The complete amino acid sequences of the V_L and C_L regions of the NNA7 L chain and the complete amino acid sequences of the V_H and C_H1 regions of the NNA7 H chain Fd fragment.

The PDB numbering scheme is provided over the sequence and the Kabat numbering scheme is provided under the sequence. The positions of the H and L chain CDRs are also indicated under the sequence. The sequences at the N-termini of the L and H chains differ from those found in the mouse germline because they result from the primer sequences used for the initial cloning of the N92 and NNA7 Fab fragments; similarly, the amino acids at the C-terminus of the H chain (PDB positions 224-230) result from the insertion of a hexahistidyl tag used for affinity purification. These sequences have been deposited in GenBank: NNA7 L chain (AF005351, DQ140176); NNA7 H chain (DQ075213).

NNA7 L chain
V_L

Seq	Code	3-letter	Kabat
1	A	ala	0
2	E	glu	1
3	L	leu	2
4	V	val	3
5	M	met	4
6	T	thr	5
7	Q	gln	6
8	S	ser	7
9	P	pro	8
10	L	leu	9
11	S	ser	10
12	L	leu	11
13	P	pro	12
14	V	val	13
15	S	ser	14
16	L	leu	15
17	G	gly	16
18	D	asp	17
19	Q	gln	18
20	A	ala	19
21	S	ser	20
22	I	ile	21
23	S	ser	22
24	C	cys	23
25	R	arg	24
26	S	ser	25
27	S	ser	26
28	Q	gln	27
29	S	ser	27A
30	L	leu	27B
31	V	val	27C
32	H	his	27D
33	S	ser	27E
34	S	ser	28
35	G	gly	29
36	N	asn	30
37	T	thr	31
38	Y	tyr	32
39	L	leu	33
40	H	his	34
41	W	trp	35
42	Y	tyr	36
43	L	leu	37
44	Q	gln	38
45	K	lys	39
46	P	pro	40
47	G	gly	41
48	Q	gln	42
49	S	ser	43
50	P	pro	44
51	K	lys	45
52	L	leu	46
53	L	leu	47
54	I	ile	48
55	Y	tyr	49
56	K	lys	50
57	V	val	51
58	S	ser	52
59	N	asn	53
60	R	arg	54
61	F	phe	55
62	S	ser	56
63	G	gly	57
64	V	val	58
65	P	pro	59
66	D	asp	60
67	R	arg	61
68	F	phe	62
69	S	ser	63
70	G	gly	64
71	S	ser	65
72	G	gly	66
73	S	ser	67
74	G	gly	68
75	T	thr	69
76	D	asp	70
77	F	phe	71
78	T	thr	72
79	L	leu	73
80	K	lys	74
81	I	ile	75
82	S	ser	76
83	R	arg	77
84	V	val	78
85	E	glu	79
86	A	ala	80
87	E	glu	81
88	D	asp	82
89	L	leu	83
90	G	gly	84
91	V	val	85
92	Y	tyr	86
93	Y	tyr	87
94	C	cys	88
95	F	phe	89
96	Q	gln	90
97	G	gly	91
98	S	ser	92
99	H	his	93
100	V	val	94
101	P	pro	95
102	L	leu	96
103	T	thr	97
104	F	phe	98
105	G	gly	99
106	A	ala	100
107	G	gly	101
108	T	thr	102
109	K	lys	103
110	L	leu	104
111	E	glu	105
112	L	leu	106
113	K	lys	107

Region markers: CDR1 (positions 24–34), CDR2 (positions 50–56), CDR3 (positions 89–97).

C_L

114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133
R	A	D	A	A	P	T	V	S	I	F	P	P	S	S	E	Q	L	T	S
arg	ala	asp	ala	ala	pro	thr	val	ser	ile	phe	pro	pro	ser	ser	glu	gln	leu	thr	ser
108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127
134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153
G	G	A	S	V	V	C	F	L	N	N	F	Y	P	K	D	I	N	V	K
gly	gly	ala	ser	val	val	cys	phe	leu	asn	asn	phe	tyr	pro	lys	asp	ile	asn	val	lys
128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147
154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173
W	K	I	D	G	S	E	R	Q	N	G	V	L	N	S	W	T	D	Q	D
trp	lys	ile	asp	gly	ser	glu	arg	gln	asn	gly	val	lys	asn	ser	trp	thr	asp	gln	asp
148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167
174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193
S	K	D	S	T	Y	S	M	S	S	T	L	T	L	T	K	D	E	Y	E
ser	lys	asp	ser	thr	tyr	ser	met	ser	ser	thr	leu	thr	leu	thr	lys	asp	glu	tyr	glu
168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187
194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213
R	H	N	S	Y	T	C	E	A	T	H	K	T	S	T	S	P	I	V	K
arg	his	asn	ser	tyr	thr	cys	glu	ala	thr	his	lys	thr	ser	thr	ser	pro	ile	val	lys
188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207

214	215	216	217	218	219	220
S	F	N	R	N	E	C
ser	phe	asn	arg	asn	glu	cys
208	209	210	211	212	213	214

NNA7 H chain
V_H

Seq	Code	Residue	Kabat
1	E	glu	0
2	V	val	1
3	Q	gln	2
4	L	leu	3
5	L	leu	4
6	E	glu	5
7	E	glu	6
8	S	ser	7
9	G	gly	8
10	P	pro	9
11	G	gly	10
12	L	leu	11
13	V	val	12
14	Q	gln	13
15	P	pro	14
16	S	ser	15
17	Q	gln	16
18	S	ser	17
19	L	leu	18
20	S	ser	19
21	I	ile	20
22	T	thr	21
23	C	cys	22
24	T	thr	23
25	V	val	24
26	S	ser	25
27	G	gly	26
28	F	phe	27
29	S	ser	28
30	L	leu	29
31	T	thr	30
32	S	ser	31
33	Y	tyr	32
34	G	gly	33
35	V	val	34
36	H	his	35
37	W	trp	36
38	V	val	37
39	R	arg	38
40	Q	gln	39
41	S	ser	40
42	P	pro	41
43	G	gly	42
44	K	lys	43
45	G	gly	44
46	L	leu	45
47	E	glu	46
48	W	trp	47
49	L	leu	48
50	G	gly	49
51	V	val	50
52	I	ile	51
53	W	trp	52
54	S	ser	53
55	G	gly	54
56	G	gly	55
57	S	ser	56
58	T	thr	57
59	D	asp	58
60	Y	tyr	59
61	N	asn	60
62	A	ala	61
63	A	ala	62
64	F	phe	63
65	I	ile	64
66	S	ser	65
67	R	arg	66
68	L	leu	67
69	S	ser	68
70	I	ile	69
71	S	ser	70
72	K	lys	71
73	D	asp	72
74	N	asn	73
75	S	ser	74
76	K	lys	75
77	S	ser	76
78	Q	gln	77
79	V	val	78
80	F	phe	79
81	F	phe	80
82	K	lys	81
83	M	met	82
84	N	asn	82a
85	S	ser	82b
86	L	leu	82c
87	Q	gln	83
88	A	ala	84
89	D	asp	85
90	D	asp	86
91	T	thr	87
92	A	ala	88
93	I	ile	89
94	Y	tyr	90
95	Y	tyr	91
96	C	cys	92
97	A	ala	93
98	R	arg	94
99	N	asn	95
100	R	arg	96
101	G	gly	97
102	Y	tyr	98
103	S	ser	100a
104	Y	tyr	100b
105	A	ala	100c
106	M	met	100d
107	D	asp	101
108	S	ser	102
109	W	trp	103
110	G	gly	104
111	Q	gln	105
112	G	gly	106
113	T	thr	107
114	S	ser	108
115	V	val	109
116	T	thr	110
117	V	val	111
118	S	ser	112
119	S	ser	113

CDR1 (around Kabat 31–35)
CDR2 (around Kabat 50–65)
CDR3 (around Kabat 95–102)

NNA7 H chain C_H1

120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139
A	K	T	T	P	P	S	V	Y	P	L	A	P	G	S	A	A	Q	T	N
ala	lys	thr	thr	pro	pro	ser	val	tyr	pro	leu	ala	pro	gly	ser	ala	ala	gln	thr	asn
114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133

140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159
S	M	V	T	L	G	C	L	V	K	G	Y	F	P	E	P	V	T	V	T
ser	met	val	thr	leu	gly	cys	leu	val	lys	gly	tyr	phe	pro	glu	pro	val	thr	val	thr
134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153

160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179
W	N	S	G	S	L	S	S	G	V	H	T	F	P	A	V	L	Q	S	D
trp	asn	ser	gly	ser	leu	ser	ser	gly	val	his	thr	phe	pro	ala	val	leu	gln	ser	asp
154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173

180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199
L	Y	T	L	S	S	S	V	T	V	P	S	S	T	W	P	S	E	T	V
leu	tyr	thr	leu	ser	ser	ser	val	thr	val	pro	ser	ser	thr	trp	pro	ser	glu	thr	val
174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193

200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219
T	C	N	V	A	H	P	A	S	S	T	K	V	D	K	K	I	V	P	R
thr	cys	asn	val	ala	his	pro	ala	ser	ser	thr	lys	val	asp	lys	lys	ile	val	pro	arg
194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213

220	221	222	223	224	225	226	227	228	229	230
D	C	T	S	H	H	H	H	H	H	G
asp	cys	thr	ser	his	his	his	his	his	his	gly
214	215	216	217	218	219	220	221	222	223	224