

ERRATUM

The Editors apologize to the readers of the paper J. Kubrycht *et al.* "Sequence Similarities of Protein Kinase Peptide Substrates and Inhibitors: Comparison of Their Primary Structures with Immunoglobulin Repeats" printed in *Folia Microbiol.* 47 (issue 4) where, on p. 336, an error crept into the table; it should read as shown below.

Table VI. Comparison of the PKSI motif with immunoglobulin sequences of different domains^a

Peptides or motifs	Sequences
PKSI motif (simplified version)^b	
Main chain	S-R---T-LR-RLAI-----G---E---Y-AR 4 6 5 8x z4533 3 3 2 22
Questionable aa	IIS/-----SS-----A-----SED-----D 222 22 3 332 2
Maximal extent of mutations	II-----D [†] ---G [†] 23 5 5
Immunoglobulin sequences^{c,d}	
1 hu κII	21-I-SCRSS-QS-L---L---H-SX-D---GN--D---YL-N*
2 hu λII	21-I-SC---T---G---T---SS-D-V-GG-----YN-V*
3 mu κ	21-I-SCRAS-QS-L---L-----SSKD---GV-S---YL-N*
4 mu λ	**20-TLTCRSS-T---GA--VT-T-SNY--ANWVQ-E--K-P-D*
5 hu subgroup III	19-RLSC-A-A-SGFT-F--STYAMSWVRQAPGKGLE-W--V-V*
6 mu subgroup III	19-RLSC-A--TS---GF---T--F-S-D--FY-M-E-W--V-R
7 CH1 domains	132-PTS--GS-TVAL-G-CLVKGYP-E---P-VTVVTWNY-QN*
8 hinge regions	241D-PKSC-D--TPPPCPRCPEPK---SCDT-P-P-P---C-PR*
9 CH2 domains	266-I-S-R---TPEVT--CVVVDV--SEDD-P---E---VQF*
10 CH3 domains	383-KKS--VS---LT--CLVXG-FYPSD--IAVTIE-W--E-S*
11 CH4 domains	517-RES--A--T--LT--CLVTG-FSPAD--ISV--Q-WL-MQR
12 CH4 extra long	**638-CYS--AXVT--L--F-KVKWIFSS---V--V--E--L-KQT*
nonrandomly repeated aa	
Accumulation constant/variable	v vv v ccv C cv cv v C
Accumulation light/heavy	l L l nhn n n n n
Ig motif	IISCRAS-TS-LTGFLVTG-FSS-D--PGV--E-W-YVQR 4 b7455 84 644 5565 576 8 446 6 5 5 4
The most important structures derived from PKSI peptides and immunoglobulin segments^d	
working motifs	
<i>primary derived (PM, initiating structure)</i>	
accumulation	vL C C v V
homologous aa	--S-R---T-L-R _C -V _A T _I -----D _G [†] -G _D [†] -----
single mutations	-----R _C -V _A T _I -----D _G [†] -G _D [†] -----
questionable	I-----L-----S-----E--YV-R
<i>revised (RM, linked to length and reference set restrictions)</i>	
RM quasimotif	I-S-R---T-L--R _C LV _A T _I -S---D _G [†] -----
RM derived template	PI-SGR---T-L--R _C LV _A T _I HS---D _G [†] -----
helper motifs	
HMC	--S-R---T-L--R _C LV _A /T/S---D-----
HMV	IIS-R---T---G---V _A T-----D-----
final motifs	
FMC regular motif	--S-----T-L--R _C LV _A ---S---D-----
FMV conditioned motif	IIS-R---T-----T _I -----D-----
FMV derived template	IIS-R---T---G---V _A T _I H-----D-----