

IMGT Collier de Perles: the New Look for IgSF and MhcSF in IMGT®

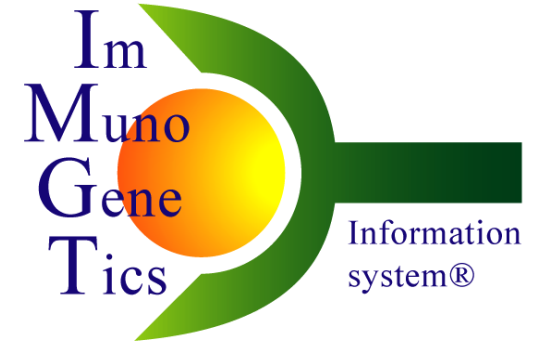
<http://imgt.cines.fr>

Quentin Kaas and Marie-Paule Lefranc

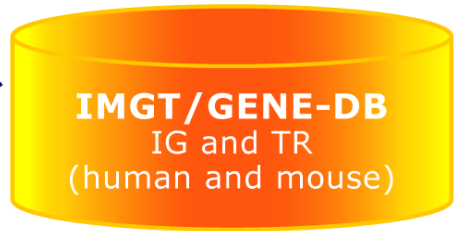
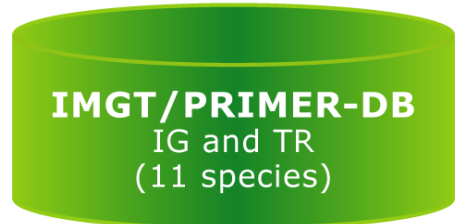
Laboratoire d'ImmunoGénétique Moléculaire
Université Montpellier, UPR CNRS 1142, IGH
Institut Universitaire de France

2nd Basic and Clinical Immunogenomics and 3rd Immunoinformatics (Immunomics) Conferences
BCII'06, October 8-12, 2006, Budapest, Hungary

Sequences

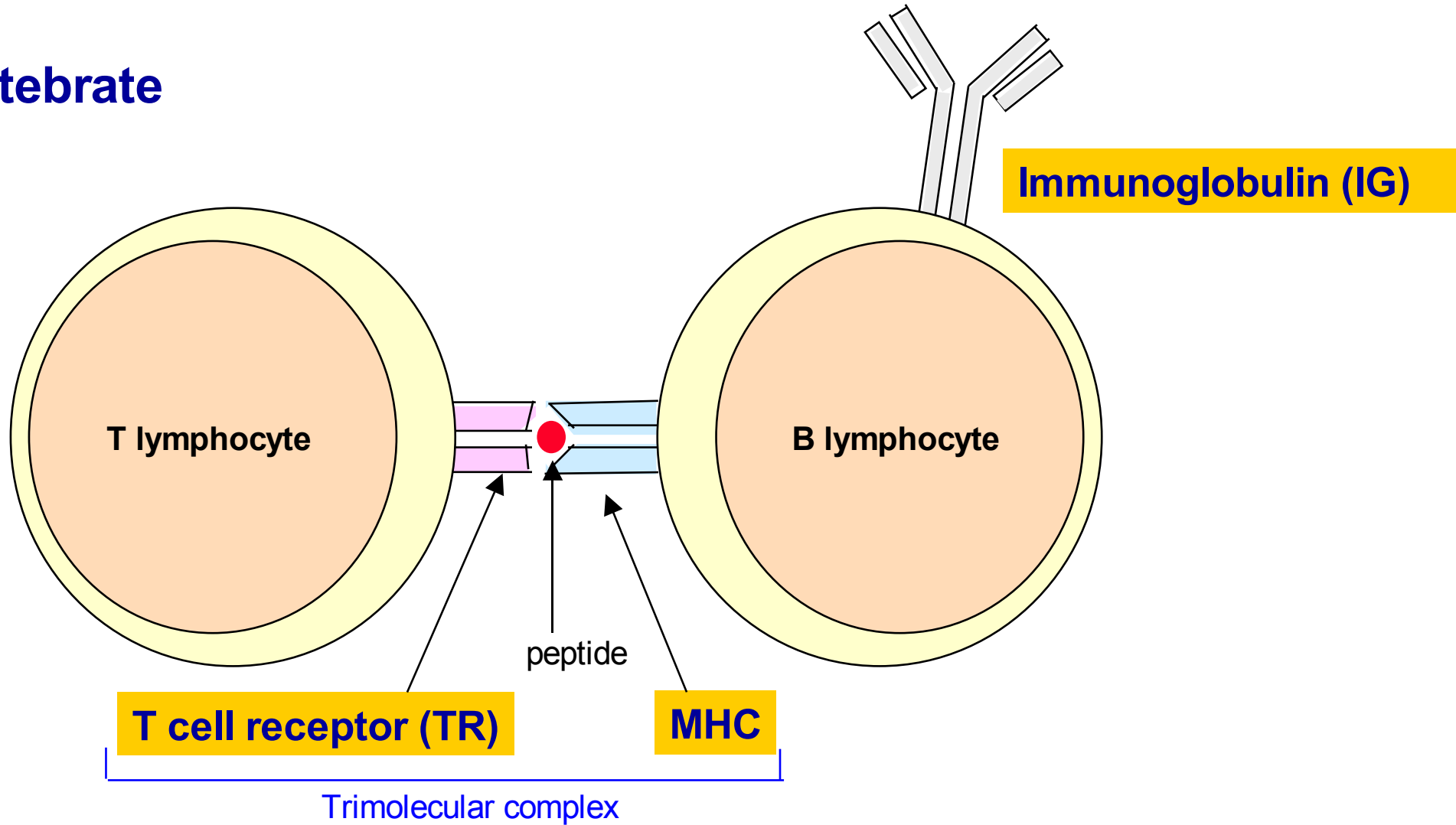


<http://imgt.cines.fr>



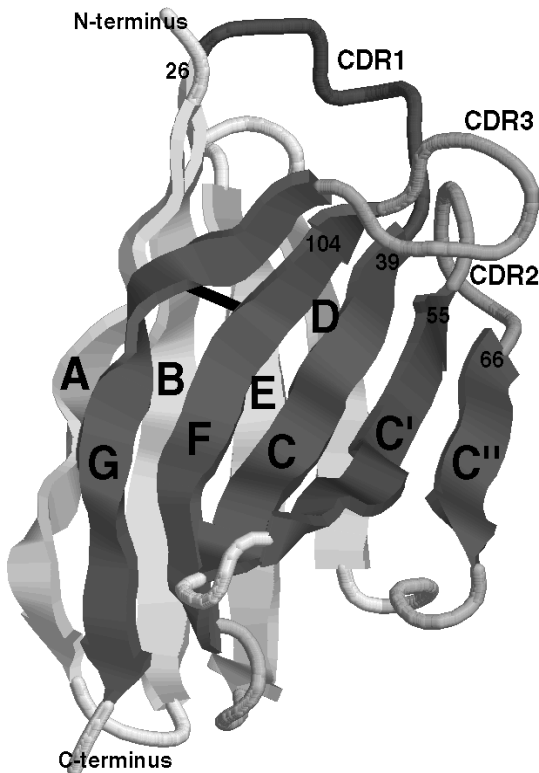
2D and 3D structures

Vertebrate S



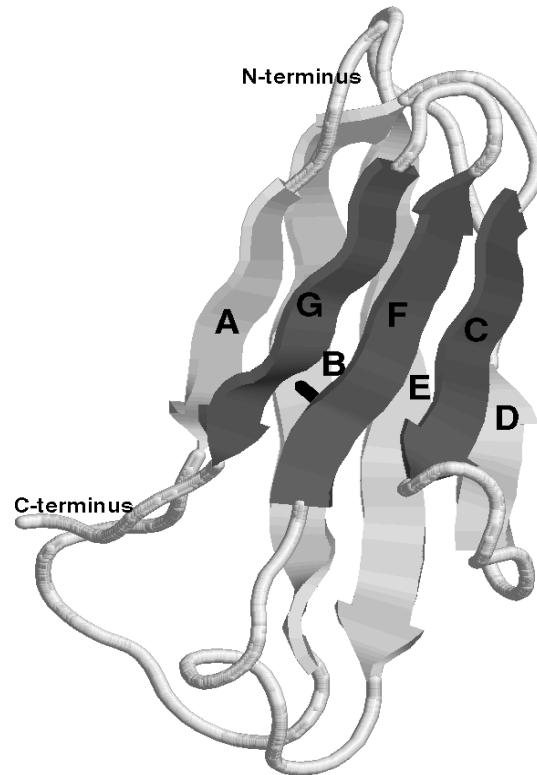
IMGT unique numbering

V-DOMAIN (IG,TR)
AND
V-LIKE-DOMAIN
(other than IG,TR)

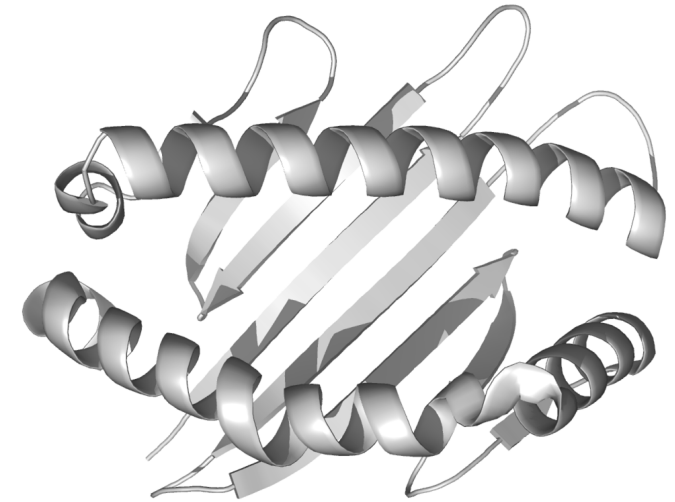


Immunoglobulin superfamily (IgSF)

C-DOMAIN (IG,TR)
AND
C-LIKE-DOMAIN
(other than IG,TR)



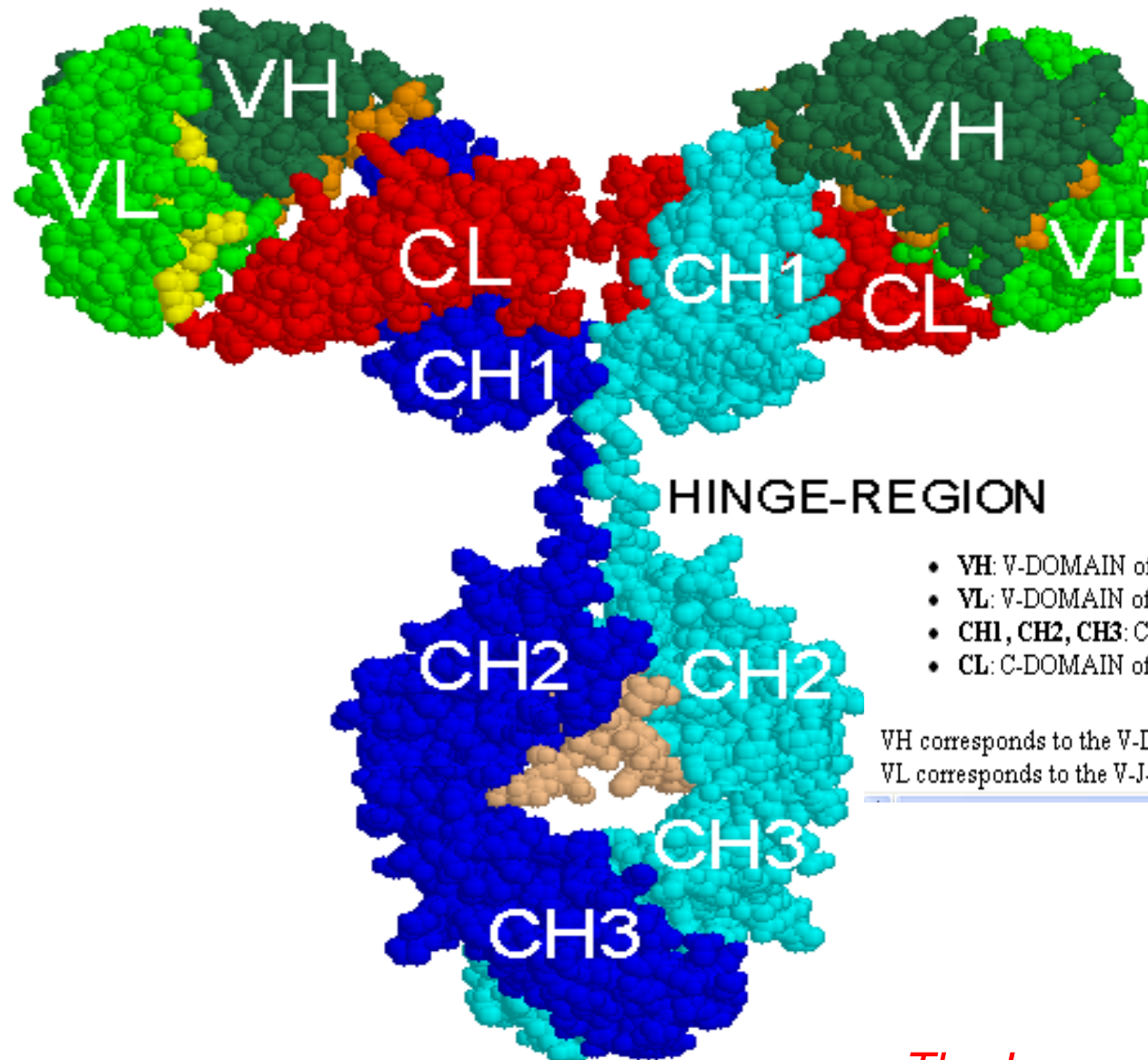
G-DOMAIN (MHC)
AND
G-LIKE-DOMAIN
(other than MHC)



MHC superfamily (MhcSF)

V-DOMAIN and C-DOMAIN

IgG1

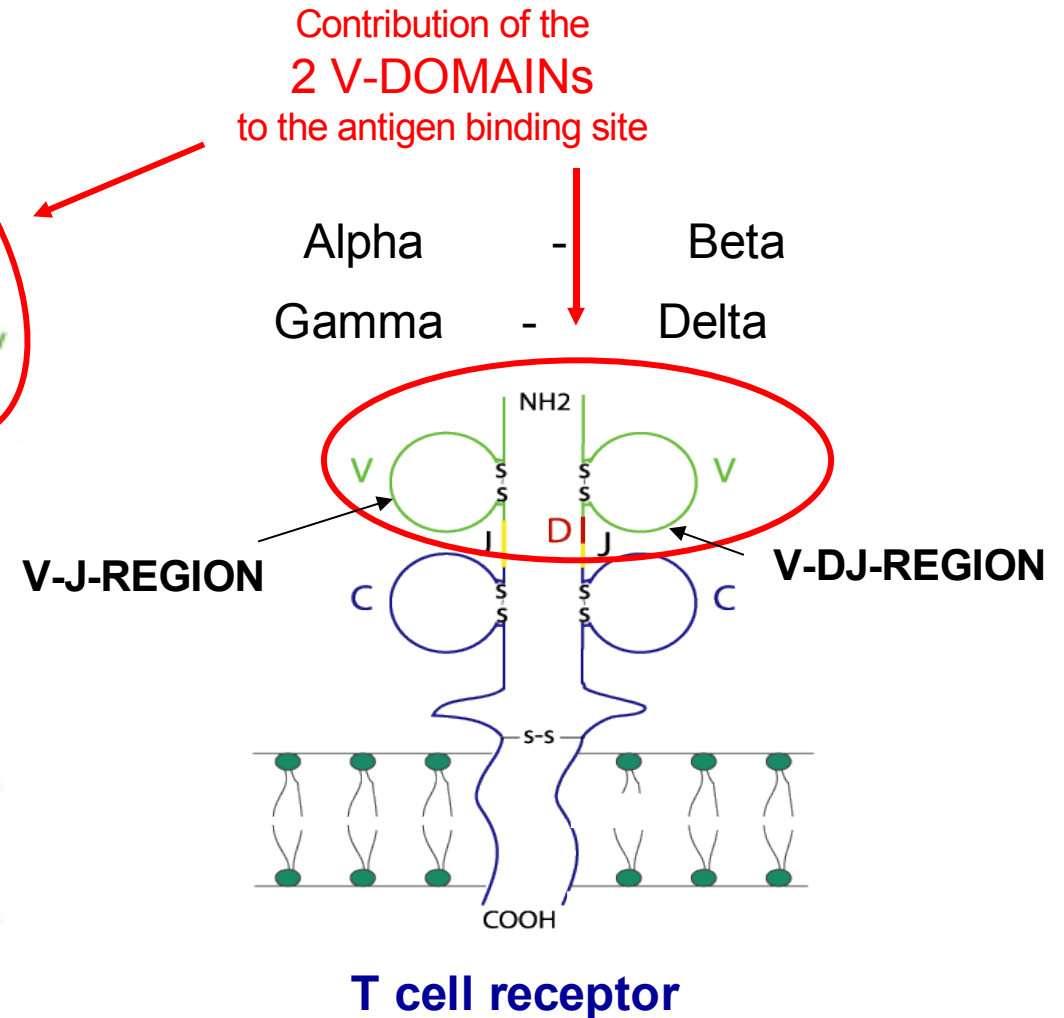
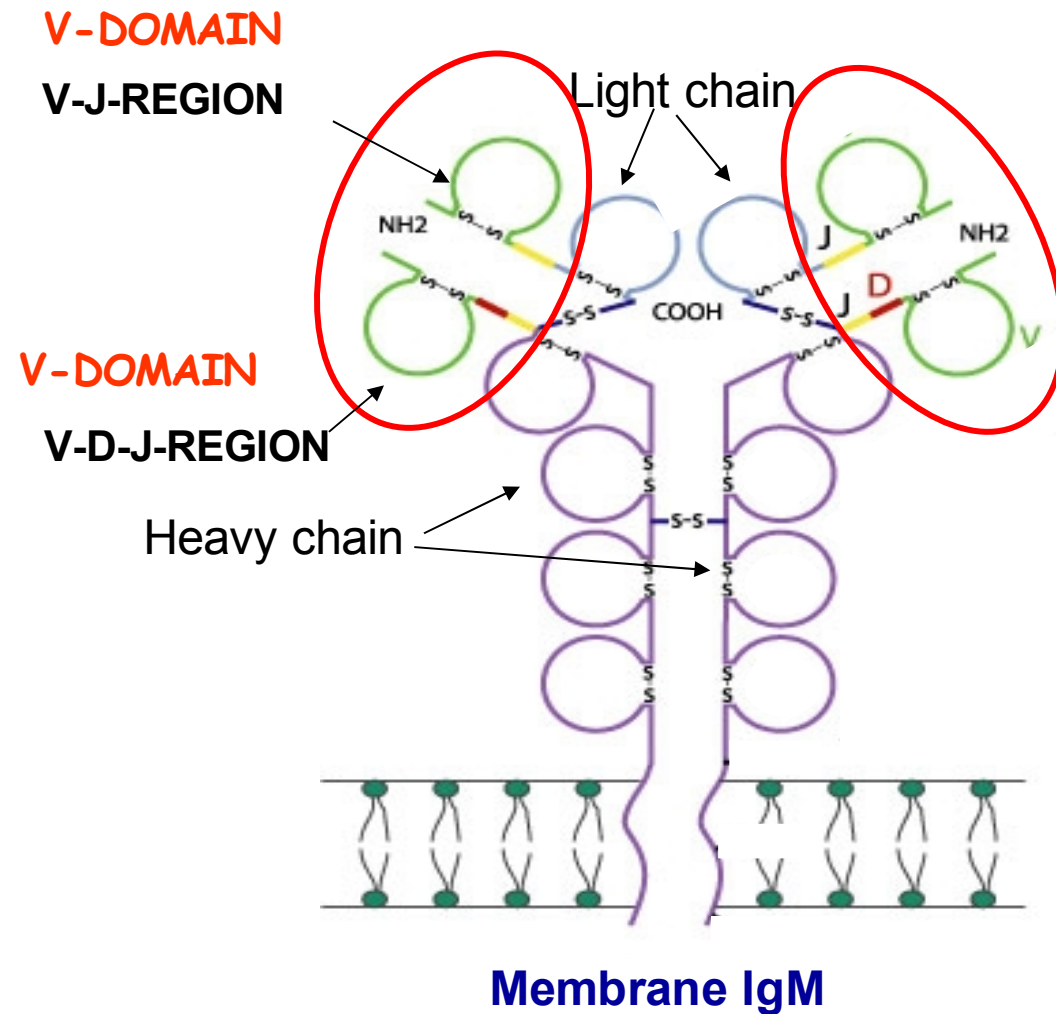


- VH: V-DOMAIN of the immunoglobulin heavy chain
- VL: V-DOMAIN of the immunoglobulin light chain
- CH1, CH2, CH3: C-DOMAIN of the immunoglobulin heavy chain
- CL: C-DOMAIN of the immunoglobulin light chain

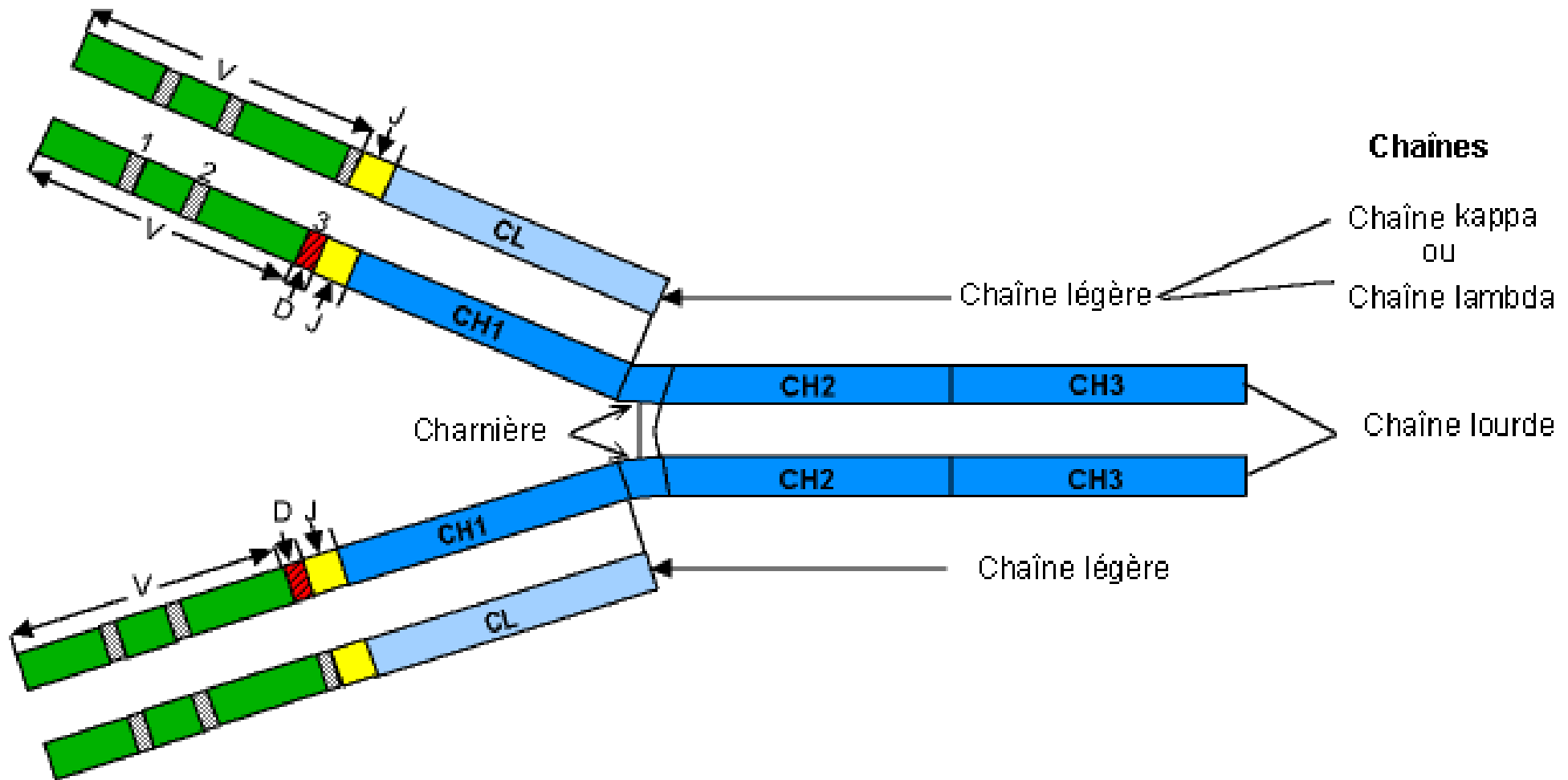
VH corresponds to the V-D-J-REGION (in green (V), orange (DJ)) of the heavy chain.
VL corresponds to the V-J-REGION (in green (V) and yellow (J)) of the light chain.

Immunoglobulin (IG)

T cell receptor (TR)

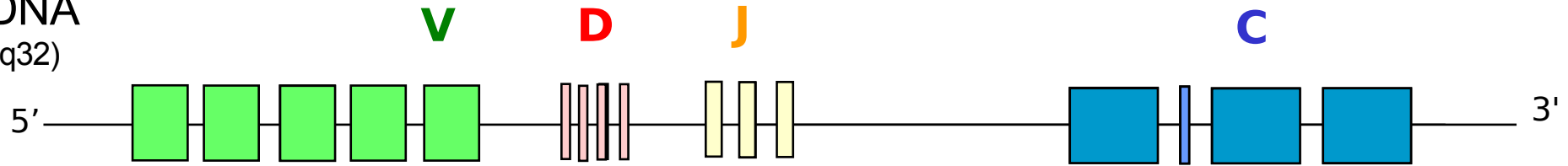


Immunoglobulin IgG



Immunoglobulin (IG) synthesis

genomic DNA
(IGH Locus 14q32)

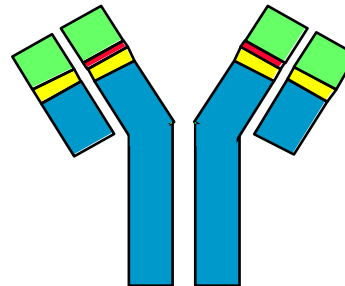


rearranged
DNA



mRNA

2×10^{12} different IG
per individual



ImMunoGeneTics
Information system®

CDR3-IMGT= Complementarity determining region (105-117)
V-J junction (104-118)
V-D-J junction (104-118)



Generation of the JUNCTION diversity

3'V-REGION

N-REGION

D-REGION

N-REGION

5'J-REGION

tgtgCGaaaga



tacc



agcatattgtg

gtggTgactgctat tcc



gat



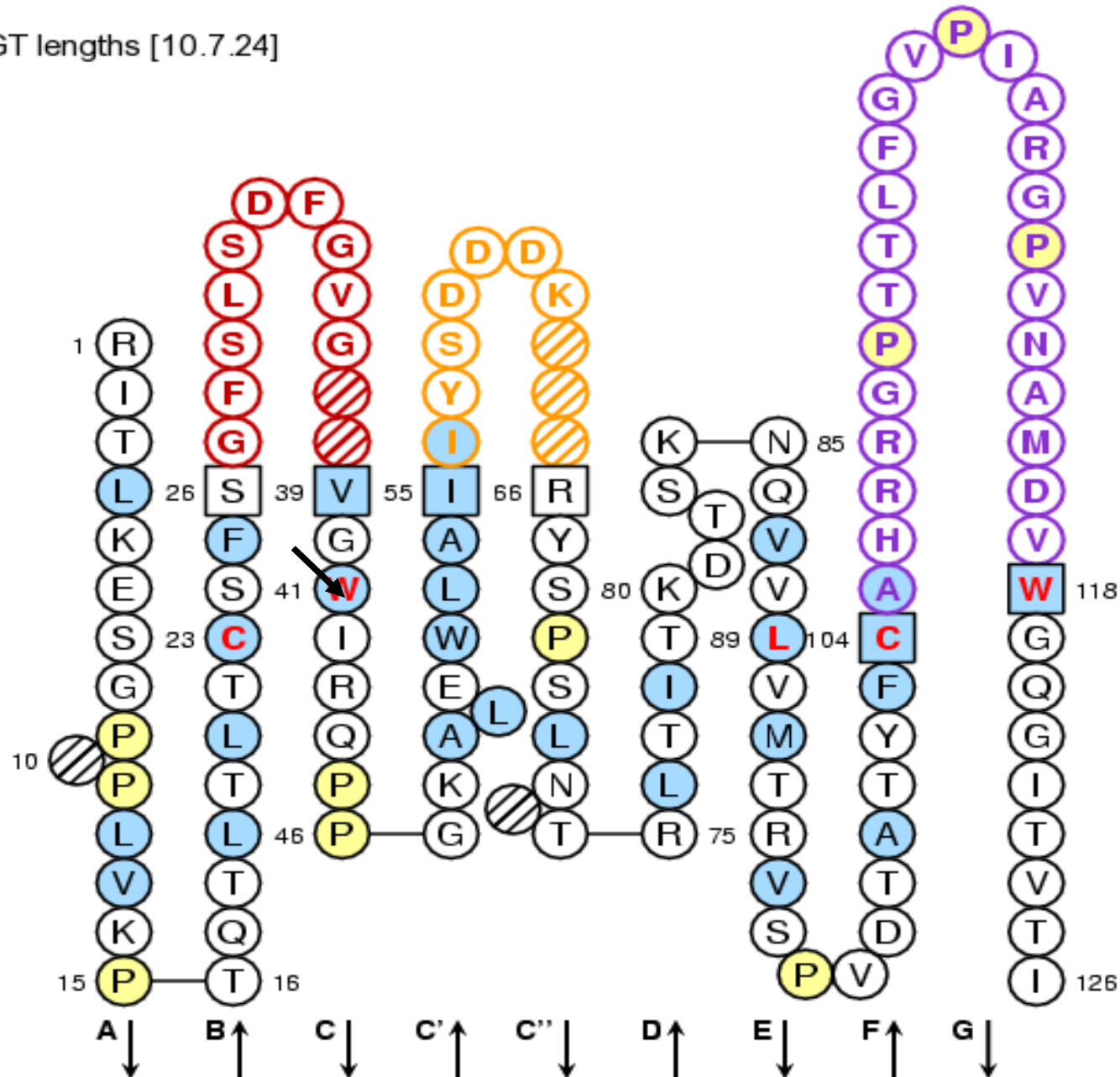
acaactggTtcg actcctgg

JUNCTION

C A P Y R G D T Y D Y S

V tgt gcg cca tac cgg ggt gac act tat gat tac tcc tgg

CDR-IMGT lengths [10.7.24]



IMGT Residue@Position contacts

41V - TRP (W)

chain : 1u8k_B

Secondary structure	Extended conformation
Phi	-122.64
Psi	137.12
ASA	0.0

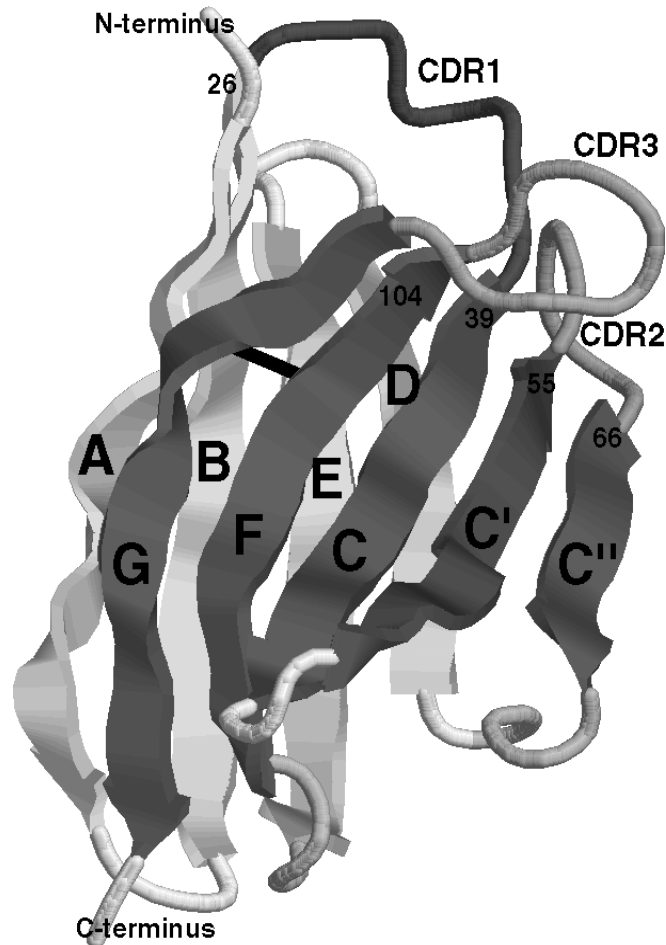
Residue local structure

	IMGT Num	Code 1C	Code 3C	Chain	Domain	Tot	NCov	Pol	HB	NPol	Cov	SS
Info	6V1	E	GLU	1u8k_B	VH	6	6	0	0	6	0	0
Info	21V1	L	LEU	1u8k_B	VH	17	17	0	0	17	0	0
Info	22V1	T	THR	1u8k_B	VH	8	8	0	0	8	0	0
Info	23V1	C	CYS	1u8k_B	VH	10	10	0	0	10	0	0
Info	39V1	V	VAL	1u8k_B	VH	2	2	1	0	1	0	0
Info	43V1	R	ARG	1u8k_B	VH	2	2	1	0	1	0	0
Info	51V1	E	GLU	1u8k_B	VH	2	2	1	0	1	0	0
Info	52V1	W	TRP	1u8k_B	VH	11	11	3	0	8	0	0
Info	53V1	L	LEU	1u8k_B	VH	15	15	1	1	14	0	0
Info	54V1	A	ALA	1u8k_B	VH	18	18	4	2	14	0	0
Info	55V1	I	ILE	1u8k_B	VH	2	2	1	0	1	0	0
Info	78V1	I	ILE	1u8k_B	VH	5	5	0	0	5	0	0
Info	87V1	V	VAL	1u8k_B	VH	11	11	1	0	10	0	0
Info	88V1	V	VAL	1u8k_B	VH	6	6	2	0	4	0	0
Info	89V1	L	LEU	1u8k_B	VH	33	33	1	0	32	0	0
Info	102V1	Y	TYR	1u8k_B	VH	5	5	0	0	5	0	0
Info	103V1	F	PHE	1u8k_B	VH	18	18	2	0	16	0	0
Info	104V1	C	CYS	1u8k_B	VH	26	26	0	0	26	0	0
Info	105V1	A	ALA	1u8k_B	VH	1	1	1	0	0	0	0

Tot	Total number of atomic pair contacts
NCo	Number of non covalent atomic
Pol	Number of polar atomic pair contacts
HB	Number of hydrogen bonds
NPol	Number of non polar atomic pair contacts
Cov	Number of covalent links (other than chain covalent links)
SS	Number of disulfide bridges

V-DOMAIN

The 3D structure of a **V-DOMAIN** (IG or TR)



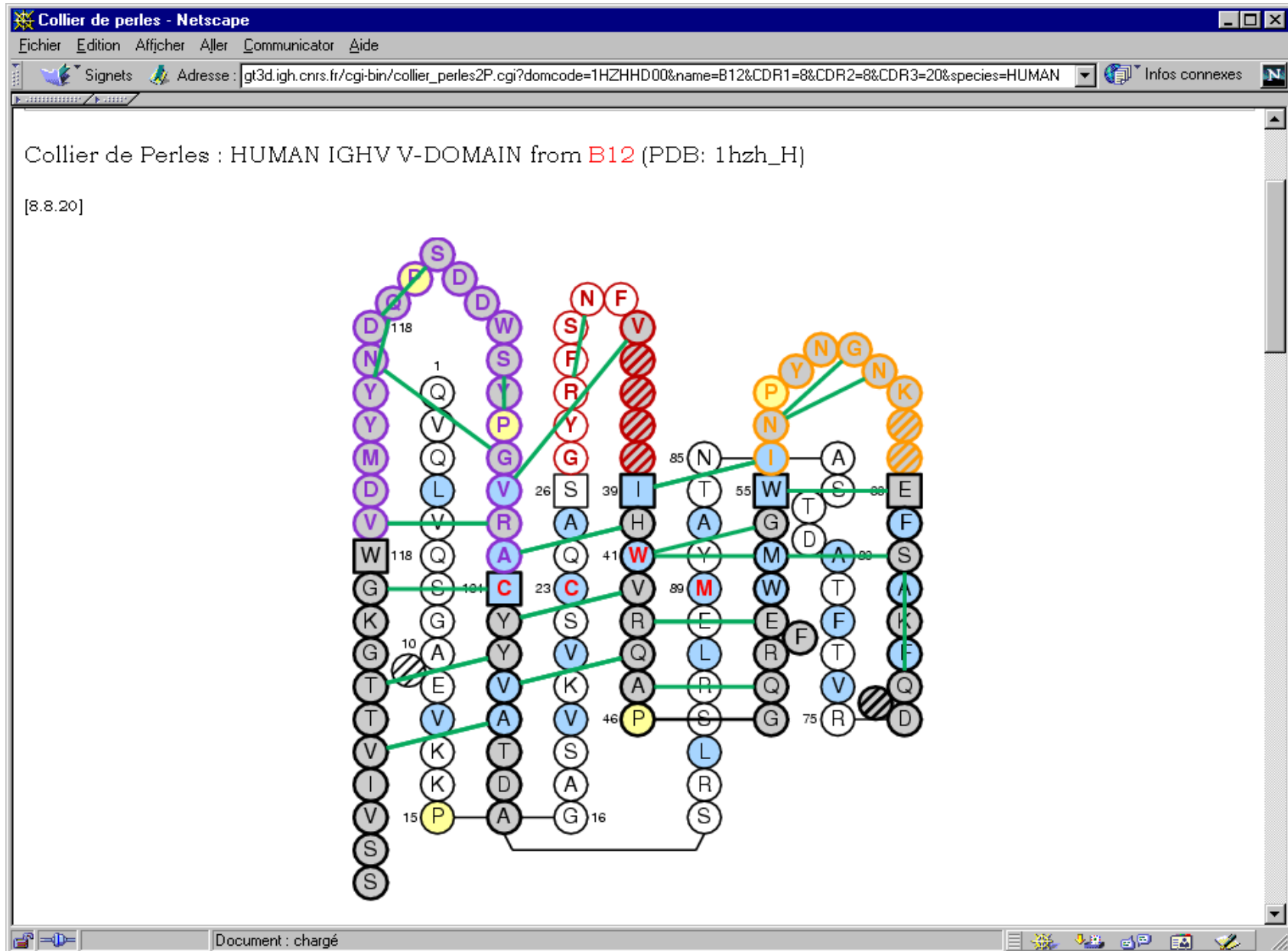
9 antiparallel beta strands:
A, B, C, C', C'', D, E, F and G

linked by **beta turns**:
AB, CC', C''D, DE and EF
and **loops**:

BC or CDR1-IMGT
C'C'' or CDR2-IMGT and
FG or CDR3-IMGT

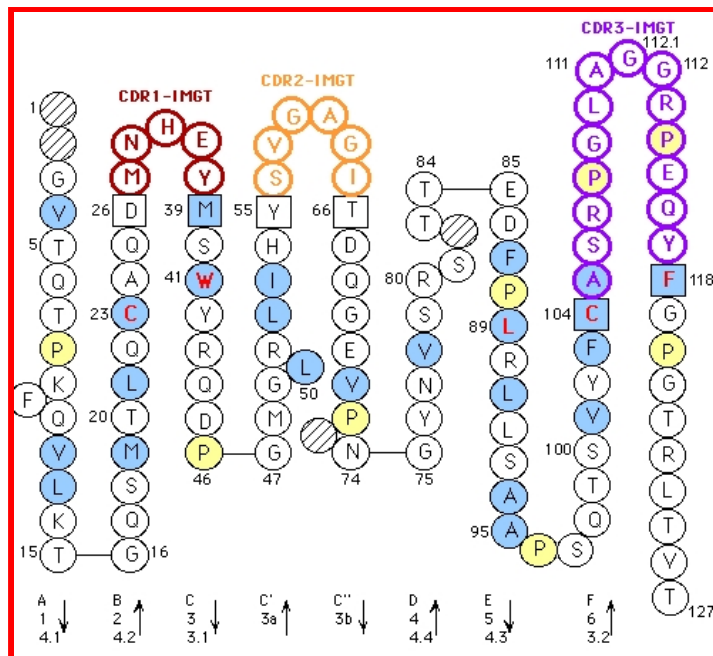
forming a sandwich of two sheets
[ABED][GFCC'C''].

IMGT Collier de Perles on two layers



IMGT Web resources: 8 000 pages HTML

IMGT
Collier
de
Perles



	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
X02850 ,TRAV8-6*01	A	Q	S	V	T	Q	L	D	S	Q	V	P	V	F	E	E	A	P	V	E
AE000659,TRAV8-6*02	CCC	CAG	TCT	GTG	ACC	CAG	CTT	GAC	AGC	CAR	CTC	CCT	GTG	TTT	GAR	GAR	GCC	CCT	GTG	GAG
M86361 ,TRAV8-6*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
X02850 ,TRAV8-6*01	L	R	C	N	V	S	S	S	V	S	V	V	V	L	L	L	L	L	L	F
AE000659,TRAV8-6*02	CTG	AGG	TGC	ARC	TAC	TCA	TGG	TCT	GTT	TCA	GTG	TAT	---	---	---	---	---	---	---	---
M86361 ,TRAV8-6*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
X02850 ,TRAV8-6*01	W	Y	V	Q	Y	P	N	Q	Q	L	Q	L	L	L	L	K	V	L	S	G
AE000659,TRAV8-6*02	TGG	TAT	GTG	CAR	TAC	CCC	ARC	CAR	GGA	CTC	CAG	CTT	CTG	CTG	AGG	TAT	TTA	TCA	GGA	TCC
M86361 ,TRAV8-6*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
X02850 ,TRAV8-6*01	T	L	L	L	L	V	E	S	I	N	---	---	---	---	---	---	---	---	---	---
AE000659,TRAV8-6*02	ACC	CTG	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
M86361 ,TRAV8-6*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	81	82	83	84	84A	84B	84C	85	86	87	88	89	90	91	92	93	94	95	96	97
X02850 ,TRAV8-6*01	A	E	F	N	K	S	Q	T	S	F	H	L	R	K	P	S	V	M	I	S
AE000659,TRAV8-6*02	GCT	GAA	TTT	ACC	AGG	AGT	CAA	ACT	TCC	TTC	CAC	TTG	AGG	AAA	CCC	TCA	CTC	CAT	ATA	AGC
M86361 ,TRAV8-6*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
	101	102	103	104	105	106	107	108	---	---	---	---	---	---	---	---	---	---	---	---
X02850 ,TRAV8-6*01	E	Y	F	C	A	V	S	---	---	---	---	---	---	---	---	---	---	---	---	---
AE000659,TRAV8-6*02	GAG	TAC	TTC	TGT	GCT	GTG	AGT	GA	---	---	---	---	---	---	---	---	---	---	---	---
M86361 ,TRAV8-6*02	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

IMGT
Alignment
of alleles

IMGT
Protein
Display

TRAV gene	FR1-IMGT (1-26)	CDR1-IMGT (27-38)	FR2-IMGT (39-55)	CDR2-IMGT (56-65)	FR3-IMGT (66-104)	CDR3-IMGT (105-115)
AE000658, TRAV1-1	GQSLEQ.PSEVTAVEGAIVQINCTYQ	TSGFYG.....	LSWYQQHGGGAPTFLSY	NALDG.....	LEETG.....	RFSSFLSRSDSYGYLLLQELQMKDSASYFC
AE000658, TRAV1-2	GQNIDQ.PIEMTATEGAIVQINCTYQ	TSGFNG.....	LFWYQQHAGEAPTFLSY	NVLDG.....	LEEKQ.....	RFSSFLSRSGYSYLLLQELQMKDSASYLC
AE000658, TRAV2	KDQVFQ.PSTVASSEGAIVVEIFCNHS	VSNAYN.....	FFWYLFHPGCGAPRLLVK	GSK.....	PSQQG.....	RYNMTYER.FSSSLLILQVREADAAVYFC
AE000658, TRAV3	AQSVAQPEDQVNVAEGNPLTVKCTYS	VSGNPY.....	LFWYVQYPNRLQLFLK	YITGDNL.....	VKGSY.....	GFEAEFNKSQTSFHLKPKSALVSDSALYFC
AE000658, TRAV4	LAKITQ.PISMDSYEGQEVNITCSHN	NIATNDY.....	ITWYQQFPSPQGRFIIQ	GYKT.....	KVTNE.....	VASLFIADPKSSTLSLPRVSLSDTAVYFC
AE000659, TRAV5	GEDVEQS.LFLSVREGDSSVINCTYT	DSSSTY.....	LYWYKQEPGAGLQLLTY	IFSNMD.....	MKQDQ.....	RLTVLLNKKDKHLRLRIADTQTGDSAIYFC
AE000659, TRAV6	SQKIEQNSEALNIQEGKTATLTCONYT	NYSPAY.....	LQWYRQDPGRGPVFLLL	IRENEK.....	EKRKE.....	RLKVTFTDTLLKQSLFHITASQPADSATYLC
AE000659, TRAV7	ENQVEHSPHFLGPQQGDVASMCTYS	VSRFNN.....	LQWYRQNTGMGPKHLLS	MYSAGY.....	EKQKG.....	RLNATLLK.NGSSLYITAVQPEDSATYFC
AE000659, TRAV8-1	AQSVSQHNHHVILSEASLELGCNYS	YGGTVN.....	LFWYVQYPGQHLQLLLK	YFSGDPL.....	VKGIK.....	GFEAEFIKSKFSFNLKPKSVQWSDTAEYFC
AE000659, TRAV8-2	AQSVTQLDSHVSVEGTPVLLRCNYS	SSYSPS.....	LFWYVQHPNKGQLQLLLK	YTSAAITL.....	VKGIN.....	GFEAEFKKSETSFHLTKPSAHMSDAAEYFC
AE000659, TRAV8-3	AQSVTQPDHITVSEGASLELRCNYS	YGATPY.....	LFWYVQSPGQGLQLLLK	YFSGDITL.....	VQGIK.....	GFEAEFKKSSFNLRKPSVHWSDAEYFC
AE000659, TRAV8-4	AQSVTQLDSHVSVEGALVLLRCNYS	SSVPPY.....	LFWYVQYPNQLQLLLK	YTSAAITL.....	VKGIN.....	GFEAEFKKSETSFHLTKPSAHMSDAAEYFC
X02850, TRAV8-6	AQSVTQLDSQVPVFEEAPVELRCNYS	SSVSFY.....	LFWYVQYPNQLQLLLK	YLSGSL.....	VESIN.....	GFEAEFNKSQTSFHLKPKSVHISDTAEYFC
AE000660, TRAV8-7	TQSVTQLDGHITVSEEAPELKCNY	YSGVPS.....	LFWYVQYSSQSLQLLLK	DLTEATQ.....	VKGIR.....	GFEAEFKKSETSFYLRKPSHVSDAEYFC
AE000659, TRAV9-1	GDQSVVOTFGQWLPSEFQSLIVNCSYF	TTQVPS.....	LFWYVQYPPGFGPOLH.K	AMKAND.....	KGRNK.....	GFEAMRYRKFTTSFHLKPKSVQFSDSAVYFC

IMGT tools for V-DOMAIN sequences:

1. IMGT/V-QUEST

Alignment for V-GENE

<u>AF402940</u>		score	GTGCAGCTGCTCGAGCAGTCTGGGGCT___GAGGTGAGCAAGCCTGGGGCCTCAGTAAAGGTTTCCTGCA
<u>X62109</u>	IGHV1-3*01	1146	CA.GTC.A...T.T.....AG.....G.....
<u>X62107</u>	IGHV1-3*02	1110	CA.GTT.A...G.T.....AG.....G.....
<u>M99637</u>	IGHV1-8*01	957	CA.GT..A...G.T.....AG.....G....C.....
<u>L06612</u>	IGHV1-46*03	948	CA.GT..A...G.T.....AG.....G.....
<u>X92343</u>	IGHV1-46*01	948	CA.GT..A...G.T.....AG.....G.....

Alignment for J-GENE

<u>AF402940</u>		score	CTTCACGGGGCGGGACGCTTTGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
<u>J00256</u>	IGHJ3*01	181	_____.T.....T..T.....A.T.....T...G
<u>X86355</u>	IGHJ6*02	179	T.A.TACTACTACT...G.A.....
<u>X86355</u>	IGHJ3*02	172	_____.T.....T..TA.....A.T.....T...G



V-GENE

JUNCTION

J-GENE

Translation

```

<----- F R 1 - I M G T -----
1          5          10          15
input      E V Q L L E S G G G L V Q P G G S
           GAG GTG CAG CTG TTG GAG TCG GGG GGA ... GGC TTG GTA CAG CCT GGG GGG TCC

M99660 IGHV3-23*01
           --- --- --- --- --- --T --- ... --- --- --- --- ---

----->
          20          25          30          35
input      L R L S C A A S G F T F S S F A
           CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTT AGC AGC TTT GCC ... ...
                                     Y
M99660 IGHV3-23*01
           --- --- --- --- --- --- --- --- --A- --- ... ...

          <----- F R 2 - I M G T -----
          40          45          50
input      M S W V R Q A P G K G L D W V S
           ... ... ATG AGC TGG GTC CGC CAG GCT CCT GGG AAG GGG CTG GAC TGG GTC TCA
                                     E
M99660 IGHV3-23*01
           ... ... --- --- --- --- --- --A --- --- --G --- ---

-->
          CDR2 - IMGT
          55          60          65          70
input      E I S G S G G T T Y Y A G S V K
           GAA ATT AGT GGT AGT GGC GGT ACC ACA ... ... TAT TAC GCA GGC TCC GTG AAG
           A S D
M99660 IGHV3-23*01
           -CT --- --- --- --- --T --- -G- --- ... .. --C --- --- --A- --- ---

```

IMGT tools for V-DOMAIN sequences:

2. IMGT/JunctionAnalysis

IMGT/JunctionAnalysis - Mozilla Firefox

Echier Edition Affichage Aller à Marque-pages Outils ?

IMGT/JunctionAnalysis Results

Locus IGH
Species Homo sapiens
IMGTrepertoire link [Locus representation](#)

Maximum number of mutations :
V-REGION : 2; D-REGION : 4; J-REGION : 2
Deletion criterium : Using patterns
Best D gene choice for a same score : Less mutations

Description of the JUNCTIONS

Click on mutated (underscored) nucleotid to see the original one

	Input	V name	V-REGION	P	N1	D-REGION	N2	P	J-REGION	J name	D name	Vmut	Dmut	Jmut	Ngc
#1	Z70256	IGHV2-26*01	tgtgtacg....		tgttgt	gcagcgctgttac	ccaaatac		...actttgaccactgg	IGHJ4*02	IGHD6-13*01	1	2	1	5/15
#2	Z70257	IGHV3-7*02	tgtgcgag		ggatgg	cagctcttatgcc	cgccc		ctactggtacttcgatctctgg	IGHJ2*01	IGHD2-2*01	0	2	0	9/11
#3	Z70606	IGHV4-31*03			c	.gactacg.....	cact		..atgcttttgatgtctgg	IGHJ3*01	IGHD4-17*01	0	0	0	3/5
#4	Z70608	IGHV4-39*05			cagagta	acgatttttgagtggttatt....	ccccggggga		..atgcttttgatatctgg	IGHJ3*02	IGHD3-3*01	0	0	0	12/17
#5	Z70610	IGHV4-34*09	tgtgcgagag.		tcgggag	cgatttttgagtggttatt....	cccgca	ca	tgatgcttttgatatctgg	IGHJ3*02	IGHD3-3*01	0	0	0	9/12
#6	Z70611	IGHV4-59*01	tgtgcgaga..		ca	tggttaactataa.	tgccggcgcttg		...actggttcgacccctgg	IGHJ5*02	IGHD3-9*01	0	2	0	9/13
#7	Z70613	IGHV4-59*01				ctgttac	ctc		gactactgg	IGHJ4*02	IGHD6-13*01	0	0	0	4/6
#8	Z70614	IGHV4-59*01			actataa	acttat.....	ccc		gactactgg	IGHJ4*02	IGHD3-16*01	0	2	0	7/14
#9	Z70615	IGHV4-59*01	tgtgcgagag.		ggctg	gtaaagaggg.....	tttcggaa		.tactggtacttcgatctctgg	IGHJ2*01	IGHD5-24*01	0	2	0	7/13
#10	Z70616	IGHV4-34*01	tgtgcgagag.		cgg	gtttggg.....	ttccc		...actggttcgacccctgg	IGHJ5*02	IGHD3-16*01	0	0	0	6/8
#11	Z70620	IGHV4-30-4*01	tgtgcgagaga		cc	ggggcgggatggtt....	cgg		.gatgcttttgatatctgg	IGHJ3*02	IGHD3-16*01	1	4	0	5/5
#12	Z70621	IGHV4-39*01	tgtgcgagaca		ccacgatttatgg	ttcggggagtt.....	tgaccccc		ttgactactgg	IGHJ4*02	IGHD3-16*01	0	1	0	12/21
#13	Z70622	IGHV4-39*06	tgtgcgagaga	t	tgccccgcctcctgcaaaat	gtattactatggttcgggga.....	tatgtacg		ttgactactgg	IGHJ4*03	IGHD3-10*01	0	0	0	15/28

Terminé

The eleven IMGT amino acid classes according to the physico-chemical properties

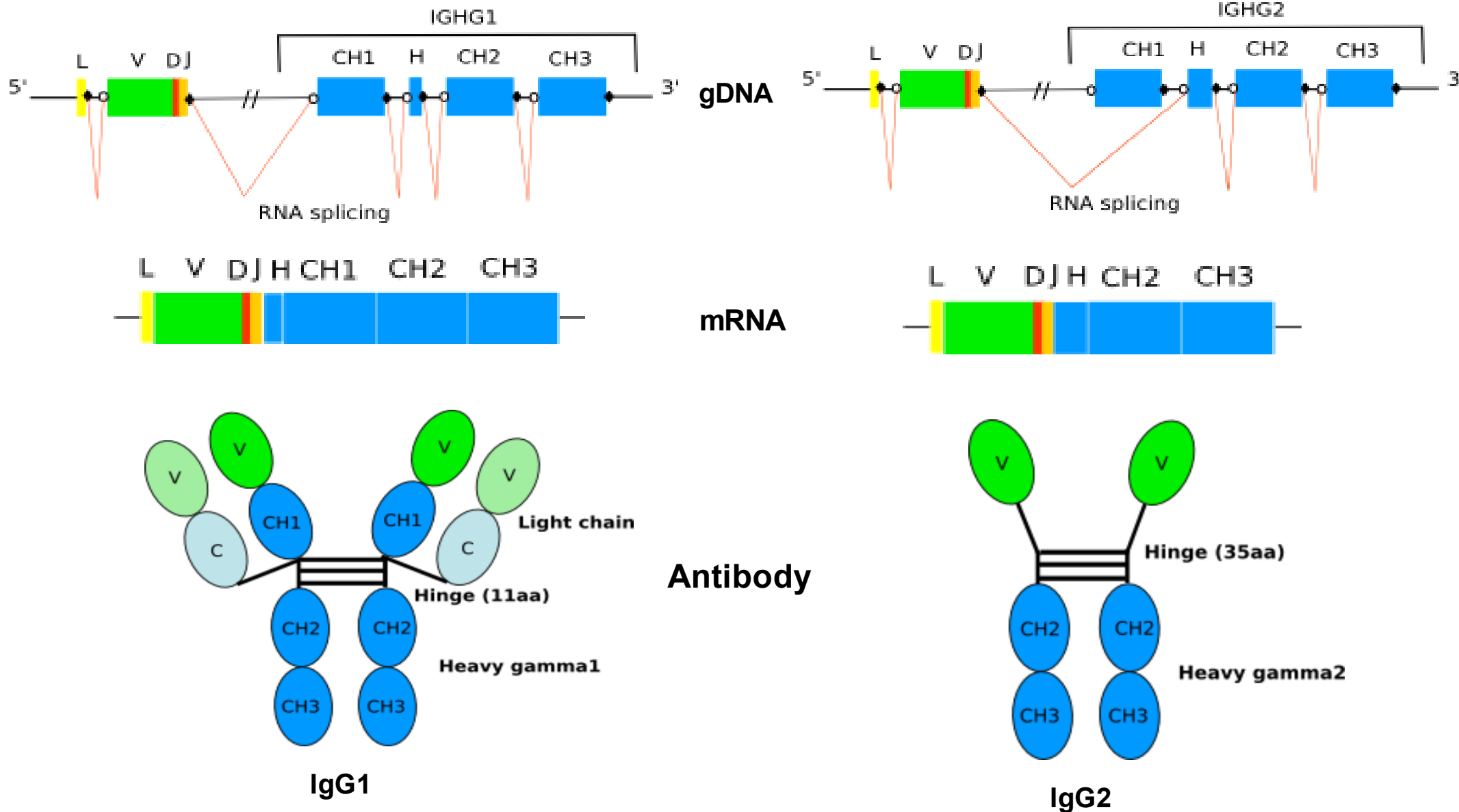
'Volume' classes		'Hydropathy' classes				
	in Å ³	Hydrophobic		Neutral		Hydrophilic
Very large	189-228	F	W	Y		
Large	162-174	I L	M			K R
Medium	138-154	V			H	E Q
Small	108-117		C	P T		D N
Very small	60-90	A		G S		
		Aliphatic		Sulfur		
				Hydroxyl		
				Basic		
				Acidic		
				Amide		
				Uncharged	Charged	Uncharged
		Nonpolar		Polar		

JUNCTION alignments

Click on mutated (underscored) amino acid to see the original one:

		104	105	106	107	108	109	110	111	111.1	111.2	111.3	111.4	112.5	112.4	112.3	112.2	112.1	112	113	114	115	116	117	118	Frame	CDR3-IMGT length	Molecular mass	
#1	Z70256	C	<u>V</u>	R	V	V	Q	<u>R</u>	L	V								P	K	Y	H	F	D	<u>H</u>	W	+	15	2,438.76	
	tgt	gta	cgt	gtt	gtg	cag	cgc	ctg	gta	...	...	...	...	...	...	...	ccc	aaa	tat	cac	ttt	gac	cac	tgg					
#2	Z70257	C	A	R	D	G	S	<u>S</u>	Y	A							R	P	Y	W	Y	F	D	L	W	+	16	2,256.49	
	tgt	gcg	agg	gat	ggc	agc	tct	tat	gcc	...	...	...	...	...	...	cgc	ccc	tac	tgg	tac	ttc	gat	ctc	tgg					
#3	Z70606	C	A	R	A	T	T	H												Y	A	F	D	V	W	+	11	1,604.77	
	tgt	gcg	aga	gcg	act	acg	cac	...	...	...	...	...	...	...	...	...	...	...	tat	gct	ttt	gat	gtc	tgg					
#4	Z70608	C	A	R	V	T	I	F	G	V	V						I	P	R	G	N	A	F	D	I	W	+	18	2,426.78
	tgt	gcc	aga	gta	acg	att	ttt	gga	gtg	gtt	...	...	...	...	att	ccc	cgg	ggg	aat	gct	ttt	gat	atc	tgg					
#5	Z70610	C	A	R	V	G	S	D	F	W	S	G					Y	S	R	H	D	A	F	D	I	W	+	19	2,539.73
	tgt	gcg	aga	gtc	ggg	agc	gat	ttt	tgg	agt	ggt	...	...	...	tat	tcc	cga	cat	gat	gct	ttt	gat	atc	tgg					
#6	Z70611	C	A	R	H	G	<u>N</u>	Y	N	A								G	V	D	W	F	D	P	W	+	15	2,072.21	
	tgt	gcg	aga	cat	ggt	aac	tat	aat	gcc	...	...	...	...	...	...	...	ggc	gtt	gac	tgg	ttc	gac	ccc	tgg					
#7	Z70613	C	A	R	A	A	A	G											T	S	L	F	D	Y	W	+	12	1,531.71	
	tgt	gcg	aga	gca	gca	gct	ggt	...	...	...	...	...	...	...	...	...	...	acc	tcc	ctc	ttt	gac	tac	tgg					
#8	Z70614	C	A	R	H	Y	N	<u>S</u>	G										T	Y	P	L	D	Y	W	+	13	1,846.01	
	tgt	gcg	aga	cac	tat	aat	tcg	ggg	...	...	...	...	...	...	...	...	...	act	tat	ccc	ctc	gac	tac	tgg					
#9	Z70615	C	A	R	G	L	V	<u>K</u>	<u>R</u>	V							S	E	Y	W	Y	F	D	L	W	+	16	2,419.75	
	tgt	gcg	aga	ggg	ctg	gta	aag	agg	gtt	...	...	...	...	...	...	...	tcg	gaa	tac	tgg	tac	ttc	gat	ctc	tgg				
#10	Z70616	C	A	R	A	G	L	G											S	H	W	F	D	P	W	+	12	1,602.8	
	tgt	gcg	aga	gcg	ggt	ttg	ggt	...	...	...	...	...	...	...	...	...	...	...	tcc	cac	tgg	ttc	gac	ccc	tgg				
#11	Z70620	C	A	R	D	R	G	<u>G</u>	M										V	R	D	A	F	D	I	W	+	14	1,932.17
	tgt	gcg	aga	gac	cgg	ggc	ggg	atg	...	...	...	...	...	...	...	...	...	gtt	cgg	gat	gct	ttt	gat	atc	tgg				
#12	Z70621	C	A	R	H	H	D	L	W	F							G	E	F	D	P	L	D	Y	W	+	16	2,307.53	
	tgt	gcg	aga	cac	cac	gat	tta	tgg	ttc	...	...	...	...	...	...	...	ggg	gag	ttt	gac	ccc	ctt	gac	tac	tgg				
		C	A	R	D	C	P	A	P	A	K	M	Y	Y	Y	G	S	G	I	C	T	F	D	Y	W				

Camelidae (camel, llama) antibodies

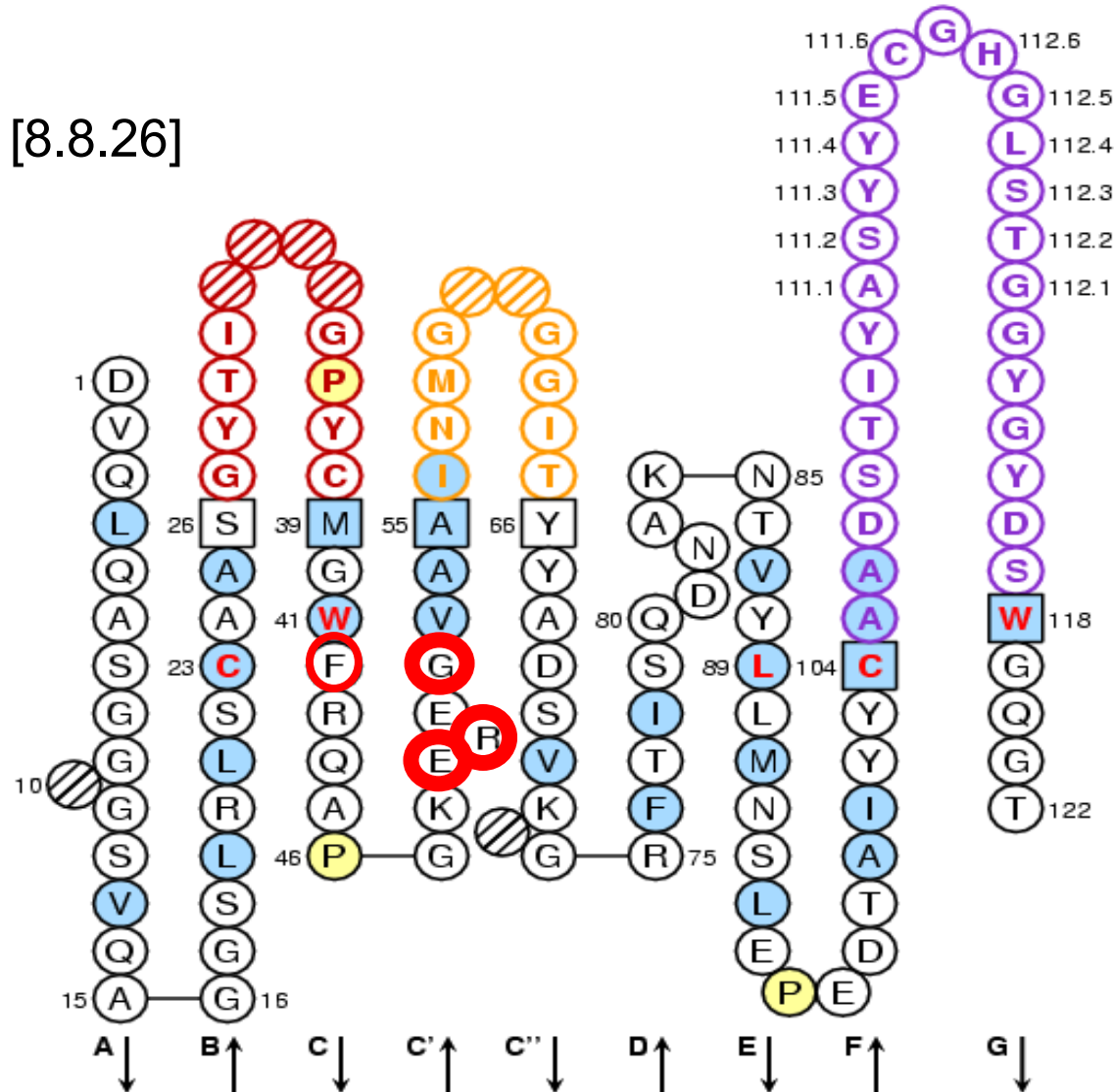


IMGT Collier de Perles

Camelus dromedarius (Camel) VH Single-Domain Antibody (1jto_A)

CDR-IMGT lengths [8.8.26]

42: F, Y
49: E, Q
50: R, C
52: G, F, L, W



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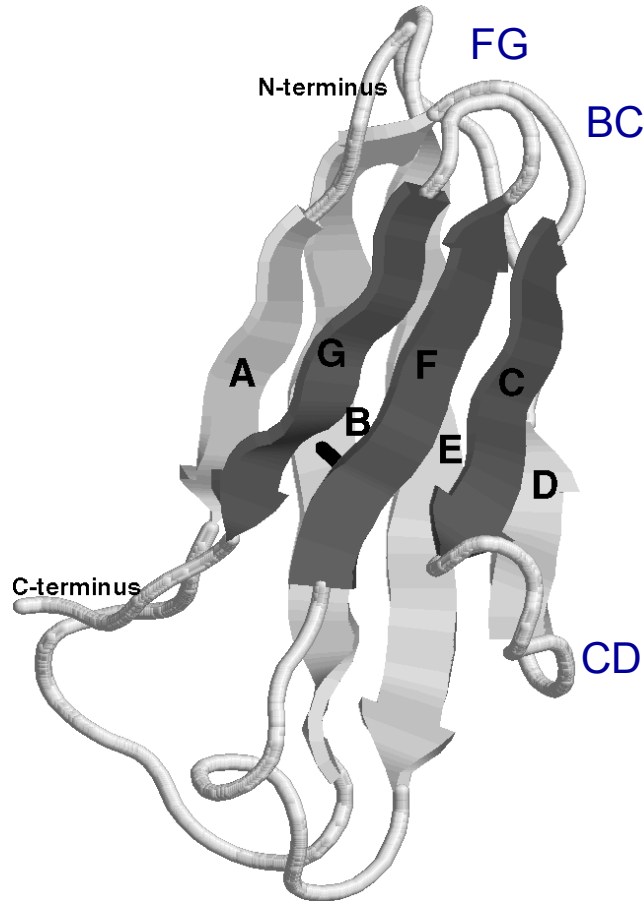
CDR-IMGT lengths [9.6.9]



Duprat, E. et al., Recent Res. Develop. Human Genet., 2, 111-136 (2004)

C-DOMAIN and C-LIKE-DOMAIN

The 3D structure of a **C-LIKE-DOMAIN** (IgSF other than IG or TR) is similar to that of a **C-DOMAIN** (IG or TR)



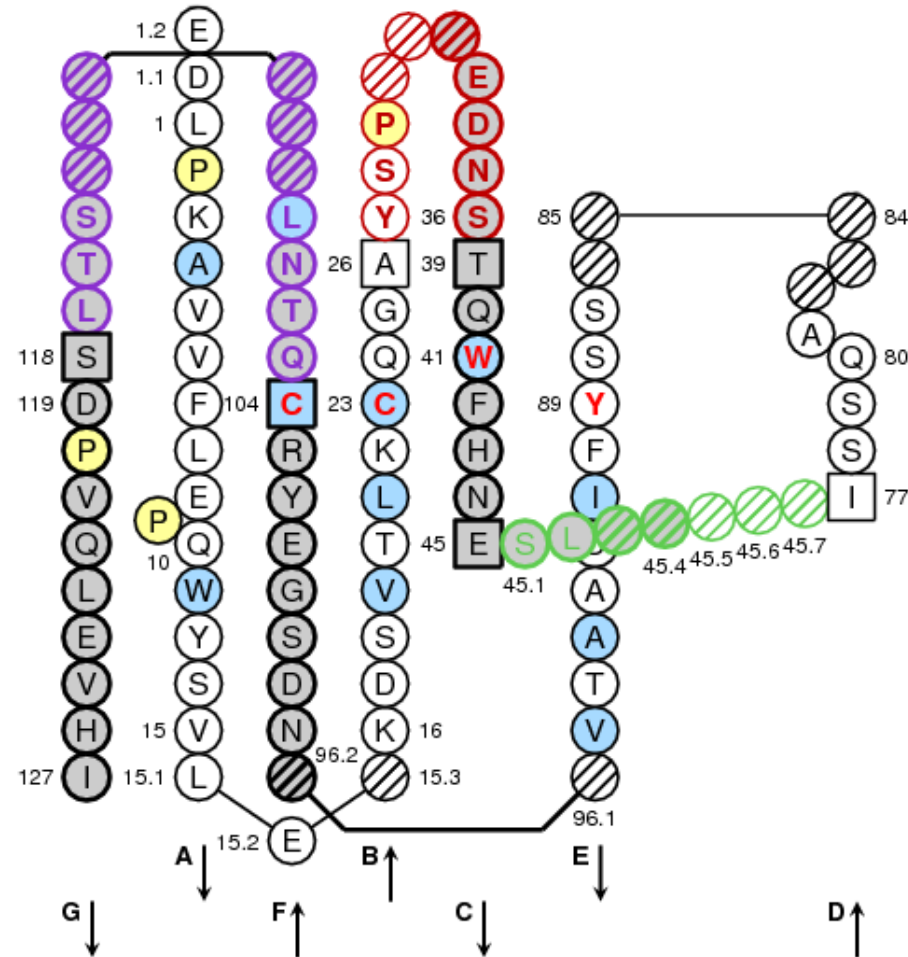
7 antiparallel beta strands:
A, B, C, D, E, F and G

linked by beta turns:
AB, DE and EF
transversal strand: CD
or loops:
BC or CDR1-IMGT and
FG or CDR3-IMGT

forming a sandwich of two sheets
[ABED][GFCD] or [ABE][GFCD]

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FCGR3B



The distinction between C1 and C2 becomes unnecessary as discussed in *Dev. Comp. Immunol.* 29, 185-203 (2005).

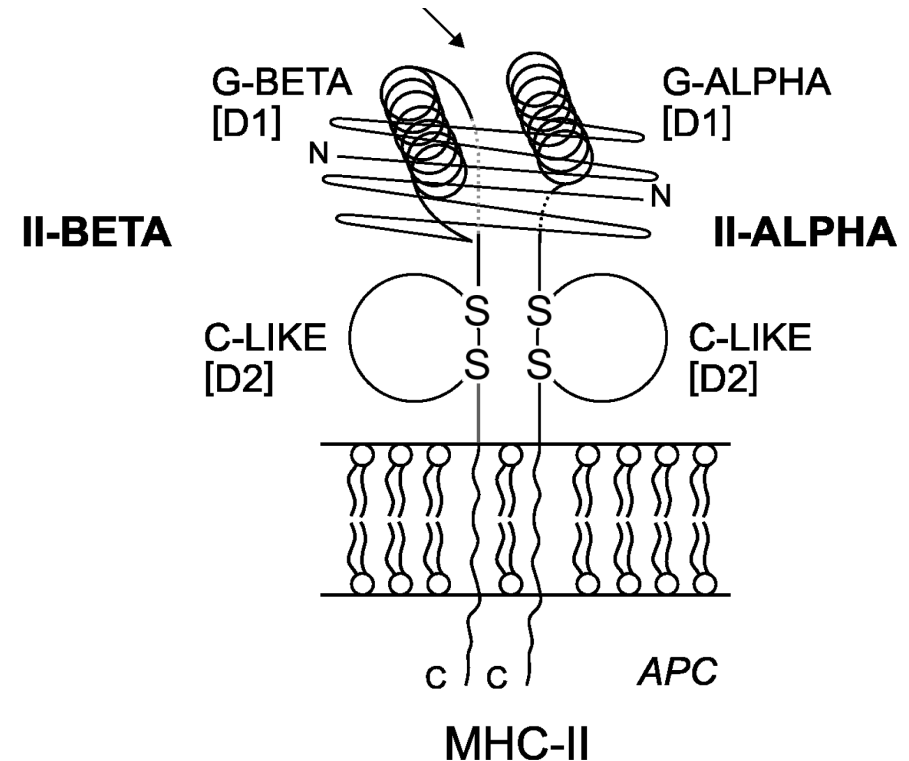
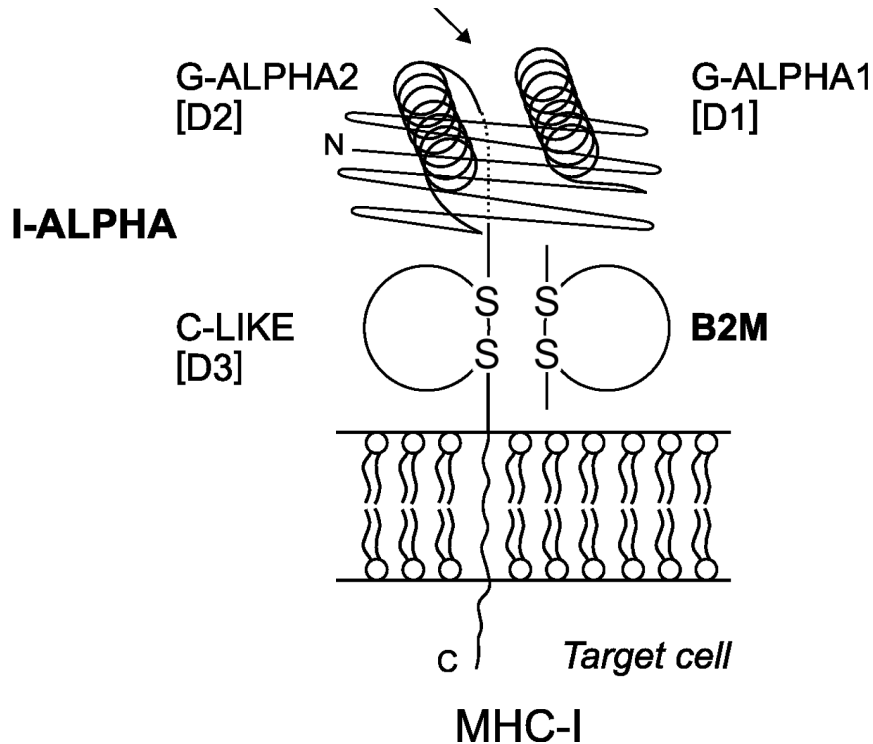
Bertrand G. et al., Tissue Antigens, 64, 119-131 (2004)

MHC class I and MHC class II

The groove is made by two G-DOMAINS that belong

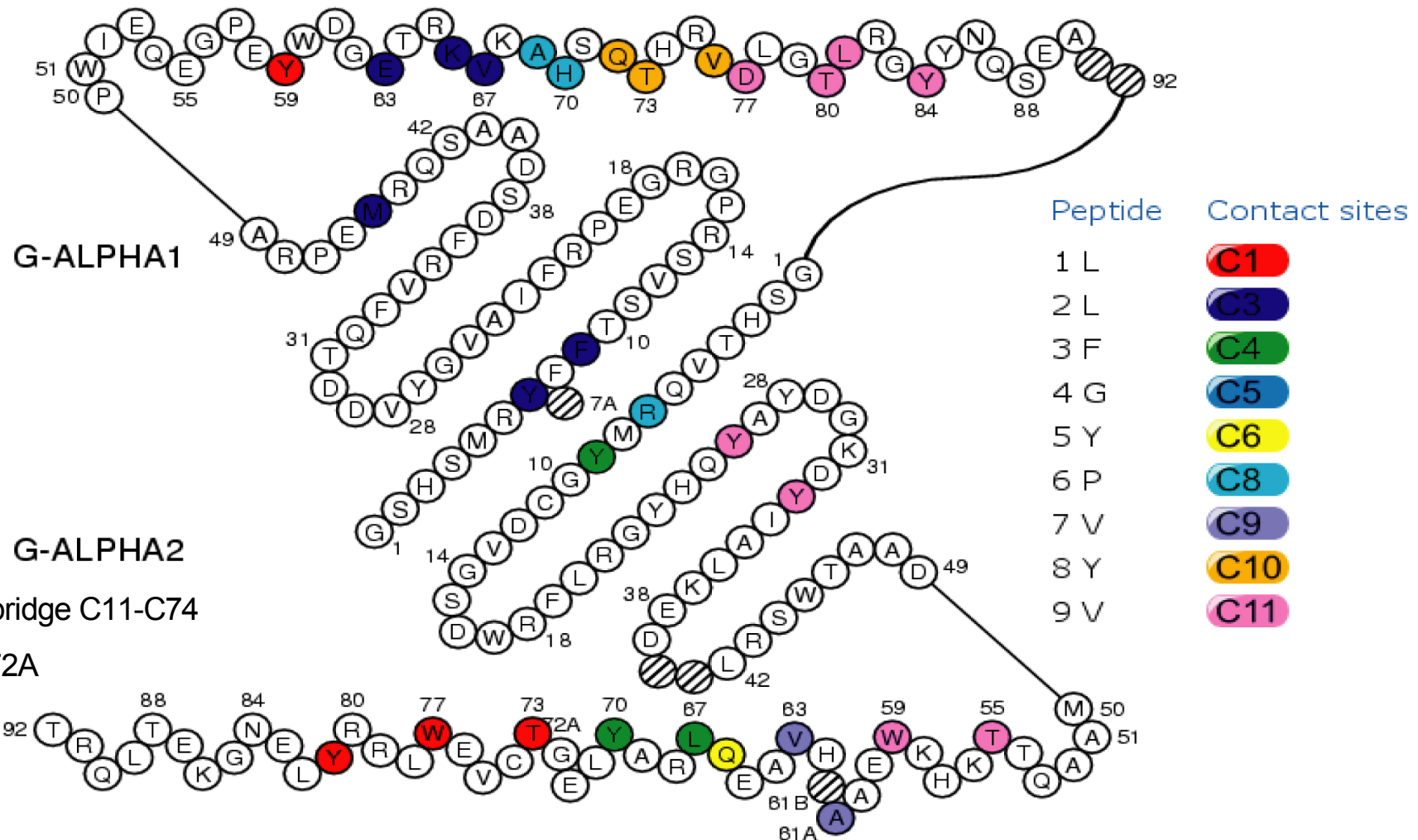
both to the same chain
I-ALPHA
in MHC class I

each one to a different chain
II-ALPHA and II-BETA
in MHC class II



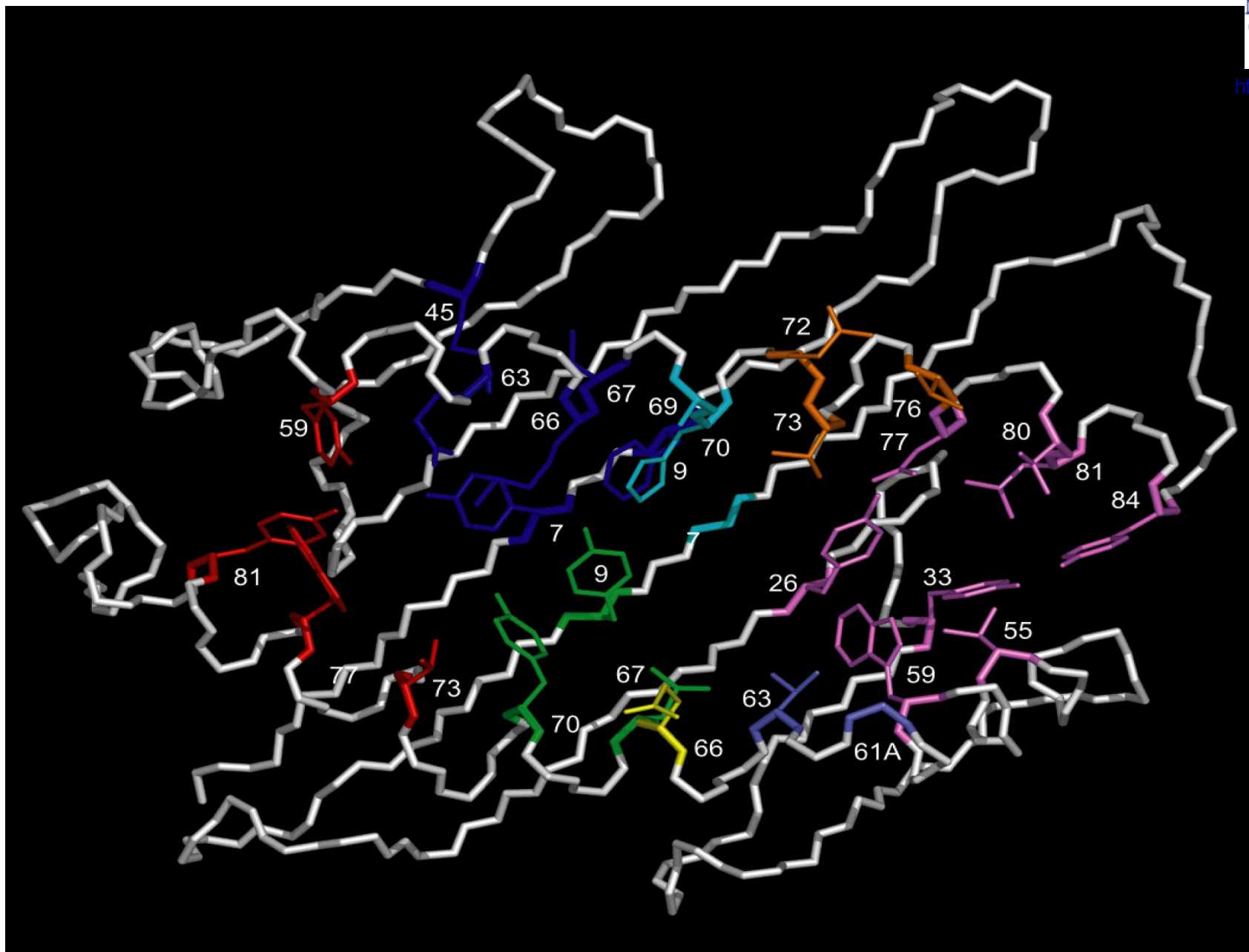
IMGT Colliers de Perles for G-DOMAIN

IMGT pMHC contact sites: MHC class I (1ao7)



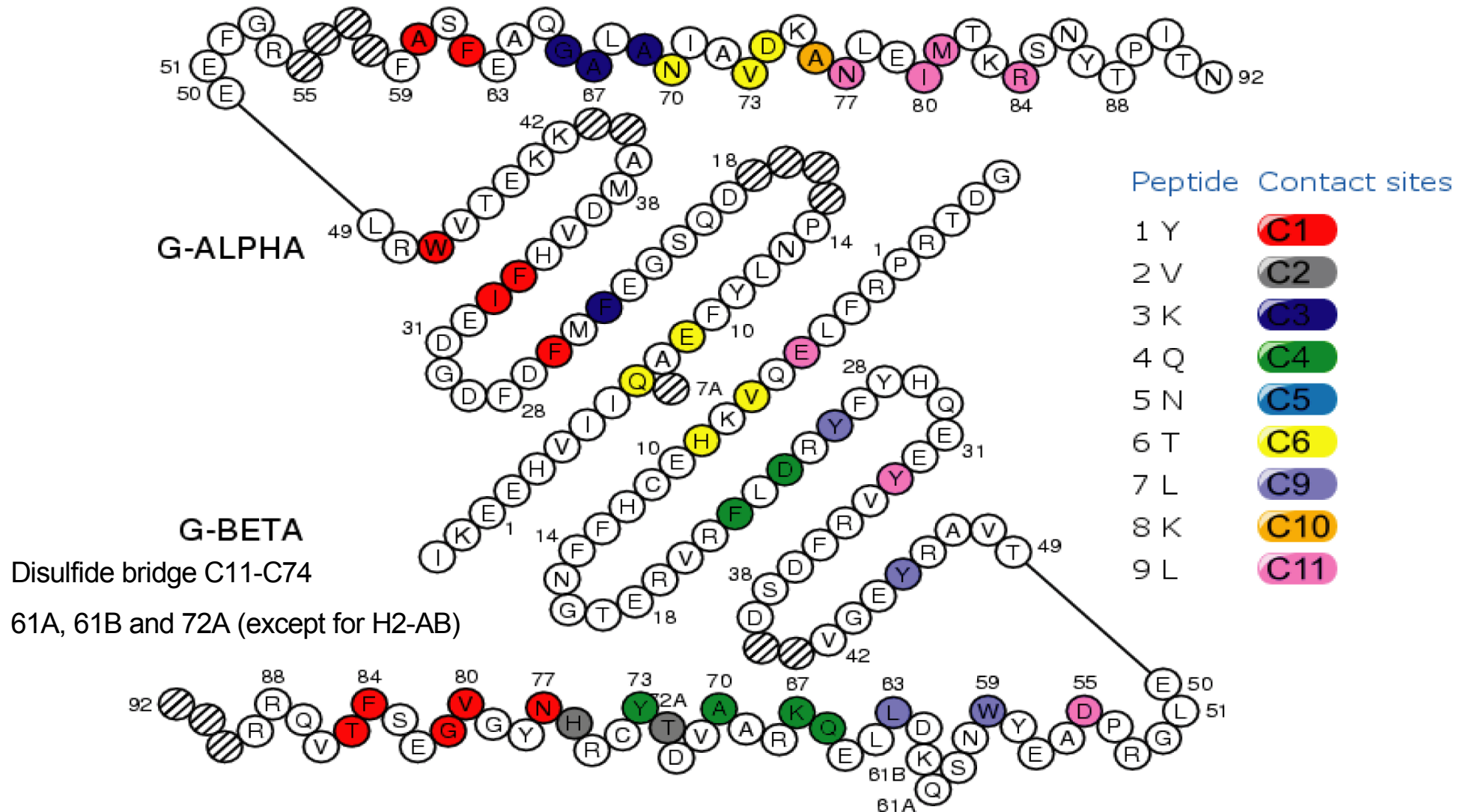
Can be compared with the 'IMGT reference pMHC contact sites' for pMHC-I with 9-aa peptides: 74 structures

1ao7



IMGT Colliers de Perles for G-DOMAIN

IMGT pMHC contact sites: MHC class II (1j8h)



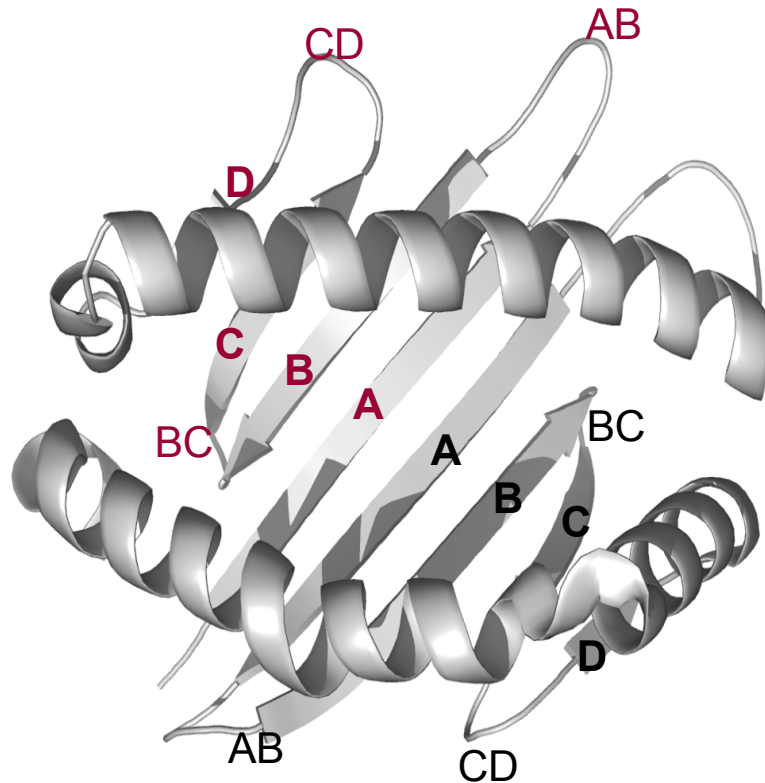
Can be compared with the 'IMGT reference pMHC contact sites' for pMHC-II and the 9 aa in the groove: 44 structures



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G-DOMAIN and G-LIKE-DOMAIN

The 3D structure of a **G-LIKE-DOMAIN** (MhcSF other than MHC) is similar to that of a **G-DOMAIN** (MHC)



4 antiparallel beta strands:

A, B, C, D

linked by beta turns:

AB, BC and CD

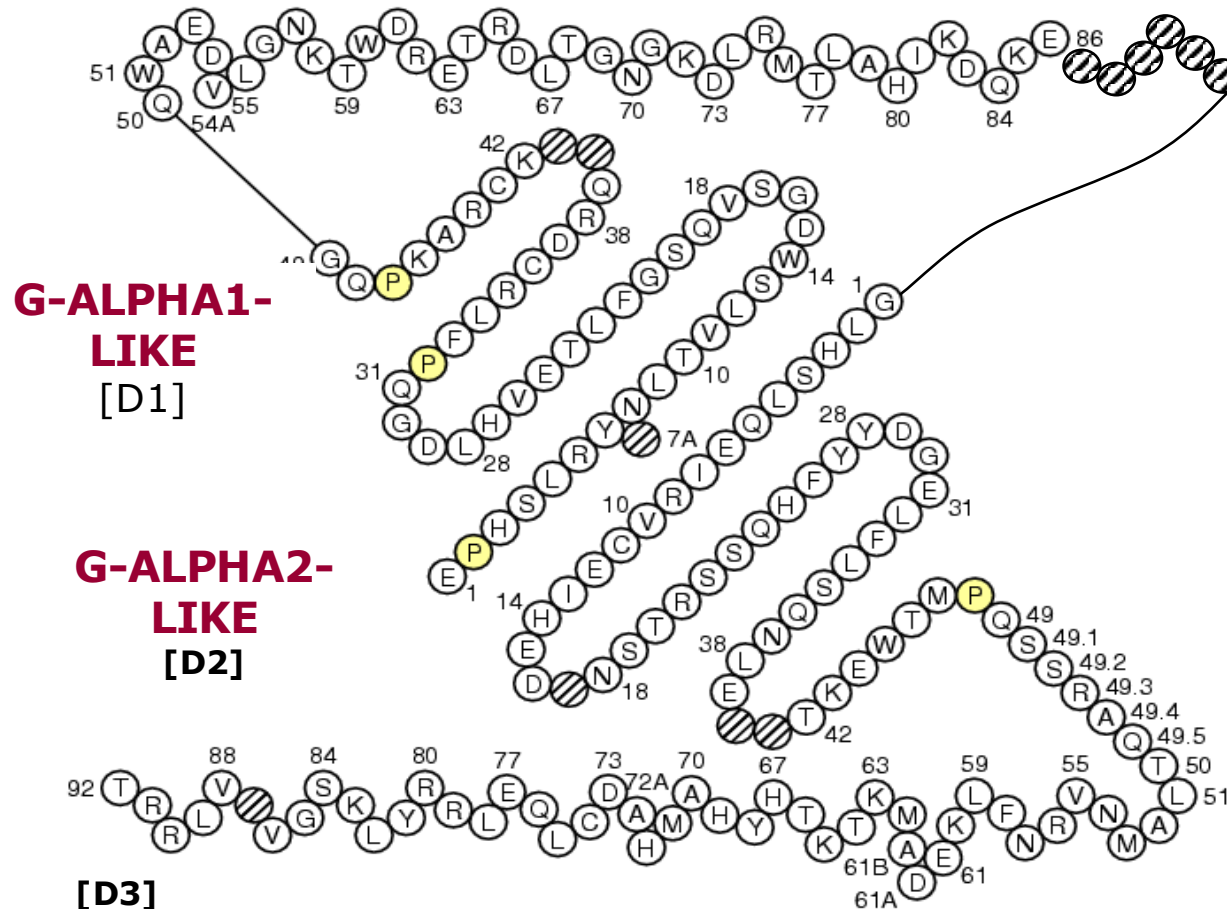
(« floor » of the groove or platform)

one long helix

(« wall » of the groove)

G-LIKE-DOMAIN

MICA

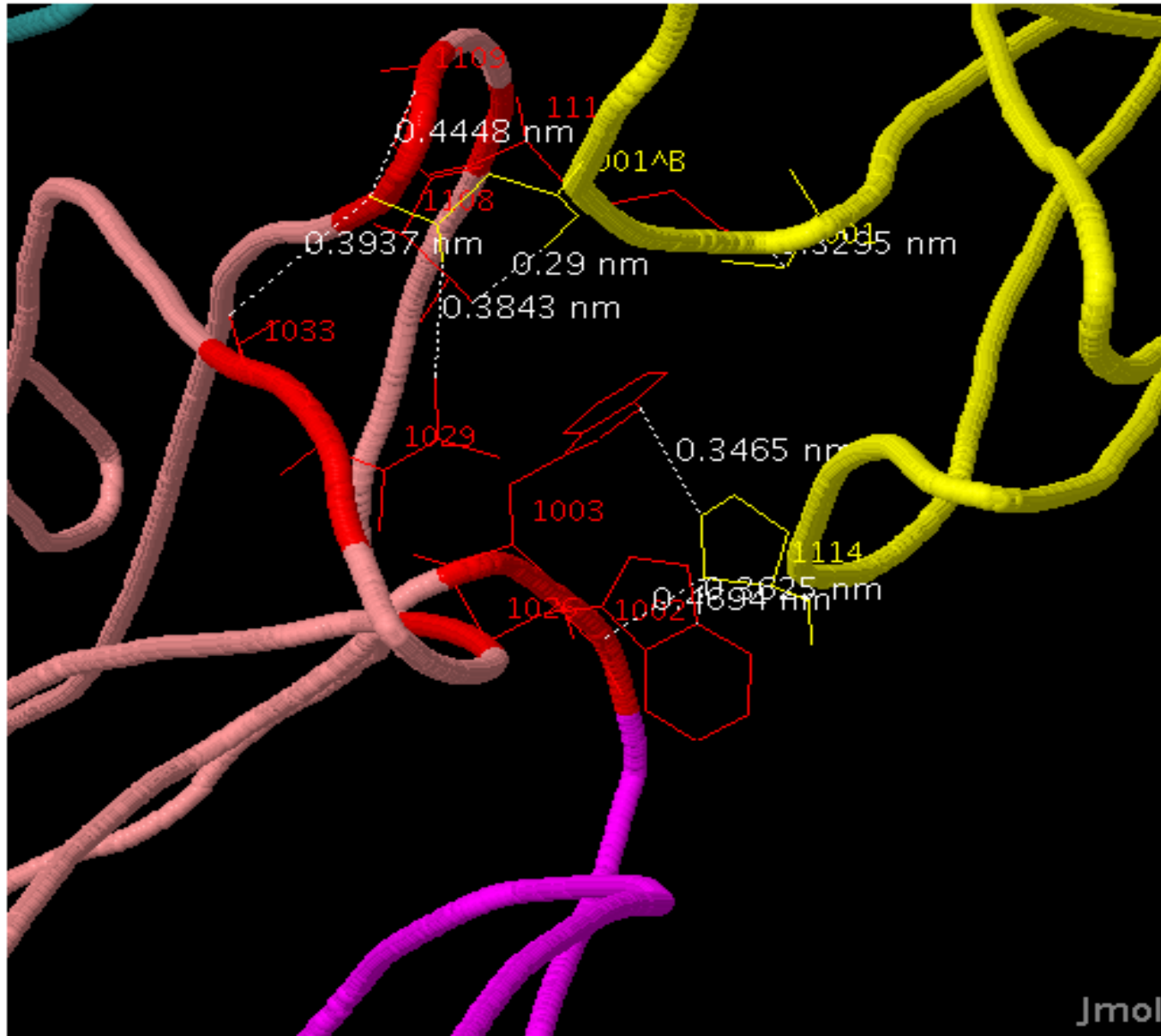


Position 54A is characteristics of the G-ALPHA1-LIKE of MHC I-like

Interactions between domains

FCGR3
B

[D2]
D-LIKE-
DOMAIN



[D1] C-LIKE-DOMAIN

IGHG1
(FC-GAMMA1)

CH2
C-DOMAIN



IMGT-ONTOLOGY concepts: *IMGT Scientific chart rules*

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CINECA, Bologna, Italy

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CNR, Italy

CNRS, France

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University of Bologna, Italy

University of Catania, Italy



The IMGT team at Montpellier



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Gene
Tics

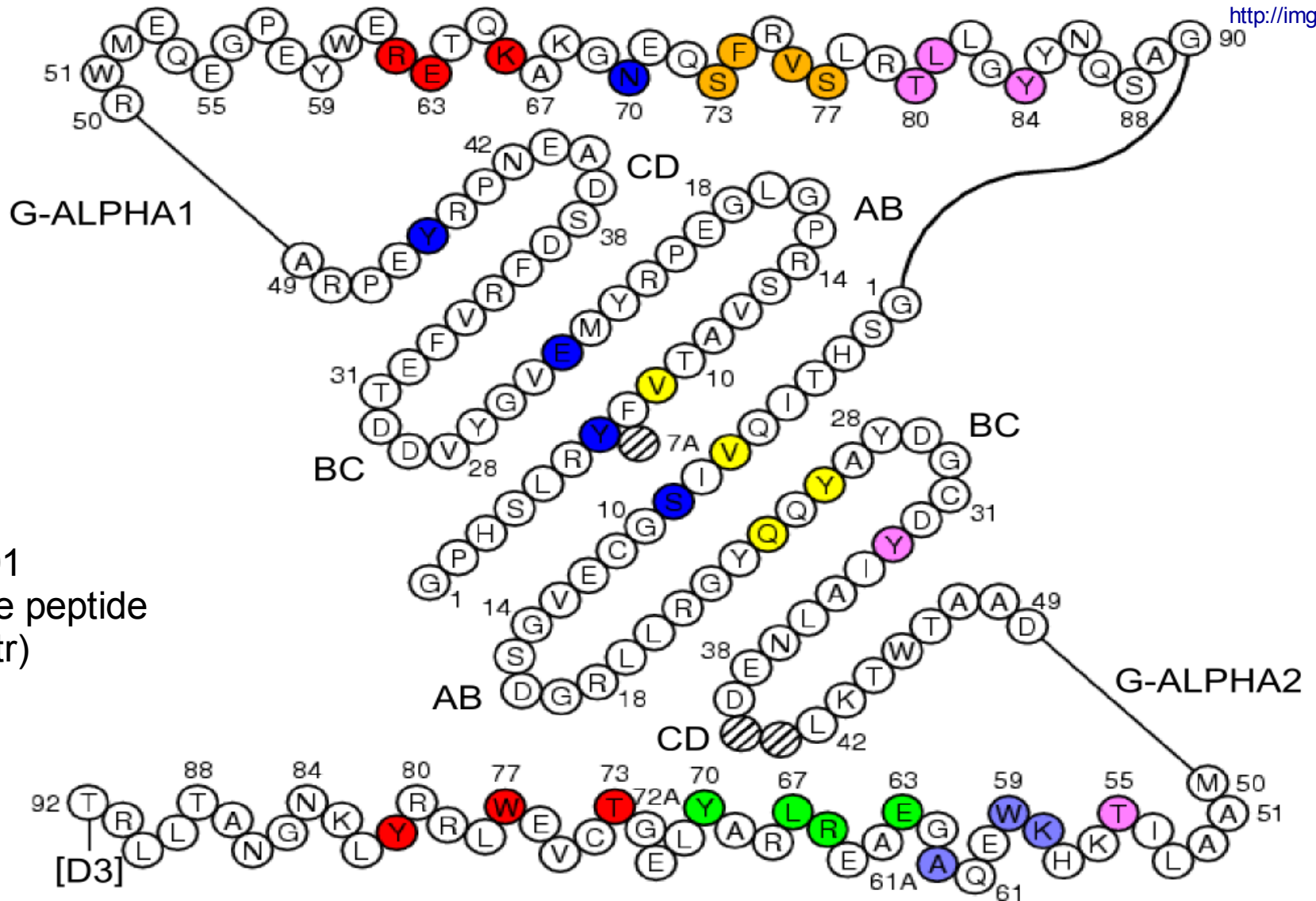
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<http://imgt.cines.fr>

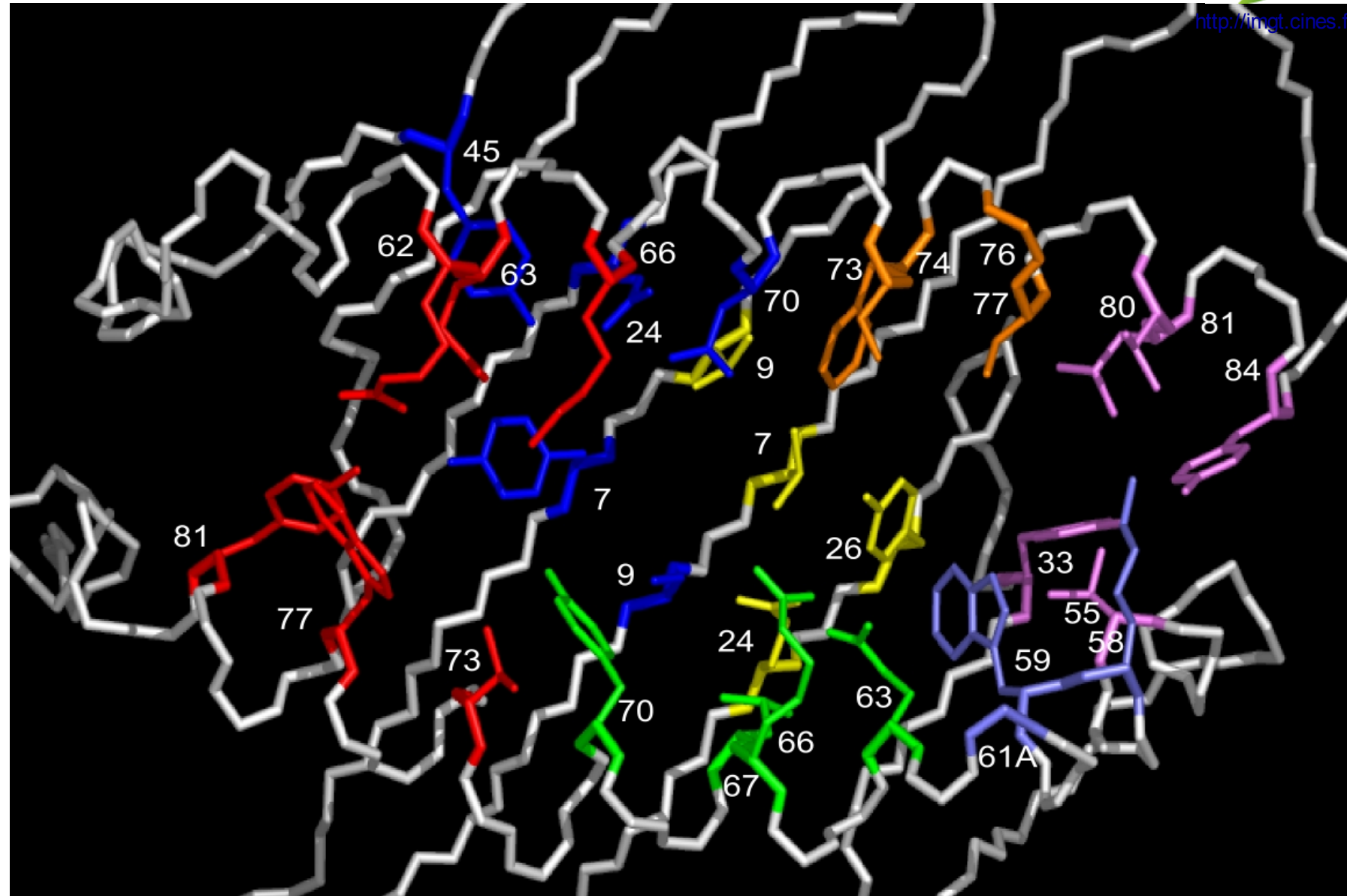
IMGT pMHC contact sites

C1	1 E
C2	--
C3	2 Q
C4	3 Y
C5	(4 K)
C6	5 F
C7	--
C8	--
C9	6 Y
C10	7 S
C11	8 V

H2-K1*01
8 residue peptide
(code 1jtr)



IMGT pMHC contact sites



H2-K1*01
(code 1jtr)
8 residue peptide