
45	VH_3_15	VK_3_11	5,5	99	76	31,2	100	79,5	8,9
46	VH_3_15	VK_3_15	6	100	77	20	100	80	9,2
47	VH_3_15	VL_1-40	10,5	100	73.5 / 73.6	32	99	80,3	8,9
48	VH_3_15	VL_1-47	9	99	72.6 / 72.9	61,8	99	78	9,3
49	VH_3_15	VL_1-51	6	100	74,11	46	100	78,9	9,1
50	VH_3_15	VL_2-14	3.0 / 3.5 / 3.0	96.0 / 98.0 / 100	72.3 / 72.2	61	99	75,5	8,9
51	VH_3_21	VK_1_06	2	98	72.9 / 73.1	56	100	74,7	9,2
52	VH_3_21	VK_1_12	5,5	100	73,6	45,6	100	77,2	9,1
53	VH_3_21	VK_1_27	3	98	74.0 / 73.4	47,6	100	77,8	9
54	VH_3_21	VL_2-11	4	98	73.0 / 73.1	49,5	99	80	8,9
55	VH_3_21	VL_2-14	3.5 / 5.5	98.0 / 99.0	72.6 / 72.0	61	98	77	8,7
56	VH_3_21	VL_2-23	3,5	99	72.4 / 72.6	40	97	77,3	8,9
57	VH_3_21	VL_3-1	3.4 / 2.5	87.0 / 88.0	60,66	48	97	77,5	7,9
58	VH_3_23	VK_1_39	3	98	75,6	43,8	100	83,8	8,9
59	VH_3_23	VK_3_15	6	99	76,45	30	100	85	8,9
60	VH_3_23	VK_3_20	4,5	97	77,4	34,5	100	82	8,7
61	VH_3_23	VL_2-11	3	96	71,3	45,5	99	82,6	8,7
62	VH_3_23	VL_2-14	3,5	97	71,5	53,3	99	78	8,3
63	VH_3_23	VL_2-23	3,5	98	71.7 / 72.4	52,7	99	79	8,7
64	VH_3_23	VL_3-1	3	98	71,5	40	100	81	7,6

Figure 18

No.	VH	VL	Purified fab expression mg/L	Purified Fab % monomer	Purified Fab Thermo-fluor	Purified IgG1 expression mg/L	Purified IgG1 % monomer	Purified IgG1 Thermafluor	IgG1 Isoelectric point
65	VH_3_23	VL_3-21	5,5	97	72,05	34,5	100	79,1	8,3
66	VH_3_30	VK_3_15	7	98	71,3	27,8	100	80,7	9,2
67	VH_3_30	VK_3_20	3	97/100	72,5	31,7	100	81	9,1
68	*VH_3_30*	*VL_2-23*	3,5	98	72.0 / 72.2	45,7	96	80,5	9
69	VH_3_30	VL_3-1	2.4 / 1.0	94		57,1	98	79,5	8,2
70	VH_3_30	VL_3-21	4,5	97	72.6 / 72.0	50	100	78	8,9
71	VH_3_53	VK_1_39	5,5	98	68,8	57,1	100	74,1	8,9
72	VH_3_53	VK_3_15	4,5	100	70,05	61	100	73,8	8,9
73	VH_3_53	VL_2-11	7,5	100	71	50	100	74,3	8,7
74	VH_3_53	VL_2-23	6	100	67,98	40	99	80,8	8,7
75	*VH_3_53*	*VL_3-1*	2,5	97	70,18	49,5	96	81,2	7,6
76	VH_3_74	VK_1_05	4	99	72,9	61,8	100	75,5	8,7
77	VH_3_74	VK_1_06	3,5	99	74,01	52,2	100	77	9,2
78	VH_3_74	VK_1_12	5,5	99	74,48	62	100	78,5	9,1
79	VH_3_74	VK_1_27	3,5	98	76,02	56	100	78,5	9,1
80	VH_3_74	VK_3_20	3,5	100	73	43,8	100	80,1	8,9
81	VH_3_74	VL_1-51	4,5	98	72,25	62,9	99	80,9	8,9
82	*VH_3_74*	*VL_3-1*	2.4 / 3.5	98.0 / 81.0	71,84	53,9	95	79	7,9
83	VH_5_51	VK_1_39	2,5	99	70,08	36,4	100	73,3	8,9
84	VH_5_51	VL_1-40	4	99	73,09	38,3	99	77,7	8,3
85	VH_5_51	VL_1-47	6	99	73,3	40	97	76,5	9
86	VH_5_51	VL_1-51	5,5	100	72,47	59	99	75,4	8,6
87	VH_5_51	VL_3-1	2	100		34	97	76	7,6
88	*VH_6_1*	*VK_1_06*	2	98	71,97	80	100	n.a.	9,3
89	VH_6_1	VK_1_09	7	99	76,4	66,7	100	80,3	9,2
90	VH_6_1	VK_1_27	7.5 / 5.0	100 / 80	76,13	84	99	80,2	9,2
91	VH_6_1	VK_3_15	6	100	75,75	38,3	100	76,4	9,2
92	VH_6_1	VK_3_20	8	100	72,69	70,5	100	77,5	9,1
93	VH_6_1	VL_1-47	7,5	100	70,28	38	98	73,9	9,3
94	VH_6_1	VL_1-51	8	100	73,6	62,9	99	76,9	9
95	VH_6_1	VL_3-1	2.3 / 3.0	97.0 / 98.0	70,9	26	97	n.a.	8,2

Figure 19

No.	VH	VL	Tm before Acid	Tm after Acid	Change	Absorption Inital	Absorption 15 min Acid	Absorption 100 min Acid	Absorption neutralization
1	VH_1_18	VK_1_39		79,2		0,041	0,061	0,05	0,042
2	VH_1_18	VK_3_11							
3	VH_1_18	VK_3_15	81,9	81,9	0	0,036	0,054	0,042	0,038
4	VH_1_18	VK_3_20		77,7		0,037	0,043	0,042	0,037
5	VH_1_18	VL_1-40	83,7	84	-0,3	0,036	0,051	0,039	0,038
6	VH_1_18	VL_1-47	84,2	84,2	0	0,036	0,051	0,04	0,038
7	VH_1_18	VL_2-23	80,9	80,7	0,2	0,036	0,049	0,04	0,039
8	VH_1_18	VL_3-1	84,9	84,7	0,2	0,036	0,049	0,04	0,038
9	VH_1_46	VK_1_09	78,2	78,1	0,1	0,036	0,053	0,045	0,042
10	VH_1_46	VK_3_15	77,4	77,6	-0,2	0,036	0,045	0,041	0,037
11	VH_1_46	VL_1-40	80,6	80,7	-0,1	0,036	0,045	0,04	0,039
12	VH_1_46	VL_1-51	79,4	79,3	0,1	0,036	0,04	0,039	0,038
13	VH_1_46	VL_2-23	78,7	78,6	0,1	0,037	0,057	0,041	0,038
14	VH_1_46	VL_3-1	76	75,9	0,1	0,043	0,062	0,067	0,096
15	VH_1_46	VL_3-21	74	74,2	-0,2	0,039	0,044	0,042	0,043
16	VH_1_69*01	VK_1_27							
17	VH_1_69*01	VK_3_11	77,6	78	0	0,037	0,048	0,039	0,038
18	VH_1_69*01	VL_1-40	81,7	81,7	0	0,039	0,05	0,048	0,042
19	VH_1_69*01	VL_1-51	78,2	78,1	0,1	0,037	0,045	0,042	0,04
20	VH_1_69*01	VL_3-1	79,2	79,1	0,1	0,041	0,047	0,046	0,048
21	VH_1_69*01	VL_3-21	78,4	76,4	2	0,04	0,06	0,045	0,038
22	VH_3_07	VK_1_12	77,8	78,2	-0,4	0,036	0,047	0,041	0,037
23	VH_3_07	VK_1_16		74,4		0,036	0,046	0,043	0,038
24	VH_3_07	VK_1_27	80,2	80,4	-0,2	0,039	0,041	0,04	0,04
25	VH_3_07	VK_1_39	80	80,2	-0,2	0,037	0,038	0,038	0,039
26	VH_3_07	VK_3_15	79,5	79,7	-0,2	0,037	0,038	0,037	0,038
27	VH_3_07	VK_3_20	78,5	78,9	-0,4	0,038	0,042	0,043	0,041
28	VH_3_07	VL_1-47	78,8	79,1	-0,3	0,037	0,039	0,037	0,037
29	VH_3_07	VL_1-51	79,8	79,8	0	0,039	0,041	0,041	0,04
30	VH_3_07	VL_2-23	81,2	81,2	0	0,043	0,049	0,043	0,041
31	VH_3_07	VL_3-1	81,2	81,2	0	0,036	0,042	0,037	0,038
32	VH_3_11	VK_1_05	74,5	75	-0,5	0,036	0,037	0,037	0,036

Figure 20

No.	VH	VL	Initial Radius [nm]	Initial % Poly-dispersity	Radius [nm] After acid	% Poly-dispersity After acid	Particle Staining before acid	Particle Staining after acid	**Cumulative score**
1	VH_1_18	VK_1_39	5,7	4,8	5,4	9,1	1	3,00	1050
2	VH_1_18	VK_3_11							
3	VH_1_18	VK_3_15	5,2	4,1	5,3	7,2	1	2	1100
4	VH_1_18	VK_3_20	5,4	2,8	5,3	7,1	2	3	1450
5	VH_1_18	VL_1-40	5,6	5,7	5,7	7,8	1	2	1525
6	VH_1_18	VL_1-47	5,3	4,3	5,5	7,4	1	2	1450
7	VH_1_18	VL_2-23	5,4	2,7	5,6	9,5	1	1	1450
8	VH_1_18	VL_3-1	5,4	5,5	5,5	9,5	1	1	1600
9	VH_1_46	VK_1_09	5,1	2,2	5,3	6,8	1	1	1475
10	VH_1_46	VK_3_15	5,3	6,9	5,4	10,6	1	1,5	1550
11	VH_1_46	VL_1-40	5,6	8,4	5,4	8,5	1	1	1600
12	VH_1_46	VL_1-51	5,1	2,4	5,3	7,4	2,5	3	1500
13	VH_1_46	VL_2-23	5,2	2,1	5,2	5,3	2	1	1450
14	VH_1_46	VL_3-1	12,2	39,8	39	mm	2	4	400
15	VH_1_46	VL_3-21	9,3	mm	8,3	mm	1	3	875
16	VH_1_69*01	VK_1_27							
17	VH_1_69*01	VK_3_11	5,3	5,6	5,4	11,3	1	2	1525
18	VH_1_69*01	VL_1-40	7,1	10,6	7,8	16	3	2,5	1150
19	VH_1_69*01	VL_1-51	5,3	3,6	5,3	6,3	1	1	1575
20	VH_1_69*01	VL_3-1	7,3	26,2	33	mm	1	1	575
21	VH_1_69*01	VL_3-21	5,5	8,7	5,7	16,3	1	1	1025
22	VH_3_07	VK_1_12	5,1	2,6	5,2	5,6	2,5	1	1425
23	VH_3_07	VK_1_16	5,6	14,1	5,2	5,9	1,5	2,5	1575
24	VH_3_07	VK_1_27	5,1	2,2	5,3	9	1	2	1450
25	VH_3_07	VK_1_39	5,2	2,7	5,3	6,3	1	3,5	1450
26	VH_3_07	VK_3_15	5,1	2,5	5,3	6,8	2	2,5	1500
27	VH_3_07	VK_3_20	5,3	8,8	5,3	9,4	1	2	E12
28	VH_3_07	VL_1-47	5,1	3,6	5,2	5,9	1	1	1700
29	VH_3_07	VL_1-51	5,2	4,5	5,1	4,9	1	2	1325
30	VH_3_07	VL_2-23	5,8	12,4	5,5	6,6	1	1	1600
31	VH_3_07	VL_3-1	5,3	4,1	5,4	7,3	1	1	1600
32	VH_3_11	VK_1_05	5,1	2,2	5,2	5,2	1	2	1150

Figure 21

No.	VH	VL	Tm before Acid	Tm after Acid	Change	Absorption Inital	Absorption 15 min Acid	Absorption 100 min Acid	Absorption neutralization
33	VH_3_11	VK_1_39	79	79,5	-0,5	0,037	0,04	0,038	0,044
34	VH_3_11	VK_3_15	78,8	79	-0,2	0,04	0,042	0,041	0,041
35	VH_3_11	VL_1-40		79,1		0,037	0,051	0,049	0,044
36	VH_3_11	VL_1-47	77,1	77,1	0	0,036	0,042	0,04	0,039
37	VH_3_11	VL_1-51	76,9	77	-0,1	0,036	0,04	0,038	0,039
38	VH_3_11	VL_2-23	74,3	74,3	0	0,036	0,038	0,039	0,038
39	VH_3_15	VK_1_05	76,4	76,7	-0,3	0,037	0,047	0,043	0,039
40	VH_3_15	VK_1_06		76,2		0,038	0,04	0,04	0,036
41	VH_3_15	VK_1_09	81,7	81,9	-0,2	0,035	0,043	0,041	0,039
42	VH_3_15	VK_1_12	78,6	79,6	-1	0,036	0,038	0,037	0,037
43	VH_3_15	VK_1_16	76,4	76,7	-0,3	0,038	0,046	0,042	0,04
44	VH_3_15	VK_1_27		80,1		0,043	0,05	0,045	0,037
45	VH_3_15	VK_3_11		79,9		0,043	0,045	0,045	0,044
46	VH_3_15	VK_3_15	80,3	80,5	-0,2	0,04	0,045	0,044	0,043
47	VH_3_15	VL_1-40	80,4	80,4	0	0,036	0,046	0,04	0,037
48	VH_3_15	VL_1-47	78,1	80,3	-2,2	0,035	0,038	0,038	0,036
49	VH_3_15	VL_1-51		78,8		0,035	0,046	0,047	0,036
50	VH_3_15	VL_2-14	75,5	75,7	-0,2	0,036	0,037	0,037	0,037
51	VH_3_21	VK_1_06	74,5	75,7	-1,2	0,036	0,041	0,043	0,039
52	VH_3_21	VK_1_12		77,2		0,036	0,042	0,041	0,038
53	VH_3_21	VK_1_27	77,6	78,1	-0,5	0,036	0,041	0,047	0,045
54	VH_3_21	VL_2-11	79,7	79,8	-0,1	0,037	0,049	0,045	0,042
55	VH_3_21	VL_2-14	76,4	76,6	-0,2	0,037	0,058	0,046	0,042
56	VH_3_21	VL_2-23	76,6	77	-0,4	0,037	0,044	0,04	0,038
57	VH_3_21	VL_3-1	77,4	77,3	0,1	0,038	0,046	0,048	0,047
58	VH_3_23	VK_1_39	83,7	83,9	-0,2	0,037	0,044	0,04	0,037
59	VH_3_23	VK_3_15		85		0,039	0,045	0,05	0,047
60	VH_3_23	VK_3_20	82,3	82,3	0	0,036	0,04	0,038	0,037
61	VH_3_23	VL_2-11	82,5	82,8	-0,3	0,035	0,041	0,038	0,036
62	VH_3_23	VL_2-14	78,1	78,1	0	0,036	0,039	0,038	0,037
63	VH_3_23	VL_2-23	79	79	0	0,036	0,039	0,038	0,038
64	VH_3_23	VL_3-1	80,9	80,1	0,8	0,037	0,041	0,038	0,037

Figure 22

No.	VH	VL	Initial Radius [nm]	Initial % Poly-dispersity	Radius [nm] After acid	% Poly-dispersity After acid	Particle Staining before acid	Particle Staining after acid	**Cumulative score**
33	VH_3_11	VK_1_39	5,2	2,9	5,5	17,2	2	2	1075
34	VH_3_11	VK_3_15	5,2	5,6	5,2	5,7	1	2	1050
35	VH_3_11	VL_1-40	5,1	2,4	5,1	5,1	1	1	1550
36	VH_3_11	VL_1-47	5,2	6	5,2	7,4	1	3,5	1550
37	VH_3_11	VL_1-51	5,1	1,9	5,1	4,8	1	1	1675
38	VH_3_11	VL_2-23	5,1	2,4	5,2	8,7	1	1	1750
39	VH_3_15	VK_1_05	5,1	3	5,2	8,3	2	2	1575
40	VH_3_15	VK_1_06	5,1	2,3	5,2	3,8	1	2	1400
41	VH_3_15	VK_1_09	7	22	5,4	14,4	2,5	2	1175
42	VH_3_15	VK_1_12	5,1	2,2	5,2	4,6	2	2	1575
43	VH_3_15	VK_1_16	5,2	3,5	5,2	3,7	3	2	1025
44	VH_3_15	VK_1_27	5,1	3	5,3	9,2	1	2	1450
45	VH_3_15	VK_3_11	5,2	5,3	5,3	13,1	2	2	1225
46	VH_3_15	VK_3_15	5,4	17,7	5,5	16,4	1	2,5	1025
47	VH_3_15	VL_1-40	5,3	11,3	5,2	7,9	3	1	1000
48	VH_3_15	VL_1-47	5,1	4	5,2	5	1	2	1150
49	VH_3_15	VL_1-51	5,6	14,1	5,2	5,9	1	2	1275
50	VH_3_15	VL_2-14	5,5	20,7	5,5	13,1	2	1	1425
51	VH_3_21	VK_1_06	5,1	2	5,2	6	1	3	1300
52	VH_3_21	VK_1_12	5,2	3,6	5,7	16,8	3	2	1500
53	VH_3_21	VK_1_27	5,2	3,3	5,3	7,6	1	2	1475
54	VH_3_21	VL_2-11	5,1	2	5,2	6	2	2	1375
55	VH_3_21	VL_2-14	5,4	5,8	5,3	5	1	2	1525
56	VH_3_21	VL_2-23	5,3	4,7	5,2	4,8	1	1	1650
57	VH_3_21	VL_3-1	8	mm	PD	mm	1	2	675
58	VH_3_23	VK_1_39	5,3	6,3	5,2	5,3	2	2	1250
59	VH_3_23	VK_3_15	5,1	2,5	5,2	6	1	2	1375
60	VH_3_23	VK_3_20	5,2	4,4	5,2	6,2	1	2,5	1300
61	VH_3_23	VL_2-11	5,2	3,6	5,3	7,5	2	2	1375
62	VH_3_23	VL_2-14	5,1	3,2	5,2	5,1	2	2	1375
63	VH_3_23	VL_2-23	5,1	2,3	5,2	6,2	1	2	1325
64	VH_3_23	VL_3-1	5,2	6	5,3	5,9	1	2	1750

Figure 23

No.	VH	VL	Tm before Acid	Tm after Acid	Change	Absorption Inital	Absorption 15 min Acid	Absorption 100 min Acid	Absorption neutralization
65	VH_3_23	VL_3-21	79	79,2	-0,2	0,036	0,041	0,038	0,037
66	VH_3_30	VK_3_15	81,1	81,2	-0,1	0,037	0,039	0,038	0,037
67	VH_3_30	VK_3_20	80,9	81,2	-0,3	0,037	0,043	0,043	0,044
68	VH_3_30	VL_2-23	80	80	0	0,036	0,041	0,039	0,037
69	VH_3_30	VL_3-1	79,7	79,6	0,1	0,039	0,046	0,049	0,054
70	VH_3_30	VL_3-21	78	78,2	-0,2	0,039	0,043	0,042	0,041
71	VH_3_53	VK_1_39	73,8	74,5	-0,7	0,042	0,047	0,045	0,044
72	VH_3_53	VK_3_15	73,6	74,1	-0,5	0,037	0,041	0,039	0,038
73	VH_3_53	VL_2-11	73,6	73,8	-0,2	0,036	0,038	0,043	0,037
74	VH_3_53	VL_2-23	69,6	69,6	0	0,036	0,042	0,039	0,037
75	VH_3_53	VL_3-1	72,6	73	-0,4	0,036	0,04	0,038	0,039
76	VH_3_74	VK_1_05	75	75,6	-0,6	0,036	0,043	0,039	0,04
77	VH_3_74	VK_1_06	77,8	77,9	-0,1	0,037	0,039	0,038	0,037
78	VH_3_74	VK_1_12	79	79,8	-0,8	0,038	0,04	0,039	0,038
79	VH_3_74	VK_1_27	78	78,3	-0,3	0,037	0,049	0,041	0,038
80	VH_3_74	VK_3_20	80,3	80	0,3	0,036	0,039	0,038	0,037
81	VH_3_74	VL_1-51	80,7	80,5	0,2	0,036	0,04	0,04	0,038
82	VH_3_74	VL_3-1	78,8	78,6	0,2	0,036	0,041	0,038	0,04
83	VH_5_51	VK_1_39	73	73,6	-0,6	0,039	0,045	0,043	0,041
84	VH_5_51	VL_1-40	77,6	77,8	-0,2	0,037	0,04	0,039	0,038
85	VH_5_51	VL_1-47	76,4	76,7	-0,3	0,036	0,041	0,038	0,037
86	VH_5_51	VL_1-51	75,7	75,6	0,1	0,035	0,04	0,04	0,04
87	VH_5_51	VL_3-1		75,5		0,036	0,047	0,042	0,04
88	VH_6_1	VK_1_06	73,6	73,3	0,3	0,037	0,038	0,037	0,037
89	VH_6_1	VK_1_09	80	80,3	-0,3	0,038	0,04	0,04	0,039
90	VH_6_1	VK_1_27	80,2	80,4	-0,2	0,037	0,037	0,039	0,038
91	VH_6_1	VK_3_15		78,1		0,04	0,046	0,045	0,042
92	VH_6_1	VK_3_20	77,2	77,4	-0,2	0,036	0,038	0,038	0,038
93	VH_6_1	VL_1-47	73,6	73,8	-0,2	0,046	0,081	0,078	0,094
94	VH_6_1	VL_1-51	76,6	76,6	0	0,036	0,039	0,037	0,038
95	VH_6_1	VL_3-1	69,4	69,9	-0,5	0,047	0,075	0,072	0,113

Figure 24

No.	VH	VL	Initial Radius [nm]	Initial % Poly-dispersity	Radius [nm] After acid	% Poly-dispersity After acid	Particle Staining before acid	Particle Staining after acid	**Cumulative score**
65	VH_3_23	VL_3-21	5,4	6,2	5,4	5,7	2	1	1700
66	VH_3_30	VK_3_15	5,1	2,3	5,2	5,8	2	2	1575
67	VH_3_30	VK_3_20	5,3	5,9	5,3	7,7	2	2,5	1275
68	VH_3_30	VL_2-23	5,2	2,9	5,4	9	2	1	1725
69	VH_3_30	VL_3-1	13,9	mm	12	mm	2	2	525
70	VH_3_30	VL_3-21	5,1	2,8	5,2	4,6	2	2	1600
71	VH_3_53	VK_1_39	5,2	3,6	5,4	9,3	2	2	1375
72	VH_3_53	VK_3_15	5,2	4,2	5,2	6,3	1	1	1275
73	VH_3_53	VL_2-11	5,1	2,8	5,1	5,3	2	1	1275
74	VH_3_53	VL_2-23	5,1	2,4	5,3	6,2	2	1	1250
75	VH_3_53	VL_3-1	5,4	7	6,1	26,6	3	2,5	1475
76	VH_3_74	VK_1_05	5,1	2,2	5,2	5,7	2	1	1450
77	VH_3_74	VK_1_06	5,1	2	5,2	5,4	2,5	2	1725
78	VH_3_74	VK_1_12	5,1	2,1	5,3	6,7	2	1	1650
79	VH_3_74	VK_1_27	5,2	3,6	5,3	5,8	2	2	1525
80	VH_3_74	VK_3_20	5,1	2,4	5,6	18,9	2	2	1525
81	VH_3_74	VL_1-51	5,1	4,9	5,2	6,6	2,5	2	1325
82	VH_3_74	VL_3-1	5,3	3,2	5,5	8,6	2	2	1650
83	VH_5_51	VK_1_39	5,8	19,6	5,3	8,1	1,5	2	1650
84	VH_5_51	VL_1-40	5,5	13,6	5,3	6,7	2,5	2	1625
85	VH_5_51	VL_1-47	5,3	8	5,4	11,9	2	2	1575
86	VH_5_51	VL_1-51	5,1	2,7	5,2	6,2	1	2,5	1375
87	VH_5_51	VL_3-1	5,4	8,5	5,5	11,4	1,5	3	1300
88	VH_6_1	VK_1_06	5,2	2,5	5,2	4,2	2,5	1,5	1600
89	VH_6_1	VK_1_09	5,1	2,6	5,3	5,5	3	1	1450
90	VH_6_1	VK_1_27	5,3	4,3	5,5	8,4	2	1	1450
91	VH_6_1	VK_3_15	5,6	11,7	5,3	7,9	1	2	1075
92	VH_6_1	VK_3_20	5,2	5,1	5,2	5	2	2	1450
93	VH_6_1	VL_1-47	29,4	mm	100	mm	2,5	4	150
94	VH_6_1	VL_1-51	5	3,1	5,5	15,7	1	1	1725
95	VH_6_1	VL_3-1	30	33	na	na	2	4	375

Figure 25

Kabat CDRs	FRAMEWORK1																												HCDR1						
Kabat No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	35a	35b
VH1-18	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S	V	K	V	S	C	K	A	S	G	Y	T	F	T	S			Y	G	I	S
VH1-46	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S	V	K	V	S	C	K	A	S	G	Y	T	F	T	S			Y	Y	M	H
VH1-69*01	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	S	C	K	A	S	G	G	T	F	S	S			Y	A	I	S
VH3-07	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	S			Y	W	M	S
VH3-11	Q	V	Q	L	V	E	S	G	G	G	L	V	K	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	D			Y	Y	M	S
VH3-15	E	V	Q	L	V	E	S	G	G	G	L	V	K	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	N			A	W	M	S
VH3-21	E	V	Q	L	V	E	S	G	G	G	L	V	K	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	S			Y	S	M	N
VH3-23	E	V	Q	L	L	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	S			Y	A	M	S
VH3-30	Q	V	Q	L	V	E	S	G	G	G	V	V	Q	P	G	R	S	L	R	L	S	C	A	A	S	G	F	T	F	S	S	.	.	Y	A	M	H
VH3-53	E	V	Q	L	V	E	S	G	G	G	L	I	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	V	S	S			N	Y	M	S
VH3-74	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	S			Y	W	M	H
VH5-51	E	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	E	S	L	K	I	S	C	K	G	S	G	Y	S	F	T	S			Y	W	I	G
VH6-01	Q	V	Q	L	Q	Q	S	G	P	G	L	V	K	P	S	Q	T	L	S	L	T	C	A	I	S	G	D	S	V	S	S	N	S	A	A	W	N

Kabat No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	35a	35b
VH1-18	CAG	GTG	CAG	CTG	GTG	CAG	AGC	GGT	GCC	GAA	GTG	AAA	AAA	CCA	GGC	GCC	AGC	GTG	AAA	GTT	AGC	TGC	AAA	GCC	AGC	GGC	TAT	ACC	TTT	ACC	AGC			TAT	GGC	ATT	AGC
VH1-46	CAG	GTG	CAG	CTG	GTG	CAG	AGC	GGT	GCC	GAA	GTG	AAA	AAA	CCA	GGC	GCC	AGC	GTG	AAA	GTT	AGC	TGC	AAA	GCC	AGC	GGC	TAT	ACC	TTC	ACC	AGC			TAC	TAT	ATG	CAT
VH1-69*01	CAG	GTG	CAG	CTG	GTG	CAG	AGC	GGT	GCC	GAA	GTG	AAA	AAA	CCA	GGC	AGC	AGC	GTG	AAA	GTG	AGC	TGT	AAA	GCC	AGC	GGT	GGC	ACC	TTT	AGC	AGC			TAT	GCC	ATT	AGC
VH3-07	GAA	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	CTG	GTG	CAG	CCA	GGT	GGT	AGC	CTG	CGC	CTG	AGC	TGC	GCC	GCC	AGC	GGC	TTT	ACC	TTT	AGC	AGC			TAT	TGG	ATG	AGC
VH3-11	CAG	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	CTG	GTG	AAA	CCA	GGC	GGT	AGC	CTG	CGC	CTG	AGC	TGC	GCC	GCC	AGC	GGC	TTT	ACC	TTT	AGC	GAT			TAC	TAC	ATG	AGC
VH3-15	GAA	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	CTG	GTG	AAA	CCA	GGC	GGT	AGC	CTG	CGC	CTG	AGC	TGC	GCC	GCC	AGC	GGC	TTT	ACC	TTT	AGC	AAC			GCC	TGG	ATG	AGC
VH3-21	GAA	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	CTG	GTG	AAA	CCA	GGC	GGT	AGC	CTG	CGC	CTG	AGC	TGC	GCC	GCC	AGC	GGC	TTT	ACC	TTT	AGC	AGC			TAT	AGC	ATG	AAC
VH3-23	GAA	GTG	CAG	CTG	CTG	GAA	AGC	GGT	GGC	GGT	CTG	GTG	CAG	CCA	GGT	GGT	AGC	CTG	CGC	CTG	AGC	TGT	GCC	GCA	AGC	GGC	TTT	ACC	TTT	AGC	AGC			TAT	GCC	ATG	AGC
VH3-30	CAG	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	GTT	GTG	CAG	CCA	GGT	CGC	AGT	CTG	CGC	CTG	AGC	TGT	GCC	GCC	AGC	GGC	TTT	ACC	TTT	AGC	AGC			TAT	GCC	ATG	CAT
VH3-53	GAA	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	CTG	ATT	CAG	CCA	GGC	GGT	AGC	CTG	CGC	CTG	AGC	TGT	GCC	GCC	AGC	GGC	TTT	ACC	GTT	AGC	AGC			AAC	TAT	ATG	AGC
VH3-74	GAA	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	CTG	GTG	CAG	CCA	GGT	GGT	AGC	CTG	CGC	CTG	AGC	TGC	GCC	GCC	AGC	GGC	TTT	ACC	TTT	AGC	AGC			TAT	TGG	ATG	CAT
VH5-51	GAA	GTG	CAG	CTG	GTG	CAG	AGC	GGT	GCC	GAA	GTG	AAA	AAA	CCG	GGC	GAA	AGC	CTG	AAA	ATC	AGC	TGC	AAA	GGC	AGC	GGC	TAT	AGC	TTT	ACC	AGC			TAT	TGG	ATT	GGC
VH6-01	CAG	GTG	CAG	CTG	CAA	CAG	AGC	GGC	CCA	GGC	CTG	GTT	AAA	CCG	AGC	CAG	ACC	CTG	AGC	CTG	ACC	TGC	GCC	ATT	AGC	GGC	GAT	AGC	GTT	AGC	AGC	AAC	AGC	GCC	GCC	TGG	AAC

Figure 26

Kabat CDRs	FRAMEWORK2														HCDR2																
Kabat No.	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	52a	52b	52c	53	54	55	56	57	58	59	60	61	62	63	64	65
VH1-18	W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	W	I	S	A			Y	N	G	N	T	N	Y	A	Q	K	L	Q	G
VH1-46	W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	I	I	N	P			S	G	G	S	T	S	Y	A	Q	K	F	Q	G
VH1-69*01	W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	G	I	I	P			I	F	G	T	A	N	Y	A	Q	K	F	Q	G
VH3-07	W	V	R	Q	A	P	G	K	G	L	E	W	V	A	N	I	K	Q			D	G	S	E	K	Y	Y	V	D	S	V	K	G
VH3-11	W	I	R	Q	A	P	G	K	G	L	E	W	V	S	Y	I	S	S			S	G	S	T	I	Y	Y	A	D	S	V	K	G
VH3-15	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	R	I	K	S	K	T	D	G	G	T	T	D	Y	A	A	P	V	K	G
VH3-21	W	V	R	Q	A	P	G	K	G	L	E	W	V	S	S	I	S	S			S	S	S	Y	I	Y	Y	A	D	S	V	K	G
VH3-23	W	V	R	Q	A	P	G	K	G	L	E	W	V	S	A	I	S	G			S	G	G	S	T	Y	Y	A	D	S	V	K	G
VH3-30	W	V	R	Q	A	P	G	K	G	L	E	W	V	A	V	I	S	Y	.	.	D	G	S	N	K	Y	Y	A	D	S	V	K	G
VH3-53	W	V	R	Q	A	P	G	K	G	L	E	W	V	S	V	I	Y	S				G	G	S	T	Y	Y	A	D	S	V	K	G
VH3-74	W	V	R	Q	A	P	G	K	G	L	V	W	V	S	R	I	N	S			D	G	S	S	T	S	Y	A	D	S	V	K	G
VH5-51	W	V	R	Q	M	P	G	K	G	L	E	W	M	G	I	I	Y	P			G	D	S	D	T	R	Y	S	P	S	F	Q	G
VH6-01	W	I	R	Q	S	P	S	R	G	L	E	W	L	G	R	T	Y	Y	R		S	K	W	Y	N	D	Y	A	V	S	V	K	S

Kabat No.	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	52a	52b	52c	53	54	55	56	57	58	59	60	61	62	63	64	65
VH1-18	TGG	GTT	CGC	CAG	GCC	CCA	GGC	CAG	GGT	CTG	GAA	TGG	ATG	GGC	TGG	ATT	AGC	GCC			TAT	AAC	GGC	AAC	ACC	AAC	TAC	GCC	CAG	AAA	CTG	CAA	GGC
VH1-46	TGG	GTT	CGC	CAG	GCC	CCA	GGC	CAG	GGT	CTG	GAA	TGG	ATG	GGC	ATT	ATT	AAC	CCG			AGC	GGC	GGC	AGC	ACC	AGC	TAT	GCA	CAG	AAA	TTT	CAG	GGC
VH1-69*01	TGG	GTT	CGC	CAG	GCA	CCA	GGT	CAG	GGT	CTG	GAA	TGG	ATG	GGT	GGC	ATT	ATT	CCG			ATT	TTT	GGC	ACC	GCC	AAC	TAT	GCC	CAG	AAA	TTT	CAG	GGT
VH3-07	TGG	GTT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTG	GCG	AAC	ATC	AAA	CAG			GAT	GGC	AGC	GAG	AAA	TAC	TAT	GTG	GAT	AGC	GTG	AAA	GGC
VH3-11	TGG	ATT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTT	AGC	TAT	ATT	AGC	AGC			AGT	GGC	AGC	ACC	ATC	TAT	TAC	GCC	GAT	AGC	GTG	AAA	GGC
VH3-15	TGG	GTT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTT	GGC	CGC	ATC	AAA	AGC	AAA	ACC	GAT	GGC	GGC	ACC	ACC	GAT	TAT	GCC	GCC	CCA	GTG	AAA	GGC
VH3-21	TGG	GTT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTT	AGC	AGC	ATC	AGC	AGC			AGT	AGC	AGC	TAT	ATC	TAT	TAC	GCC	GAT	AGC	GTG	AAA	GGC
VH3-23	TGG	GTG	CGC	CAA	GCA	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTG	AGC	GCC	ATT	AGC	GGC			AGC	GGT	GGC	AGC	ACC	TAT	TAT	GCC	GAT	AGC	GTG	AAA	GGT
VH3-30	TGG	GTT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTG	GCC	GTG	ATT	AGC	TAT			GAT	GGC	AGC	AAC	AAA	TAT	TAC	GCC	GAT	AGC	GTG	AAA	GGC
VH3-53	TGG	GTT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTT	AGC	GTG	ATC	TAT	AGC				GGC	GGC	AGC	ACC	TAT	TAT	GCC	GAT	AGC	GTG	AAA	GGC
VH3-74	TGG	GTT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GTT	TGG	GTT	AGC	CGC	ATT	AAC	AGC			GAC	GGC	AGC	AGC	ACC	AGC	TAT	GCC	GAT	AGC	GTG	AAA	GGC
VH5-51	TGG	GTT	CGC	CAG	ATG	CCG	GGC	AAA	GGC	CTG	GAA	TGG	ATG	GGC	ATT	ATC	TAT	CCG			GGC	GAT	AGC	GAT	ACC	CGC	TAT	AGC	CCG	AGC	TTT	CAG	GGC
VH6-01	TGG	ATT	CGC	CAG	AGC	CCG	AGC	CGC	GGT	CTG	GAA	TGG	CTG	GGC	CGC	ACC	TAT	TAT		CGC	AGC	AAA	TGG	TAC	AAC	GAT	TAC	GCC	GTT	AGC	GTG	AAA	AGC

Figure 27

Kabat CDRs	FRAMEWORK3																														
Kabat No.	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	82A	82B	82C	83	84	85	86	87	88	89	90	91	92	93	94
VH1-18	R	V	T	M	T	T	D	T	S	T	S	T	A	Y	M	E	L	R	S	L	R	S	D	D	T	A	V	Y	Y	C	A	R
VH1-46	R	V	T	M	T	R	D	T	S	T	S	T	V	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R
VH1-69*01	R	V	T	I	T	A	D	E	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R
VH3-07	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH3-11	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH3-15	R	F	T	I	S	R	D	D	S	K	N	T	L	Y	L	Q	M	N	S	L	K	T	E	D	T	A	V	Y	Y	C	A	R
VH3-21	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH3-23	R	F	T	I	S	R	D	N	S	K	N	T	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH3-30	R	F	T	I	S	R	D	N	S	K	N	T	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH3-53	R	F	T	I	S	R	D	N	S	K	N	T	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH3-74	R	F	T	I	S	R	D	N	A	K	N	T	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH5-51	Q	V	T	I	S	A	D	K	S	I	S	T	A	Y	L	Q	W	S	S	L	K	A	S	D	T	A	M	Y	Y	C	A	R
VH6-01	R	I	T	I	N	P	D	T	S	K	N	Q	F	S	L	Q	L	N	S	V	T	P	E	D	T	A	V	Y	Y	C	A	R

Kabat No.	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	82A	82B	82C	83	84	85	86	87	88	89	90	91	92	93	94
VH1-18	CG	C	GTG	ACC	ATG	ACC	ACC	GAT	AC	C	AGC	AC	C	AGC	ACC	GCC	TAT	ATG	GAA	CTG	CGC	TCC	CTG	CGC	AGC	GAC	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH1-46	CG	C	GTG	ACC	ATG	ACC	CGC	GAT	AC	C	AGC	AC	C	AGC	ACC	GTG	TAT	ATG	GAA	CTG	AGC	AGC	CTG	CGC	AGC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH1-69*01	CG	C	GTG	ACC	ATT	ACC	GCA	GAT	GA	A	AGC	AC	C	AGC	ACC	GCC	TAT	ATG	GAA	CTG	AGC	AGC	CTG	CGC	AGC	GAA	GAT	A	CC	GCA	G	TG	TAT	TAT	T	GC	GCG	C	GG
VH3-07	CG	C	TTT	ACC	ATT	AGC	CGC	GAT	AA	C	GCC	AA	A	AAC	AGC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH3-11	CG	C	TTT	ACC	ATT	AGC	CGC	GAT	AA	C	GCC	AA	A	AAC	AGC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH3-15	CG	C	TTT	ACC	ATT	AGC	CGC	GAC	GA	T	AGC	AA	A	AAC	ACC	CTG	TAC	CTG	CAA	ATG	AAC	AGC	CTG	AAA	ACC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH3-21	CG	C	TTT	ACC	ATT	AGC	CGC	GAT	AA	C	GCC	AA	A	AAC	AGC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH3-23	CG	C	TTT	ACC	ATT	AGT	CGC	GAT	AA	C	AGC	AA	A	AAC	ACC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCA	GAA	GAT	A	CC	GCA	G	TT	TAT	TAT	T	GC	GCG	C	GG
VH3-30	CG	C	TTT	ACC	ATT	AGC	CGC	GAT	AA	C	AGC	AA	A	AAC	ACC	CTG	TAC	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH3-53	CG	C	TTT	ACC	ATT	AGC	CGC	GAT	AA	C	AGC	AA	A	AAC	ACC	CTG	TAC	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH3-74	CG	C	TTT	ACC	ATT	AGC	CGC	GAT	AA	C	GCC	AA	A	AAC	ACC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH5-51	CA	G	GTT	ACA	ATT	AGC	GCC	GAC	AA	A	AGC	AT	C	AGC	ACC	GCC	TAT	CTG	CAA	TGG	AGC	AGC	CTG	AAA	GCC	AGC	GAT	A	CC	GCC	A	TG	TAT	TAT	T	GC	GCG	C	GT
VH6-01	CG	C	ATT	ACC	ATT	AAC	CCG	GAT	AC	C	AGC	AA	A	AAC	CAG	TTC	AGC	CTG	CAA	CTG	AAC	AGC	GTG	ACC	CCG	GAA	GAT	A	CC	GCC	G	TG	TAT	TAC	T	GC	GCG	C	GT

Figure 28

Kabat CDRs	FRAMEWORK1																						LCDR1																
Kabat No	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	27a	27b	27c	27d	27e	27f	28	29	30	31	32	33	34
VK1-05	D	I	Q	M	T	Q	S	P	S	T	L	S	A	S	V	G	D	R	V	T	I	T	C	R	A	S	Q	S	I	S	.	.	.	.	.	.	S	W	L	A
VK1-06	A	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	A	S	Q	G	I	R	.	.	.	.	.	.	N	D	L	G
VK1-09	D	I	Q	L	T	Q	S	P	S	F	L	S	A	S	V	G	D	R	V	T	I	T	C	R	A	S	Q	G	I	S	.	.	.	.	.	.	S	Y	L	A
VK1-12	D	I	Q	M	T	Q	S	P	S	S	V	S	A	S	V	G	D	R	V	T	I	T	C	R	A	S	Q	G	I	S	.	.	.	.	.	.	S	W	L	A
VK1-16	D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	A	S	Q	G	I	S	.	.	.	.	.	.	N	Y	L	A
VK1-27	D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	A	S	Q	G	I	S	.	.	.	.	.	.	N	Y	L	A
VK1-39	D	I	Q	M	T	Q	S	P	S	S	L	S	A	S	V	G	D	R	V	T	I	T	C	R	A	S	Q	S	I	S	.	.	.	.	.	.	S	Y	L	N
VK3-11	E	I	V	L	T	Q	S	P	A	T	L	S	L	S	P	G	E	R	A	T	L	S	C	R	A	S	Q	S	V	S	.	.	.	.	.	.	S	Y	L	A
VK3-15	E	I	V	M	T	Q	S	P	A	T	L	S	V	S	P	G	E	R	A	T	L	S	C	R	A	S	Q	S	V	S	.	.	.	.	.	.	S	N	L	A
VK3-20	E	I	V	L	T	Q	S	P	G	T	L	S	L	S	P	G	E	R	A	T	L	S	C	R	A	S	Q	S	V	S	S	.	.	.	.	.	S	Y	L	A

Kabat No	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	27a	27b	27c	27d	27e	27f	28	29	30	31	32	33	34
VK1-05	GAT	ATT	CAG	ATG	ACC	CA	G	AGC	CC	G	AGC	ACC	CTG	AGC	GCA	AGC	GTG	GGC	GAT	CGC	GTG	ACC	ATT	AC	C	TGC	CGC	GCC	AGT	CAG	AGC	ATT	AGC					AGC	TGG	CTG	GCC
VK1-06	GCC	ATT	CAG	ATG	ACC	CA	G	AGC	CC	G	AGC	AGC	CTG	AGC	GCA	AGC	GTG	GGC	GAT	CGC	GTG	ACC	ATT	AC	C	TGC	CGC	GCC	AGC	CAG	GGC	ATT	CGC					AAC	GAT	CTG	GGC
VK1-09	GAT	ATT	CAG	CTG	ACC	CA	G	AGC	CC	G	AGC	TTT	CTG	AGC	GCC	AGC	GTG	GGC	GAT	CGC	GTG	ACC	ATT	AC	C	TGC	CGC	GCC	AGC	CAG	GGC	ATT	AGC					AGC	TAT	CTG	GCC
VK1-12	GAT	ATT	CAG	ATG	ACC	CA	G	AGC	CC	G	AGC	AGC	GTT	AGC	GCC	AGC	GTG	GGC	GAT	CGC	GTG	ACC	ATT	AC	C	TGC	CGC	GCC	AGT	CAG	GGC	ATT	AGC					AGC	TGG	CTG	GCC
VK1-16	GAT	ATT	CAG	ATG	ACC	CA	G	AGC	CC	G	AGC	AGC	CTG	AGC	GCA	AGC	GTG	GGC	GAT	CGC	GTG	ACC	ATT	AC	C	TGC	CGC	GCC	AGC	CAG	GGC	ATT	AGC					AAC	TAT	CTG	GCA
VK1-27	GAT	ATT	CAG	ATG	ACC	CA	G	AGC	CC	G	AGC	AGC	CTG	AGC	GCA	AGC	GTG	GGC	GAT	CGC	GTG	ACC	ATT	AC	C	TGC	CGC	GCC	AGC	CAG	GGC	ATT	AGC					AAC	TAT	CTG	GCC
VK1-39	GAT	ATT	CAG	ATG	ACC	CA	G	AGC	CC	G	AGC	AGC	CTG	AGC	GCC	AGC	GTG	GGT	GAT	CGC	GTG	ACC	ATT	AC	C	TGT	CGC	GCA	AGC	CAG	AGC	ATT	AGC					AGC	TAT	CTG	AAC
VK3-11	GAA	ATT	GTG	CTG	ACC	CA	G	AGC	CC	A	GCC	ACC	CTG	AGC	CTG	AGC	CCA	GGT	GAA	CGC	GCA	ACC	CTG	AG	C	TGT	CGC	GCA	AGC	CAG	AGC	GTG	AGC					AGC	TAT	CTG	GCC
VK3-15	GAA	ATT	GTG	ATG	ACC	CA	G	AGC	CC	G	GCC	ACC	CTG	AGC	GTT	AGC	CCA	GGC	GAA	CGC	GCA	ACC	CTG	AG	C	TGT	CGC	GCC	AGT	CAG	AGC	GTT	AGC					AGC	AAC	CTG	GCC
VK3-20	GAA	ATT	GTG	CTG	ACC	CA	G	AGC	CC	G	GGC	ACC	CTG	AGC	CTG	AGC	CCA	GGC	GAA	CGC	GCA	ACC	CTG	AG	C	TGT	CGC	GCC	AGT	CAG	AGC	GTT	AGC	AGC				AGC	TAT	CTG	GCC

Figure 29

Kabat CDRs	FRAMEWORK2															LCDR2						
Kabat No	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56
VK1-05	W	Y	Q	Q	K	P	G	K	A	P	K	L	L	I	Y	D	A	S	S	L	E	S
VK1-06	W	Y	Q	Q	K	P	G	K	A	P	K	L	L	I	Y	A	A	S	S	L	Q	S
VK1-09	W	Y	Q	Q	K	P	G	K	A	P	K	L	L	I	Y	A	A	S	T	L	Q	S
VK1-12	W	Y	Q	Q	K	P	G	K	A	P	K	L	L	I	Y	A	A	S	S	L	Q	S
VK1-16	W	F	Q	Q	K	P	G	K	A	P	K	S	L	I	Y	A	A	S	S	L	Q	S
VK1-27	W	Y	Q	Q	K	P	G	K	V	P	K	L	L	I	Y	A	A	S	T	L	Q	S
VK1-39	W	Y	Q	Q	K	P	G	K	A	P	K	L	L	I	Y	A	A	S	S	L	Q	S
VK3-11	W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y	D	A	S	N	R	A	T
VK3-15	W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y	G	A	S	T	R	A	T
VK3-20	W	Y	Q	Q	K	P	G	Q	A	P	R	L	L	I	Y	G	A	S	S	R	A	T

Kabat No	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56
VK1-05	T	GG	TAT	C	AG	CAG	AAA	CCG	GGC	AAA	GCC	CCG	AAA	CT G	CTG	AT C	TAT	GAT	GCC	AGC	AGC	CTG	GAA	AGC
VK1-06	T	GG	TAT	C	AG	CAG	AAA	CCG	GGC	AAA	GCC	CCG	AAA	CT G	CTG	AT C	TAT	GCC	GCC	AGC	AGC	CTG	CAA	AGC
VK1-09	T	GG	TAT	C	AG	CAG	AAA	CCG	GGC	AAA	GCC	CCG	AAA	CT G	CTG	AT C	TAT	GCC	GCC	AGC	ACC	CTG	CAA	AGC
VK1-12	T	GG	TAT	C	AG	CAG	AAA	CCG	GGC	AAA	GCC	CCG	AAA	CT G	CTG	AT C	TAT	GCC	GCC	AGC	AGC	CTG	CAA	AGC
VK1-16	T	GG	TTT	C	AG	CAG	AAA	CCG	GGC	AAA	GCC	CCG	AAA	AG C	CTG	AT C	TAT	GCC	GCC	AGC	AGT	CTG	CAA	AGC
VK1-27	T	GG	TAT	C	AG	CAG	AAA	CCG	GGC	AAA	GTG	CCG	AAA	CT G	CTG	AT C	TAT	GCC	GCC	AGC	ACC	CTG	CAA	AGC
VK1-39	T	GG	TAT	C	AG	CAG	AAA	CCA	GGC	AAA	GCC	CCA	AAA	CT G	CTG	AT T	TAT	GCC	GCA	AGC	AGC	CTG	CAA	AGC
VK3-11	T	GG	TAT	C	AA	CAG	AAA	CCA	GGC	CAG	GCA	CCA	CGC	CT G	CTG	AT T	TAT	GAT	GCC	AGC	AAT	CGC	GCA	ACC
VK3-15	T	GG	TAT	C	AG	CAG	AAA	CCG	GGT	CAG	GCC	CCA	CGC	CT G	CTG	AT C	TAT	GGT	GCC	AGC	ACC	CGC	GCC	ACC
VK3-20	T	GG	TAT	C	AG	CAG	AAA	CCG	GGC	CAG	GCC	CCA	CGC	CT G	CTG	AT C	TAT	GGT	GCC	AGC	AGC	CGC	GCC	ACC

Figure 30

Kabat CDRs	FRAMEWORK3																													
Kabat No	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88
VK1-05	G	V	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	P	E	D	F	A	T	Y	Y	C
VK1-06	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q	P	E	D	F	A	T	Y	Y	C
VK1-09	G	V	P	S	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	P	E	D	F	A	T	Y	Y	C
VK1-12	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q	P	E	D	F	A	T	Y	Y	C
VK1-16	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q	P	E	D	F	A	T	Y	Y	C
VK1-27	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q	P	E	D	V	A	T	Y	Y	C
VK1-39	G	V	P	S	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	Q	P	E	D	F	A	T	Y	Y	C
VK3-11	G	I	P	A	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	S	L	E	P	E	D	F	A	V	Y	Y	C
VK3-15	G	I	P	A	R	F	S	G	S	G	S	G	T	E	F	T	L	T	I	S	S	L	Q	S	E	D	F	A	V	Y	Y	C
VK3-20	G	I	P	D	R	F	S	G	S	G	S	G	T	D	F	T	L	T	I	S	R	L	E	P	E	D	F	A	V	Y	Y	C

Kabat No	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88
VK1-05	GGC	GTG	CCG	AGC	CGC	TTT	AGC	GGC	AGC	GGT	AGC	GGC	ACC	GAG	TTC	ACC	CTG	ACC	ATT	AGC	AGC	CTG	CAA	CCG	GAA	GAC	TTT	GCC	ACC	TAT	TAT	TGC
VK1-06	GGC	GTG	CCA	AGT	CGC	TTT	AGC	GGC	AGC	GGT	AGC	GGC	ACC	GAT	TTC	ACC	CTG	ACC	ATT	AGC	AGT	CTG	CAA	CCG	GAA	GAC	TTT	GCC	ACC	TAT	TAT	TGC
VK1-09	GGC	GTG	CCA	AGC	CGC	TTT	AGC	GGC	AGC	GGT	AGC	GGC	ACC	GAG	TTC	ACC	CTG	ACC	ATT	AGC	AGC	CTG	CAA	CCG	GAA	GAC	TTT	GCC	ACC	TAT	TAT	TGC
VK1-12	GGC	GTG	CCA	AGT	CGC	TTT	AGC	GGC	AGC	GGT	AGC	GGC	ACC	GAT	TTC	ACC	CTG	ACC	ATT	AGC	AGT	CTG	CAA	CCG	GAA	GAC	TTT	GCC	ACC	TAT	TAT	TGC
VK1-16	GGC	GTG	CCA	AGT	CGC	TTT	AGC	GGC	AGC	GGT	AGC	GGC	ACC	GAT	TTC	ACC	CTG	ACC	ATT	AGC	AGC	CTG	CAA	CCG	GAA	GAC	TTT	GCC	ACC	TAT	TAT	TGC
VK1-27	GGC	GTG	CCA	AGT	CGC	TTT	AGC	GGC	AGC	GGT	AGC	GGC	ACC	GAT	TTC	ACC	CTG	ACC	ATT	AGC	AGC	CTG	CAA	CCG	GAA	GAC	GTG	GCG	ACC	TAT	TAT	TGC
VK1-39	GGT	GTG	CCG	AGC	CGC	TTT	AGC	GGC	AGC	GGT	AGC	GGC	ACC	GAT	TTT	ACC	CTG	ACC	ATT	AGT	AGC	CTG	CAA	CCG	GAA	GAC	TTT	GCC	ACC	TAT	TAT	TGC
VK3-11	GGC	ATT	CCG	GCA	CGC	TTT	AGC	GGC	AGC	GGT	AGC	GGC	ACC	GAT	TTT	ACC	CTG	ACC	ATT	AGC	AGC	CTG	GAA	CCG	GAA	GAC	TTT	GCC	GTG	TAT	TAT	TGC
VK3-15	GGC	ATT	CCA	GCA	CGC	TTT	AGC	GGC	AGC	GGT	AGC	GGC	ACC	GAG	TTC	ACC	CTG	ACC	ATT	AGC	AGC	CTG	CAA	AGC	GAA	GAC	TTT	GCC	GTG	TAT	TAT	TGC
VK3-20	GGC	ATT	CCA	GAT	CGC	TTT	AGC	GGC	AGC	GGT	AGC	GGC	ACC	GAT	TTC	ACC	CTG	ACC	ATT	AGC	CGC	CTG	GAA	CCG	GAA	GAC	TTT	GCC	GTG	TAT	TAT	TGC

Figure 31

Kabat CDRs	FRAMEWORK1																						LCDR1																
Kabat No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	27a	27b	27c	27d	27e	27f	28	29	30	31	32	33	34
VL1-40	Q	S	V	L	T	Q	P	P	S	.	V	S	G	A	P	G	Q	R	V	T	I	S	C	T	G	S	S	S	N	I	G	A	G	.	.	.	Y	D	V	H
VL1-47	Q	S	V	L	T	Q	P	P	S	.	A	S	G	T	P	G	Q	R	V	T	I	S	C	S	G	S	S	S	N	I	G	S	.	.	.	.	N	Y	V	Y
VL1-51	Q	S	V	L	T	Q	P	P	S	.	V	S	A	A	P	G	Q	K	V	T	I	S	C	S	G	S	S	S	N	I	G	N	.	.	.	.	N	Y	V	S
VL2-11	Q	S	A	L	T	Q	P	R	S	.	V	S	G	S	P	G	Q	S	V	T	I	S	C	T	G	T	S	S	D	V	G	G	Y	.	.	.	N	Y	V	S
VL2-14	Q	S	A	L	T	Q	P	A	S	.	V	S	G	S	P	G	Q	S	I	T	I	S	C	T	G	T	S	S	D	V	G	G	Y	.	.	.	N	Y	V	S
VL2-23	Q	S	A	L	T	Q	P	A	S	.	V	S	G	S	P	G	Q	S	I	T	I	S	C	T	G	T	S	S	D	V	G	S	Y	.	.	.	N	L	V	S
VL3-1	S	Y	E	L	T	Q	P	P	S	.	V	S	V	S	P	G	Q	T	A	S	I	T	C	S	G	D	K	L	G	D	.	.	.	.	.	.	K	Y	A	Y
VL3-21	S	Y	V	L	T	Q	P	P	S	.	V	S	V	A	P	G	K	T	A	R	I	T	C	G	G	N	N	I	G	S	.	.	.	.	.	.	K	S	V	H

Kabat No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	27a	27b	27c	27d	27e	27f	28	29	30	31	32	33	34
VL1-40	CAG	AGC	GTG	CTG	ACC	CAG	CCA	CCA	AGC		GTG	AGC	GGT	GCA	CCA	GGT	CAG	CGC	GTG	ACC	ATT	AGC	TGC	ACC	GGC	AGC	AGC	AGC	AAC	ATT	GGC	GCA	GGC				TAT	GAT	GTG	CAT
VL1-47	CAG	AGC	GTG	CTG	ACC	CAG	CCA	CCA	AGC		GCA	AGC	GGC	ACC	CCA	GGC	CAG	CGC	GTG	ACC	ATT	AGC	TGT	AGC	GGC	AGC	AGC	AGC	AAC	ATT	GGC	AGC					AAC	TAT	GTG	TAC
VL1-51	CAG	AGC	GTG	CTG	ACC	CAG	CCG	CCG	AGC		GTT	AGC	GCC	GCA	CCA	GGC	CAG	AAA	GTG	ACC	ATT	AGC	TGT	AGC	GGC	AGC	AGC	AGC	AAC	ATC	GGC	AAC					AAC	TAC	GTT	AGC
VL2-11	CAG	AGC	GCC	CTG	ACC	CAG	CCA	CGC	AGC		GTT	AGC	GGT	AGC	CCA	GGC	CAG	AGC	GTG	ACC	ATT	AGC	TGC	ACC	GGC	ACC	AGC	AGC	GAC	GTG	GGC	GGC	TAT				AAC	TAC	GTT	AGC
VL2-14	CAG	AGC	GCC	CTG	ACC	CAG	CCA	GCC	AGC		GTT	AGC	GGT	AGC	CCA	GGC	CAG	AGC	ATT	ACC	ATT	AGC	TGC	ACC	GGC	ACC	AGC	AGC	GAC	GTG	GGC	GGC	TAT				AAC	TAC	GTT	AGC
VL2-23	CAG	AGC	GCC	CTG	ACC	CAG	CCA	GCC	AGC		GTT	AGC	GGT	AGC	CCA	GGC	CAG	AGC	ATT	ACC	ATT	AGC	TGC	ACC	GGC	ACC	AGC	AGC	GAC	GTG	GGC	AGC	TAT				AAC	CTG	GTT	AGC
VL3-1	AGC	TAT	GAA	CTG	ACC	CAG	CCG	CCG	AGC		GTT	AGC	GTT	AGC	CCA	GGC	CAG	ACC	GCC	AGC	ATT	ACC	TGT	AGC	GGC	GAC	AAA	CTG	GGC	GAC							AAA	TAC	GCC	TAC
VL3-21	AGC	TAT	GTG	CTG	ACC	CAG	CCG	CCG	AGC		GTT	AGC	GTG	GCC	CCA	GGC	AAA	ACC	GCC	CGC	ATT	ACC	TGC	GGC	GGC	AAC	AAC	ATT	GGC	AGC							AAA	AGC	GTG	CAC

Figure 32

Kabat CDRs	FRAMEWORK2															LCDR2						
Kabat No.	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56
VL1-40	W	Y	Q	Q	L	P	G	T	A	P	K	L	L	I	Y	G	N	S	N	R	P	S
VL1-47	W	Y	Q	Q	L	P	G	T	A	P	K	L	L	I	Y	R	N	N	Q	R	P	S
VL1-51	W	Y	Q	Q	L	P	G	T	A	P	K	L	L	I	Y	D	N	N	K	R	P	S
VL2-11	W	Y	Q	Q	H	P	G	K	A	P	K	L	M	I	Y	D	V	S	K	R	P	S
VL2-14	W	Y	Q	Q	H	P	G	K	A	P	K	L	M	I	Y	E	V	S	N	R	P	S
VL2-23	W	Y	Q	Q	H	P	G	K	A	P	K	L	M	I	Y	E	G	S	K	R	P	S
VL3-1	W	Y	Q	Q	K	P	G	Q	S	P	V	L	V	I	Y	Q	D	S	K	R	P	S
VL3-21	W	Y	Q	Q	K	P	G	Q	A	P	V	L	V	I	Y	Y	D	S	D	R	P	S

Kabat No.	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56
VL1-40	T GG	TAT	C AG	CAG	CTG	CCA	GGC	AC C	GCA	CC G	AAA	CTG	CTG	ATT	TAT	GGC	AAC	AGC	AAT	CGC	CCA	AGC
VL1-47	T GG	TAT	C AG	CAG	CTG	CCG	GGC	AC C	GCC	CC G	AAA	CTG	CTG	ATC	TAT	CGC	AAC	AAC	CAG	CGC	CCG	AGC
VL1-51	T GG	TAT	C AG	CAG	CTG	CCG	GGC	AC C	GCC	CC G	AAA	CTG	CTG	ATC	TAT	GAT	AAC	AAC	AAA	CGC	CCG	AGC
VL2-11	T GG	TAT	C AG	CAG	CAT	CCG	GGC	AA A	GCC	CC G	AAA	CTG	ATG	ATC	TAT	GAT	GTT	AGC	AAA	CGC	CCG	AGC
VL2-14	T GG	TAT	C AG	CAG	CAT	CCG	GGC	AA A	GCC	CC G	AAA	CTG	ATG	ATC	TAT	GAA	GTT	AGC	AAC	CGC	CCG	AGC
VL2-23	T GG	TAT	C AG	CAG	CAT	CCG	GGC	AA A	GCC	CC G	AAA	CTG	ATG	ATC	TAT	GAA	GGC	AGC	AAA	CGC	CCG	AGC
VL3-1	T GG	TAT	C AG	CAG	AAA	CCG	GGC	CA G	AGC	CC G	GTG	CTG	GTT	ATC	TAT	CAG	GAT	AGC	AAA	CGC	CCG	AGC
VL3-21	T GG	TAT	C AG	CAG	AAA	CCG	GGC	CA G	GCC	CC G	GTG	CTG	GTT	ATC	TAT	TAT	GAT	AGC	GAT	CGC	CCG	AGC

Figure 33

	FRAMEWORK3																													
Kabat No.	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88
VL1-40	G	V	P	D	R	F	S	G	S	K	S	G	T	S	A	S	L	A	I	T	G	L	Q	A	E	D	E	A	D	Y	Y	C
VL1-47	G	V	P	D	R	F	S	G	S	K	S	G	T	S	A	S	L	A	I	S	G	L	R	S	E	D	E	A	D	Y	Y	C
VL1-51	G	I	P	D	R	F	S	G	S	K	S	G	T	S	A	T	L	G	I	T	G	L	Q	T	E	D	E	A	D	Y	Y	C
VL2-11	G	V	P	D	R	F	S	G	S	K	S	G	N	T	A	S	L	T	I	S	G	L	Q	A	E	D	E	A	D	Y	Y	C
VL2-14	G	V	S	N	R	F	S	G	S	K	S	G	N	T	A	S	L	T	I	S	G	L	Q	A	E	D	E	A	D	Y	Y	C
VL2-23	G	V	S	N	R	F	S	G	S	K	S	G	N	T	A	S	L	T	I	S	G	L	Q	A	E	D	E	A	D	Y	Y	C
VL3-1	G	I	P	E	R	F	S	G	S	N	S	G	N	T	A	T	L	T	I	S	G	T	Q	A	E	D	E	A	D	Y	Y	C
VL3-21	G	I	P	E	R	F	S	G	S	N	S	G	N	T	A	T	L	T	I	S	R	V	E	A	E	D	E	A	D	Y	Y	C

Kabat No.	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88
VL1-40	GGT	GTG	CCG	GAT	CGC	TTT	AGC	GGC	AGC	AAA	AGC	GGC	ACC	AGC	GCC	AGC	CTG	GCG	ATT	ACC	GGT	CTG	CAA	GCC	GAA	GAC	GAA	GCC	GAT	TAT	TAC	TGC
VL1-47	GGC	GTG	CCA	GAT	CGC	TTT	AGC	GGT	AGC	AAA	AGC	GGC	ACC	AGC	GCA	AGC	CTG	GCG	ATT	AGC	GGC	CTG	CGC	AGC	GAA	GAC	GAA	GCC	GAT	TAT	TAC	TGC
VL1-51	GGC	ATC	CCG	GAT	CGC	TTT	AGC	GGT	AGC	AAA	AGC	GGC	ACC	AGC	GCC	ACC	CTG	GGC	ATT	ACC	GGC	CTG	CAA	ACC	GAA	GAC	GAA	GCC	GAT	TAT	TAC	TGC
VL2-11	GGC	GTG	CCG	GAT	CGC	TTT	AGC	GGC	AGC	AAA	AGC	GGC	AAC	ACC	GCC	AGC	CTG	ACC	ATC	AGC	GGC	CTG	CAA	GCC	GAA	GAC	GAA	GCC	GAT	TAT	TAC	TGC
VL2-14	GGC	GTT	AGC	AAT	CGC	TTT	AGC	GGC	AGC	AAA	AGC	GGC	AAC	ACC	GCC	AGC	CTG	ACC	ATT	AGC	GGC	CTG	CAA	GCC	GAA	GAC	GAA	GCC	GAT	TAT	TAC	TGC
VL2-23	GGC	GTT	AGC	AAC	CGC	TTT	AGT	GGC	AGC	AAA	AGC	GGC	AAC	ACC	GCC	AGC	CTG	ACC	ATT	AGC	GGC	CTG	CAA	GCC	GAA	GAC	GAA	GCC	GAT	TAT	TAC	TGC
VL3-1	GGC	ATT	CCA	GAA	CGC	TTT	AGC	GGC	AGC	AAC	AGC	GGC	AAC	ACC	GCC	ACC	CTG	ACC	ATT	AGC	GGC	ACC	CAG	GCC	GAA	GAC	GAA	GCC	GAT	TAT	TAC	TGC
VL3-21	GGC	ATT	CCA	GAA	CGC	TTT	AGC	GGC	AGC	AAC	AGC	GGC	AAC	ACC	GCC	ACC	CTG	ACC	ATT	AGC	CGC	GTG	GAA	GCC	GAA	GAC	GAA	GCC	GAT	TAT	TAC	TGC

Figure 34 Low Post Translational Modification VHs

Kabat CDRs	FRAMEWORK1																												HCDR1						
Kabat No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	35a	35b
VH1-18	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S	V	K	V	S	C	K	A	S	G	Y	T	F	T	S			Y	G	I	S
VH1-46	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S	V	K	V	S	C	K	A	S	G	Y	T	F	T	S			Y	Y	I	H
VH1-69*01	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	S	S	V	K	V	S	C	K	A	S	G	Y	T	F	S	S			Y	A	I	S
VH3-07	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	S			Y	W	I	S
VH3-11	Q	V	Q	L	V	E	S	G	G	G	L	V	K	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	D			H	Y	I	S
VH3-15	E	V	Q	L	V	E	S	G	G	G	L	V	K	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	N			Y	W	I	S
VH3-21	E	V	Q	L	V	E	S	G	G	G	L	V	K	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	S			Y	S	I	N
VH3-23	E	V	Q	L	L	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	S			Y	A	I	S
VH3-30	Q	V	Q	L	V	E	S	G	G	G	V	V	Q	P	G	R	S	L	R	L	S	C	A	A	S	G	F	T	F	S	S			Y	A	I	H
VH3-53	E	V	Q	L	V	E	S	G	G	G	L	I	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	V	S	S			H	Y	I	S
VH3-74	E	V	Q	L	V	E	S	G	G	G	L	V	Q	P	G	G	S	L	R	L	S	C	A	A	S	G	F	T	F	S	S			Y	W	I	H
VH5-51	E	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	E	S	L	K	I	S	C	K	G	S	G	Y	S	F	T	S			Y	W	I	S
VH6-01	Q	V	Q	L	Q	Q	S	G	P	G	L	V	K	P	S	Q	T	L	S	L	T	C	A	I	S	G	G	S	V	S	T	S	S	A	A	W	N

Kabat No.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	35a	35b
VH1-18	CAG	GTG	CAG	CTG	GTG	CAG	AGC	GGT	GCC	GAA	GTG	AAA	AAA	CCA	GGC	GCC	AGC	GTG	AAA	GTT	AGC	TGC	AAA	GCC	AGC	GGC	TAT	ACC	TTT	ACC	AGC			TAT	GGC	ATT	AGC
VH1-46	CAG	GTG	CAG	CTG	GTG	CAG	AGC	GGT	GCC	GAA	GTG	AAA	AAA	CCA	GGC	GCC	AGC	GTG	AAA	GTT	AGC	TGC	AAA	GCC	AGC	GGC	TAT	ACC	TTC	ACC	AGC			TAC	TAT	ATT	CAT
VH1-69*01	CAG	GTG	CAG	CTG	GTG	CAG	AGC	GGT	GCC	GAA	GTG	AAA	AAA	CCA	GGC	AGC	AGC	GTG	AAA	GTG	AGC	TGT	AAA	GCC	AGC	GGT	TAT	ACC	TTT	AGC	AGC			TAT	GCC	ATT	AGC
VH3-07	GAA	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	CTG	GTG	CAG	CCA	GGT	GGT	AGC	CTG	CGC	CTG	AGC	TGC	GCC	GCC	AGC	GGC	TTT	ACC	TTT	AGC	AGC			TAT	TGG	ATT	AGC
VH3-11	CAG	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	CTG	GTG	AAA	CCA	GGC	GGT	AGC	CTG	CGC	CTG	AGC	TGC	GCC	GCC	AGC	GGC	TTT	ACC	TTT	AGC	GAT			CAT	TAC	ATT	AGC
VH3-15	GAA	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	CTG	GTG	AAA	CCA	GGC	GGT	AGC	CTG	CGC	CTG	AGC	TGC	GCC	GCC	AGC	GGC	TTT	ACC	TTT	AGC	AAC			TAT	TGG	ATT	AGC
VH3-21	GAA	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	CTG	GTG	AAA	CCA	GGC	GGT	AGC	CTG	CGC	CTG	AGC	TGC	GCC	GCC	AGC	GGC	TTT	ACC	TTT	AGC	AGC			TAT	AGC	ATT	AAC
VH3-23	GAA	GTG	CAG	CTG	CTG	GAA	AGC	GGT	GGC	GGT	CTG	GTG	CAG	CCA	GGT	GGT	AGC	CTG	CGC	CTG	AGC	TGT	GCC	GCA	AGC	GGC	TTT	ACC	TTT	AGC	AGC			TAT	GCC	ATT	AGC
VH3-30	CAG	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	GTT	GTG	CAG	CCA	GGT	CGC	AGT	CTG	CGC	CTG	AGC	TGT	GCC	GCC	AGC	GGC	TTT	ACC	TTT	AGC	AGC			TAT	GCC	ATT	CAT
VH3-53	GAA	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	CTG	ATT	CAG	CCA	GGC	GGT	AGC	CTG	CGC	CTG	AGC	TGT	GCC	GCC	AGC	GGC	TTT	ACC	GTT	AGC	AGC			CAT	TAT	ATT	AGC
VH3-74	GAA	GTG	CAG	CTG	GTG	GAA	AGC	GGC	GGT	GGC	CTG	GTG	CAG	CCA	GGT	GGT	AGC	CTG	CGC	CTG	AGC	TGC	GCC	GCC	AGC	GGC	TTT	ACC	TTT	AGC	AGC			TAT	TGG	ATT	CAT
VH5-51	GAA	GTG	CAG	CTG	GTG	CAG	AGC	GGT	GCC	GAA	GTG	AAA	AAA	CCG	GGC	GAA	AGC	CTG	AAA	ATC	AGC	TGC	AAA	GGC	AGC	GGC	TAT	AGC	TTT	ACC	AGC			TAT	TGG	ATT	AGC
VH6-01	CAG	GTG	CAG	CTG	CAA	CAG	AGC	GGC	CCA	GGC	CTG	GTT	AAA	CCG	AGC	CAG	ACC	CTG	AGC	CTG	ACC	TGC	GCC	ATT	AGC	GGC	GGC	AGC	GTT	AGC	ACC	AGC	AGC	GCC	GCC	TGG	AAC

Figure 35 Low Post Translational Modification VHs

Kabat CDRs	FRAMEWORK2														HCDR2																
Kabat No.	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	52a	52b	52c	53	54	55	56	57	58	59	60	61	62	63	64	65
VH1-18	W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	W	I	S	A			Y	G	G	N	T	N	Y	A	Q	K	L	Q	G
VH1-46	W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	I	I	N	P			S	G	G	S	T	S	Y	A	Q	K	F	Q	G
VH1-69*01	W	V	R	Q	A	P	G	Q	G	L	E	W	M	G	G	I	I	P			I	F	G	T	A	N	Y	A	Q	K	F	Q	G
VH3-07	W	V	R	Q	A	P	G	K	G	L	E	W	V	A	N	I	K	Q			S	G	S	E	T	Y	Y	V	E	S	V	K	G
VH3-11	W	I	R	Q	A	P	G	K	G	L	E	W	V	S	Y	I	S	S			S	G	S	T	T	Y	Y	A	E	S	V	K	G
VH3-15	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	R	I	K	S	K	T	Y	G	G	T	T	D	Y	A	E	P	V	K	G
VH3-21	W	V	R	Q	A	P	G	K	G	L	E	W	V	S	S	I	S	S			S	S	S	Y	T	Y	Y	A	E	S	V	K	G
VH3-23	W	V	R	Q	A	P	G	K	G	L	E	W	V	S	A	I	S	G			S	G	G	S	T	Y	Y	A	E	S	V	K	G
VH3-30	W	V	R	Q	A	P	G	K	G	L	E	W	V	A	V	I	S	Y			S	G	S	N	K	Y	Y	A	E	S	V	K	G
VH3-53	W	V	R	Q	A	P	G	K	G	L	E	W	V	S	V	I	Y	S				G	G	S	T	Y	Y	A	E	S	V	K	G
VH3-74	W	V	R	Q	A	P	G	K	G	L	V	W	V	S	R	I	T	S			S	G	S	S	T	S	Y	A	E	S	V	K	G
VH5-51	W	V	R	Q	M	P	G	K	G	L	E	W	M	G	I	I	Y	P			G	T	S	Y	T	R	Y	S	P	S	F	Q	G
VH6-01	W	I	R	Q	S	P	S	R	G	L	E	W	L	G	R	I	Y	Y	R		S	K	W	Y	N	D	Y	A	V	S	V	K	S

Kabat No.	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	52a	52b	52c	53	54	55	56	57	58	59	60	61	62	63	64	65
VH1-18	TGG	GTT	CGC	CAG	GCC	CCA	GGC	CAG	GGT	CTG	GAA	TGG	ATG	GGC	TGG	ATT	AGC	GCC			TAT	GGC	GGC	AAC	ACC	AAC	TAC	GCC	CAG	AAA	CTG	CAA	GGC
VH1-46	TGG	GTT	CGC	CAG	GCC	CCA	GGC	CAG	GGT	CTG	GAA	TGG	ATG	GGC	ATT	ATT	AAC	CCG			AGC	GGC	GGC	AGC	ACC	AGC	TAT	GCA	CAG	AAA	TTT	CAG	GGC
VH1-69*01	TGG	GTT	CGC	CAG	GCA	CCA	GGT	CAG	GGT	CTG	GAA	TGG	ATG	GGT	GGC	ATT	ATT	CCG			ATT	TTT	GGC	ACC	GCC	AAC	TAT	GCC	CAG	AAA	TTT	CAG	GGT
VH3-07	TGG	GTT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTG	GCG	AAC	ATC	AAA	CAG			AGC	GGC	AGC	GAG	ACC	TAC	TAT	GTG	GAG	AGC	GTG	AAA	GGC
VH3-11	TGG	ATT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTT	AGC	TAT	ATT	AGC	AGC			AGT	GGC	AGC	ACC	ACC	TAT	TAC	GCC	GAG	AGC	GTG	AAA	GGC
VH3-15	TGG	GTT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTT	GGC	CGC	ATC	AAA	AGC	AAA	ACC	TAT	GGC	GGC	ACC	ACC	GAT	TAT	GCC	GAG	CCA	GTG	AAA	GGC
VH3-21	TGG	GTT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTT	AGC	AGC	ATC	AGC	AGC			AGT	AGC	AGC	TAT	ACC	TAT	TAC	GCC	GAG	AGC	GTG	AAA	GGC
VH3-23	TGG	GTG	CGC	CAA	GCA	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTG	AGC	GCC	ATT	AGC	GGC			AGC	GGT	GGC	AGC	ACC	TAT	TAT	GCC	GAG	AGC	GTG	AAA	GGT
VH3-30	TGG	GTT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTG	GCC	GTG	ATT	AGC	TAT			AGC	GGC	AGC	AAC	AAA	TAT	TAC	GCC	GAG	AGC	GTG	AAA	GGC
VH3-53	TGG	GTT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GAA	TGG	GTT	AGC	GTG	ATC	TAT	AGC				GGC	GGC	AGC	ACC	TAT	TAT	GCC	GAG	AGC	GTG	AAA	GGC
VH3-74	TGG	GTT	CGC	CAG	GCC	CCA	GGC	AAA	GGC	CTG	GTT	TGG	GTT	AGC	CGC	ATT	ACC	AGC			AGC	GGC	AGC	AGC	ACC	AGC	TAT	GCC	GAG	AGC	GTG	AAA	GGC
VH5-51	TGG	GTT	CGC	CAG	ATG	CCG	GGC	AAA	GGC	CTG	GAA	TGG	ATG	GGC	ATT	ATC	TAT	CCG			GGC	ACC	AGC	TAT	ACC	CGC	TAT	AGC	CCG	AGC	TTT	CAG	GGC
VH6-01	TGG	ATT	CGC	CAG	AGC	CCG	AGC	CGC	GGT	CTG	GAA	TGG	CTG	GGC	CGC	ATT	TAT	TAT	CGC		AGC	AAA	TGG	TAC	AAC	GAT	TAC	GCC	GTT	AGC	GTG	AAA	AGC

Figure 36 Low Post Translational Modification VHs

FRAMEWORK3																															
Kabat No.	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	82A	82B	82C	83	84	85	86	87	88	89	90	91	92	93	94
VH1-18	R	V	T	M	T	T	D	T	S	T	S	T	A	Y	M	E	L	R	S	L	R	S	D	D	T	A	V	Y	Y	C	A	R
VH1-46	R	V	T	M	T	R	D	T	S	T	S	T	V	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R
VH1-69*01	R	V	T	I	T	A	D	E	S	T	S	T	A	Y	M	E	L	S	S	L	R	S	E	D	T	A	V	Y	Y	C	A	R
VH3-07	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH3-11	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH3-15	R	F	T	I	S	R	D	D	S	K	N	T	L	Y	L	Q	M	N	S	L	K	T	E	D	T	A	V	Y	Y	C	A	R
VH3-21	R	F	T	I	S	R	D	N	A	K	N	S	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH3-23	R	F	T	I	S	R	D	N	S	K	N	T	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH3-30	R	F	T	I	S	R	D	N	S	K	N	T	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH3-53	R	F	T	I	S	R	D	N	S	K	N	T	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH3-74	R	F	T	I	S	R	D	N	A	K	N	T	L	Y	L	Q	M	N	S	L	R	A	E	D	T	A	V	Y	Y	C	A	R
VH5-51	Q	V	T	I	S	A	D	K	S	I	S	T	A	Y	L	Q	W	S	S	L	K	A	S	D	T	A	M	Y	Y	C	A	R
VH6-01	R	I	T	I	N	P	D	T	S	K	N	Q	F	S	L	Q	L	N	S	V	T	P	E	D	T	A	V	Y	Y	C	A	R

Kabat No.	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	82A	82B	82C	83	84	85	86	87	88	89	90	91	92	93	94
VH1-18	CG	C	GTG	ACC	ATG	ACC	ACC	GAT	AC	C	AGC	AC	C	AGC	ACC	GCC	TAT	ATG	GAA	CTG	CGC	TCC	CTG	CGC	AGC	GAC	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH1-46	CG	C	GTG	ACC	ATG	ACC	CGC	GAT	AC	C	AGC	AC	C	AGC	ACC	GTG	TAT	ATG	GAA	CTG	AGC	AGC	CTG	CGC	AGC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH1-69*01	CG	C	GTG	ACC	ATT	ACC	GCA	GAT	GA	A	AGC	AC	C	AGC	ACC	GCC	TAT	ATG	GAA	CTG	AGC	AGC	CTG	CGC	AGC	GAA	GAT	A	CC	GCA	G	TG	TAT	TAT	T	GC	GCG	C	GG
VH3-07	CG	C	TTT	ACC	ATT	AGC	CGC	GAT	AA	C	GCC	AA	A	AAC	AGC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH3-11	CG	C	TTT	ACC	ATT	AGC	CGC	GAT	AA	C	GCC	AA	A	AAC	AGC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH3-15	CG	C	TTT	ACC	ATT	AGC	CGC	GAC	GA	T	AGC	AA	A	AAC	ACC	CTG	TAC	CTG	CAA	ATG	AAC	AGC	CTG	AAA	ACC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH3-21	CG	C	TTT	ACC	ATT	AGC	CGC	GAT	AA	C	GCC	AA	A	AAC	AGC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH3-23	CG	C	TTT	ACC	ATT	AGT	CGC	GAT	AA	C	AGC	AA	A	AAC	ACC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCA	GAA	GAT	A	CC	GCA	G	TT	TAT	TAT	T	GC	GCG	C	GG
VH3-30	CG	C	TTT	ACC	ATT	AGC	CGC	GAT	AA	C	AGC	AA	A	AAC	ACC	CTG	TAC	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH3-53	CG	C	TTT	ACC	ATT	AGC	CGC	GAT	AA	C	AGC	AA	A	AAC	ACC	CTG	TAC	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH3-74	CG	C	TTT	ACC	ATT	AGC	CGC	GAT	AA	C	GCC	AA	A	AAC	ACC	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	CGG	GCC	GAA	GAT	A	CC	GCC	G	TG	TAT	TAT	T	GC	GCG	C	GT
VH5-51	CA	G	GTT	ACA	ATT	AGC	GCC	GAC	AA	A	AGC	AT	C	AGC	ACC	GCC	TAT	CTG	CAA	TGG	AGC	AGC	CTG	AAA	GCC	AGC	GAT	A	CC	GCC	A	TG	TAT	TAT	T	GC	GCG	C	GT
VH6-01	CG	C	ATT	ACC	ATT	AAC	CCG	GAT	AC	C	AGC	AA	A	AAC	CAG	TTC	AGC	CTG	CAA	CTG	AAC	AGC	GTG	ACC	CCG	GAA	GAT	A	CC	GCC	G	TG	TAT	TAC	T	GC	GCG	C	GT

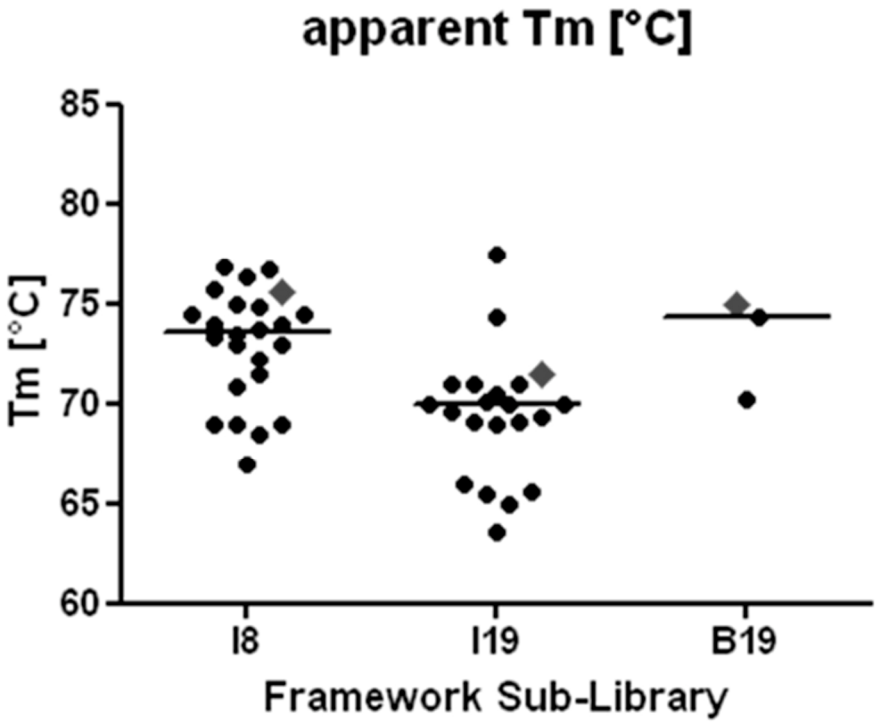
Figure 37

			HCDR3	LCDR3	Fab		IgG			
VH	VL	Target	Length [aa]	Length [aa]	Tm [°C]	affinity [nM]	pI	expression [mg/L]	Tm [°C]	SEC monomer [%]
VH3-23	VK1-39	DKK3	6	8	76,8	nd	9,2	28,5	81,8	97
VH3-23	VK1-39	DKK3	7	8	73,4	nd	9,3	40,9	81,4	100
VH3-23	VK1-39	DKK3	8	8	72,9	nd	9,1	36,4	77,0	98
VH3-23	VK1-39	DKK3	8	8	74,0	nd	9,4	26,0	78,8	99
VH3-23	VK1-39	DKK3	8	8	75,0	nd	9,4	20,5	79,0	99
VH3-23	VK1-39	DKK3	6	8	76,3	nd	9,2	17,1	83,5	98
VH3-23	VK1-39	DKK3	9	8	75,7	nd	9,2	32,0	81,6	97
VH3-23	VK1-39	DKK3	8	8	72,2	nd	9,4	22,9	76,0	100
VH3-23	VL3-1	DKK3	6	8	65,6	nd	8,9	19,0	70,5	96
VH3-23	VL3-1	DKK3	7	8	63,6	nd	8,7	36,4	68,9	100
VH3-23	VL3-1	DKK3	7	8	70,1	nd	7,9	29,1	69,1	97
VH3-23	VK1-39	DKK3	11	8	nd	nd	9,4	26,7	79,5	100
VH3-23	VK1-39	DKK3	6	8	74,5	nd	9,3	30,0	82,1	97
VH3-23	VK1-39	DKK3	6	8	73,0	nd	9,1	22,0	77,3	96
VH3-23	VK1-39	DKK3	11	8	74,0	nd	9,2	23,6	87,0	98
VH3-23	VL3-1	DKK3	12	9	nd	nd	8,7	25,6	74,7	98
VH3-23	VL3-1	DKK3	7	8	71,0	nd	8,7	45,5	76,9	97
VH3-23	VL3-1	DKK3	5	8	nd	nd	8,7	32,0	68,7	97
VH3-23	VL3-1	DKK3	7	8	65,0	nd	8,7	28,8	70,1	90
VH3-23	VL3-1	DKK3	7	8	70,5	nd	8,9	31,1	74,1	99

Figure 38

			HCDR3	LCDR3	Fab		IgG			
VH	VL	Target	Length [aa]	Length [aa]	Tm [°C]	affinity [nM]	pI	expression [mg/L]	Tm [°C]	SEC monomer [%]
VH3-23	VK1-39	ErbB4/Her4	16	8	75,0	nd	8,7	31,8	85,4	99
VH3-23	VK1-39	ErbB4/Her4	12	8	75,0	nd	9,0	36,4	82,0	100
VH3-23	VK1-39	ErbB4/Her4	15	8	74,8	*61*	8,3	50,0	85,6	99
VH3-23	VK1-39	ErbB4/Her4	13	8	68,4	*22*	9,2	17,5	77,4	99
VH3-23	VK1-39	ErbB4/Her4	11	8	71,4	*59*	8,7	32,7	77,6	99
VH3-23	VK1-39	ErbB4/Her4	15	8	69,0	14	9,1	28,5	74,1	100
VH3-23	VK1-39	ErbB4/Her4	13	8	69,0	8,4	8,9	34,5	81,4	100
VH3-23	VK1-39	ErbB4/Her4	16	8	73,3	20	8,9	25,3	83,2	nsp
VH3-23	VK1-39	ErbB4/Her4	19	8	70,8	30	9,0	26,0	86,5	100
VH3-23	VK1-39	ErbB4/Her4	17	8	76,7	14	8,7	35,0	78,6	99
VH3-23	VK1-39	ErbB4/Her4	14	8	68,9	*12*	8,9	32,5	87,9	100
VH3-23	VK1-39	ErbB4/Her4	19	8	74,5	nd	8,3	19,1	84,4	99
VH3-23	VL3-1	ErbB4/Her4	17	8	77,5	2,1	7,4	41,8	74,3	99
VH3-23	VL3-1	ErbB4/Her4	11	8	70,0	nd	7,4	36,1	76,0	98
VH3-23	VK1-39	ErbB4/Her4	11	8	67,0	*86*	9,2	33,3	87,0	97
VH3-23	VL3-1	ErbB4/Her4	15	8	69,1	1,2	8,3	42,0	69,6	99
VH3-23	VL3-1	ErbB4/Her4	15	9	74,3	nd	7,6	26,0	69,1	98
VH3-23	VL3-1	ErbB4/Her4	12	8	65,9	24	8,3	42,5	70,3	97
VH3-23	VL3-1	ErbB4/Her4	18	10	69,0	13	8,7	31,1	72,6	99
VH3-23	VL3-1	ErbB4/Her4	11	8	65,5	*45*	7,1	38,0	75,7	99
VH3-23	VL3-1	ErbB4/Her4	12	10	69,9	*55*	7,6	29,4	79,0	97
VH3-23	VL3-1	ErbB4/Her4	14	8	71,0	*36*	7,1	24,2	68,4	99
VH3-23	VL3-1	ErbB4/Her4	15	8	71,0	*48*	8,0	26,9	73,4	99
VH3-23	VL3-1	ErbB4/Her4	13	8	69,1	*95*	7,4	20,0	69,4	96

Figure 39



Key: Apparent midpoints of unfolding of selected Fabs as determined by Differential Scanning Fluorimetry (DSF) as described in Example 9.1.2. Each dot represents one unique Fab. Squares indicate the control Fabs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

B19 represents VH1-18/VL3-1

Figure 40

Heavy Chain Framework 4: JH4

Kabat No.	103	104	105	106	107	108	109	110	111	112	113
FWR4 aa	W	G	Q	G	T	L	V	T	V	S	S
FWR4 nt	TGG	GGC	CAG	GGC	ACC	CTG	GTT	ACT	GTC	TCG	AGC

OR

Kabat No.	103	104	105	106	107	108	109	110	111	112	113
FWR4 aa	W	G	Q	G	T	L	V	T	V	S	S
FWR4 nt	TGG	GGC	CAG	GGC	ACC	CTG	GTT	ACT	GTC	TCG	AGC

XhoI restriction site CTCGAG

Light Chain Kappa Framework 4: Jk1

	Kabat No.	98	99	100	101	102	103	104	105	106	106A	107	108	109
	FWR4 aa	F	G	Q	G	T	K	V	E	I		K	R	T
pJP_h_Igkappa vector	FWR4 nt	TTC	GGC	CAG	GGT	ACC	AAA	GTG	GAA	ATC		AAG	CGC	ACC
pJPx1 vector	FWR4 nt	TTC	GGC	CAG	GGT	ACC	AAA	GTT	GAA	ATT		AAA	CGC	ACC
or														
pJPx1 vector	FWR4 nt	TTC	GGC	CAG	GGT	ACC	AAA	GTG	GAA	ATT		AAA	CGC	ACC

KpnI/Acc65I restriction site GGTACC

Key: pJPx1 vector is an expression vector for Fab expression in E. coli
pJP_h_Igkappa vector is an expression vector for human kappa light chain expression in mammalian cells

Light Chain Lambda Framework 4: Jλ2/3

	Kabat No.	98	99	100	101	102	103	104	105	106	106A	107	108
	FWR4 aa	F	G	G	G	T	K	L	T	V	L	G	Q
pJP_h_Iglambda2	FWR4 nt	TTT	GGC	GGC	GGT	ACC	AAG	CTG	ACC	GTG	CTC	GGC	CAG
pJPx1	FWR4 nt	TTT	GGC	GGC	GGT	ACC	AAA	CTC	ACT	GTC	CTG	GGC	CAG
or													
pJPx1 vector	FWR4 nt	TTT	GGC	GGC	GGT	ACC	AAA	CTG	ACC	GTG	CTG	GGC	CAG

KpnI/Acc65I restriction site GGTACC

Key: pJPx1 vector is an expression vector for Fab expression in E. coli
pJP_h_Iglambda2 vector is an expression vector for human lambda light chain expression in mammalian cells

Figure 41A IgG1 Fc heavy

		114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142
IgG1	pJP_h_IgIgG1f	CH1																												
	CH1 to CH3	A	S	T	K	G	P	S	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L	G	C	L	V
		GCG	TCG	ACC	AAA	GGC	CCC	AGC	GTG	TTC	CCT	CTG	GCC	CCC	AGC	AGC	AAG	AGC	ACC	TCT	GGC	GGA	ACA	GCC	GCC	CTG	GGC	TGC	CTG	GTC

143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177
CH1																																		
K	D	Y	F	P	E	P	V	T	V	S	W	N	S	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G	L	Y	S
AAG	GAC	TAC	TTC	CCC	GAG	CCC	GTG	ACC	GTG	TCC	TGG	AAC	TCT	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTT	CCA	GCC	GTG	CTC	CAG	AGC	AGC	GGC	CTG	TAC	AGC

178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211
CH1																																	
L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q	T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	R	V
CTG	AGC	AGC	GTC	GTG	ACC	GTG	CCC	AGC	AGC	AGC	CTG	GGC	ACC	CAG	ACC	TAC	ATC	TGC	AAC	GTG	AAC	CAC	AAG	CCC	AGC	AAC	ACA	AAG	GTG	GAC	AAG	CGG	GTG

212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245
Hinge															CH2																		
E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P	E	L	L	G	G	P	S	V	F	L	F	P	P	K	P	K	D
GAA	CCC	AAG	AGC	TGC	GAC	AAG	ACC	CAC	ACC	TGT	CCC	CCC	TGC	CCT	GCC	CCT	GAA	CTG	CTG	GGA	GGC	CCC	TCC	GTG	TTC	CTG	TTC	CCC	CCA	AAG	CCT	AAG	GAC

246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280
CH2																																		
T	L	M	I	S	R	T	P	E	V	T	C	V	V	V	D	V	S	H	E	D	P	E	V	K	F	N	W	Y	V	D	G	V	E	V
ACC	CTG	ATG	ATC	AGC	CGG	ACC	CCC	GAA	GTG	ACC	TGC	GTG	GTG	GTG	GAC	GTG	TCC	CAC	GAG	GAC	CCT	GAA	GTG	AAG	TTT	AAT	TGG	TAC	GTG	GAC	GGC	GTG	GAA	GTG

The nucleic acid sequences shown have been codon optimized

Figure 41B IgG1 Fc heavy

281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315
CH2																																		
H	N	A	K	T	K	P	R	E	E	Q	Y	N	S	T	Y	R	V	V	S	V	L	T	V	L	H	Q	D	W	L	N	G	K	E	Y
CAC	AAC	GCC	AAG	ACC	AAG	CCC	AGA	GAG	GAA	CAG	TAC	AAC	AGC	ACC	TAC	CGG	GTG	GTG	TCC	GTG	CTG	ACC	GTG	CTG	CAC	CAG	GAC	TGG	CTG	AAC	GGC	AAA	GAG	TAC

316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350
CH3																																		
K	C	K	V	S	N	K	A	L	P	A	P	I	E	K	T	I	S	K	A	K	G	Q	P	R	E	P	Q	V	Y	T	L	P	P	S
AAG	TGC	AAG	GTG	TCC	AAC	AAG	GCC	CTG	CCT	GCC	CCC	ATC	GAG	AAA	ACC	ATC	AGC	AAG	GCC	AAA	GGC	CAG	CCC	CGC	GAG	CCC	CAG	GTG	TAC	ACA	CTG	CCC	CCT	AGC

351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385
CH3																																		
R	E	E	M	T	K	N	Q	V	S	L	T	C	L	V	K	G	F	Y	P	S	D	I	A	V	E	W	E	S	N	G	Q	P	E	N
CGG	GAA	GAG	ATG	ACC	AAG	AAC	CAG	GTG	TCC	CTG	ACC	TGC	CTC	GTG	AAG	GGC	TTC	TAC	CCC	AGC	GAC	ATT	GCC	GTG	GAA	TGG	GAG	AGC	AAC	GGC	CAG	CCC	GAG	AAC

386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420
CH3																																		
N	Y	K	T	T	P	P	V	L	D	S	D	G	S	F	F	L	Y	S	K	L	T	V	D	K	S	R	W	Q	Q	G	N	V	F	S
AAC	TAC	AAG	ACC	ACC	CCC	CCT	GTG	CTG	GAC	AGC	GAC	GGC	TCA	TTC	TTC	CTG	TAC	AGC	AAG	CTG	ACC	GTG	GAC	AAG	AGC	CGG	TGG	CAG	CAG	GGC	AAC	GTG	TTC	AGC

421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443
CH3																						
C	S	V	M	H	E	A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P	G	K
TGC	TCC	GTG	ATG	CAC	GAG	GCC	CTG	CAC	AAC	CAC	TAC	ACC	CAG	AAG	TCC	CTG	AGC	CTG	AGC	CCC	GGC	AAG

Figure 42 Fab Fc heavy

		114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142
Fab	pJPx1	CH1																												
	CH1 - Flag+His Tag	A	S	T	K	G	P	S	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L	G	C	L	V
		GCG	TCG	ACC	AAA	GGC	CCG	AGC	GTG	TTT	CCG	CTG	GCC	CCG	AGC	AGC	AAA	AGC	ACC	AGC	GGC	GGC	ACC	GCC	GCA	CTG	GGC	TGC	CTG	GTG

143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177
CH1																																		
K	D	Y	F	P	E	P	V	T	V	S	W	N	S	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G	L	Y	S
AAA	GAT	TAT	TTC	CCG	GAA	CCA	GTG	ACC	GTG	AGC	TGG	AAC	AGC	GGT	GCC	CTG	ACC	AGC	GGC	GTG	CAT	ACC	TTT	CCG	GCG	GTG	CTG	CAA	AGC	AGC	GGC	CTG	TAT	AGC

178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211
CH1																																	
L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q	T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K	V
CTG	AGC	AGC	GTT	GTG	ACC	GTG	CCG	AGC	AGC	AGC	CTG	GGC	ACC	CAG	ACC	TAT	ATT	TGC	AAC	GTC	AAC	CAT	AAA	CCG	AGC	AAC	ACC	AAA	GTC	GAT	AAA	AAA	GTC

212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234
						FLAG (M2) Tag											6xHIS Tag					
E	P	K	S	E	F	D	Y	K	D	D	D	D	K	G	A	P	H	H	H	H	H	H
GAA	CCG	AAA	AGC	GAA	TTC	GAC	TAT	AAA	GAT	GAC	GAT	GAC	AAA	GGG	GCG	CCG	CAC	CAT	CAT	CAC	CAT	CAC

The nucleic acid sequences shown have been codon optimized

Figure 43

IgG Fc kappa light

IgG	pJP_h_Igkappa	V	A	A	P	S	V	F	I	F	P	P	S	D	E	Q	L	K	S	G	T	A	S	V	V	C	L
	Ckappa =IGKC	GTG	GCC	GCT	CCC	TCC	GTG	TTC	ATC	TTC	CCA	CCC	AGC	GAC	GAG	CAG	CTG	AAG	TCC	GGC	ACA	GCC	AGC	GTC	GTG	TGC	CTG

L	N	N	F	Y	P	R	E	A	K	V	Q	W	K	V	D	N	A	L	Q	S	G	N	S	Q	E	S	V	T	E	Q
CTG	AAC	AAC	TTC	TAC	CCC	CGC	GAG	GCC	AAA	GTG	CAG	TGG	AAG	GTG	GAC	AAC	GCC	CTC	CAG	AGC	GGC	AAC	AGC	CAG	GAA	AGC	GTC	ACC	GAG	CAG

D	S	K	D	S	T	Y	S	L	S	S	T	L	T	L	S	K	A	D	Y	E	K	H	K	V	Y	A	C	E	V	T
GAC	AGC	AAG	GAC	TCC	ACC	TAC	AGC	CTG	AGC	AGC	ACC	CTG	ACC	CTG	AGC	AAG	GCC	GAC	TAC	GAG	AAG	CAC	AAG	GTG	TAC	GCC	TGC	GAA	GTG	ACC

H	Q	G	L	S	S	P	V	T	K	S	F	N	R	G	E	C
CAC	CAG	GGC	CTG	TCC	AGC	CCC	GTG	ACC	AAG	AGC	TTC	AAC	CGG	GGC	GAG	TGC

Fab Fc kappa light

Fab	pJPx1	V	A	A	P	S	V	F	I	F	P	P	S	D	E	Q	L	K	S	G	T	A	S	V	V	C	L
	Ckappa	GTG	GCC	GCA	CCG	AGC	GTG	TTT	ATC	TTT	CCG	CCG	AGC	GAT	GAA	CAG	CTG	AAA	AGC	GGC	ACC	GCC	AGC	GTG	GTG	TGC	CTG

L	N	N	F	Y	P	R	E	A	K	V	Q	W	K	V	D	N	A	L	Q	S	G	N	S	Q	E	S	V	T	E	Q
CTG	AAC	AAC	TTT	TAT	CCG	CGC	GAA	GCC	AAA	GTG	CAG	TGG	AAA	GTG	GAT	AAC	GCC	CTG	CAA	AGC	GGC	AAC	AGC	CAG	GAA	AGC	GTT	ACC	GAA	CAG

D	S	K	D	S	T	Y	S	L	S	S	T	L	T	L	S	K	A	D	Y	E	K	H	K	V	Y	A	C	E	V	T
GAT	AGC	AAA	GAT	AGC	ACC	TAC	AGC	CTG	AGC	AGC	ACC	CTG	ACC	CTG	AGC	AAA	GCC	GAT	TAT	GAA	AAA	CAT	AAA	GTG	TAT	GCC	TGC	GAA	GTG	ACC

H	Q	G	L	S	S	P	V	T	K	S	F	N	R	G	E	A
CAT	CAG	GGC	CTG	AGC	AGC	CCA	GTG	ACC	AAA	AGT	TTT	AAC	CGC	GGC	GAG	GCC

Figure 44

IgG Fc lambda light

IgG	pJP_h_lglambda2	P	K	A	A	P	S	V	T	L	F	P	P	S	S	E	E	L	Q	A	N	K	A	T	L	V	C
	Clambda2	CCC	AAA	GCC	GCC	CCT	AGC	GTG	ACC	CTG	TTC	CCC	CCA	AGC	AGC	GAG	GAA	CTC	CAG	GCC	AAC	AAG	GCC	ACC	CTC	GTG	TGC

L	I	S	D	F	Y	P	G	A	V	T	V	A	W	K	A	D	S	S	P	V	K	A	G	V	E	T	T	T	P	S
CTG	ATC	AGC	GAC	TTC	TAC	CCT	GGC	GCC	GTG	ACC	GTG	GCC	TGG	AAG	GCC	GAT	AGC	AGC	CCT	GTG	AAG	GCC	GGC	GTG	GAA	ACC	ACC	ACC	CCC	AGC

K	Q	S	N	N	K	Y	A	A	S	S	Y	L	S	L	T	P	E	Q	W	K	S	H	R	S	Y	S	C	Q	V	T
AAG	CAG	AGC	AAC	AAC	AAA	TAC	GCC	GCC	AGC	AGC	TAC	CTG	AGC	CTG	ACC	CCC	GAG	CAG	TGG	AAG	TCC	CAC	AGA	TCC	TAC	AGC	TGC	CAG	GTC	ACA

H	E	G	S	T	V	E	K	T	V	A	P	T	E	C	S
CAC	GAG	GGC	AGC	ACC	GTG	GAA	AAG	ACC	GTG	GCC	CCC	ACC	GAG	TGC	AGC

Fab Fc lambda light

Fab	pJPx1	P	K	A	A	P	S	V	T	L	F	P	P	S	S	E	E	L	Q	A	N	K	A	T	L	V	C
	Clambda2	CCG	AAA	GCC	GCC	CCA	AGC	GTG	ACC	CTG	TTT	CCG	CCG	AGC	AGC	GAA	GAA	CTG	CAA	GCC	AAC	AAA	GCC	ACC	CTG	GTT	TGC

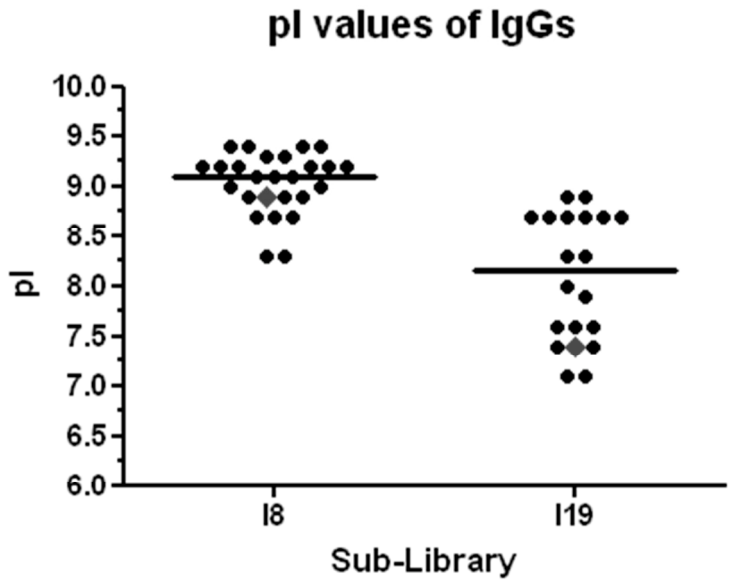
L	I	S	D	F	Y	P	G	A	V	T	V	A	W	K	A	D	S	S	P	V	K	A	G	V	E	T	T	T	P	S
CTG	ATC	AGC	GAT	TTT	TAT	CCG	GGT	GCC	GTG	ACC	GTG	GCC	TGG	AAA	GCC	GAT	AGC	AGC	CCG	GTG	AAA	GCC	GGC	GTG	GAA	ACC	ACC	ACC	CCG	AGC

K	Q	S	N	N	K	Y	A	A	S	S	Y	L	S	L	T	P	E	Q	W	K	S	H	R	S	Y	S	C	Q	V	T
AAA	CAG	AGC	AAC	AAC	AAA	TAT	GCC	GCC	AGC	AGC	TAT	CTG	AGC	CTG	ACC	CCG	GAA	CAG	TGG	AAA	AGC	CAT	CGC	AGC	TAT	AGT	TGT	CAA	GTG	ACC

H	E	G	S	T	V	E	K	T	V	A	P	T	E	A
CAT	GAA	GGC	AGC	ACC	GTG	GAA	AAA	ACC	GTG	GCC	CCG	ACC	GAG	GCC

The nucleic acid sequences shown have been codon optimized

Figure 45

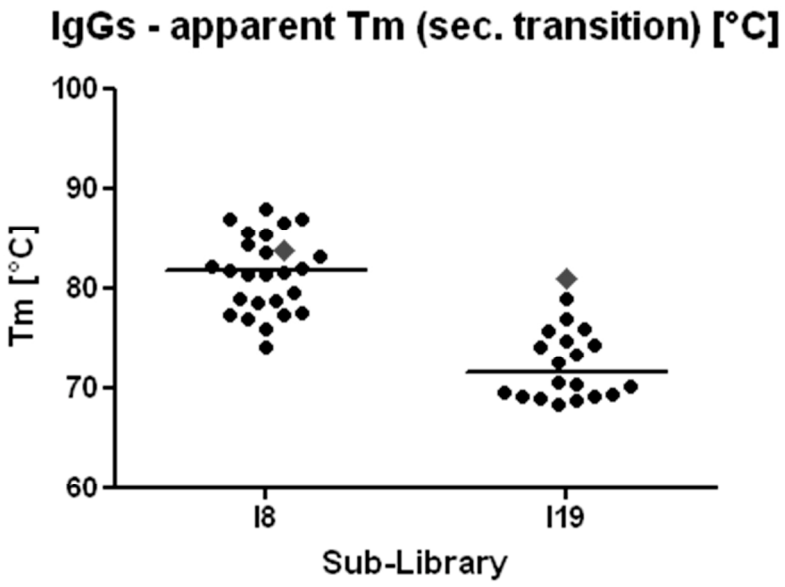


Key: pI values of selected IgGs as described in Example 9.2.4. Each dot represents one unique IgG. Squares indicate the control IgGs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

Figure 46

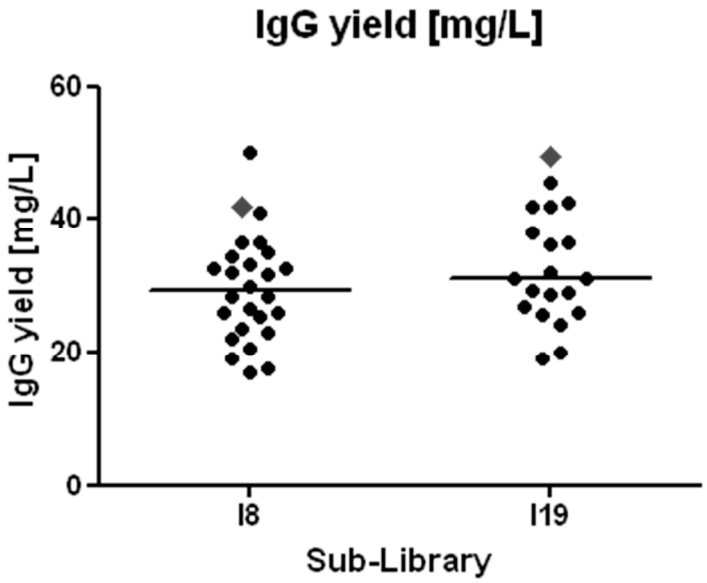


Key: Apparent midpoints of unfolding of selected IgGs as determined by Differential Scanning Fluorimetry (DSF) as described in Example 9.2.2. Each dot represents one unique IgG. Squares indicate the control IgGs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

Figure 47

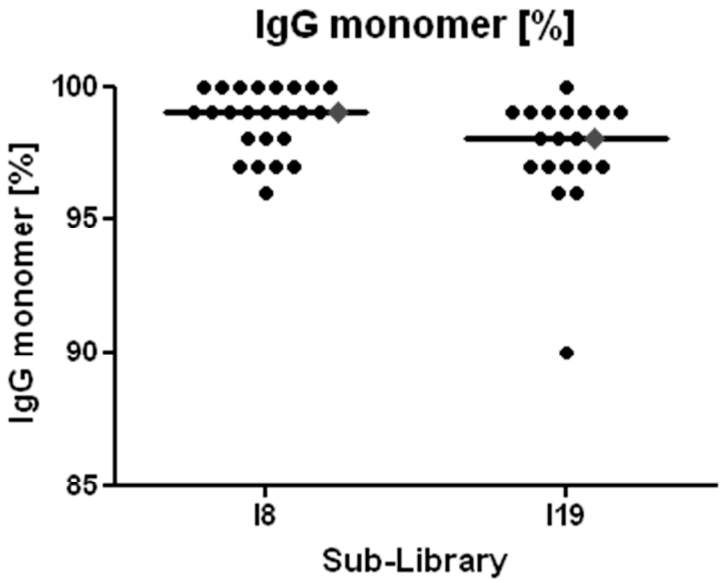


Key: Expression yields of selected IgGs as determined by UV-spectrophotometry as described in Example 9.2.1. Each dot represents one unique IgG. Squares indicate the control IgGs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

Figure 48



Key: Monomer content of selected IgGs as determined by size exclusion chromatography (SEC) as described in Example 9.2.3. Each dot represents one unique IgG. Squares indicate the control IgGs as described in Example 9 with the constant CDR3s as described in Ewert S. et al.(2004), J. Mol. Biol. 325, p. 531ff. Bars indicate the Median.

I8 represents VH3-23/VK1-39

I19 represents VH3-23/VL3-1

Figure 49

Agitation			Absorption at 320 nm					
No.	VH	VL	Inital	after 45 min agitation at RT	after 1,5 h agitation at RT	After 2,5 H agitation at RT	After 3,5 h agitiation at RT	After 24 h agitation at RT
1	VH_1_18	VK_1_39	0,041	0,049	0,054	0,056	0,059	0,1
2	VH_1_18	VK_3_11						
3	VH_1_18	VK_3_15	0,042	0,051	0,044	0,046	0,051	0,102
4	VH_1_18	VK_3_20	0,037	0,04	0,041	0,043	0,043	0,06
5	VH_1_18	VL_1-40	0,040	0,044	0,041	0,043	0,043	0,048
6	VH_1_18	VL_1-47	0,039	0,043	0,042	0,043	0,043	0,052
7	VH_1_18	VL_2-23	0,041	0,054	0,042	0,044	0,043	0,050
8	VH_1_18	VL_3-1	0,039	0,043	0,041	0,042	0,041	0,043
9	VH_1_46	VK_1_09	0,038	0,041	0,040	0,041	0,039	0,053
10	VH_1_46	VK_3_15	0,037	0,041	0,040	0,039	0,040	0,044
11	VH_1_46	VL_1-40	0,036	0,042	0,040	0,041	0,040	0,043
12	VH_1_46	VL_1-51	0,040	0,043	0,042	0,042	0,043	0,048
13	VH_1_46	VL_2-23	0,042	0,047	0,044	0,043	0,047	0,051
14	VH_1_46	VL_3-1	0,046	0,059	0,051	0,052	0,055	0,063
15	VH_1_46	VL_3-21	0,042	0,103	0,057	0,062	0,066	0,058
16	VH_1_69*01	VK_1_27						
17	VH_1_69*01	VK_3_11	0,037	0,044	0,041	0,043	0,042	0,049
18	VH_1_69*01	VL_1-40	0,040	0,042	0,041	0,043	0,040	0,045
19	VH_1_69*01	VL_1-51	0,040	0,042	0,041	0,042	0,041	0,044
20	VH_1_69*01	VL_3-1	0,042	0,068	0,060	0,069	0,076	0,113
21	VH_1_69*01	VL_3-21	0,041	0,063	0,050	0,056	0,062	0,069
22	VH_3_07	VK_1_12	0,041	0,043	0,042	0,044	0,043	0,052
23	VH_3_07	VK_1_16	0,036	0,037	0,038	0,040	0,039	0,05
24	VH_3_07	VK_1_27	0,036	0,040	0,040	0,043	0,042	0,047
25	VH_3_07	VK_1_39	0,043	0,045	0,045	0,045	0,058	0,052
26	VH_3_07	VK_3_15	0,041	0,043	0,043	0,043	0,042	0,049
27	VH_3_07	VK_3_20	0,040	0,061	0,045	0,045	0,045	0,066
28	VH_3_07	VL_1-47	0,038	0,041	0,040	0,040	0,040	0,045
29	VH_3_07	VL_1-51	0,042	0,043	0,042	0,044	0,044	0,054
30	VH_3_07	VL_2-23	0,036	0,040	0,038	0,039	0,038	0,043
31	VH_3_07	VL_3-1	0,037	0,041	0,041	0,042	0,041	0,051
32	VH_3_11	VK_1_05	0,043	0,050	0,051	0,053	0,054	0,083

Figure 50

Agitation			Tm after agitation stress	DLS		Particle Staining	
No.	VH	VL	apparent Tm [°C]	Radius [nm]	% Poly-dispersity	IgGs before stress Categorized from 1-4	IgGs Post stress categorized from 1-4
1	VH_1_18	VK_1_39	79,7	5,6	21,3		4
2	VH_1_18	VK_3_11					
3	VH_1_18	VK_3_15	81,6	60	50	1,00	4,00
4	VH_1_18	VK_3_20	78	5,6	8,9		4
5	VH_1_18	VL_1-40	83,9	6	16	1	3
6	VH_1_18	VL_1-47	84,0	6,1	21	1,00	2,5
7	VH_1_18	VL_2-23	80,4	5,9	22	1,00	3,0
8	VH_1_18	VL_3-1	84,7	5,5	8,5	1,00	3,0
9	VH_1_46	VK_1_09	77,8	6	23	1,00	3,5
10	VH_1_46	VK_3_15	77,4	6	36,4	1,00	3,5
11	VH_1_46	VL_1-40	80,7	5,9	19,5	1	3,0
12	VH_1_46	VL_1-51	79,4	5,4	15,5	2,50	2,0
13	VH_1_46	VL_2-23	78,5	5,5	14,2	2,00	2,0
14	VH_1_46	VL_3-1	76,0	60	50	2,00	2,5
15	VH_1_46	VL_3-21	74,1	5,7	19,2	1,00	2,5
16	VH_1_69*01	VK_1_27					
17	VH_1_69*01	VK_3_11	77,8	5,8	22,6	1,00	3,0
18	VH_1_69*01	VL_1-40	81,6	7,3	13,2	3,00	2,5
19	VH_1_69*01	VL_1-51	78,1	5,3	4,1	1	2,5
20	VH_1_69*01	VL_3-1	79,5	60	50	1	3,5
21	VH_1_69*01	VL_3-21	76,2	6	31,6	1	3,5
22	VH_3_07	VK_1_12	78,1	5,4	22,5	2,50	3,0
23	VH_3_07	VK_1_16	75,2	5,3	4,7		2,5
24	VH_3_07	VK_1_27	80,2	6,2	50	1	2
25	VH_3_07	VK_1_39	80,0	5,3	7,1	1,00	1,5
26	VH_3_07	VK_3_15	79,2	5,9	29	2,00	2,5
27	VH_3_07	VK_3_20	78,3	60	50	1,00	3,5
28	VH_3_07	VL_1-47	78,8	5,5	19,3	1,00	2,0
29	VH_3_07	VL_1-51	79,7	60	50	1,00	3,0
30	VH_3_07	VL_2-23	81,2	5,8	18,7	1	2,5
31	VH_3_07	VL_3-1	80,9	5,7	23,8	1	3,0
32	VH_3_11	VK_1_05	74,8	60	50	1	3,5

Figure 51

Agitation			Absorption at 320 nm					
No.	VH	VL	Inital	after 45 min agitation at RT	after 1,5 h agitation at RT	After 2,5 H agitation at RT	After 3,5 h agitiation at RT	After 24 h agitation at RT
33	VH_3_11	VK_1_39	0,039	0,045	0,047	0,050	0,050	0,070
34	VH_3_11	VK_3_15	0,042	0,048	0,048	0,052	0,053	0,099
35	VH_3_11	VL_1-40	0,037	0,039	0,039	0,041	0,040	0,05
36	VH_3_11	VL_1-47	0,036	0,037	0,039	0,040	0,040	0,05
37	VH_3_11	VL_1-51	0,040	0,043	0,041	0,041	0,042	0,045
38	VH_3_11	VL_2-23	0,037	0,041	0,040	0,040	0,039	0,044
39	VH_3_15	VK_1_05	0,040	0,042	0,042	0,041	0,041	0,044
40	VH_3_15	VK_1_06	0,038	0,039	0,040	0,042	0,045	0,07
41	VH_3_15	VK_1_09	0,040	0,042	0,041	0,042	0,043	0,048
42	VH_3_15	VK_1_12	0,039	0,041	0,040	0,041	0,041	0,053
43	VH_3_15	VK_1_16	0,039	0,044	0,045	0,049	0,049	0,096
44	VH_3_15	VK_1_27	0,043	0,037	0,037	0,038	0,039	0,05
45	VH_3_15	VK_3_11	0,043	0,037	0,038	0,041	0,042	0,06
46	VH_3_15	VK_3_15	0,038	0,046	0,048	0,052	0,054	0,101
47	VH_3_15	VL_1-40	0,045	0,051	0,051	0,053	0,054	0,092
48	VH_3_15	VL_1-47	0,043	0,048	0,049	0,050	0,051	0,087
49	VH_3_15	VL_1-51	0,035	0,041	0,042	0,043	0,044	0,07
50	VH_3_15	VL_2-14	0,036	0,039	0,041	0,044	0,044	0,058
51	VH_3_21	VK_1_06	0,040	0,045	0,047	0,050	0,050	0,059
52	VH_3_21	VK_1_12	0,036	0,041	0,042	0,042	0,042	0,05
53	VH_3_21	VK_1_27	0,040	0,042	0,042	0,041	0,042	0,045
54	VH_3_21	VL_2-11	0,039	0,043	0,039	0,040	0,040	0,045
55	VH_3_21	VL_2-14	0,038	0,040	0,040	0,041	0,040	0,045
56	VH_3_21	VL_2-23	0,037	0,041	0,039	0,042	0,040	0,043
57	VH_3_21	VL_3-1	0,040	0,047	0,051	0,058	0,058	0,068
58	VH_3_23	VK_1_39	0,037	0,043	0,043	0,045	0,046	0,051
59	VH_3_23	VK_3_15	0,039	0,038	0,039	0,041	0,042	0,08
60	VH_3_23	VK_3_20	0,035	0,041	0,041	0,043	0,043	0,062
61	VH_3_23	VL_2-11	0,035	0,040	0,040	0,043	0,043	0,053
62	VH_3_23	VL_2-14	0,036	0,040	0,039	0,041	0,044	0,068
63	VH_3_23	VL_2-23	0,037	0,042	0,042	0,045	0,046	0,079
64	VH_3_23	VL_3-1	0,037	0,040	0,039	0,039	0,038	0,043

Figure 52

Agitation			Tm after agitation stress	DLS		Particle Staining	
No.	VH	VL	apparent Tm [°C]	Radius [nm]	% Poly-dispersity	IgGs before stress Categorized from 1-4	IgGs Post stress categorized from 1-4
33	VH_3_11	VK_1_39	79,2	60	50	2	3,5
34	VH_3_11	VK_3_15	79,0	60	50	1	3,5
35	VH_3_11	VL_1-40	80,5	5,1	3,1		3,0
36	VH_3_11	VL_1-47	80,5	5,1	2,7		4,0
37	VH_3_11	VL_1-51	77,1	5,4	9,9	1	2,0
38	VH_3_11	VL_2-23	74,1	5,6	22,4	1	2,5
39	VH_3_15	VK_1_05	76,0	6	24,9	2	2,0
40	VH_3_15	VK_1_06	79,0	25	50		4,0
41	VH_3_15	VK_1_09	81,4	60	50	2,5	3,5
42	VH_3_15	VK_1_12	79,5	5,6	17,2	2	3,5
43	VH_3_15	VK_1_16	76,7	60	50	3	4,0
44	VH_3_15	VK_1_27	77,4	6,8	25		3,0
45	VH_3_15	VK_3_11		25	50		3,0
46	VH_3_15	VK_3_15	80,3	291	23,7	1	4,0
47	VH_3_15	VL_1-40	80,7	60	50	3	3,5
48	VH_3_15	VL_1-47	77,8	60	50	1	3,5
49	VH_3_15	VL_1-51		25	50		2,5
50	VH_3_15	VL_2-14	75,5	60	50	2	3,0
51	VH_3_21	VK_1_06	75,5	6	23,8	1	2,5
52	VH_3_21	VK_1_12		5,7	17,9		2,0
53	VH_3_21	VK_1_27	77,6	5,5	16,9	1	2,5
54	VH_3_21	VL_2-11	79,7	6,4	31,6	2	2,5
55	VH_3_21	VL_2-14	76,4	6	24,7	1	3,0
56	VH_3_21	VL_2-23	76,9	6	25,2	1	2,5
57	VH_3_21	VL_3-1	77,4	6,4	44,4	1	3,0
58	VH_3_23	VK_1_39	83,4	60,00	50,00	2	3,0
59	VH_3_23	VK_3_15		5,9	27,6		4
60	VH_3_23	VK_3_20	82,0	60,00	50,00	1	3,5
61	VH_3_23	VL_2-11	82,5	60,00	50,00	2	3,5
62	VH_3_23	VL_2-14	78,1	60,00	50,00	2	3,5
63	VH_3_23	VL_2-23	78,8	60,00	50,00	1	3,5
64	VH_3_23	VL_3-1	80,9	5,70	16,20	1	2,0

Figure 53

Agitation			Absorption at 320 nm					
No.	VH	VL	Inital	after 45 min agitation at RT	after 1,5 h agitation at RT	After 2,5 H agitation at RT	After 3,5 h agitiation at RT	After 24 h agitation at RT
65	VH_3_23	VL_3-21	0,040	0,041	0,040	0,041	0,043	0,045
66	VH_3_30	VK_3_15	0,038	0,044	0,040	0,040	0,041	0,046
67	VH_3_30	VK_3_20	0,040	0,044	0,041	0,043	0,046	0,050
68	VH_3_30	VL_2-23	0,037	0,040	0,039	0,039	0,039	0,043
69	VH_3_30	VL_3-1	0,042	0,065	0,080	0,093	0,098	0,183
70	VH_3_30	VL_3-21	0,036	0,039	0,039	0,039	0,038	0,052
71	VH_3_53	VK_1_39	0,036	0,040	0,041	0,042	0,041	0,047
72	VH_3_53	VK_3_15	0,036	0,042	0,043	0,046	0,048	0,085
73	VH_3_53	VL_2-11	0,037	0,044	0,043	0,045	0,049	0,074
74	VH_3_53	VL_2-23	0,035	0,042	0,043	0,047	0,047	0,082
75	VH_3_53	VL_3-1	0,036	0,039	0,038	0,041	0,040	0,047
76	VH_3_74	VK_1_05	0,037	0,041	0,039	0,040	0,040	0,049
77	VH_3_74	VK_1_06	0,035	0,039	0,038	0,038	0,038	0,043
78	VH_3_74	VK_1_12	0,039	0,044	0,042	0,041	0,040	0,045
79	VH_3_74	VK_1_27	0,038	0,044	0,041	0,043	0,041	0,047
80	VH_3_74	VK_3_20	0,036	0,038	0,038	0,040	0,039	0,044
81	VH_3_74	VL_1-51	0,037	0,039	0,039	0,040	0,041	0,067
82	VH_3_74	VL_3-1	0,036	0,039	0,038	0,040	0,039	0,045
83	VH_5_51	VK_1_39	0,036	0,039	0,037	0,037	0,038	0,038
84	VH_5_51	VL_1-40	0,036	0,041	0,038	0,040	0,039	0,042
85	VH_5_51	VL_1-47	0,035	0,041	0,039	0,041	0,041	0,047
86	VH_5_51	VL_1-51	0,037	0,044	0,043	0,045	0,046	0,059
87	VH_5_51	VL_3-1	0,036	0,041	0,042	0,044	0,046	0,08
88	VH_6_1	VK_1_06	0,037	0,042	0,040	0,040	0,039	0,045
89	VH_6_1	VK_1_09	0,039	0,061	0,042	0,043	0,040	0,046
90	VH_6_1	VK_1_27	0,039	0,060	0,042	0,042	0,044	0,067
91	VH_6_1	VK_3_15	0,04	0,045	0,049	0,056	0,054	0,11
92	VH_6_1	VK_3_20	0,038	0,044	0,039	0,039	0,043	0,052
93	VH_6_1	VL_1-47	0,048	0,058	0,061	0,067	0,072	0,164
94	VH_6_1	VL_1-51	0,036	0,042	0,039	0,039	0,038	0,043
95	VH_6_1	VL_3-1	0,048	0,056	0,051	0,053	0,052	0,061

Figure 54

Agitation			Tm after agitation stress	DLS		Particle Staining	
No.	VH	VL	apparent Tm [°C]	Radius [nm]	% Poly-dispersity	IgGs before stress Categorized from 1-4	IgGs Post stress categorized from 1-4
65	VH_3_23	VL_3-21	79,0	5,30	10,60	2	2,0
66	VH_3_30	VK_3_15	80,9	5,70	24,60	2	2,5
67	VH_3_30	VK_3_20	80,9	6,70	50,00	2	3,0
68	VH_3_30	VL_2-23	80,2	5,90	23,70	2	2,5
69	VH_3_30	VL_3-1	79,5	94,00	50	2	4,0
70	VH_3_30	VL_3-21	77,8	5,70	21,60	2	3,0
71	VH_3_53	VK_1_39	74,1	5,90	24,60	2	3,0
72	VH_3_53	VK_3_15	73,8	60,00	50,00	1	3,5
73	VH_3_53	VL_2-11	73,8	60,00	50,00	2	3,0
74	VH_3_53	VL_2-23	69,6	60,00	50,00	2	3,5
75	VH_3_53	VL_3-1	73,1	5,40	12,00	3	2,5
76	VH_3_74	VK_1_05	75,5	6,10	42,20	2	2,5
77	VH_3_74	VK_1_06	77,8	5,50	18,10	2,5	2,0
78	VH_3_74	VK_1_12	79,3	5,30	12,60	2	2,0
79	VH_3_74	VK_1_27	78,1	5,50	15,70	2	2,0
80	VH_3_74	VK_3_20	79,7	60,00	50,00	2	2,5
81	VH_3_74	VL_1-51	80,7	60,00	50,00	2,5	3,0
82	VH_3_74	VL_3-1	79,0	5,50	15,60	2	2,5
83	VH_5_51	VK_1_39	73,6	5,30	10,50	1,5	3,0
84	VH_5_51	VL_1-40	77,6	5,70	23,10	2,5	2,5
85	VH_5_51	VL_1-47	76,4	5,80	21,80	2	3,0
86	VH_5_51	VL_1-51	75,7	5,60	22,70	1	2,5
87	VH_5_51	VL_3-1	77,1	7,4	24,4		2,5
88	VH_6_1	VK_1_06	73,6	5,80	17,40	2,5	2,5
89	VH_6_1	VK_1_09	79,6	5,30	10,50	3	2,5
90	VH_6_1	VK_1_27	80,0	6,30	22,60	2	3,5
91	VH_6_1	VK_3_15	78,4	8,8	26,8		4,0
92	VH_6_1	VK_3_20	77,1	60,00	50,00	2	3,0
93	VH_6_1	VL_1-47	73,6	60,00	44,6	2,5	3,0
94	VH_6_1	VL_1-51	76,7	5,70	22,80	1	2,5
95	VH_6_1	VL_3-1	69,6	40,00	50,00	2	2,0

Figure 55

Cumulative Score Calculation			Score Absorption data acid treatment				Score DLS Data before and after acid treatment				Score Particle staining before and after acid	
No.	VH	VL	Inital	15 min Acid treatment	100 min Acid treatment	After neutralization	Initial Radius [nm]	Initial % Poly-dispersity	After acid treatment Radius [nm]	After acid treatment % Polydispersity	IgGs before Categorized from 1-4	IgGs Post acid categorized from 1-4
1	VH_1_18	VK_1_39	75	0	25	75	100	100	100	100	100	25
2	VH_1_18	VK_3_11										
3	VH_1_18	VK_3_15	100	25	75	100	100	100	100	100	100	75
4	VH_1_18	VK_3_20	100	75	75	100	100	100	100	100	75	25
5	VH_1_18	VL_1-40	100	25	100	100	100	100	100	100	100	75
6	VH_1_18	VL_1-47	100	25	75	100	100	100	100	100	100	75
7	VH_1_18	VL_2-23	100	25	75	100	100	100	100	100	100	100
8	VH_1_18	VL_3-1	100	25	75	100	100	100	100	100	100	100
9	VH_1_46	VK_1_09	100	25	25	75	100	100	100	100	100	100
10	VH_1_46	VK_3_15	100	25	75	100	100	100	100	100	100	100
11	VH_1_46	VL_1-40	100	25	75	100	100	100	100	100	100	100
12	VH_1_46	VL_1-51	100	75	100	100	100	100	100	100	25	25
13	VH_1_46	VL_2-23	100	25	75	100	100	100	100	100	75	100
14	VH_1_46	VL_3-1	75	0	0	0	50	25	25	0	75	0
15	VH_1_46	VL_3-21	100	75	75	75	50	0	50	0	100	25
16	VH_1_69*01	VK_1_27										
17	VH_1_69*01	VK_3_11	100	25	100	100	100	100	100	100	100	75
18	VH_1_69*01	VL_1-40	100	25	25	75	50	100	50	75	25	25
19	VH_1_69*01	VL_1-51	100	25	75	75	100	100	100	100	100	100
20	VH_1_69*01	VL_3-1	75	25	25	25	50	75	25	0	100	100
21	VH_1_69*01	VL_3-21	75	0	25	100	100	100	100	75	100	100
22	VH_3_07	VK_1_12	100	25	75	100	100	100	100	100	25	100
23	VH_3_07	VK_1_16	100	25	75	100	100	100	100	100	100	25
24	VH_3_07	VK_1_27	100	75	75	75	100	100	100	100	100	75
25	VH_3_07	VK_1_39	100	100	100	100	100	100	100	100	100	0
26	VH_3_07	VK_3_15	100	100	100	100	100	100	100	100	75	25
27	VH_3_07	VK_3_20	100	75	75	75	100	100	100	100	100	75
28	VH_3_07	VL_1-47	100	100	100	100	100	100	100	100	100	100
29	VH_3_07	VL_1-51	100	75	75	75	100	100	100	100	100	75
30	VH_3_07	VL_2-23	75	25	75	75	100	100	100	100	100	100
31	VH_3_07	VL_3-1	100	75	100	100	100	100	100	100	100	100
32	VH_3_11	VK_1_05	100	100	100	100	100	100	100	100	100	75

Figure 56

Cumulative Score Calculation			Score Absorption data during and after agitation						Score DLS data after agitation		Particle staining	
No.	**VH**	**VL**	Inital	after 45 min agitation at RT	after 1,5 h agitation at RT	After 2,5 H agitation at RT	After 3,5 h agitiation at RT	After 24 h agitation at RT	Radius [nm]	% Poly-dispersity	Particle staining after agitation	**Cumul-ative Score**
1	VH_1_18	VK_1_39	75	25	25	25	25	0	100	75	0	1050
2	VH_1_18	VK_3_11										
3	VH_1_18	VK_3_15	75	25	75	25	25	0	0	0	0	1100
4	VH_1_18	VK_3_20	100	75	75	75	75	0	100	100	0	1450
5	VH_1_18	VL_1-40	100	75	75	75	75	25	100	75	25	1525
6	VH_1_18	VL_1-47	100	75	75	75	75	25	50	75	25	1450
7	VH_1_18	VL_2-23	75	25	75	75	75	25	100	75	25	1450
8	VH_1_18	VL_3-1	100	75	75	75	75	75	100	100	25	1600
9	VH_1_46	VK_1_09	100	75	100	75	100	25	100	75	0	1475
10	VH_1_46	VK_3_15	100	75	100	100	75	75	100	25	0	1550
11	VH_1_46	VL_1-40	100	75	75	75	100	75	100	75	25	1600
12	VH_1_46	VL_1-51	100	75	75	75	75	25	100	75	75	1500
13	VH_1_46	VL_2-23	75	25	75	75	25	25	100	100	75	1450
14	VH_1_46	VL_3-1	25	25	25	25	25	0	0	0	25	400
15	VH_1_46	VL_3-21	75	0	25	0	0	25	100	75	25	875
16	VH_1_69*01	VK_1_27										
17	VH_1_69*01	VK_3_11	100	75	75	75	75	25	100	75	25	1525
18	VH_1_69*01	VL_1-40	100	75	75	75	75	25	50	100	25	1150
19	VH_1_69*01	VL_1-51	100	75	75	75	75	75	100	100	25	1575
20	VH_1_69*01	VL_3-1	75	0	0	0	0	0	0	0	0	575
21	VH_1_69*01	VL_3-21	75	0	25	25	0	0	100	25	0	1025
22	VH_3_07	VK_1_12	75	75	75	75	75	25	100	75	25	1425
23	VH_3_07	VK_1_16	100	100	100	100	100	25	100	100	25	1575
24	VH_3_07	VK_1_27	100	75	75	75	75	25	50	0	75	1450
25	VH_3_07	VK_1_39	75	25	75	25	25	25	100	100	100	1450
26	VH_3_07	VK_3_15	75	75	75	75	75	25	100	75	25	1500
27	VH_3_07	VK_3_20	100	0	75	75	25	0	0	0	0	1175
28	VH_3_07	VL_1-47	100	75	75	75	100	25	100	75	75	1700
29	VH_3_07	VL_1-51	75	75	75	75	75	25	0	0	25	1325
30	VH_3_07	VL_2-23	100	75	100	100	100	75	100	75	25	1600
31	VH_3_07	VL_3-1	100	75	75	75	75	25	100	75	25	1600
32	VH_3_11	VK_1_05	75	25	25	25	25	0	0	0	0	1150

Figure 57

Cumulative Score Calculation			Score Absorption data acid treatment				Score DLS Data before and after acid treatment				Score Particle staining before and after acid treatment	
No.	VH	VL	Inital	15 min Acid treatment	100 min Acid treatment	After neutralization	Initial Radius [nm]	Initial % Poly-dispersity	After acid treatment Radius [nm]	After acid treatment % Polydispersity	IgGs before Categorized from 1-4	IgGs Post acid categorized from 1-4
33	VH_3_11	VK_1_39	100	75	100	75	100	100	100	75	75	75
34	VH_3_11	VK_3_15	75	75	75	75	100	100	100	100	100	75
35	VH_3_11	VL_1-40	100	25	25	75	100	100	100	100	100	100
36	VH_3_11	VL_1-47	100	75	75	75	100	100	50	75	100	100
37	VH_3_11	VL_1-51	100	75	100	100	100	100	100	100	100	100
38	VH_3_11	VL_2-23	100	100	100	100	100	100	100	100	100	100
39	VH_3_15	VK_1_05	100	25	75	100	100	100	100	100	75	75
40	VH_3_15	VK_1_06	100	75	75	100	100	100	100	100	100	75
41	VH_3_15	VK_1_09	100	75	75	100	50	75	100	100	25	75
42	VH_3_15	VK_1_12	100	100	100	100	100	100	100	100	75	75
43	VH_3_15	VK_1_16	100	25	75	75	100	100	100	100	25	75
44	VH_3_15	VK_1_27	75	25	25	100	100	100	100	100	100	75
45	VH_3_15	VK_3_11	75	25	25	75	100	100	100	100	75	75
46	VH_3_15	VK_3_15	75	25	75	75	100	75	100	75	100	25
47	VH_3_15	VL_1-40	100	25	75	100	100	100	100	100	25	100
48	VH_3_15	VL_1-47	100	100	100	100	100	100	100	100	100	75
49	VH_3_15	VL_1-51	100	25	25	100	100	100	100	100	100	75
50	VH_3_15	VL_2-14	100	100	100	100	100	100	75	100	75	100
51	VH_3_21	VK_1_06	100	75	75	100	100	100	100	100	100	25
52	VH_3_21	VK_1_12	100	75	75	100	100	100	100	75	25	75
53	VH_3_21	VK_1_27	100	75	25	25	100	100	100	100	100	75
54	VH_3_21	VL_2-11	100	25	25	75	100	100	100	100	75	75
55	VH_3_21	VL_2-14	100	25	25	75	100	100	100	100	100	75
56	VH_3_21	VL_2-23	100	75	75	100	100	100	100	100	100	100
57	VH_3_21	VL_3-1	100	25	25	25	50	0	0	0	100	75
58	VH_3_23	VK_1_39	100	75	75	100	100	100	100	100	100	75
59	VH_3_23	VK_3_15	100	25	25	25	100	100	100	100	100	75
60	VH_3_23	VK_3_20	100	75	100	100	100	100	100	100	100	25
61	VH_3_23	VL_2-11	100	75	100	100	100	100	100	100	75	75
62	VH_3_23	VL_2-14	100	100	100	100	100	100	100	100	75	75
63	VH_3_23	VL_2-23	100	100	100	100	100	100	100	100	100	75
64	VH_3_23	VL_3-1	100	75	100	100	100	100	100	100	100	75

Figure 58

Cumulative Score Calculation			Score Absorption data during and after agitation						Score DLS data after agitation		Particle staining	
No.	**VH**	**VL**	Inital	after 45 min agitation at RT	after 1,5 h agitation at RT	After 2,5 H agitation at RT	After 3,5 h agitiation at RT	After 24 h agitation at RT	Radius [nm]	% Poly-dispersity	Particle staining after agitation	**Cumul-ative Score**
33	VH_3_11	VK_1_39	100	25	25	25	25	0	0	0	0	1075
34	VH_3_11	VK_3_15	75	25	25	25	25	0	0	0	0	1050
35	VH_3_11	VL_1-40	100	100	100	75	100	25	100	100	25	1550
36	VH_3_11	VL_1-47	100	100	100	100	75	25	100	100	0	1550
37	VH_3_11	VL_1-51	100	75	75	75	75	25	100	100	75	1675
38	VH_3_11	VL_2-23	100	75	100	100	100	75	100	75	25	1750
39	VH_3_15	VK_1_05	100	75	75	75	75	75	100	75	75	1575
40	VH_3_15	VK_1_06	100	100	100	75	75	0	25	0	0	1400
41	VH_3_15	VK_1_09	75	75	75	75	75	25	0	0	0	1175
42	VH_3_15	VK_1_12	100	75	100	75	75	25	100	75	0	1575
43	VH_3_15	VK_1_16	100	75	25	25	25	0	0	0	0	1025
44	VH_3_15	VK_1_27	75	100	100	100	100	25	50	75	25	1450
45	VH_3_15	VK_3_11	75	100	100	75	75	0	25	0	25	1225
46	VH_3_15	VK_3_15	100	25	25	25	25	0	25	75	0	1025
47	VH_3_15	VL_1-40	75	25	25	25	25	0	0	0	0	1000
48	VH_3_15	VL_1-47	75	25	25	25	25	0	0	0	0	1150
49	VH_3_15	VL_1-51	100	75	75	75	75	0	25	0	25	1275
50	VH_3_15	VL_2-14	100	100	75	75	75	25	0	0	25	1425
51	VH_3_21	VK_1_06	100	25	25	25	25	25	100	75	25	1300
52	VH_3_21	VK_1_12	100	75	75	75	75	25	100	75	75	1500
53	VH_3_21	VK_1_27	100	75	75	75	75	75	100	75	25	1475
54	VH_3_21	VL_2-11	100	75	100	75	75	75	50	25	25	1375
55	VH_3_21	VL_2-14	100	100	100	75	75	75	100	75	25	1525
56	VH_3_21	VL_2-23	100	75	100	75	75	75	100	75	25	1650
57	VH_3_21	VL_3-1	100	25	25	25	25	0	50	0	25	675
58	VH_3_23	VK_1_39	100	75	75	25	25	25	0	0	25	1250
59	VH_3_23	VK_3_15	100	100	100	75	75	0	100	75	0	1375
60	VH_3_23	VK_3_20	100	75	75	75	75	0	0	0	0	1300
61	VH_3_23	VL_2-11	100	100	75	75	75	25	0	0	0	1375
62	VH_3_23	VL_2-14	100	75	100	75	75	0	0	0	0	1375
63	VH_3_23	VL_2-23	100	75	75	75	25	0	0	0	0	1325
64	VH_3_23	VL_3-1	100	75	100	100	100	75	100	75	75	1750

Figure 59

Cumulative Score Calculation			Score Absorption data acid treatment				Score DLS Data before and after acid treatment				Score Particle staining before and after acid treatment	
No.	VH	VL	Inital	15 min Acid treatment	100 min Acid treatment	After neutralization	Initial Radius [nm]	Initial % Poly-dispersity	After acid treatment Radius [nm]	After acid treatment % Polydispersity	IgGs before Categorized from 1-4	IgGs Post acid categorized from 1-4
65	VH_3_23	VL_3-21	100	75	100	100	100	100	100	100	75	100
66	VH_3_30	VK_3_15	100	100	100	100	100	100	100	100	75	75
67	VH_3_30	VK_3_20	100	75	75	75	100	100	100	100	75	25
68	VH_3_30	VL_2-23	100	75	100	100	100	100	100	100	75	100
69	VH_3_30	VL_3-1	100	25	25	25	50	0	50	0	75	75
70	VH_3_30	VL_3-21	100	75	75	75	100	100	100	100	75	75
71	VH_3_53	VK_1_39	75	25	25	75	100	100	100	100	75	75
72	VH_3_53	VK_3_15	100	75	100	100	100	100	100	100	100	100
73	VH_3_53	VL_2-11	100	100	75	100	100	100	100	100	75	100
74	VH_3_53	VL_2-23	100	75	100	100	100	100	100	100	75	100
75	VH_3_53	VL_3-1	100	75	100	100	100	100	50	75	25	25
76	VH_3_74	VK_1_05	100	75	100	75	100	100	100	100	75	100
77	VH_3_74	VK_1_06	100	100	100	100	100	100	100	100	25	75
78	VH_3_74	VK_1_12	100	75	100	100	100	100	100	100	75	100
79	VH_3_74	VK_1_27	100	25	75	100	100	100	100	100	75	75
80	VH_3_74	VK_3_20	100	100	100	100	100	100	100	75	75	75
81	VH_3_74	VL_1-51	100	75	75	100	100	100	100	100	25	75
82	VH_3_74	VL_3-1	100	75	100	75	100	100	100	100	75	75
83	VH_5_51	VK_1_39	100	25	75	75	100	100	75	100	100	75
84	VH_5_51	VL_1-40	100	75	100	100	100	100	100	100	25	75
85	VH_5_51	VL_1-47	100	75	100	100	100	100	100	100	75	75
86	VH_5_51	VL_1-51	100	75	75	75	100	100	100	100	100	25
87	VH_5_51	VL_3-1	100	25	75	75	100	100	100	100	100	25
88	VH_6_1	VK_1_06	100	100	100	100	100	100	100	100	25	100
89	VH_6_1	VK_1_09	100	75	75	100	100	100	100	100	25	100
90	VH_6_1	VK_1_27	100	100	100	100	100	100	100	100	75	100
91	VH_6_1	VK_3_15	75	25	25	75	100	100	100	100	100	75
92	VH_6_1	VK_3_20	100	100	100	100	100	100	100	100	75	75
93	VH_6_1	VL_1-47	25	0	0	0	25	0	0	0	25	0
94	VH_6_1	VL_1-51	100	100	100	100	100	100	100	75	100	100
95	VH_6_1	VL_3-1	25	0	0	0	0	25	25	0	75	0

Figure 60

Cumulative Score Calculation			Score Absorption data during and after agitation						Score DLS data after agitation		Particle staining	
No.	**VH**	**VL**	Inital	after 45 min agitation at RT	after 1,5 h agitation at RT	After 2,5 H agitation at RT	After 3,5 h agitiation at RT	After 24 h agitation at RT	Radius [nm]	% Poly-dispersity	Particle staining after agitation	**Cumul-ative Score**
65	VH_3_23	VL_3-21	100	75	75	75	75	75	100	100	75	1700
66	VH_3_30	VK_3_15	100	75	75	75	75	25	100	75	25	1575
67	VH_3_30	VK_3_20	100	75	75	75	25	25	50	0	25	1275
68	VH_3_30	VL_2-23	100	100	100	100	100	75	100	75	25	1725
69	VH_3_30	VL_3-1	75	0	0	0	0	0	25	0	0	525
70	VH_3_30	VL_3-21	100	100	100	100	100	25	100	75	25	1600
71	VH_3_53	VK_1_39	100	75	75	75	75	25	100	75	25	1375
72	VH_3_53	VK_3_15	100	75	75	25	25	0	0	0	0	1275
73	VH_3_53	VL_2-11	100	75	75	25	25	0	0	0	25	1275
74	VH_3_53	VL_2-23	100	75	75	25	25	0	0	0	0	1250
75	VH_3_53	VL_3-1	100	100	100	75	100	25	100	100	25	1475
76	VH_3_74	VK_1_05	100	75	100	75	75	25	50	0	25	1450
77	VH_3_74	VK_1_06	100	100	100	100	100	75	100	75	75	1725
78	VH_3_74	VK_1_12	100	75	75	75	75	25	100	100	75	1650
79	VH_3_74	VK_1_27	100	75	75	75	75	25	100	75	75	1525
80	VH_3_74	VK_3_20	100	100	100	100	100	75	0	0	25	1525
81	VH_3_74	VL_1-51	100	100	100	75	75	0	0	0	25	1325
82	VH_3_74	VL_3-1	100	100	100	75	100	75	100	75	25	1650
83	VH_5_51	VK_1_39	100	100	100	100	100	100	100	100	25	1650
84	VH_5_51	VL_1-40	100	75	100	100	100	75	100	75	25	1625
85	VH_5_51	VL_1-47	100	75	100	75	75	25	100	75	25	1575
86	VH_5_51	VL_1-51	100	75	75	25	25	25	100	75	25	1375
87	VH_5_51	VL_3-1	100	75	75	75	25	0	50	75	25	1300
88	VH_6_1	VK_1_06	100	75	100	75	100	25	100	75	25	1600
89	VH_6_1	VK_1_09	100	0	75	75	75	25	100	100	25	1450
90	VH_6_1	VK_1_27	100	25	75	75	75	0	50	75	0	1450
91	VH_6_1	VK_3_15	75	25	25	25	25	0	50	75	0	1075
92	VH_6_1	VK_3_20	100	75	100	100	75	25	0	0	25	1450
93	VH_6_1	VL_1-47	25	25	0	0	0	0	0	0	25	150
94	VH_6_1	VL_1-51	100	75	100	100	100	75	100	75	25	1725
95	VH_6_1	VL_3-1	25	25	25	25	25	0	25	0	75	375

Figure 61 A

					ELISA hits per 368			
Germline protein pair composition	**Target**	**Antigen immobilization**	**Blocking**	**# clones screened**	>10X Background	5-10X Background	**# clones sequenced**	# unique antibodies
VH3-23 K1-39	FZD4-Fc	Fc capture	Milk powder and Fc blocking	368	149	0	85	19
VH1-69 L1-51 VH3-07 L1-51 VH3-15 L1-51 VH5-51 L1-51 VH6-1 L1-51	GFP	Epoxy M450 beads	Chemiblocker	368	132	24	34	21
VH3-23 K1-39 VH3-74 K1-06	GFP	Epoxy M450 beads	Chemiblocker	368	6	11	10	7
VH1-69 L1-51 VH3-07 L1-51 VH3-15 L1-51 VH5-51 L1-51 VH6-1 L1-51	HER4-Fc	Epoxy M450 beads	Chemiblocker + 50 µg/ml irrelevant Fc fusion protein	368	223	31	25	21
VH3-23 K1-39 VH3-74 K1-06	HER4-Fc	Epoxy M450 beads	Chemiblocker + 50 µg/ml irrelevant Fc fusion protein	368	69	38	27	8
VH1-69 L1-51 VH3-07 L1-51 VH3-15 L1-51 VH5-51 L1-51 VH6-1 L1-51	FZD4-Fc	Epoxy M450 beads	Chemiblocker + 50 µg/ml irrelevant Fc fusion protein	368	64	19	24	15
VH3-23 K1-39 VH3-74 K1-06	FZD4-Fc	Epoxy M450 beads	Chemiblocker + 50 µg/ml irrelevant Fc fusion protein	368	97	44	42	28
VH1-18 VK3-20 VH3-07 VK1-12 VH3-15 VK1-05 VH3-15 VK1-06 VH3-15 VK1-12 VH3-21 VK1-12	GFP	Epoxy M450 beads	Chemiblocker	368	5	2	7	4

Figure 61 B

					ELISA hits per 368			
Germline protein pair composition	**Target**	**Antigen immobilization**	**Blocking**	**# clones screened**	>10X Background	5-10X Background	**# clones sequenced**	# unique antibodies
VH3-23 VL3-1	GFP	Epoxy M450 beads	Chemiblocker	368	10	16	26	17
VH1-18 VK3-20 VH3-07 VK1-12 VH3-15 VK1-05 VH3-15 VK1-06 VH3-15 VK1-12 VH3-21 VK1-12	HER4-Fc	Epoxy M450 beads	Chemiblocker + irrelevant Fc fusion protein	368	168	14	61	20
VH1-18 VK3-20 VH3-07 VK1-12 VH3-15 VK1-05 VH3-15 VK1-06 VH3-15 VK1-12 VH3-21 VK1-12	FZD4-Fc	Epoxy M450 beads	Chemiblocker + irrelevant Fc fusion protein	368	161	30	93	27
VH3-11 VL1-47 VH3-23 VL2-23 VH3-53 VL2-11 VH5-51 VL1-40 VH3-23 VL3-1	GFP	Epoxy M450 beads	Chemiblocker	368	36	16	52	43
VH1-46 VK3-15 VH3-07 VK1-27	GFP	Epoxy M450 beads	Chemiblocker	368	36	9	36	14
VH3-11 VL1-47 VH3-23 VL2-23 VH3-53 VL2-11 VH5-51 VL1-40 VH3-23 VL3-1	HER4-Fc	Epoxy M450 beads	Chemiblocker + irrelevant Fc fusion protein	368	141	38	96	26
VH1-46 VK3-15 VH3-07 VK1-27	HER4-Fc	Epoxy M450 beads	Chemiblocker + irrelevant Fc fusion protein	368	12	98	40	1
VH3-11 VL1-47 VH3-23 VL2-23 VH3-53 VL2-11 VH5-51 VL1-40 VH3-23 VL3-1	FZD4-Fc	Epoxy M450 beads	Chemiblocker + 50 µg/ml irrelevant Fc fusion protein	368	77	21	88	27

Figure 61C

					ELISA hits per 368			
Germline protein pair composition	**Target**	**Antigen immobilization**	**Blocking**	**# clones screened**	>10X Background	5-10X Background	**# clones sequenced**	# unique antibodies
VH5-51 VK1-39 VH3-74 VK1-12 VH3-15 VK3-11 VH3-74 VK3-20 VH6-1 VK3-20 VH1-18 VK3-20	HER4-Fc	Epoxy M450 beads	Chemiblocker + irrelevant Fc fusion protein	368	12	5	11	8
VH5-51 VK1-39 VH3-74 VK1-12 VH3-15 VK3-11 VH3-74 VK3-20 VH6-1 VK3-20 VH1-18 VK3-20	FZD4-Fc	Epoxy M450 beads	Chemiblocker + irrelevant Fc fusion protein	368	15	1	9	8
VH3-23 VK3-15 VH3-53 VK3-15 VH3-07 VK3-15 VH6-01 VK1-09 VH3-15 VK1-27 VH3-74 VK1-05 VH3-07 VK1-12	HER4-Fc	Epoxy M450 beads	Chemiblocker + irrelevant Fc fusion protein	368	5	2	6	5

Figure 61D

					ELISA hits per 368			
Germline protein pair composition	**Target**	**Antigen immobilization**	**Blocking**	**# clones screened**	>10X Background	5-10X Background	**# clones sequenced**	# unique antibodies
VH3-11 VL1-40 VH3-07 VL1-47 VH1-46 VL1-51 VH3-11 VL1-51 VH3-11 VL2-23 VH5-51 VL1-51	GFP	Epoxy M450 beads	Chemiblocker	368	14	1	6	4
VH3-11 VL1-40 VH3-07 VL1-47 VH1-46 VL1-51 VH3-11 VL1-51 VH3-11 VL2-23 VH5-51 VL1-51	HER4-Fc	Epoxy M450 beads	Chemiblocker + irrelevant Fc fusion protein	368	13	3	8	4
VH3-11 VL1-40 VH3-07 VL1-47 VH1-46 VL1-51 VH3-11 VL1-51 VH3-11 VL2-23 VH5-51 VL1-51	FZD4-Fc	Epoxy M450 beads	Chemiblocker + irrelevant Fc fusion protein	368	4	0	2	2

Figure 62A

VH	VL	Target	HCDR3 Kabat Length [aa]	LCDR3 SAS Length [aa]	pI	expression [mg/L]	Tm [°C]	SEC monomer [%]
VH3-23	VK1-39	rhErbB4/HER4-Fc	10	8	8,7	27,3	81,8	99
VH3-23	VK1-39	rhErbB4/HER4-Fc	8	8	9,4	3,5	79,1	na
VH3-23	VK1-39	rhErbB4/HER4-Fc	12	8	9,2	22,0	77,8	99
VH3-23	VK1-39	rhErbB4/HER4-Fc	14	8	8,7	26,0	86,1	99
VH3-23	VK1-39	rhErbB4/HER4-Fc	10	8	9,3	13,8	81,2	98
VH1-69	VL1-51	rhErbB4/HER4-Fc	9	9	9,2	37,6	75,5	87
VH1-69	VL1-51	rhErbB4/HER4-Fc	8	10	8,9	36,0	69,8	97
VH1-69	VL1-51	rhErbB4/HER4-Fc	9	11	9,1	26,4	75,0	89
VH1-69	VL1-51	rhErbB4/HER4-Fc	9	11	8,6	33,5	68,9	95
VH1-69	VL1-51	rhErbB4/HER4-Fc	9	10	9,1	18,0	75,0	92
VH3-23	VK1-39	rhFZD4-Fc	11	8	9,2	15,4	86,3	98
VH3-23	VK1-39	rhFZD4-Fc	10	8	9,1	18,9	78,5	100
VH3-23	VK1-39	rhFZD4-Fc	11	8	9,1	1,0	79,6	na
VH3-23	VK1-39	rhFZD4-Fc	8	8	9,1	13,8	81,9	99
VH3-23	VK1-39	rhFZD4-Fc	10	8	9,2	21,6	81,8	100
VH3-23	VK1-39	rhFZD4-Fc	10	8	8,9	14,7	78,1	100
VH3-23	VK1-39	rhFZD4-Fc	10	8	9,1	17,6	78,9	100
VH3-23	VK1-39	rhFZD4-Fc	10	8	9,2	11,4	82,1	100
VH3-23	VK1-39	rhFZD4-Fc	10	8	9,2	1,6	76,7	na
VH3-23	VK1-39	rhFZD4-Fc	10	8	9,2	7,0	83,7	na
VH3-23	VK1-39	eGFP	10	8	8,7	17,2	81,8	99
VH3-23	VK1-39	eGFP	10	8	9,2	13,2	81,8	100
VH3-23	VK1-39	eGFP	14	8	9,0	17,5	81,0	97
VH5-51	VL1-51	eGFP	15	11	9,3	38,2	67,0	98
VH5-51	VL1-51	eGFP	15	11	9,2	34,0	67,3	98
VH5-51	VL1-51	eGFP	16	11	9,0	30,5	76,7	93
VH5-51	VL1-51	eGFP	17	11	9,0	21,8	63,0	95
VH5-51	VL1-51	eGFP	15	12	9,2	9,0	71,7	na

Figure 62B

VH	VL	Target	HCDR3 Kabat Length [aa]	LCDR3 SAS Length [aa]	pI	expression [mg/L]	Tm [°C]	SEC monomer [%]
VH1-46	VK3-15	eGFP	12	9	9,3	10,5	68,9	96
VH1-46	VK3-15	eGFP	11	9	9,4	4	75,2	100
VH1-46	VK3-15	eGFP	11	9	9,4	10,5	79,4	74/78
VH3-15	VK1-05	rhErbB4/HER4-Fc	10	8	9,2	48,3	80,4	100
VH3-21	VK1-12	rhErbB4/HER4-Fc	14	8	9,4	30,5	73,6	100
VH3-21	VK1-12	rhErbB4/HER4-Fc	15	8	9,4	13,8	73,6	96/95
VH3-21	VK1-12	rhErbB4/HER4-Fc	11	8	9,2	20	nsp	100
VH5-51	VL1-40	rhErbB4/HER4-Fc	10	10	9	27,6	66	91/93
VH5-51	VL1-40	rhErbB4/HER4-Fc	10	10	8,7	35,2	73,2	94/95
VH3-21	VK1-12	rhFZD4-Fc	12	8	9,4	31,3	79,5	99
VH3-21	VK1-12	rhFZD4-Fc	10	8	9,1	21,9	76,2	100
VH3-23	VL3-1	rhFZD4-Fc	12	10	8,9	4,4	nsp	85
VH3-23	VL3-1	rhFZD4-Fc	13	10	8,9	14,7	66,2	85/91
VH3-23	VL3-1	rhFZD4-Fc	13	10	8,7	40,8	75,5	93/97
VH1-69	VL1-51	rhErbB4/HER4-Fc	7	11	8,9	20,7	69,2	93/93
VH1-69	VL1-51	rhErbB4/HER4-Fc	9	11	9,1	28,6	69,6	91/91
VH1-69	VL1-51	rhErbB4/HER4-Fc	9	11	9,1	33	76,1	95/96
VH1-69	VL1-51	rhErbB4/HER4-Fc	10	11	8,9	34,5	74	88/90

Figure 62C

VH	VL	Target	HCDR3 Kabat Length [aa]	LCDR3 SAS Length [aa]	pI	expression [mg/L]	Tm [°C]	SEC monomer [%]
VH1-69	VL1-51	rhErbB4/HER4-Fc	9	10	8,9	29,9	76,2	88/90
VH1-69-low	VL1-51	rhErbB4/HER4-Fc	7	11	9,1	34	71	98
VH1-69-low	VL1-51	rhErbB4/HER4-Fc	10	10	8,9	61,8	77,5	95
VH1-69-low	VL1-51	rhErbB4/HER4-Fc	9	10	9,1	40	79	93
VH1-69-low	VL1-51	rhErbB4/HER4-Fc	7	10	9,2	37,8	78,9	97/98
VH3-23	VL1-47	eGFP	9	11	9,4	46,1	67,8	100
VH3-23	VL1-47	eGFP	9	9	9,5	39,8	66,5	100
VH3-23	VL1-47	eGFP	9	11	9,4	4,1	70,4	97
VH3-23	VL1-47	eGFP	9	11	9,5	52,2	68,5	94/96
VH3-53	VL2-11	rhErbB4/HER4-Fc	6	9	9,2	12,7	75,1	100
VH3-53	VL2-11	rhErbB4/HER4-Fc	14	10	9,4	37,8	73,6	96
VH3-53	VL2-11	rhErbB4/HER4-Fc	7	10	9,2	48,3	75,6	98/99
VH3-07	VK1-27	rhErbB4/HER4-Fc	10	8	9	25,5	82,9	100
VH3-53	VL2-11	rhFZD4-Fc	11	9	9,1	56	70,7	98

VH1-69-low means the low PTM VHs shown in Figures 34-36