

Supplementary Table 2. Unique peptides detected in each chain by proteomic analyses.

Chain	Sequence	Origin (band No.)	N hit	LC hit	ratio
$\alpha 1, \alpha 2$ chain	(K)AVGDKLPECEADDGCPK(P)	1	0	2	-
	(K)LRTEGDGVYTLNNEK(Q)	1,2,3	1	6	6.0
	(K)LPECEAVCGKPK(N)	2,3	4	4	1.0
	(K)LPECEADDGCPKPPEIAHGYVEHSVR(Y)	2,3	1	2	2.0
	(K)AVGDKLPECEAVCGKPK(N)	2,3	7	22	3.14
	(K)AVGDKLPECEAVCGK(P)	2,3	1	6	6.0
	(R)TEGDGVYTLNNEK(Q)	2,3	4	6	1.5
	(K)LRTEGDGVYTLNNEKQWINK(A)	3	0	1	-
$\alpha 2$ chain	(K)LRTEGDGVYTLNDKK(Q)	12,3	13	37	2.85
	(K)LRTEGDGVYTLNDK(K)	2,3	6	12	2
	(K)AVGDKLPECEADDGCPKPPEIAHGYVEHSVR(Y)	2	0	6	-
	(R)TEGDGVYTLNDK(K)	2,3	2	4	2.0
	(R)TEGDGVYTLNDKK(Q)	2,3	6	12	2.0
	(K)AVGDKLPECEADDGCPK(P)	3	0	1	-
β chain	(K)YVMLPVADQDQCIR(H)	1,2,3	7	20	2.86
	(K)SCAVAEYGVYVK(V)	1,3	9	22	2.44
	(R)VMPICLPSK(D)	1	0	2	-
	(K)VTSIQDWVQK(T)	1,2,3	4	22	5.5
	(K)DIAPTLTLYVGK(K)	1	2	5	2.5
	(K)SPVGVQPILNEHTFCAGMSK(Y)	1,2,3	3	24	8.0
	(R)VGYVSGWGR(N)	1,2	4	11	2.75
	(R)ILGGHLDAK(G)	1	0	4	-
	(R)HYEGSTVPEK(K)	1,3	2	2	1
	(K)VVLHPNYSQVDIGLIK(L)	1	0	3	-
	(R)VMPICLPSKDYAEVGR(V)	1	3	14	4.67
	(R)HYEGSTVPEKK(T)	1	0	2	-