IG,TR and IgSF,MHC and MhcSF:

what do we learn from the IMGT Colliers de Perles ?

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NON-HUMAN PRIMATE IMMUNOGENETICS
22nd European Immunogenetics and Histocompatibility Conference satellite session
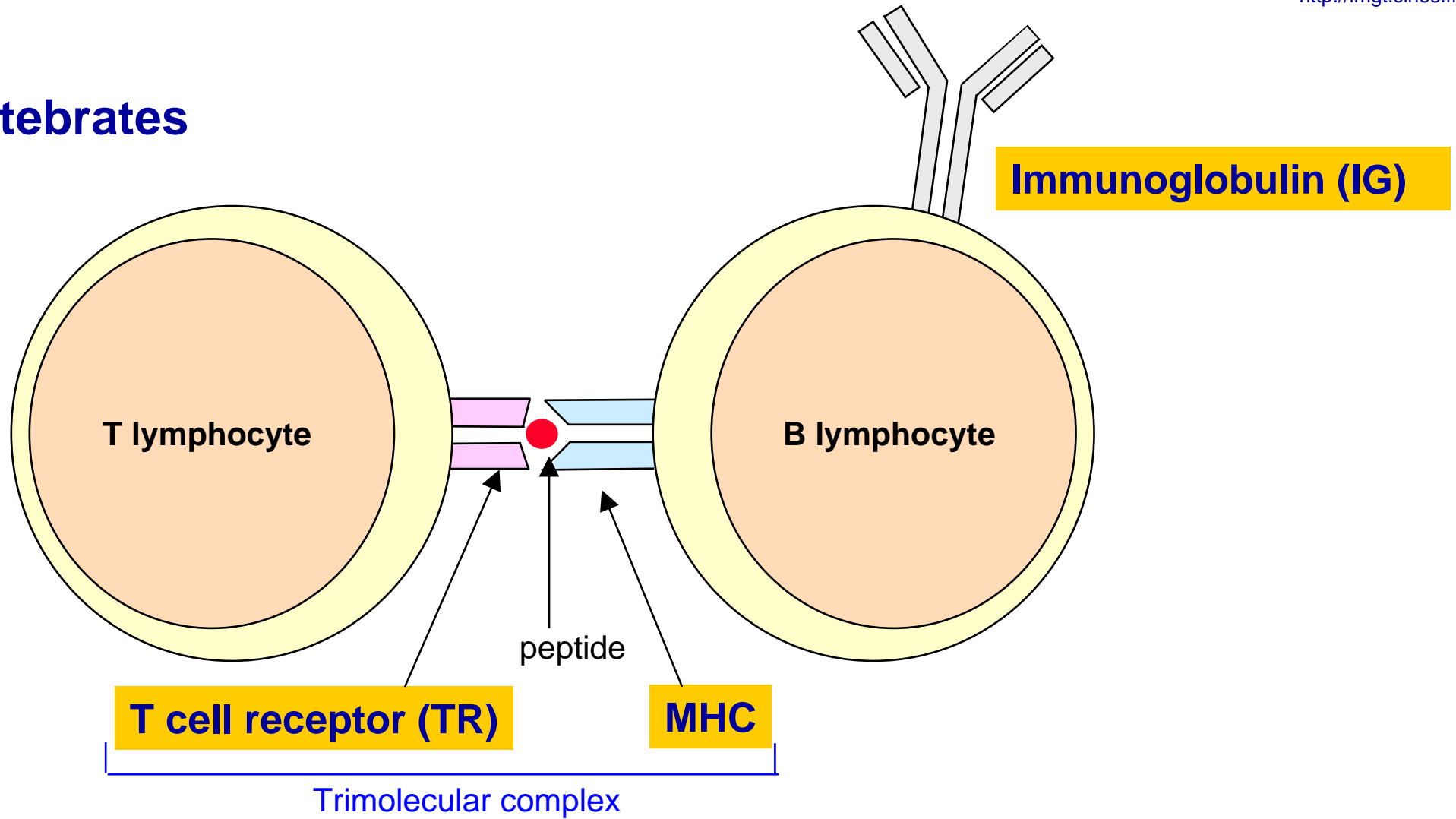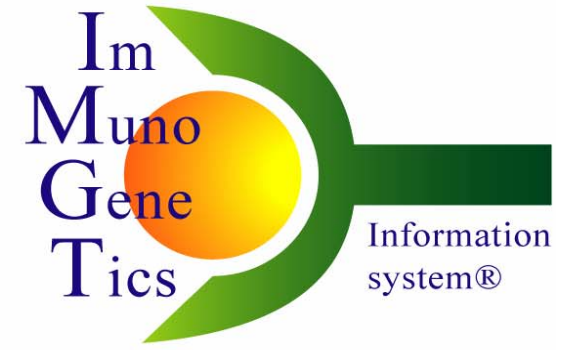**April 2, 2008**

Overview

1. **Introduction**

2. **IMGT Colliers de Perles for V-DOMAIN (IG and TR)**

3. **IMGT Colliers de Perles for C-DOMAIN (IG and TR)**

4. **IMGT Colliers de Perles for G-DOMAIN (MHC)**

5. **IMGT Colliers de Perles for IgSF and MhcSF**

6. **IMGT resources and tools**

IMGT®: the adaptive immune response

Vertebrates

Immunoglobulin (IG)

T lymphocyte

B lymphocyte

peptide

T cell receptor (TR)

MHC

Trimolecular complex

Immunoglobulin (IG)

T cell receptor (TR)

Light chain

Heavy chain
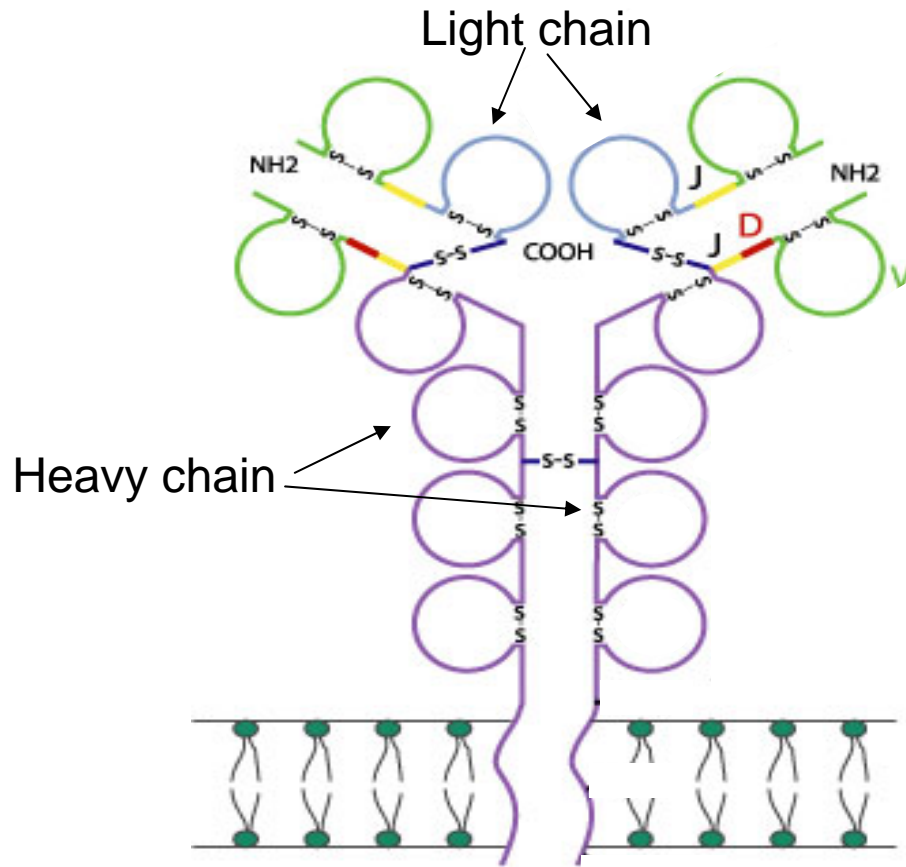
Membrane IgM

Alpha   -   Beta

Gamma   -   Delta
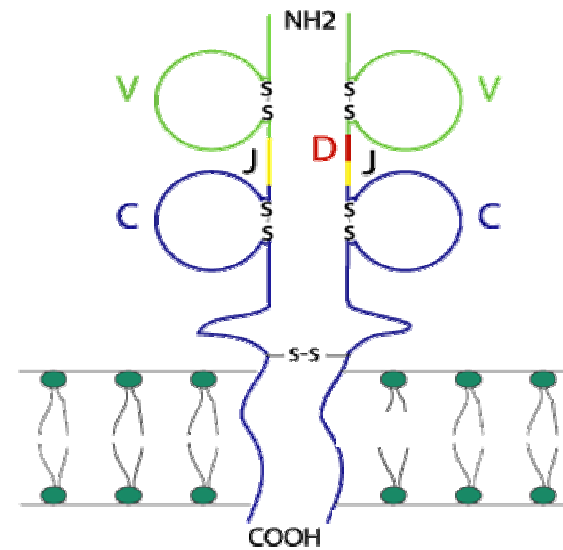
T cell receptor

Immunoglobulin (IG)

T cell receptor (TR)

V-DOMAIN

V-J-REGION

Light chain
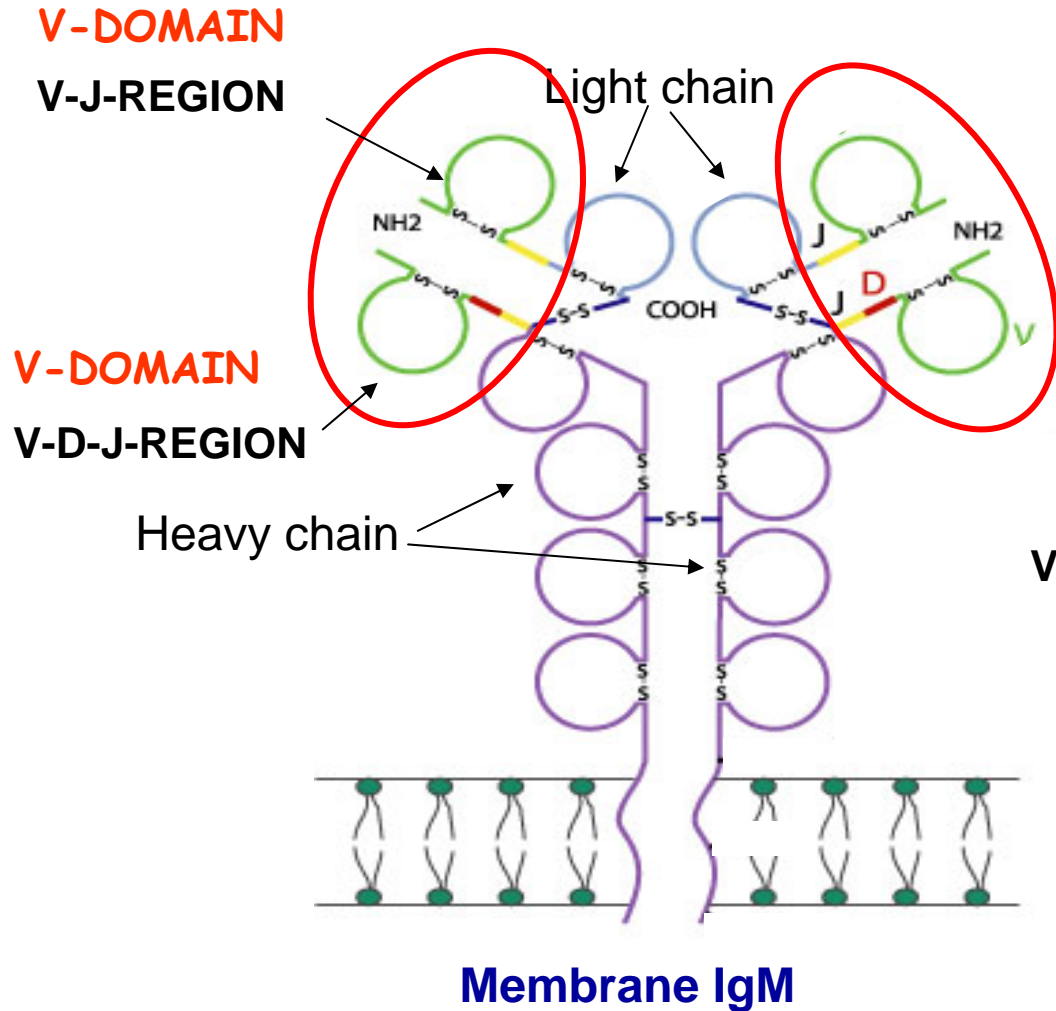
Contribution of the
2 V-DOMAINs
to the antigen binding site

NH2

NH2

J

D

J

Alpha - Beta

Gamma - Delta

V-DOMAIN

V-D-J-REGION

COOH

V

Heavy chain

S-S

NH2

V

V

D

V-J-REGION

J

J

V-D-J-REGION

C

C

S-S

S-S

Membrane IgM

COOH

T cell receptor

The Immunoglobulin FactsBook, 2001
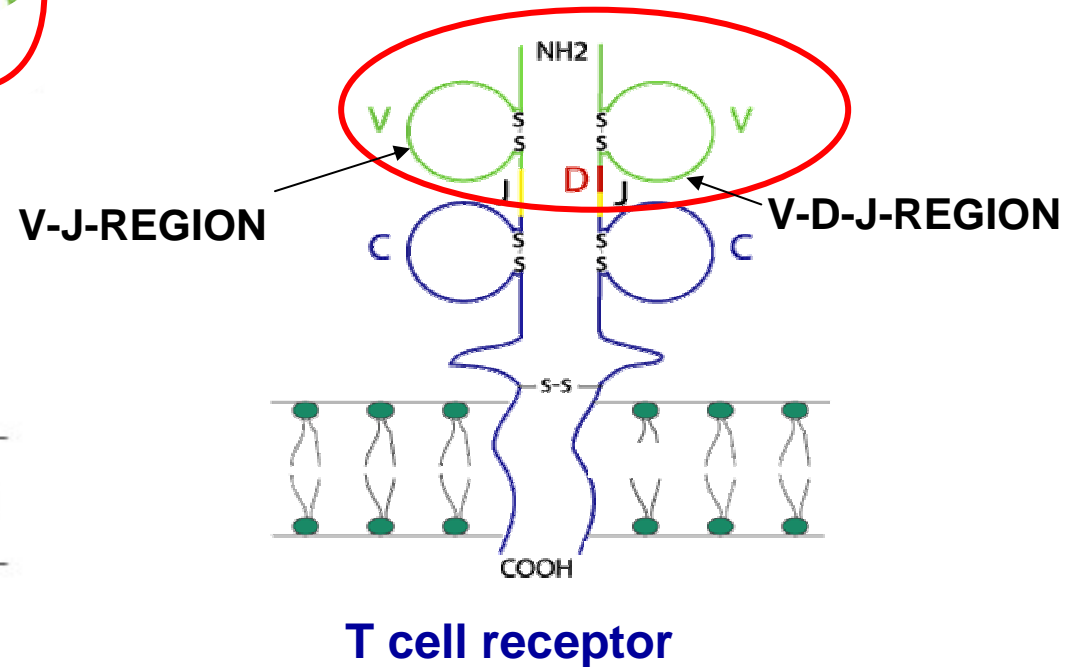
Immunoglobulin V-DOMAINs

http://imgt.cines.fr

VH   **V-KAPPA**

V-D-J junction   **V-J junction**

1ao7_E
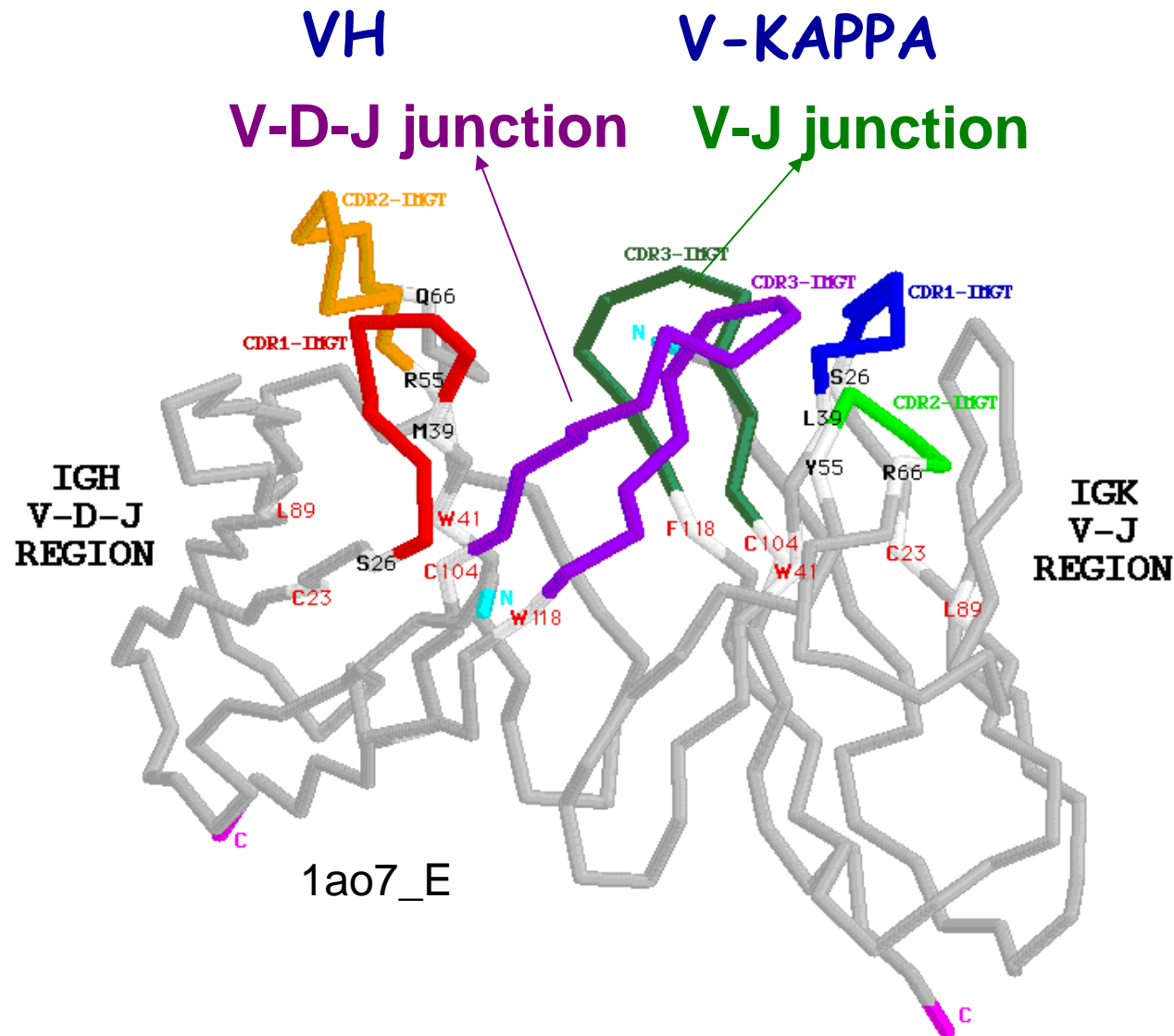
Side view of the V-DOMAINs

CDR: complementarity determining region

IMGT Repertoire, http://imgt.cines.fr

IMGT Colliers de Perles for V-DOMAIN (IG and TR)

http://imgt.cines.fr

The 3D structure of a **V-DOMAIN**
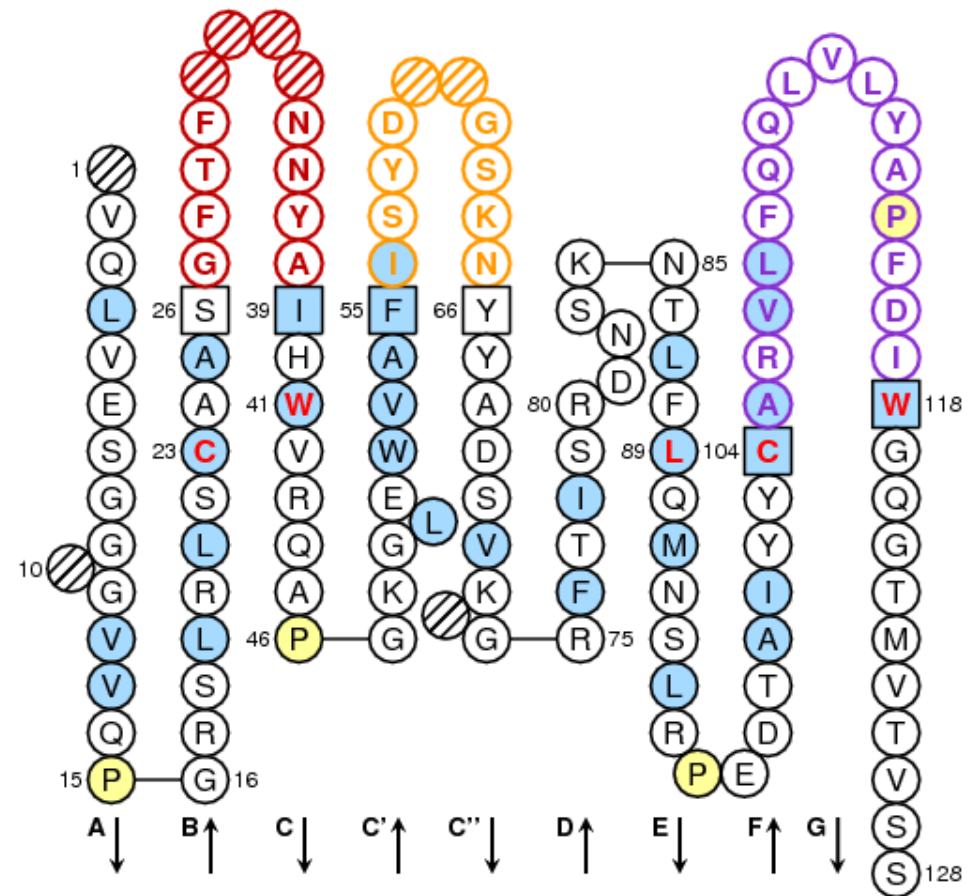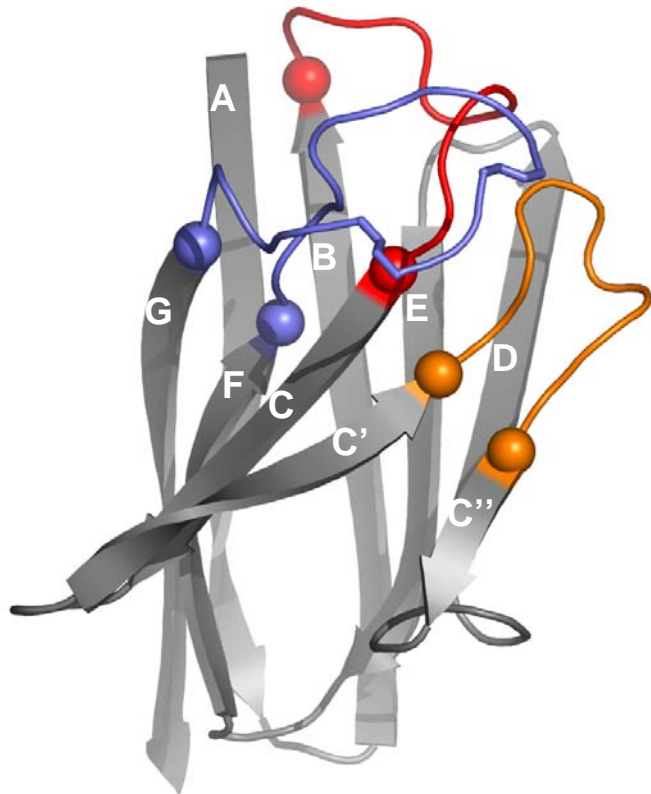
IGHV V-DOMAIN from B7-15A2 (1aqk_H)

CDR-IMGT lengths [8.8.16]

IMGT Colliers de Perles for C-DOMAIN (IG and TR)

The 3D structure of a **C-DOMAIN**

http://imgt.cines.fr
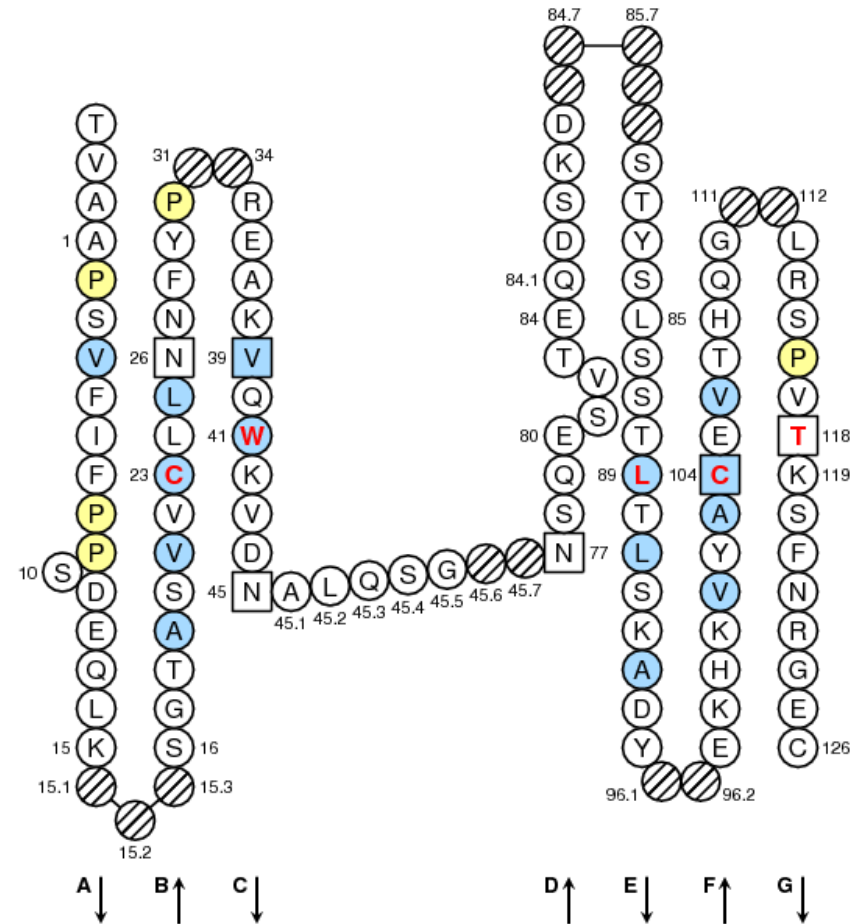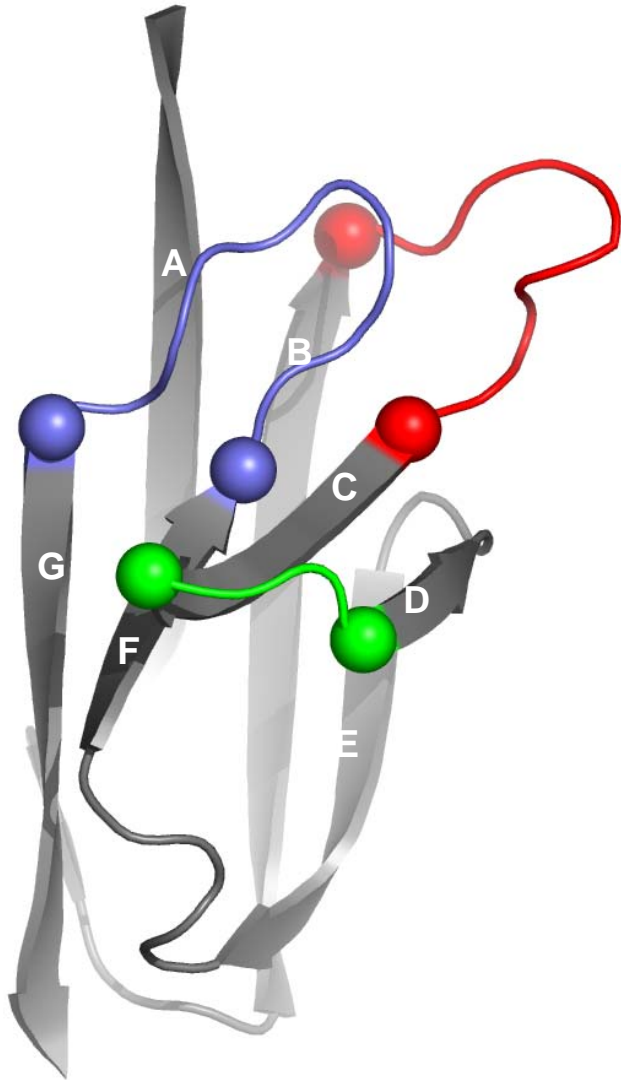
Homo sapiens (Human) IGKC C-DOMAIN
from b12 (1hzh_L)

MHC class I and MHC class II

Im
Muno
Gene
Tics
Information
system®

http://imgt.cines.fr

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

G-ALPHA2 [D2]   G-ALPHA1 [D1]   N
I-ALPHA
C-LIKE [D3]   B2M
C   Target cell
MHC-I

G-BETA [D1]   G-ALPHA [D1]   N   N
II-BETA   II-ALPHA
C-LIKE [D2]   C-LIKE [D2]
c   c   APC
MHC-II
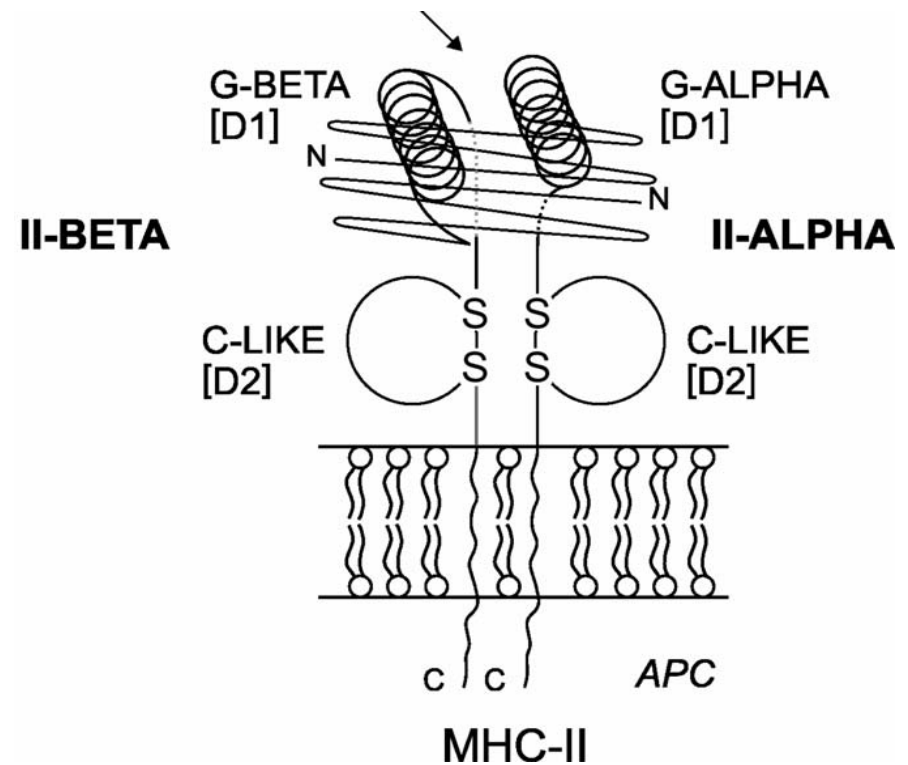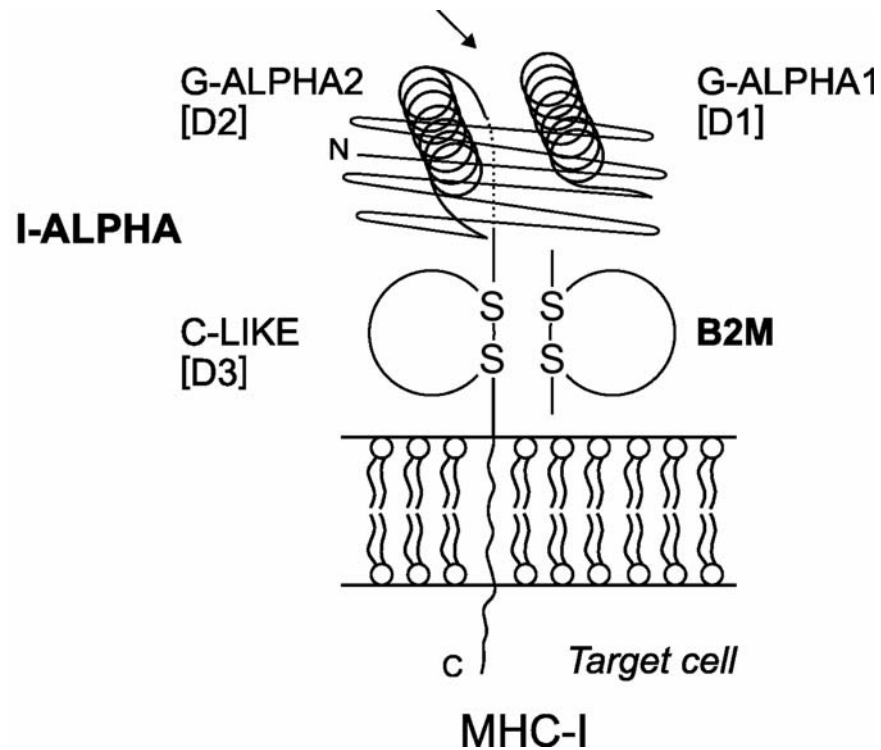
IMGT Colliers de Perles for G-DOMAIN (MHC-I)

The 3D structure
of **G-DOMAINs**
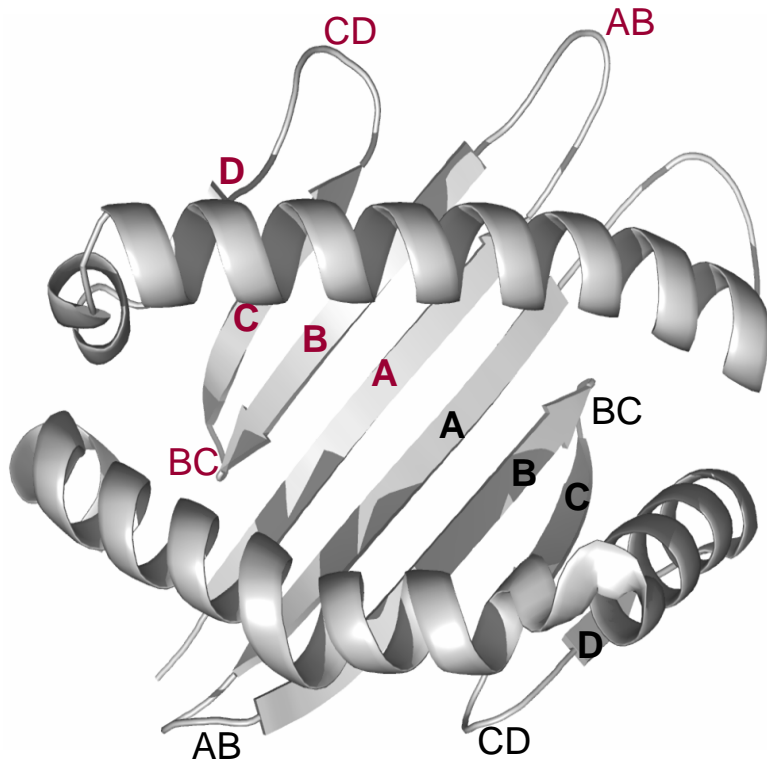
MHC-I
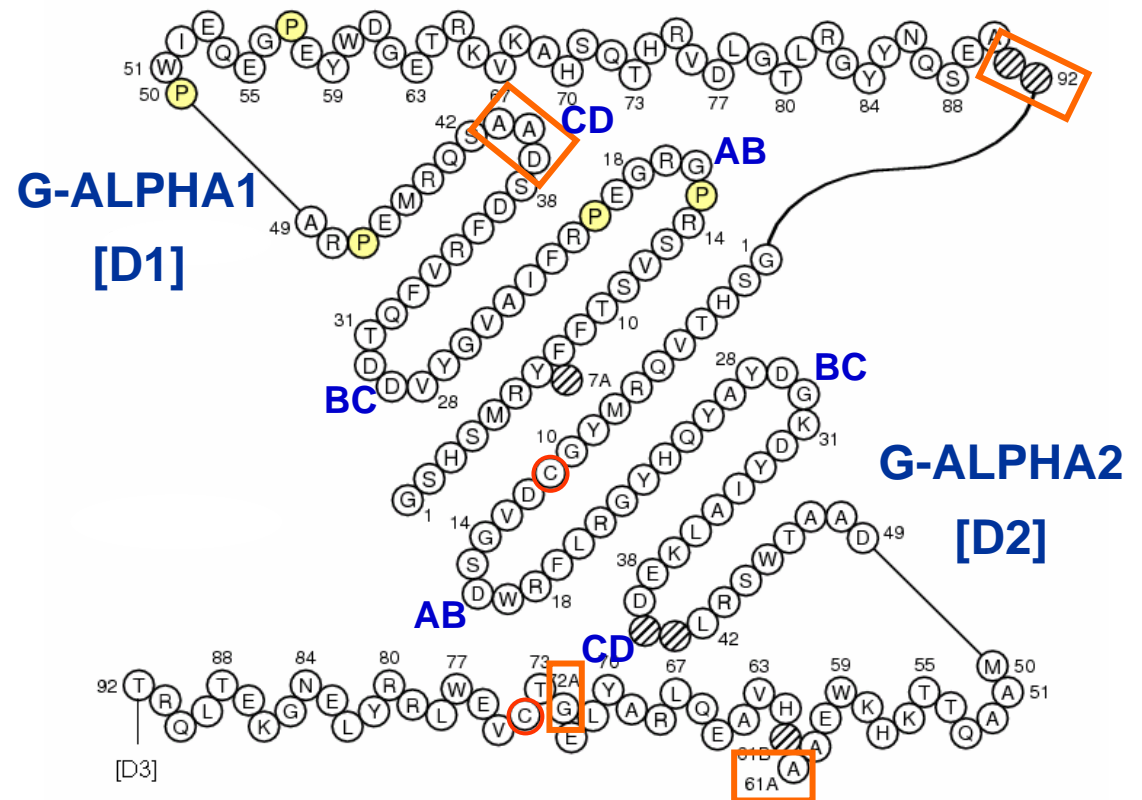
Lefranc et al., Dev. Comp. Immunol. 29, 917-938 (2005)

IMGT Colliers de Perles for G-DOMAIN (MHC-II)

MHC-II

G-ALPHA

[D1]

G-BETA

[D1]
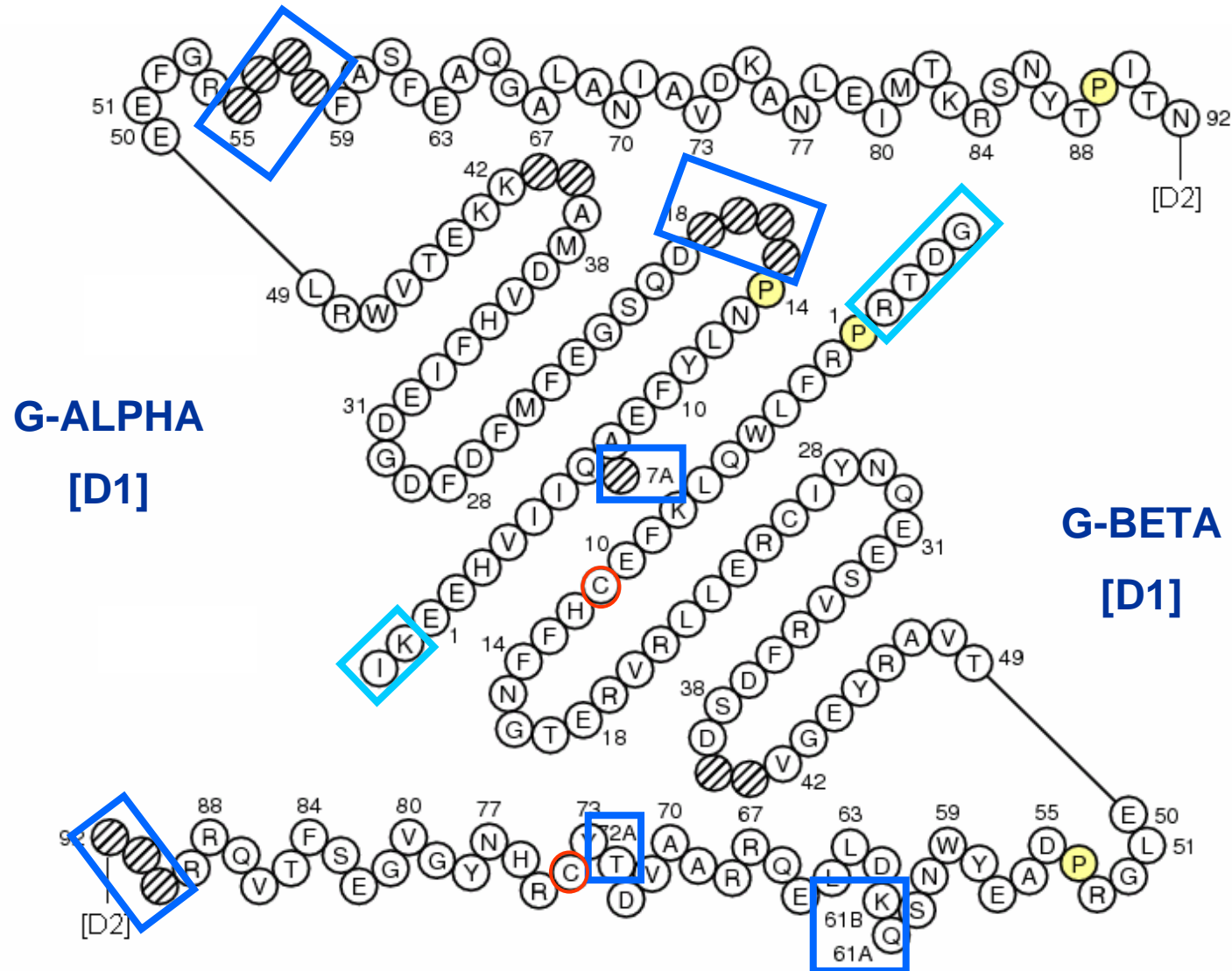
Lefranc et al., Dev. Comp. Immunol. 29, 917-938 (2005)

Comparison of strand, turn and helix lengths Of G-DOMAINs

	G-ALPHA1	G-ALPHA2
A-STRAND	14	14
AB-TURN	3	3
B-STRAND	11	11
BC-TURN	2	2
C-STRAND	8	8
CD-TURN	3	1
D-STRAND	8	8
HELIX	41	45 (61A,72A)
Total	90	92

	G-ALPHA	G-BETA
A-STRAND	14- 15 (7A) +2	14 +4
AB-TURN	0	3
B-STRAND	10	11
BC-TURN	2	2
C-STRAND	8	8
CD-TURN	1	1
D-STRAND	8	8
HELIX	39	43 (61A,61B,72A)
Total	84-85	94

Lefranc et al., Dev. Comp. Immunol. 29, 917-938 (2005)

IMGT Colliers de Perles for IgSF and MhcSF

http://imgt.cines.fr

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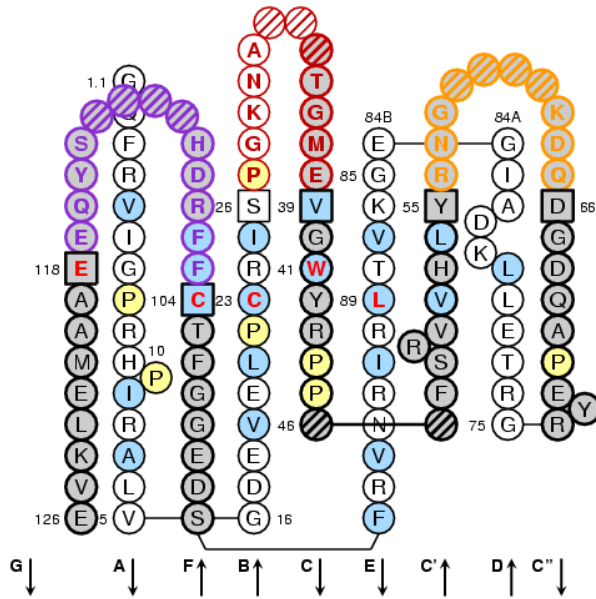
C-DOMAIN (IG,TR)
AND
C-LIKE-DOMAIN
(other than IG,TR)
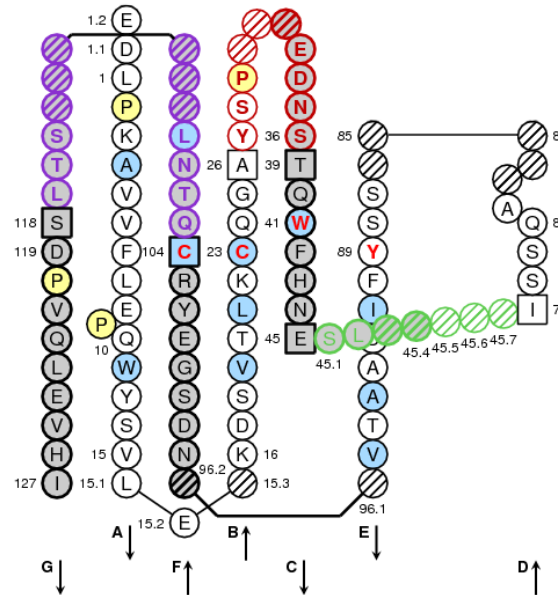
G-DOMAIN (MHC)
AND
G-LIKE-DOMAIN
(other than MHC)

MOG
(1pkq_E)

FCGR3B
(1e4k)
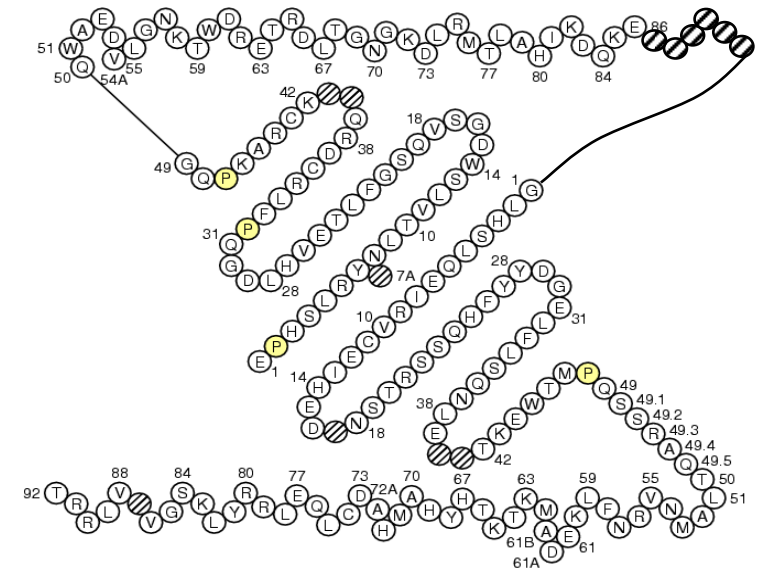
MICA
(1hyr)

Immunoglobulin superfamily (IgSF)

MHC superfamily (MhcSF)

IMGT Protein displays

Protein display: Chimpanzee *(Pan troglodytes)* IGH C-REGIONs

The IGHC protein display numbering is according to the IMGT unique numbering for C-DOMAIN and C-LIKE-DOMAIN.

Only the *01 allele of each functional or ORF C-REGION is shown.

N-glycosylation sites (NXS/T, where X is different from P) are underlined.

☞ The hinge exon(s) are shown at the end of the protein display.

```
              IGHC
              genes

                                    A           AB        B           BC          C         CD        D           DE                  E        EF      F              FG              G
                                 -------------->  --------->           ------>    ------>                                    ----------->  ------->              --------->
                                 1       10    15  16  20  23         30      36 39  41 45       77        84                      85   89    96 97      104       110         118    121      1
                                 7654321|.......|....|123|...|...|....|.....|   |.....|1234567|......|12345677654321|...........|12|....... .     .....|.......  ..|.......

CH1
    X53702   , IGHA1            (A)SPTSPKVFPLSLDSNPQ....DGNVVVACLVQ GFFPQ.EPLS     VTWSESGQGV....TATNFPPSQDASG.....DLYTTSSQLTLPATQC..LAGKSVTC HVKHY...TNPSQ DVTVPCR
    X53706   , IGHA2            (A)SPTSPKVFPLSLDSNPQ....DGNVVVACLVQ GFFPQ.EPLS     VTWSESGQNV....TATNFPPSQDASG.....DLYTTSSQLTLPATQC..LAGKSVTC HVTHY...TNPSQ DVTVPCR
    M15398   , IGHE             (A)PTRSPSLFPLTRCCKNIPSN.ATSVTLGCLAM GYFP..EPVM     VTWDAGSLNG....TTMTLPATTLTPS.....GHYATISLLTVSGAW....AKQMFTC RVAHTPSSTDWVD NKTFS
    X65284   , IGHG1  c         (A)STKGPSVFPLAPSSKSTS...GGTQALGCLVK DYFP..EPVT     VSWNSGALTS....GVHTFPAVLQSS......GLYSLSSVVTVPSSSL...GTQTYIC NVDHKP..SNTKV DKKV
    AF300436 , IGHG2                                                                             AVLQSS......GLYSLSSVVAVPSSNF...GTQTYTC NVDHKP..SNTKV DKTV
    AF300434 , IGHG3                                                                             AVLQSS......GLYSLSSVVTVPSSSL...GTQTYIC NVDHKP..SNTKV DKRV
    AF300432 , IGHG4                                                                             AVLQSS......GLYSLSSVVTVPSSSL...GTQTYTC NVDHKP..SNTKV DKTV
    AF300430 , IGHGP                                                                             AVLQSS......GLYSLSSVVTVPSSSL...GTQTYTC NVDHKP..SNTKV DKRV
CH2
    X53702   , IGHA1  (1)           CCHPRLLLHRPALEDLLL..GSEANLTCTLT GLRDA.SGAT     FTWSPSSGKS....AVQGPPERDLCG......CYSVSSVLPGCAEPW..NHGETFTC TAAYPE..SKTPL TANITKS
    X53706   , IGHA2  (1)           CCHPRLSLHRPALEDLLL..GSEANLTCTLT GLRDA.SGAT     FTWTPPSGKS....AVQGPPERDLCG......CYSVSSVLPGCAQPW..NHGETFTC TAAHPE..LKNPL TANITKS
    M15398   , IGHE           (V)CSRDFTPTVKVLQSSCDGGGHF.PPTIQLLCLVS GYTP..GTIN     ITWLEDGQVMD...VDLSTASATQEG......ELASTQSELTLSQKHW..LSDRTYTC QVTYQ....GGTF EDSTKKCA
    X61311   , IGHG1  c       (A)PELLGGPSVFLFPPKPKDTLMI.SRTPEVTCVVV DVSHEDPEVK     FNWYVDGVEVH...NAKTKPREEQYN......STYRVVSVLTVLHQDW..LNGKEYKC KVSNKA..LPAPI EKTISKAK
```

http://imgt.cines.fr/textes/IMGTrepertoire/Proteins/

IMGT/DomainGapAlign to gap the amino acid sequences of V, C and G domains

IMGT/Collier-de-Perles tool

IMGT/3Dstructure-DB

http://imgt.cines.fr

THANK YOU

for using IMGT/3Dstructure-DB

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IMGT/3Dstructure-DB card for : 1ao7
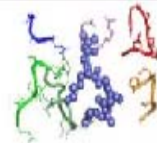
Entry code [   ] Search

Query page

IMGT protein name	IMGT receptor type	IMGT receptor description	Ligand(s)	Species	CC	Chain ID
A6	TR	TR-ALPHA_BETA-1		*Homo sapiens* (Human)	1	[1ao7 D 1ao7 E]
HLA-A*0201	MHC	MHC-I-ALPHA_B2M		*Homo sapiens* (Human)	1	[1ao7 A 1ao7 B]
		Peptide	Tax peptide 11-19 (Q82235)	Human T lymphotropic virus type 1	1	[1ao7 C]

Experimental technique **X-ray diffraction**   Resolution (in angstrom) **2.6**   PDB release date **17-SEP-97**

| Epitope and Chain details | Contact analysis | 3D visualization Jmol or QuickPDB | Renumbered IMGT file | IMGT numbering comparison | References and links | Printable card |

Reference 1ao7: *Garboczi et al., Nature 384, 134-141 (1996)*

IMGT/3Dstructure-DB: Contact Analysis

Contacts of Domain V-ALPHA with Domain G-ALPHA1

Summary:

Residue contacts	Number of residues			Atom contact types		
	Total	From 1	From 2	Total	Polar	Hydrogen
15	16	9	7	126	22	3

Contacts of

Domain	Chain
V-ALPHA 1ao7_D	

with

Domain	Chain
G-ALPHA1 1ao7_A	

List of the Residue@Position pair contacts:

Click 'R@P' for IMGT Residue@Position cards

	Order					Order					Atom contacts		
	IMGT Num	Residue		Domain	Chain		IMGT Num	Residue		Domain	Chain	Total	Polar	Hydrogen
R@P	2	LYS	K	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	7	1	0
R@P	26	SER	S	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	3	2	0
R@P	27	ASP	D	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	24	6	1
R@P	28	ARG	R	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	1	1	0
R@P	37	GLN	Q	V-ALPHA	1ao7_D	R@P	66	LYS	K	G-ALPHA1	1ao7_A	4	1	0
R@P	108	THR	T	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	5	2	1
R@P	108	THR	T	V-ALPHA	1ao7_D	R@P	66	LYS	K	G-ALPHA1	1ao7_A	1	0	0
R@P	109	ASP	D	V-ALPHA	1ao7_D	R@P	62	GLY	G	G-ALPHA1	1ao7_A	1	1	0
R@P	109	ASP	D	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	19	5	1
R@P	109	ASP	D	V-ALPHA	1ao7_D	R@P	66	LYS	K	G-ALPHA1	1ao7_A	14	1	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	12	1	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	68	LYS	K	G-ALPHA1	1ao7_A	8	0	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	69	ALA	A	G-ALPHA1	1ao7_A	16	0	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	72	GLN	Q	G-ALPHA1	1ao7_A	4	0	0
R@P	114	GLY	G	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	7	1	0

IMGT/3Dstructure-DB: Contact Analysis

Contacts of Domain V-ALPHA with Domain G-ALPHA1

Summary:

Contacts of

Residue contacts	Number of residues			Atom contact types		
	Total	From 1	From 2	Total	Polar	Hydrogen
15	16	9	7	126	22	3

Domain	Chain
V-ALPHA 1ao7_D	

with

Domain	Chain
G-ALPHA1 1ao7_A	

List of the Residue@Position pair contacts:

Click 'R@P' for IMGT Residue@Position cards

	Order					Order					Atom contacts		
	IMGT Num	Residue		Domain	Chain		IMGT Num	Residue		Domain	Chain	Total	Polar	Hydrogen
R@P	2	LYS	K	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	7	1	0
R@P	26	SER	S	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	3	2	0
R@P	27	ASP	D	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	24	6	1
R@P	28	ARG	R	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	1	1	0
R@P	37	GLN	Q	V-ALPHA	1ao7_D	R@P	66	LYS	K	G-ALPHA1	1ao7_A	4	1	0
R@P	108	THR	T	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	5	2	1
R@P	108	THR	T	V-ALPHA	1ao7_D	R@P	66	LYS	K	G-ALPHA1	1ao7_A	1	0	0
R@P	109	ASP	D	V-ALPHA	1ao7_D	R@P	62	GLY	G	G-ALPHA1	1ao7_A	1	1	0
R@P	109	ASP	D	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	19	5	1
R@P	109	ASP	D	V-ALPHA	1ao7_D	R@P	66	LYS	K	G-ALPHA1	1ao7_A	14	1	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	12	1	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	68	LYS	K	G-ALPHA1	1ao7_A	8	0	0
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R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	72	GLN	Q	G-ALPHA1	1ao7_A	4	0	0
R@P	114	GLY	G	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	7	1	0

IMGT/3Dstructure-DB: Contact Analysis

Contacts of Domain V-ALPHA with Domain G-ALPHA1

Summary:

Residue contacts	Number of residues			Atom contact types		
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15	16	9	7	126	22	3

Contacts of

Domain	Chain	with	Domain	Chain
V-ALPHA	1ao7_D		G-ALPHA1	1ao7_A

List of the Residue@Position pair contacts:

Click 'R@P' for IMGT Residue@Position cards

	Order					Order					Atom contacts		
	IMGT Num	Residue		Domain	Chain		IMGT Num	Residue		Domain	Chain	Total	Polar	Hydrogen
R@P	2	LYS	K	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	7	1	0
R@P	26	SER	S	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	3	2	0
R@P	27	ASP	D	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	24	6	1
R@P	28	ARG	R	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	1	1	0
R@P	37	GLN	Q	V-ALPHA	1ao7_D	R@P	66	LYS	K	G-ALPHA1	1ao7_A	4	1	0
R@P	108	THR	T	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	5	2	1
R@P	108	THR	T	V-ALPHA	1ao7_D	R@P	66	LYS	K	G-ALPHA1	1ao7_A	1	0	0
R@P	109	ASP	D	V-ALPHA	1ao7_D	R@P	62	GLY	G	G-ALPHA1	1ao7_A	1	1	0
R@P	109	ASP	D	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	19	5	1
R@P	109	ASP	D	V-ALPHA	1ao7_D	R@P	66	LYS	K	G-ALPHA1	1ao7_A	14	1	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	12	1	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	68	LYS	K	G-ALPHA1	1ao7_A	8	0	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	69	ALA	A	G-ALPHA1	1ao7_A	16	0	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	72	GLN	Q	G-ALPHA1	1ao7_A	4	0	0
R@P	114	GLY	G	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	7	1	0

K 2
S 26

D 27
R 28
Q 37

T 108
D 109
W 113
G 114

IMGT/3Dstructure-DB: Contact Analysis

Contacts of V-ALPHA with G-ALPHA1

http://imgt.cines.fr

Summary:

Contacts of

Residue contacts	Number of residues			Atom contact types		
	Total	From 1	From 2	Total	Polar	Hydrogen
15	16	9	7	126	22	3

Domain	Chain
V-ALPHA 1ao7_D	

with

Domain	Chain
G-ALPHA1 1ao7_A	

List of the Residue@Position pair contacts:

Click 'R@P' for IMGT Residue@Position cards

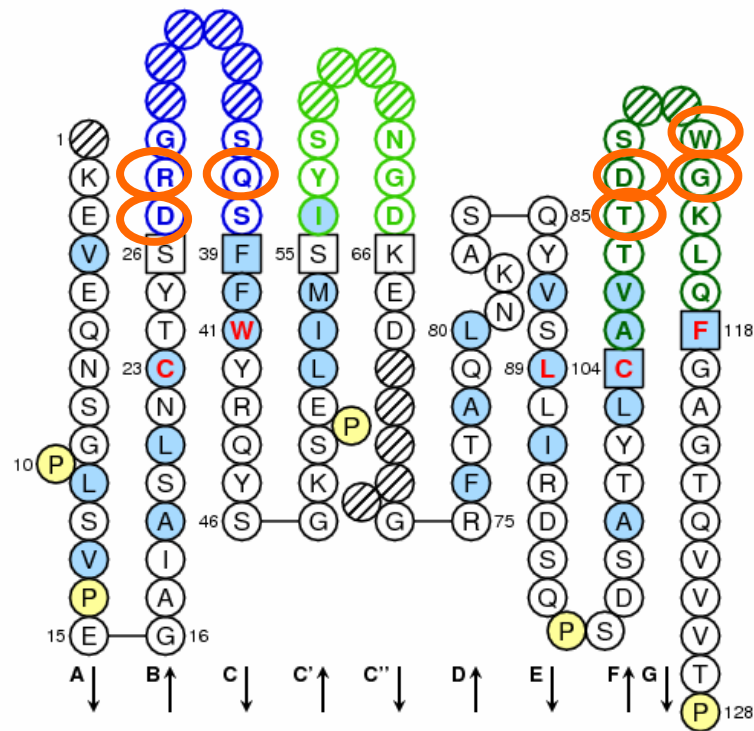|	Order					Order					Atom contacts		
	IMGT Num	Residue		Domain	Chain		IMGT Num	Residue		Domain	Chain	Total	Polar	Hydrogen
R@P	2	LYS	K	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	7	1	0
R@P	26	SER	S	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	3	2	0
R@P	27	ASP	D	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	24	6	1
R@P	28	ARG	R	V-ALPHA	1ao7_D	R@P	58	GLU	E	G-ALPHA1	1ao7_A	1	1	0
R@P	37	GLN	Q	V-ALPHA	1ao7_D	R@P	66	LYS	K	G-ALPHA1	1ao7_A	4	1	0
R@P	108	THR	T	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	5	2	1
R@P	108	THR	T	V-ALPHA	1ao7_D	R@P	66	LYS	K	G-ALPHA1	1ao7_A	1	0	0
R@P	109	ASP	D	V-ALPHA	1ao7_D	R@P	62	GLY	G	G-ALPHA1	1ao7_A	1	1	0
R@P	109	ASP	D	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	19	5	1
R@P	109	ASP	D	V-ALPHA	1ao7_D	R@P	66	LYS	K	G-ALPHA1	1ao7_A	14	1	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	12	1	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	68	LYS	K	G-ALPHA1	1ao7_A	8	0	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	69	ALA	A	G-ALPHA1	1ao7_A	16	0	0
R@P	113	TRP	W	V-ALPHA	1ao7_D	R@P	72	GLN	Q	G-ALPHA1	1ao7_A	4	0	0
R@P	114	GLY	G	V-ALPHA	1ao7_D	R@P	65	ARG	R	G-ALPHA1	1ao7_A	7	1	0

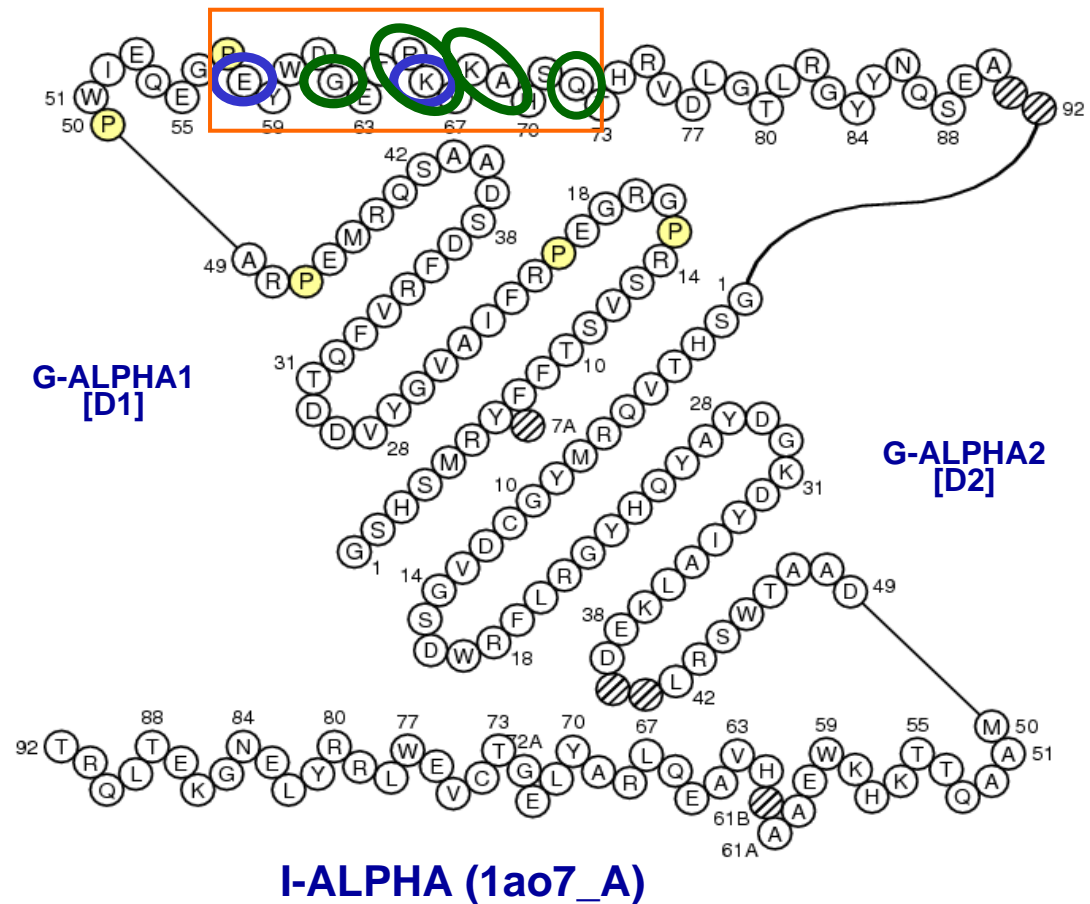E 58
G 62
R 65
K 66
K 68
A 69
Q 72

K 2
S 26

D 27
R 28
Q 37

T 108
D 109
W 113
G 114

Contacts of V-ALPHA with G-ALPHA1

The contacts involve CDR1-IMGT and CDR3-IMGT of V-ALPHA

TR V-ALPHA

(1ao7_D)

G-ALPHA1 [D1]

G-ALPHA2 [D2]

I-ALPHA (1ao7_A)

Kaas and Lefranc, In Silico Biology 5, 505-528 (2005)

Conclusion

1. IMGT Colliers de Perles are the standardized graphical 2D representations of the IMGT unique numbering for the V- and V-LIKE domains, C and C-LIKE domains, G and G-LIKE domains of the IgSF and MhcSF.

2. IMGT Colliers de Perles bridge the gaps between sequences and 3D structures. They are highly valuable in the absence of 3D structures for the delimitation of strands, turns, loops and helix, and for the display of conserved amino acids.

3. IMGT Colliers de Perles allow to compare the domains of a same type whatever the species, the chain type and the receptor type.

4. When the 3D structure is known, the IMGT Colliers de Perles describe the contacts between amino acids.

5. IMGT Colliers de Perles are particularly useful for antibody engineering : they allow to map a sequence on the domain conserved topology, in order to perform comparison with germline sequences and to determine the amino acid positions which are potentially immunogenic.

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