Figure S2

a

H-bond Distance, A		subunit 1 residue	atom		subunit2 atom	residue
2.8	3.2	Glu124	OE1	– – –	NZ	Lys110
3.3	3.2	Asp116	O	– – –	N	Lys115
3.2	3.0	Ala118	N	– – –	OD1	Asn114
2.9	2.5					
2.9	3.5	Tyr 98	OH	– – –	ND2	Asn114
2.6	3.5	Asp95	D2	– – –	ND2	Asn104
3.0	2.8	Asp93	OD1	– – –	NE	Arg107
3.1	3.1				NH1	Arg107
2.8	2.8					
3.5	3.3				OG1	Thr57
2.8	2.8		OD2	– – –	OG1	Thr58
2.7	2.6				OG1	Thr61
3.2	3.1	Gly51	O	– – –	N	Leu56
3.4	3.1	Asp83	OD1	– – –	NE1	Trp45

b

H-bond Distance, A		subunit 1 residue	atom		subunit2 atom	residue
2.9		Gln183	OE1	– – –	N	Leu184
2.9			NE2	– – –	O	Leu184
3.2		Tyr158	OH	– – –	N	Phe181

c

subunit 1					subunit 2			
Kv1.1	Kv3.1	Kv4.2	KCTD5	Interface		KCTD5	Kv4.2	Kv3.1	Kv1.1
Glu 144	Glu 87	Glu 117	Glu 124	α4-helix	α3-α4	Lys 110	Lys 103	Lys 73	Arg 130
Asn 136	Asp 79	His 109	Asp 116	α3-α4	α3-α4	Lys 115	Arg 108	Thr 78	Val 135
Asp 140				α3-α4 loop	α3-α4 loop	Val 112	His 105	His 75	Arg 132
Pro 138	Cys 81	Cys 111	Ala 118						
Ser 117	Val 61		Tyr 98	α3-helix		Asn 114	Pro 107	Pro 77	Pro 134
Arg 115	Pro 59	Pro 89		β3–α3 turn	α3-helix	Asn 104	Asn 97	Asn 67	Tyr 123
Asn 114	His 58	Asp 88	Asp 95			Gly 100	Arg 93	Gln 64	Asp 119
Asp 112	Asp 56	Asp 86	Asp 93	β3–α3 turn	α3-helix	Arg 107	Arg 100	Arg 70	Gln 126
					β2-α1 loop α1–helix	Thr 57,58 61	Thr 54 58	Thr 23 27	Thr 83 87
Ser 73	Gly 17	Ser 48	Gly 51	β1–β2 turn	β2-strand	Leu 56	Gln 53	Glu 22	Glu 78
Asn 71	Asn 15	Asn 46	Asn 49						
			Asp 83	α1–α2 loop	β1-strand	Trp 45			

L3 L2 L1

BTB segment