Figure 1.

Figure 1A.

Family 2 HCDR2

MOR#	mAb#	Family 2 HCDR2 consensus																SEQ ID NO
7702		H	I	I	P	W	F	G	W	T	Y	Y	A	Q	K	F	Q	G	
7701		M							T		F								
7708	624	R									S								
8297		R							T		S								
8298		R							Y		S								
7785	3077	S									N								
8104	7024	S							T		N								
8105		S							Y		N								
7786		Y									N								
Consensus		HMRSY							WTY		YFSD								
Formula I		Xaa_1	I	I	P	W	F	G	Xaa_2	T	Xaa_3	Y	A	Q	K	F	Q	G	35

Xaa_1 may be His, Met, Arg, Ser or Tyr;
Xaa_2 may be Trp, Thr or Tyr; and
Xaa_3 may be Tyr, Phe, Ser or Asp.

Figure 1.

Figure 1B.

Family 6a LCDR3

MOR#	mAb#	Family 6a LCDR3 consensus								SEQ ID NO
Clone 10		H	Q	F	T	I	P	S	H	
Clone 11		Q			V	T			F	
Clone 12		Q		G	N	Y	R	P	L	
Consensus		HQ		FG	TVN	ITY	PR	SP	HFL	
Formula II		Xaa_4	Q	Xaa5	Xaa6	Xaa7	Xaa8	Xaa9	Xaa10	11

Xaa4 may be His or Gln;
Xaa5 may be Phe or Gly;
Xaa6 may be Thr, Val or Asn;
Xaa7 may be Ile, Thr or Tyr;
Xaa8 may be Pro or Arg;
Xaa9 may be Ser or Pro; and
Xaa10 may be His, Phe or Leu.

Figure 1.

Figure 1C.

Family 6b LCDR3

MOR#	mAb#	Family 6B LCDR3 consensus										SEQ ID NO
Clone 13		Q	Q	S	N	H	I	P	P	A	T	
7706	4538			Y	R	S	T	L	S	L		
8299	3584			Y	R	S	T	L	S	L		
8300				Y	R	S	T	L	S	L		
8301				Y	R	S	T	L	S	L		
Clone 15				Y	V	S	L	S	F	D		
Clone 16				Y	Y	S	A		L	L		
7775	732	T		Y	Y	S	S		S	L		
8101		T		Y	Y	S	S		S	L		
8102		T		Y	Y	S	S		S	L		
8103	4168	T		Y	Y	S	S		S	L		
Consensus		QT	Q	SY	NRVY	HS	ITLAS	PLS	PSFL	ALD	T	
Formula III		Xaa11	Q	Xaa12	Xaa13	Xaa14	Xaa15	Xaa16	Xaa17	Xaa18	T	17

Xaa11 may be Gln or Thr;
Xaa12 may be Ser or Tyr;
Xaa13 may be Asn, Arg, Val or Tyr;
Xaa14 may be His or Ser;
Xaa15 may be Ile, Thr, Leu, Ala or Ser;
Xaa16 may be Pro, Leu or Ser;
Xaa17 may be Pro, Ser, Phe or Leu; and
Xaa18 may be Ala, Leu or Asp.

Figure 1.

Figure 1D.

Family 6b HCDR3

MOR#	mAb#	Family 6b HCDR3 consensus												SEQ ID NO
Clone 13		E	V	D	S	M	Y	Y	S	Y	F	D	I	
7706	4538													
8299	3584													
8300						I								
8301						L								
Clone 15						T								
Clone 16														
7775	732													
8101						I								
8102						L								
8103	4168					T								
Consensus		E	V	D	S	MILT	Y	Y	S	Y	F	D	I	
Formula IV		E	V	D	S	Xaa19	Y	Y	S	Y	F	D	I	57

Xaa19 is Met, Ile, Leu or Thr.

Figure 1.

Figure 1E.

Family 19a LCDR3

Clone	MOR#	mAb#	Family 19a consensus sequence LCDR3											SEQ ID NO
179	Clone 179		G	S	Y	D	F	F	L	G	M	I	V	
180	Clone 180													
181	7709													
182	Clone 182													
183	7700	1926												
	8095													
	8096													
	8097													
	8098													
	8141										L			
	8142										T			
	8143										Y			
	8160	7146									L			
	8161										T			
	8162										Y			
ut	8302	6785												
T	8303										T			
L		5548									L			
184	7768													
185	Clone 185													
Consensus			G	S	Y	D	F	F	L	G	MLTY	I	V	
Formula V			G	S	Y	D	F	F	L	G	Xaa20	I	V	22

Xaa20 is Met, Leu, Thr or Tyr.

Figure 1.

Figure 1F.

Family 19a HCDR2

MOR#	mAb#	Family 19a consensus sequence HCDR2																	SEQ ID
Clone 179		A	I	N	G	L	G	T	H	K	Y	Y	A	D	S	V	K	G	
Clone 180				S	M	D		G	W	T									
7709		G			K	A		Y	Y	T									
Clone 182		G		S		H		G	Y		F								
7700	1926	T		S	M	T	S	G	F	T									
8095		T		S	I	T	S	G	F	T									
8096		T		S	L	T	S	G	F	T									
8097		T		S	M	T	S	G	F	T									
8098		T		S	M	T	S	G	F	T									
8141		T		S	M	T	S	G	F	T									
8142		T		S	M	T	S	G	F	T									
8143		T		S	M	T	S	G	F	T									
8160	7146	T		S	M	T	S	G	F	T									
8161		T		S	M	T	S	G	F	T									
8162		T		S	M	T	S	G	F	T									
8302	6785	T		S	L	T	S	G	F	T									
8303		T		S	L	T	S	G	F	T									
	5548	T		S	L	T	S	G	F	T									
7768		V			K	G		D	F										
Clone 185		V		S	H	S		G	W	I	N								
Consensus		AGTV	I	NS	GMKILH	LDAHTGS	GS	TGYD	HWYF	KTI	YFN	Y	A	D	S	V	K	G	
Formula VI		Xaa21	I	Xaa22	Xaa23	Xaa24	Xaa25	Xaa26	Xaa27	Xaa28	Xaa29	Y	A	D	S	V	K	G	46

Xaa21 may be Ala, Gly, Thr or Val;
Xaa22 may be Asn or Ser;
Xaa23 may be Gly, Met, Lys, Ile, Leu or His;
Xaa24 may be Leu, Asp, Ala, His, Thr, Gly or Ser;
Xaa25 may be Gly or Ser;
Xaa26 may be Thr, Gly, Tyr or Asp;
Xaa27 may be His, Trp, Tyr or Phe;
Xaa28 may be Lys, Thr or Ile; and
Xaa29 may be Tyr, Phe or Asn.

Figure 1.

Figure 1G.

Family 19a HCDR3

MOR #	mAb #	Family 19a consensus sequence HCDR3						SEQ ID NO
Clone 179		Q	L	M	L	D	V	
Clone 180								
7709								
Clone 182								
7700	1926							
8095								
8096								
8097				L				
8098				T				
8141								
8142								
8143								
8160	7146			T				
8161				T				
8162				T				
8302	6785			T				
8303				T				
	5548			T				
7768								
Clone 185								
Consensus		Q	L	MLT	L	D	V	
Formula VII		Q	L	Xaa30	L	D	V	61

Xaa30 may be Met, Leu or Thr.

Figure 1.

Figure 1H.

Family 19b HCDR2

MOR#	mAb#	Family 19b consensus sequence HCDR2																SEQ ID NO
Clone 186		V	T	S	A	N	G	R	T	Y	Y	A	D	S	V	K	G	
Clone 187					K	M		H										
Clone 188					M	T		N										
Clone 189					H	R	D	N					G					
Consensus		V	T	S	AKMH	NMTR	GD	RHN	T	Y	Y	A	DG	S	V	K	G	
Formula VIII		V	T	S	Xaa31	Xaa32	Xaa3	Xaa34	T	Y	Y	A	Xaa35	S	V	K	G	51

Xaa31 may be Ala, Lys, Met or His;
Xaa32 may be Asn, Met, Thr or Arg;
Xaa33 may be Gly or Asp;
Xaa34 may be Arg, His or Asn; and
Xaa35 may be Asp or Gly.

Figure 2.

Figure 2A.

```
          1                              *                 *          60
6785      QSVLTQPPSVSVAPGQTARISCSGDNLGDKYANWYQQKPGQAPVLVIYDDIDRPSGIPER

IGLV3-1   SYELTQPPSVSVSPGQTASITCSGDKLGDKYACWYQQKPGQSPVLVIYQDSKRPSGIPER
IGLV3-9   SYELTQPLSVSVALGQTARITCGGNNIGSKNVHWYQQKPGQAPVLVIYRDSNRPSGIPER
IGLV3-10  SYELTQPPSVSVSPGQTARITCSGDALPKKYAYWYQQKSGQAPVLVIYEDSKRPSGIPER
IGLV3-12  SYELTQPHSVSVATAQMARITCGGNNIGSKAVHWYQQKPGQDPVLVIYSDSNRPSGIPER
IGLV3-16  SYELTQPPSVSVSLGQMARITCSGEALPKKYAYWYQQKPGQFPVLVIYKDSERPSGIPER
IGLV3-19  SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR
IGLV3-21  SYVLTQPPSVSVAPGKTARITCGGNNIGSKSVHWYQQKPGQAPVLVIYYDSDRPSGIPER
IGLV3-22  SYELTQLPSVSVSPGQTARITCSGDVLGENYADWYQQKPGQAPELVIYEDSERYPGIPER
IGLV3-25  SYELMQPPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQAPVLVIYKDSERPSGIPER
IGLV3-27  SYELTQPSSVSVSPGQTARITCSGDVLAKKYARWFQQKPGQAPVLVIYKDSERPSGIPER
IGLV3-32  SSGPTQVPAVSVALGQMARITCQGDSMEGSYEHWYQQKPGQAPVLVIYDSSDRPSRIPER

          61                           * **            108
6785      FSGSNSGNTATLTISGTQAEDEADYYCGSYDFFLGMIVFGGGTKLTVL

IGLV3-1   FSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTA
IGLV3-9   FSGSNSGNTATLTISRAQAGDEADYYCQVWDSSTA
IGLV3-10  FSGSSSGTMATLTISGAQVEDEADYYCYSTDSSGNH
IGLV3-12  FSGSNPGNTTTLTISRIEAGDEADYYCQVWDSSSDH
IGLV3-16  FSGSSSGTIVTLTISGVQAEDEADYYCLSADSSGTY
IGLV3-19  FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNH
IGLV3-21  FSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDH
IGLV3-22  FSGSTSGNTTTLTISRVLTEDEADYYCLSGDEDN
IGLV3-25  FSGSSSGTTVTLTISGVQAEDEADYYCQSADSSGTY
IGLV3-27  FSGSSSGTTVTLTISGAQVEDEADYYCYSAADNN
IGLV3-32  FSGSKSGNTTTLTITGAQAEDEADYYYQLIDNHA

IGLJ1                                       YVFGTGTKVTVL
IGLJ2                                       VVFGGGTKLTVL
IGLJ3                                       VVFGGGTKLTVL
IGLJ4                                       FVFGGGTQLIIL
IGLJ5                                       WVFGEGTELTVL
IGLJ6                                       NVFGSGTKVTVL
IGLJ7                                       AVFGGGTQLTVL
```

Figure 2.

Figure 2B.

```
          1                                                  * *  * *        70
6785      QVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISLTSGFTYYADSVKGRFTI

IGHV3-7   EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTI
IGHV3-9   EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGYADSVKGRFTI
IGHV3-11  QVQLVESGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTIYYADSVKGRFTI
IGHV3-16  EVQLVESGGGLVQPGGSLRLSCAASGFTFSNSDMNWARKAPGKGLEWVSGVSWNGSRTHYVDSVKRRFII
IGHV3-19  TVQLVESGGGLVEPGGSLRLSCAASGFTFSNSDMNWVRQAPGKGLEWVSGVSWNGSRTHYADSVKGRFII
IGHV3-20  EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGYADSVKGRFTI
IGHV3-21  EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSYIYYADSVKGRFTI
IGHV3-23  EVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTI
IGHV3-30  QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTI
IGHV3-30-3 QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTI
IGHV3-33  QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYYADSVKGRFTI
IGHV3-35  EVQLVESGGGLVQPGGSLRLSCAASGFTFSNSDMNWVHQAPGKGLEWVSGVSWNGSRTHYADSVKGRFII
IGHV3-43  EVQLVESGGVVVQPGGSLRLSCAASGFTFDDYTMHWVRQAPGKGLEWVSLISWDGGSTYYADSVKGRFTI
IGHV3-48  EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSYISSSSSTIYYADSVKGRFTI
IGHV3-64  EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEYVSAISSNGGSTYYANSVKGRFTI
IGHV3-74  EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMHWVRQAPGKGLVWVSRINSDGSSTSYADSVKGRFTI

          71                          ***          115
6785      SRDNSKNTLYLQMNSLRAEDTAVYYCARQLTLDVWGQGTLVTVSS
IGHV3-7   SRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-9   SRDNAKNSLYLQMNSLRAEDTALYYCAKD
IGHV3-11  SRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-16  SRDNSRNSLYLQKNRRRAEDMAVYYCVR
IGHV3-19  SRDNSRNFLYQQMNSLRPEDMAVYYCVR
IGHV3-20  SRDNAKNSLYLQMNSLRAEDTALYHCAR
IGHV3-21  SRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-23  SRDNSKNTLYLQMNSLRAEDTAVYYCAK
IGHV3-30  SRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-30-3 SRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-33  SRDNSKNTLYLQMNSLRAEDTAVYYCAR
IGHV3-35  SRDNSRNTLYLQTNSLRAEDTAVYYCVR
IGHV3-35  SRDNSRNTLYLQTNSLRAEDTAVYYCVR
IGHV3-43  SRDNSKNSLYLQMNSLRTEDTALYYCAKD
IGHV3-48  SRDNAKNSLYLQMNSLRAEDTAVYYCAR
IGHV3-64  SRDNSKNTLYLQMGSLRAEDMAVYYCAR
IGHV3-74  SRDNAKNTLYLQMNSLRAEDTAVYYCAR

IGHJ1                              ...AEYFQHWGQGTLVTVSS
IGHJ2                              ...YWYFDLWGRGTLVTVSS
IGHJ3                              .....AFDVWGQGTMVTVSS
IGHJ4                              .....YFDYWGQGTLVTVSS
IGHJ5                              ....NWFDSWGQGTLVTVSS
IGHJ6                             YYYYYGMDVWGQGTTVTVSS
```

Figure 3

Figure 3A.

MORmAb 8141	MORmAb 8142	MORmAb 8143	mAb 6785	Numbering			Kabat	Chothia
VL	VL	VL	VL	Sequential	Kabat	Chothia	CDR	HV
Q	Q	Q	Q	1	1	1		
S	S	S	S	2	2	2		
V	V	V	V	3	3	3		
L	L	L	L	4	4	4		
T	T	T	T	5	5	5		
Q	Q	Q	Q	6	6	6		
P	P	P	P	7	7	7		
P	P	P	P	8	8	8		
S	S	S	S	9	9	9		
V	V	V	V	10	11	11		
S	S	S	S	11	12	12		
V	V	V	V	12	13	13		
A	A	A	A	13	14	14		
P	P	P	P	14	15	15		
G	G	G	G	15	16	16		
Q	Q	Q	Q	16	17	17		
T	T	T	T	17	18	18		
A	A	A	A	18	19	19		
R	R	R	R	19	20	20		
I	I	I	I	20	21	21		
S	S	S	S	21	22	22		
C	C	C	C	22	23	23		
S	S	S	S	23	24	24		
G	G	G	G	24	25	25		
D	D	D	D	25	26	26		
N	N	N	N	26	27	27		
L	L	L	L	27	28	28		
G	G	G	G	28	29	29		
D	D	D	D	29	30	30		
K	K	K	K	30	31	31		
Y	Y	Y	Y	31	32	32		
A	A	A	A	32	33	33		
N	N	N	N	33	34	34		
W	W	W	W	34	35	35		
Y	Y	Y	Y	35	36	36		
Q	Q	Q	Q	36	37	37		
Q	Q	Q	Q	37	38	38		
K	K	K	K	38	39	39		
P	P	P	P	39	40	40		
G	G	G	G	40	41	41		
Q	Q	Q	Q	41	42	42		
A	A	A	A	42	43	43		
P	P	P	P	43	44	44		
V	V	V	V	44	45	45		
L	L	L	L	45	46	46		
V	V	V	V	46	47	47		
I	I	I	I	47	48	48		
Y	Y	Y	Y	48	49	49		
D	D	D	D	49	50	50		
D	D	D	D	50	51	51		
I	I	I	I	51	52	52		
D	D	D	D	52	53	53		
R	R	R	R	53	54	54		
P	P	P	P	54	55	55		
S	S	S	S	55	56	56		
G	G	G	G	56	57	57		

I	I	I	I	57	58	58		
P	P	P	P	58	59	59		
E	E	E	E	59	60	60		
R	R	R	R	60	61	61		
F	F	F	F	61	62	62		
S	S	S	S	62	63	63		
G	G	G	G	63	64	64		
S	S	S	S	64	65	65		
N	N	N	N	65	66	66		
S	S	S	S	66	67	67		
G	G	G	G	67	68	68		
N	N	N	N	68	69	69		
T	T	T	T	69	70	70		
A	A	A	A	70	71	71		
T	T	T	T	71	72	72		
L	L	L	L	72	73	73		
T	T	T	T	73	74	74		
I	I	I	I	74	75	75		
S	S	S	S	75	76	76		
G	G	G	G	76	77	77		
T	T	T	T	77	78	78		
Q	Q	Q	Q	78	79	79		
A	A	A	A	79	80	80		
E	E	E	E	80	81	81		
D	D	D	D	81	82	82		
E	E	E	E	82	83	83		
A	A	A	A	83	84	84		
D	D	D	D	84	85	85		
Y	Y	Y	Y	85	86	86		
Y	Y	Y	Y	86	87	87		
C	C	C	C	87	88	88		
G	G	G	G	88	89	89		
S	S	S	S	89	90	90		
Y	Y	Y	Y	90	91	91		
D	D	D	D	91	92	92		
F	F	F	F	92	93	93		
F	F	F	F	93	94	94		
L	L	L	L	94	95	95		
G	G	G	G	95	a	a		
L	T	Y	M	96	b	b		
I	I	I	I	97	96	96		
V	V	V	V	98	97	97		
F	F	F	F	99	98	98		
G	G	G	G	100	99	99		
G	G	G	G	101	100	100		
G	G	G	G	102	101	101		
T	T	T	T	103	102	102		
K	K	K	K	104	103	103		
L	L	L	L	105	104	104		
T	T	T	T	106	105	105		
V	V	V	V	107	106	106		
L	L	L	L	108	a	a		

Figure 3.

Figure 3B.

MORmAb 7709	MORmAB 7700	MORmAb 8096	mAb 6785	Numbering			Kabat	Chothia
VH	VH	VH	VH	Sequential	Kabat	Chothia	CDR	HV
Q	Q	Q	Q	1	1	1		
V	V	V	V	2	2	2		
Q	Q	Q	Q	3	3	3		
L	L	L	L	4	4	4		
L	L	L	L	5	5	5		
E	E	E	E	6	6	6		
S	S	S	S	7	7	7		
G	G	G	G	8	8	8		
G	G	G	G	9	9	9		
G	G	G	G	10	10	10		
L	L	L	L	11	11	11		
V	V	V	V	12	12	12		
Q	Q	Q	Q	13	13	13		
P	P	P	P	14	14	14		
G	G	G	G	15	15	15		
G	G	G	G	16	16	16		
S	S	S	S	17	17	17		
L	L	L	L	18	18	18		
R	R	R	R	19	19	19		
L	L	L	L	20	20	20		
S	S	S	S	21	21	21		
C	C	C	C	22	22	22		
A	A	A	A	23	23	23		
A	A	A	A	24	24	24		
S	S	S	S	25	25	25		
G	G	G	G	26	26	26		
F	F	F	F	27	27	27		
T	T	T	T	28	28	28		
F	F	F	F	29	29	29		
S	S	S	S	30	30	30		
S	S	S	S	31	31	31		
Y	Y	Y	Y	32	32	32		
A	A	A	A	33	33	33		
M	M	M	M	34	34	34		
S	S	S	S	35	35	35		
W	W	W	W	36	36	a		
V	V	V	V	37	37	36		
R	R	R	R	38	38	37		
Q	Q	Q	Q	39	39	38		
A	A	A	A	40	40	39		
P	P	P	P	41	41	40		
G	G	G	G	42	42	41		
K	K	K	K	43	43	42		
G	G	G	G	44	44	43		
L	L	L	L	45	45	44		
E	E	E	E	46	46	45		
W	W	W	W	47	47	46		
V	V	V	V	48	48	47		
S	S	S	S	49	49	48		
G	T	T	T	50	50	49		
I	I	I	I	51	51	50		
N	S	S	S	52	52	51		
K	M	L	L	53	a	52		
A	T	T	T	54	53	53		
G	S	S	S	55	54	54		
Y	G	G	G	56	55	55		
Y	F	F	F	57	56	56		
T	T	T	T	58	57	57		

Y	Y	Y	Y	59	58	58		
Y	Y	Y	Y	60	59	59		
A	A	A	A	61	60	60		
D	D	D	D	62	61	61		
S	S	S	S	63	62	62		
V	V	V	V	64	63	63		
K	K	K	K	65	64	64		
G	G	G	G	66	65	65		
R	R	R	R	67	66	66		
F	F	F	F	68	67	67		
T	T	T	T	69	68	68		
I	I	I	I	70	69	69		
S	S	S	S	71	70	70		
R	R	R	R	72	71	71		
D	D	D	D	73	72	72		
N	N	N	N	74	73	73		
S	S	S	S	75	74	74		
K	K	K	K	76	75	75		
N	N	N	N	77	76	76		
T	T	T	T	78	77	77		
L	L	L	L	79	78	78		
Y	Y	Y	Y	80	79	79		
L	L	L	L	81	80	80		
Q	Q	Q	Q	82	81	81		
M	M	M	M	83	82	82		
N	N	N	N	84	a	a		
S	S	S	S	85	b	b		
L	L	L	L	86	c	c		
R	R	R	R	87	83	83		
A	A	A	A	88	84	84		
E	E	E	E	89	85	85		
D	D	D	D	90	86	86		
T	T	T	T	91	87	87		
A	A	A	A	92	88	88		
V	V	V	V	93	89	89		
Y	Y	Y	Y	94	90	90		
Y	Y	Y	Y	95	91	91		
C	C	C	C	96	92	92		
A	A	A	A	97	93	93		
R	R	R	R	98	94	94		
Q	Q	Q	Q	99	95	95		
L	L	L	L	100	96	96		
M	M	M	T	101	97	97		
L	L	L	L	102	98	98		
D	D	D	D	103	101	101		
V	V	V	V	104	102	102		
W	W	W	W	105	103	103		
G	G	G	G	106	104	104		
Q	Q	Q	Q	107	105	105		
G	G	G	G	108	106	106		
T	T	T	T	109	107	107		
L	L	L	L	110	108	108		
V	V	V	V	111	109	109		
T	T	T	T	112	110	110		
V	V	V	V	113	111	111		
S	S	S	S	114	112	112		
S	S	S	S	115	113	113		

Figure 4.

Figure 4A.

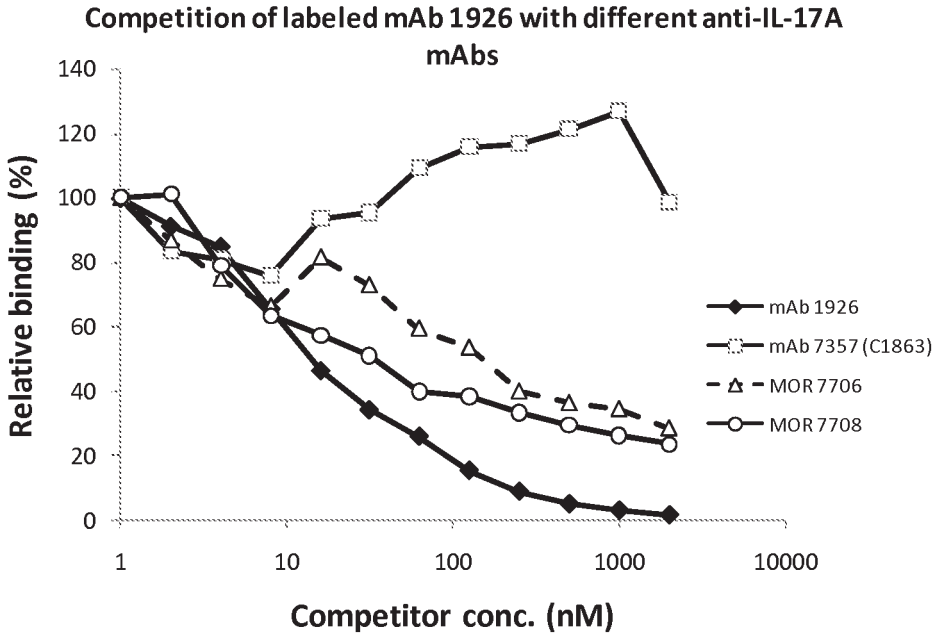


Figure 4B.

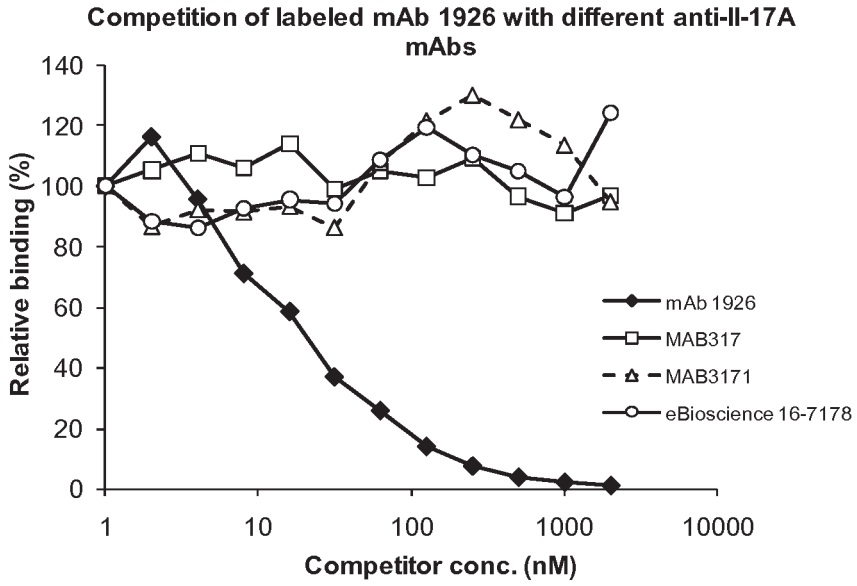


Figure 4.

Figure 4C.

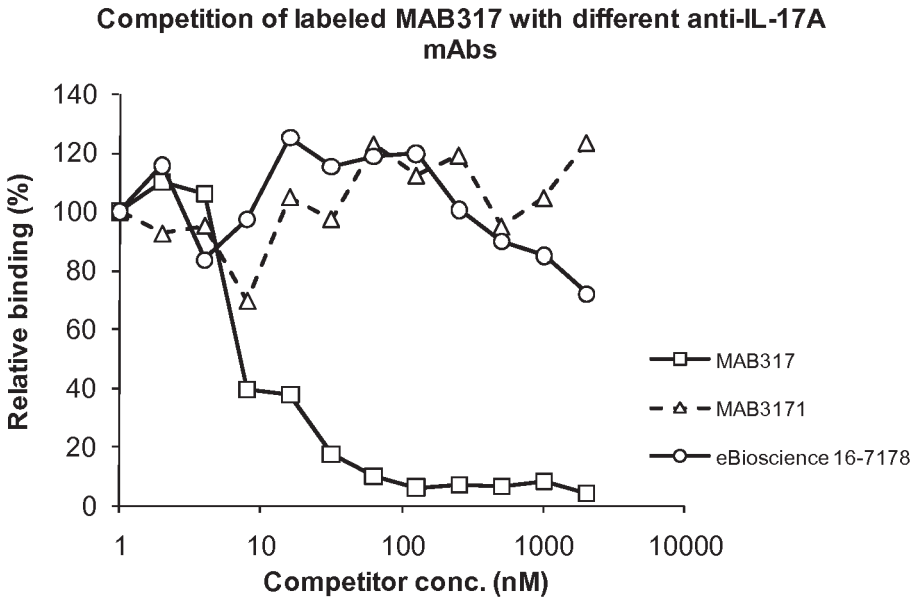


Figure 4D.

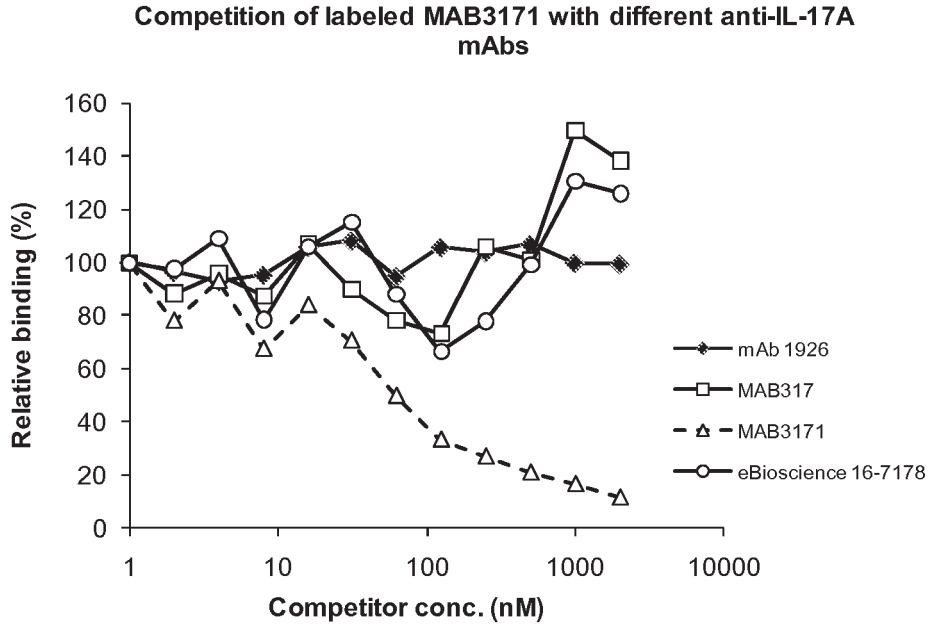


Figure 4.

Figure 4E.

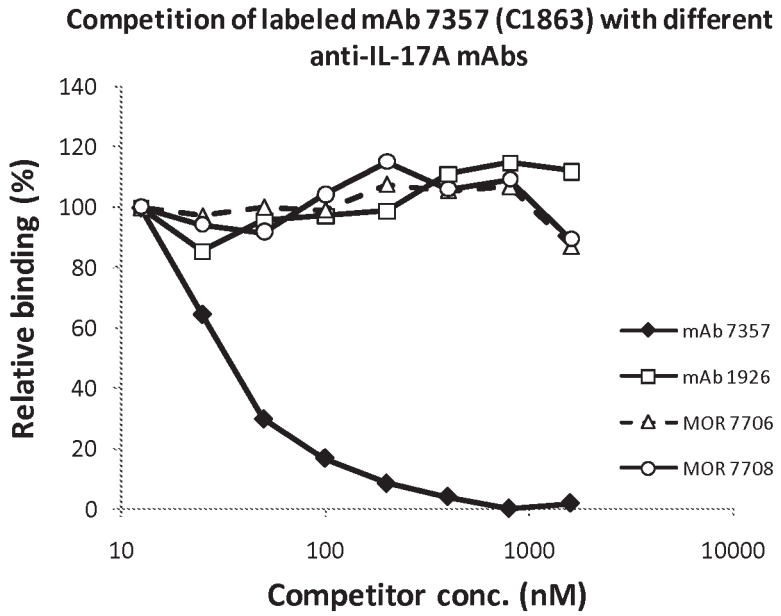


Figure 4F.

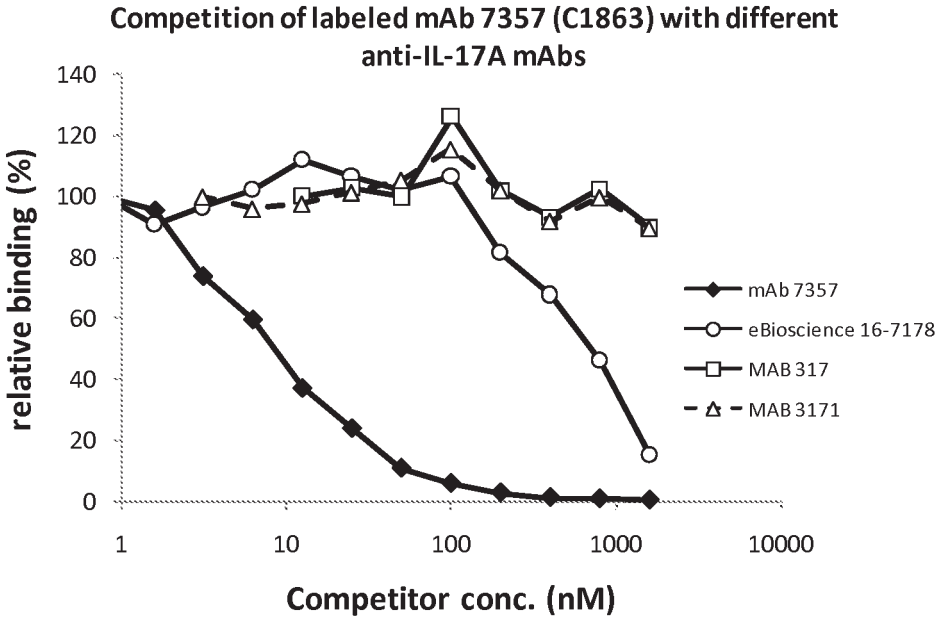


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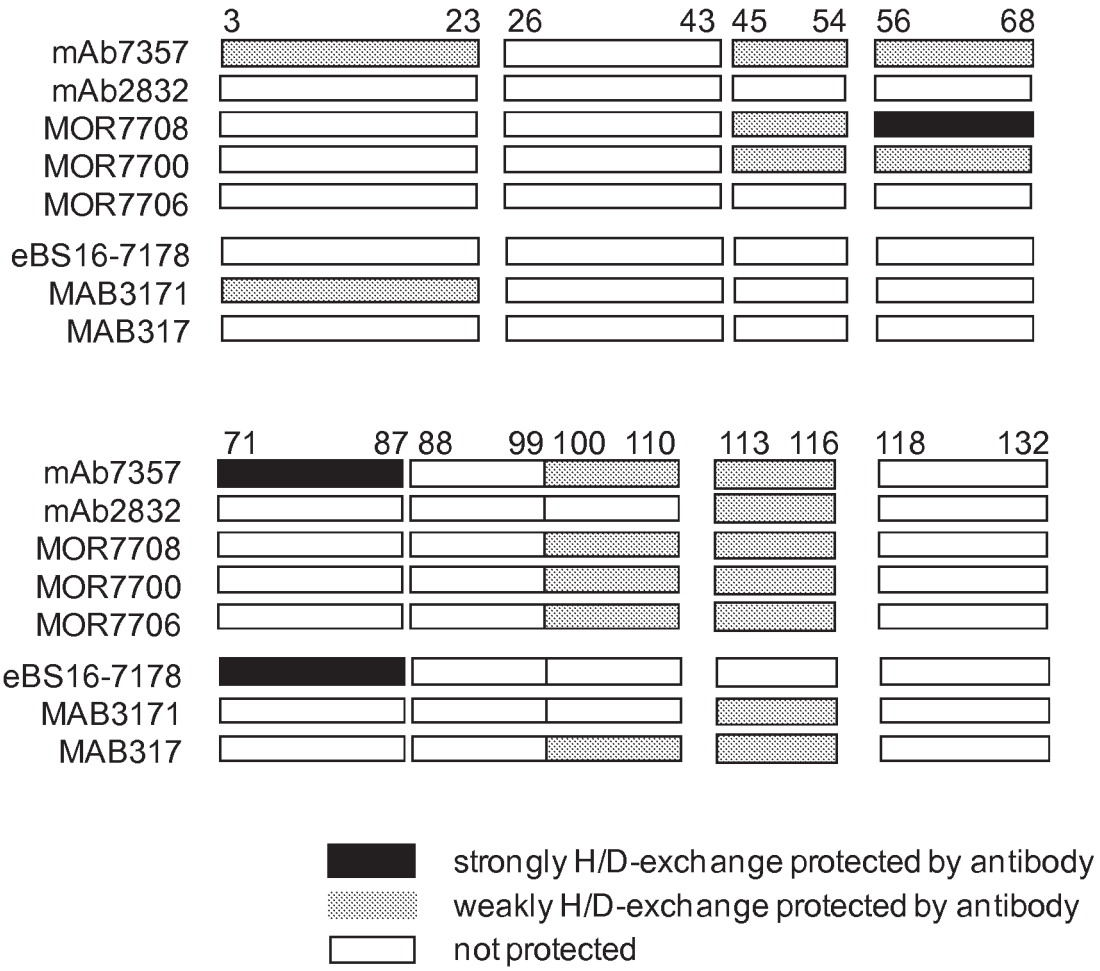

3
23
26
43
45
54
56
68
mAb7357
mAb2832
MOR7708
MOR7700
MOR7706
eBS16-7178
MAB3171
MAB317
71
87
88
99
100
110
113
116
118
132
mAb7357
mAb2832
MOR7708
MOR7700
MOR7706
eBS16-7178
MAB3171
MAB317
strongly H/D-exchange protected by antibody
weakly H/D-exchange protected by antibody
not protected

Figure 6.

Figure 6A.

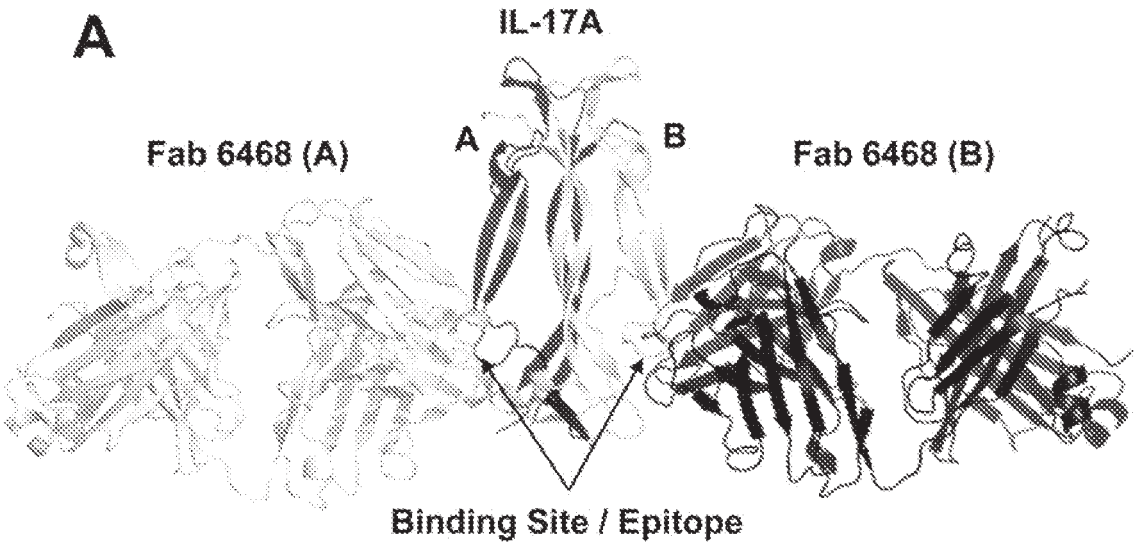


Figure 6B.



Figure 6C.



Figure 6D.



Figure 7.

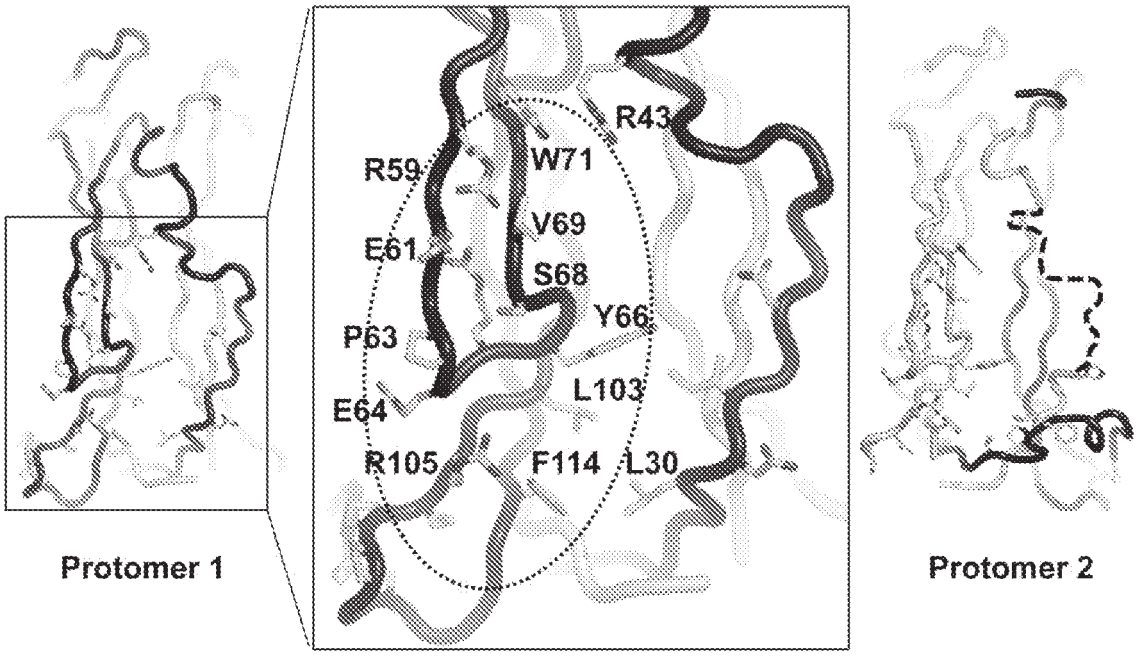

R43
R59
W71
V69
E61
S68
Y66
P63
L103
E64
R105
F114
L30
Protomer 1
Protomer 2

Figure 8.

Figure 8A.

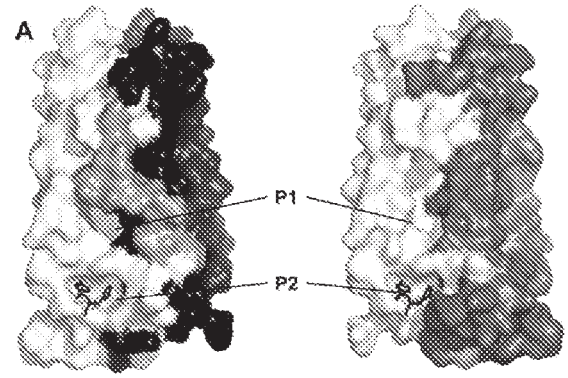


Figure 8B.

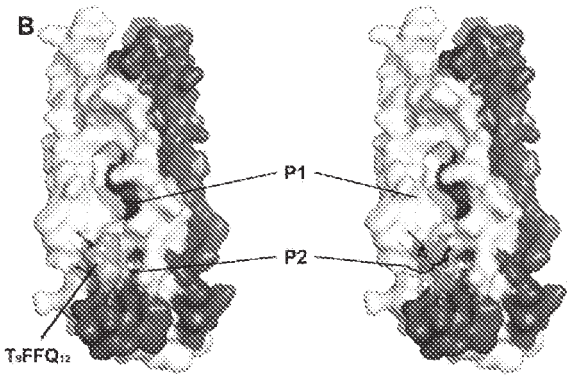


Figure 8C.

C

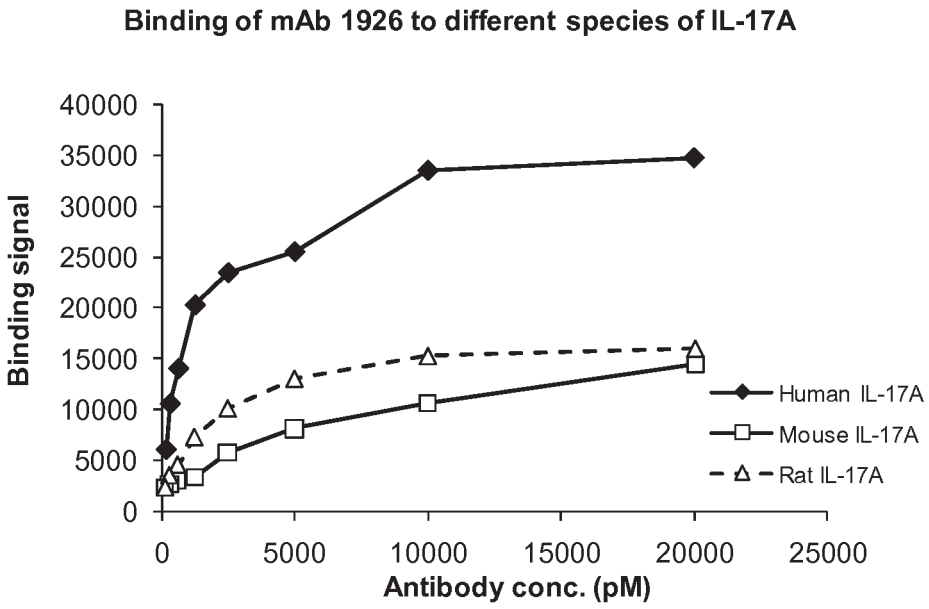
◊♦ Pocket P1 residues

△▲ Pocket P2 residues

Full and filled symbols indicate residues from the two monomers of the IL-17A dimer

```
IL-17A   (1) --IVRAGITIPRNP-GCPNSEDKNFFRTVMVNLNIHNRNTNTNPKRSSDY
IL-17F   (1) RKIPKVGHTFFQKPESCPPVPGG-------SMKLDIGIINENQRVSMSRNI
                                                ▲ ▲
                        ♦          ♦♦ ♦♦♦
IL-17A  (48) YNRSTSPWNLHRNEDPERYPSVIWEAQCRHLGCINADGNVDYHMNSVPIQ
IL-17F  (45) ESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNSVPIQ
                                    ▲
                ◊◊♦◊                      ♦ ♦
IL-17A  (98) QEILVLRREPPHCPNSFRLEKILVSVGCTCVTPIVHHVQ
IL-17F  (95) QETLVVRRKHQGCSVSFQLEKVLVTVGCTCVTPVIHHVQ
                  △ ▲ ▲          ▲ △
```

Figure 9.


Binding of mAb 1926 to different species of IL-17A
Binding signal
40000
35000
30000
25000
20000
15000
10000
5000
0
0
5000
10000
15000
20000
25000
Antibody conc. (pM)
Human IL-17A
Mouse IL-17A
Rat IL-17A