

## Supplementary material:

**Table S1: TMEM263 percent identity matrix as created by Clustal Omega 2.1**

<i>Danio rerio</i>	100.00	68.42	73.28	73.04	73.04	74.14	74.14	73.28
<i>Xenopus laevis</i>	68.42	100.00	79.82	77.88	77.88	77.19	77.19	77.19
<i>Gallus gallus</i>	73.28	79.82	100.00	88.70	88.70	89.66	89.66	89.66
<i>Rattus norvegicus</i>	73.04	77.88	88.70	100.00	100.00	96.52	96.52	97.39
<i>Mus musculus</i>	73.04	77.88	88.70	100.00	100.00	96.52	96.52	97.39
<i>Homo sapiens</i>	74.14	77.19	89.66	96.52	96.52	100.00	100.00	99.14
<i>Pan paniscus</i>	74.14	77.19	89.66	96.52	96.52	100.00	100.00	99.14
<i>Bos taurus</i>	73.28	77.19	89.66	97.39	97.39	99.14	99.14	100.00

Human TMEM 263 shares over 96% amino acid sequence identity to mouse and rat TMEM 263, and approximately 74 % to zebrafish, 77 % to chicken and almost 90 % to *Xenopus* spp.

## Proteins (co-)purified with the anti-Slick antibody identified by mass spectrometric analysis

Unique peptide sequences specifically detected by mass spectrometric sequencing respective to the corresponding protein are highlighted in yellow.

### Slick channel, Potassium channel subfamily T member 2 (1135 aa) Accession: NP\_001074496.2

GI:161168989

MVDLESEVPPLPPRYRFRDLLLGDQGWQNDQVQVEFYMNENTFKERLKLFFIKNQRSSLRIRLRFNFSLK  
LLSCLLYIIRVLLLEKPSQGSSEWSHIFWVNRSLPLWGLQVSVALISLFFETILLGYLSYKGNIEWEQILRIPF  
ILEIINAVPFIISIFWPTLRNLFVFPVFLNCLWAKHALENMINDLHRAIQRTOQSAMFNQVLILISTLLCLI  
FTCICGIQHLEIRIGKKNLFDSDLYFCIVTFSTVGFQDVTPEWSSKLFVVMAMICVALVVLPIQFEQLAYL  
WMERQKSGGNYSRHRAQTEKHVVLCVSSSLKIDLLMDFLNEFYAHPRLQDYVVVILCPTEMDVQVRRVLQI  
PMWSQRVIYLLQGSALKDQDQLLRAKMDNAEACFILSSRCEVDRTESSDHQITLRAWAVKDFAPNCPYVQIL  
KPENKFHIKFADHVVCEEEFKYAMLALNCICPATSTLITLLVHTSRGQEGQOSPEQWQKTYGRCSGNEVY  
HIVLEESTFFAEYEGKSFTYASFHAHKKFGVCLVGVRRDNKNILLNPGPRYIMNASDICFYINITKEEN  
SAFKNQDQQRKSNVRSRFSYHGSPRLPVHSIIASMGTVAIDLQDTSCRATSGPTLALPSEGGKELRRPSIA  
PVLEVADTSSIQTCDLLSDQSEDETTPEETSSNLEYAKGYPPYSPYIGSSPTFCHLLQEKVPFCCLRLD  
KSCQHNYVEDAKAYGFKNKLIIVAAETAGNGLYNFIVPLRAYYRPKKELNPIVLLLDNPPDMHFLDAICW  
FPMVYYMVGSIDNLDLRLCGVTFANMVDVDEKSTMSAEEDYMADAKTIVNVQTLFRLFPSSLSITELT  
HPANMRFMQFRAKDCYSLALSLEKKERERGSNLAFMFRLPFAAGRVSISMLDTLLYQSFVKDYMISIT  
RLLGLDTPGSGFLCSMKITEDDLWIRTYARLYQKLCSSSTGDVPIGIYRTESSQKLTTSSEQSISISVEEW  
EDTKDVKDPGHRSLHRNSTSSDQSDHPLLRKSMQWARRLSRKGPKHSGKTAEKITQQRNLNLYRRSERQ  
ELAELVKNRMKHLGLSTVGYDEMNDHQSTLSYILINPSPDTRLELNDVVYLIRPDPLSYLPNSEPSRKNS  
ICNAAVQDSREETQL

584 out of 1135 amino acids detected; 51.5 % protein coverage

### Slack channel, Potassium channel subfamily T member 1, isoform 1, Slack B (longer version, 1238 aa) Accession: NP\_001138875.1 GI: 224028216

MARAKLPRSPSEGKAGPGDTPAGAAAPEEPHGLSPLLPARGGGVSGSDVGQRLHVEDFSLDSSLSQVQVE  
FYVNENTFKERLKLFFIKNQRSSLRIRLRFNFSLKLLTCLLYIVRVLLDNPQDIGCWGCTKYNYTFNGSS  
SEFHWPILWVERKMALWVIQVIVATISFLETMLIIYLSYKGNIEWEQIFHVSFVLEMINTLPFIIITVFWP  
PLRNLFIPVFLNCLWAKHALENMINDFHRAAILRTOQSAMFNQVLILFCTLLCLVFTGTGCGIQHLEIRAGNL  
NLLTSFYFCIVTFSTVGFQDVTPKIWPSQLLVVILICVTLVVLPIQFEELVYLWMERQKSGGNYSRHRAR  
TEKHVVLCVSSSLKIDLLMDFLNEFYAHPRLQDYVVVILCPTSEMVDVQVRRVLQIPLWSQRVIYLLQGSALKD  
QDLMRAKMDNGEACFILSSRNEVDRTAADHQITLRAWAVKDFAPNCPYVQILKPENKFHVKFADHVVCE  
EECKYAMLALNCICPATSTLITLLVHTSRGQEGQESPEQWQRTYGRCSGNEVYHIRMGDSKFFREYEGKS  
FTYAFAFHAKKYGVCLIGLKREENKSILLNPGPRHILAASDTCFYINITKEENSAFIFKQEEKQKRGLA  
GQALYEGPSRLPVHSIIASMGTVAMDLQNTDCRPSQGGSGGDGKLTLPTEGSGSRRPSIAPVLELADS  
SALLPCDLLSDQSEDEVTSPDDEGLSVVEYVKGYPNSPYIGSSPTLCHLLPVKAPFCCLRLDKGCKHNS  
YEDAKAYGFKNKLIIVSAETAGNGLYNFIVPLRAYYRSRRELNPIVLLLDNPKPDHFFLEAICCFPMVYYM  
EGSVDNLDSSLQCGIYADNLVVVDKSTMSAEEDYMADAKTIVNVQTMFRLFPSSLSITTELTHPSNMRF  
MQFRAKDSYSLALSLEKQERENGSNLAFMFRLPFAAGRVSISMLDTLLYQSFVKDYMITITRLLGLD  
TTPGSGYLCAKMTEDDLWIRTYGRFLFQKLCSSSAEIPIGIYRTECHVFSEPHDVRAQSQISVNMEDCED  
TREAKGPWGTRAASGSGSTHGRHGGADPVEHPLLRKSLQWARKLSRKSTKQAGKAPVATDWTITQQRLS  
LYRRSERQELSELVKNRMKHLGLPTTGYEDVANLTASDVMNRVNLGYLQDEMNDHHTLSYVILNPPPD  
TRLEPNDIVYLIRSDPLAHVASSSQSRKSSCSNKLSSCNPETREDETQL

559 out of 1238 amino acids detected ; 45.2 % protein coverage

**Beta-synuclein (133 AA) Accession: Q91ZZ3.1 GI:81879780**

MDVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYVGSKTSQVQGVASVAEKTKEQASHLGGAVF  
SGAGNIAAATGLVKKEEFPTDLKPEEVAQEAAEPLIEPLMEPEGESYEDSPQEEYQEYEPEA

70 out of 133 amino acids detected ; 52.6 % protein coverage

**Transmembrane protein 263, TMEM 263 (115 aa), Accession: Q9DAM7.1 GI:81881684**

MNQADKNQEIPSYLSDEPPEGSMKDHPPQQPGMLSRVTGGIFSVTKGAVGATIGGVAVIGGKSLEVTKTA  
VTTVPMSGIGLVKGGVSAVAGGVTAVGSAAVVKVPLSGKKKDKSD

30 out of 133 amino acids detected; 26 % protein coverage

**Inactive dipeptidyl-peptidase 10, DPP 10 (800 aa) Accession: NP\_950186.3GI:238776842**

MTAMKQEQQPTPGARATQSQPADQELGSNSPPQRNWKGIAIALLVILVVCSLITMSVILLTPDELSTNSSE  
TRLSLEELLGKGFGLHNPEPRWINDTVVVKYKTNNGHVMKLNTESNASTLLLDNSTFVTFKASRHSLSPLD  
KYVLLAYDVKQIFHYSFTASYLIYNIHTGEVWELNPPEVEDSVLQYAAWGVQGGQLIYIFENNIYYQPDI  
KSSSLRLTSSGKEGIIFNGIADWLYEEELLHSHIAHWWSPDGERLAFLMINDSLVPMIIPRFTGALYPK  
AKQYPYKAGQANPSVKLYVVNLYGPTHLELMPPDIFKSREYYITMVKWSNTRTVVRWLNRPQNISIL  
TLCESTTGACSRKYEMTSDTWLTKQNEEPVFSRDGSKFFMTVPVKQGGGEFHHIAMFLVQSKSEQITVR  
HLTSGNWEVIRILAYDETTQKIYFLSTESSPQGRQLYSASTEGLLNRCDCISCNFMKEDCTYFDASFPMN  
QHFLLFCEGPKVPVVSLSLHITDNPSRYFLLNNSVMKETIQKKKLAKRETRILHIDYELPLQLSFPKDFM  
EKNQYALLLIMDEEPPGQMVTDKFHVDWDSVLIDTNDVIVARFDGRGSGFQGLKVLQEIHRRIQSVEAKD  
QVAVKYLLKQPYIDSKRLSIFGKGYGGYIASMILKSDEKFFKCGAVVAPISDMKLYASAFSERYLGMP  
KEESTYQASSVLHNIHGLKEENLLIHTGADTKVHFQHSALIKHLIKAGVNYTLQVYPDEGYHISDKSK  
HHFYSTILRFFSDCLKEEVSVPQEPPEDE

76 out of 800 amino acids detected; 9.5 % protein coverage

**Synapse associated protein 102,SAP 102, disks large homolog 3 isoform 1 (849) Accession:**

**NP\_058027.1GI:7949129**

MHKHQHCKCPECEYEVTRLAALRRLEPPGYGDWQVPDPYGPSSGNGASSGYGGYSSQTLPSQAGATPTPR  
TKAKLIPTGRDVGVPVPPKVPVPGKSTPKLNGSGPGWWPECTCTNRDWYEQASPAPLLVNPEALEPSLSVNG  
SDGMFKYEEIVLERGNSGLGFSIAGGIDNHPVDDPGIFITKIIPGGAAAMDGRLGVNDCVLRVNEVDVS  
EUVHSRAVEALKEAGPVVRLVVRRRQPPPETIMEVNLLKGPGLGFSIAGGIGNQHIPGDNSIYITKIIIE  
GGAAQKDGRLQIGDRLAVNNTNLQDVRHEEAVASLKNSTDMVYLKVAKPGSIHLNDMYAPPDYASTFTA  
LADNHIHNSLGLGAVESKVTPAPPQVPTRYSPIPRHMLAEEDFTREPRKIIHLKGSTGLGFNIVG  
GEDGEGIFVSFILAGGPADLSGELRRGDRILSVNGVNLRNATHEQAAAALKRAGQSVTIVAQYRPEEYSR  
FESKIHDLREQMMNSSMSSGSLRTSEKRSLYVRALFDYDRTRDSCPLSQGLSFSYGDILHVINASDDE  
WWQARLVTPHGESEQIGVIPSKRVEKKEARLKTVKFHARTGMIESNRDFPGLSDDYYGAKNLKGVTSN  
TSDSESSSKGQEDAILSYPEVTRQEIHYARPVIILGPMKDRVNDLISEFPHKFGSCVPHTRPRRDNEV  
DGQDYHFVVSREQMEKDIQDNKFIQAGQFNDNLYGTSIQSVRAVAERGHCILDVSGNAIKRLQQAQLYP  
IAIFIKPKSIEALMEMNRRQTYEQANKIFDKAMKLEQEFGEYFTAIVQGDSLEEIYNKIKQIIEQSGHY  
IWPVSPEKL

153 out of 849 detected; 18 % protein coverage

## Proteins (co-)purified with the anti-Slack antibody identified by mass spectrometric analysis

Unique peptide sequences specifically detected by mass spectrometric sequencing respective to the corresponding protein are highlighted in yellow.

### Slack channel, Potassium channel subfamily T member 1, isoform 1, Slack B (1238 aa) Accession: NP\_001138875.1 GI: 224028216

MARAKLPRSPSEGKAGPGDTPAGAAAPEEPHGLSPLL PARGGGSVGSVDVGQR LHVEDFSLDSSLSQVQVE  
FYVNENTFKERLKLFFIKNQRSSLRIRLNFNFSLKLLTCLLYIVRVLLDNDPDQIGCGWGCTKYNFTNGSS  
SEFWAPILWVERKMLWVIQVIVATISFLETMLIIYLSYKGNIEWEQIFHVSFVLEMINTLPFIITVFWP  
PLRNLFI PVFLNCWLAKHALENMINDFHRAILRQTQSAMFNQVLILFCTLLCLVFTGTTCGIQHLEERAGGNL  
NLLTSFYFCIVTFSTVGFVDVTPKIWPSQLLVVILICVTLVVLPLQFEELVYLWMERQKSGGNYSRHRAR  
TEKHVVLCVSSSLKIDLLMDFLNEFYAHPR LQDYVYVILCPSEMDVQVRRVLQIPLWSQRVIYLGQSALKD  
QDLMRKMDNGEACFILSSRNEVDRTAADHQTILRAWAVKDFAPNCPPLYVQILKPENKFHVKFADHVCE  
EECKYAMLALNCICPATSTLITLLVHTSRGQEGQESPEQWQRTYGRCSGNEVYHIRMGDSKFFREYEGKS  
FTYAAFHAHKKYGVCLIGLKREENKSILLNPGPRHILAASDTCFYINITKEENSAFIFKQEEKQKRRGLA  
GQALYEGPSRLPVHSIIASMGTVAMDLONTDCRPSQGGSGDGTCLTLPTENGSGSRRPSIAPVLELADS  
SALLPCDLLSDQSEDEVTSPDDEGLSVVEYVKGYPPNSPYIGSSPTLCHLLPVKAPFCCLRLDKGCKHNS  
YEDAKAYGFKNKLIIVSAETAGNGLYNFIVPLRAYYRSRRELNPVLLLDNKPDDHFLAICCFPMVYYM  
EGSVDNLDLQCGI IYADNLVVVDKESTMSAEEDYMADAKTIVNVQTMFRLFPSSLISITTELTHPSNMRF  
MQFRAKDSYSLALS KLEKQERENGSNLA FMFRLPFAAGR VFSISMLD TLLYQS FVKDYMITITRLLGLD  
TTPGSGYL CAMKVTEDDLWIRTYGR LFQKLCSSSAE IPIGIYRTECHVFSEPHDVR AQSQISVNMEDCED  
TREAKGPWGTRAASGSGSTHGRHGG SADPVEHPLLRKSLQWARKLSRKSTKQAGKAPVATDWITQORLS  
LYRRSERQELSELVKNRMKHLGLPTTGYEDVANLTASDVMNRVNLGYLQDEMNDHHQNTLSYVLINPPPD  
TRLEPNDIVYLIRSDPLAHVASSQSRKSSCSNKLS SSCPETRDETQL

240 out of 1238 amino acids detected; 19.4 % protein coverage

### Slick channel, Potassium channel subfamily T member 2 (1135 aa) Accession: NP\_001074496.2 GI:161168989

MVDLESEVPPLPPRYRFRDLLLLGDQGWQNDDRVQVEFYMNENTFKERLKLFFIKNQRSSLRIRLNFNFSLK  
LLSCLLYIIRVLLLEKPSQGSEWSHIFWVNRSLPLWGLQVVALISLFETILLGYLSYKGNIEWEQILRIPF  
ILEIINAVPFIISIFWPTLRNLVFPVFLNCWLAKHALENMINDLHRAIQRQTQSAMFNQVLILISTLLCLI  
FTCICGIQHLEIRIGKKNLFDLSLYFCIVTFSTVGFVDVTPETWSSKLFVAMICVALVVLPIQFEQLAYL  
WMERQKSGGNYSRHRARTEKHVVLCVSSSLKIDLLMDFLNEFYAHPR LQDYVYVILCPTEMDVQVRRVLQI  
PMWSQRVIYLGQSALKDQDLLRAKMDNAEACFILSSRCEVDRTSSDHQTILRAWAVKDFAPNCPPLYVQIL  
KPENKFHIKFADHVCEEEFKYAMLALNCICPATSTLITLLVHTSRGQEGQESPEQWQRTYGRCSGNEVY  
HIVLEESTFFAEYEGKSFTYASFHAHKKFGVCLVGVRRDNKNILLNPGPRYIMNASDICFYINITKEEN  
SAFKNQDQQRKSNVRSRFFYHGPSRLPVHSIIASMGTVAIDLQDTSCRATSGPTLALPSEGGKELRRPSIA  
PVLEVADTSSIQTCDLLSDQSEDETTDDEETSSNLEYAKGYPPSPYIGSSPTFCHLLQEKVPFCCLRLD  
KSCQHNYEDAKAYGFKNKLIIVAAETAGNGLYNFIVPLRAYYRPKKELNPVLLLDNPPDMHF LDAICW  
FPMVYYMVGSIDNLDLRCGVTFAANMVVDKESTMSAEEDYMADAKTIVNVQTLFRLFSLSISITELT  
HPANMRFMQFRAKDCYSLALS KLEKKERERGSNLA FMFRLPFAAGR VFSISMLD TLLYQS FVKDYMISIT  
RLLLGLDTPGSGFLCSMKITEDDLWIRTYARLYQKLCSSSTGDVPIGIYR TESQKLTTSSESQISISVEEW  
EDTKDVKDPGHRSLHRNSTSSDQSDHPLLRKSMQWARRLSRKGPKHSGKTAEKITQORLNLYRRSERQ  
ELAELVKNRMKHLGLSTVGYDEMNDHQSTLSYILINSPDTRLELNDVVYLIRPDPLSYLPNSEPSRKNS  
ICNAAVQDSREETQL

99 out of 1135 amino acids detected; 8.7 % protein coverage

**Beta-synuclein (133 aa) Accession: Q91ZZ3.1 GI:81879780**

MDVFMKGLSMAKEGVVAAAETKQGVTEAAEKTKEGVLYVGSKTSQVVGVASVAEKTKEQASHLGGAVF  
SGAGNIAAATGLVKKEEFPTDLKPEEVAQEAAEEPLIEPLMEPEGESYEDSPQEEYQEYEP

70 out of 133 amino acids detected; **52.6 % protein coverage**

**Transmembrane protein 263, TMEM 263 (115 aa), Accession: Q9DAM7.1 GI:81881684**

MNQADKNQEIPSYLSDEPPEGSMKDHPQQQPGMLSRVTGGIFSVTKGAVGATIGGVAWIGGKSLEVTKTA  
VTTVPSMGIGLVKGGVSAVAGGVTAVGSVVNKVPLSGKKKDKSD

46 out of 115 amino acids detected; **40% protein coverage**