

**Table S1 Tryptic peptides of *ApCatSper* 1-4,  $\beta$ ,  $\delta$  and  $\gamma$  identified by mass spectrometry.**

Protein	Peptide sequence	XCorr	Probability	Sequence coverage [%]
<i>ApCatSper1</i>	HLQGTGPVGAQDAALKK	5.31	51.8	10.1
	RQLTVGPQDIILPSHLK	4.0	35.8	
	QLTVGPQDIILPSHLK	3.1	43.9	
	LLAAIEQNAHIMR	3.89	104.9	
<i>ApCatSper2</i>	LLAAIEQNAHIM(ox)R	3.35	60.3	24.8
	KSDDWKEVVHDNLQMLVNNSPSETVWPR	5.46	116.0	
	SDDWEKVVHDNLQMLVNNSPSETVWPR	4.35	85.4	
	VVHDNLQMLVNNSPSETVWPR	5.22	106.9	
	YFQLMEALQENLQER	5.12	127.1	
	IIEDFHLLSFDDHGHSADPK	5.09	99.1	
	NGLEDPKMTSGIFDELAELIFR	4.43	58.4	
	MTSGIFDELAELIFR	4.11	115.1	
	VDLT YQDSFR	3.27	40.2	
	HGSSLTGLDGVK	3.18	89.5	
<i>ApCatSper3</i>	QDLQNLYHALLNIFDS	3.13	53.9	5.3
	KTVGSSDALFR	3.07	28.4	
<i>ApCatSper4</i>	WIRPDFFEFHR	3.64	33.0	16.4
	MSSESLPSLTR	2.99	28.3	
	KGDILSNLLELEQR	4.92	129.7	
	TDMTTQKPLHFQDFK	3.98	106.3	
	FQNYVVLLSALEDNLAEYQTIK	3.28	8.7	
	RNSSLSPSAQALIK	3.05	52.1	
	NSSLSPSAQALIK	2.77	31.6	
	LFTFDPSAVQR	2.91	30.1	
	QVENAGAAFRK	2.57	45.2	
	EVPITSVDDVMAK	2.54	51.2	
Predicted protein	Peptide sequence	XCorr	PEP ( $\times 10^{-5}$ )	Sequence coverage [%]
<i>ApCatSper <math>\beta</math></i>	TFTFGADSWNVDLGHWK	3.99	53.03	11.4
	EVVSIVDPHREPIQILR	3.19	52.15	
	FLISSLKEDR	2.45	595.8	
	NTYTENVYPHLVIR	4.92	0.36	
	LHFVYDPLVTAAEFLHGSPK	4.91	0.054	
	RLHFVYDPLVTAAEFLHGSPK	4.74	0.26	
	SIQESSHPVDSAITVEHIAATR	4.66	0.60	
	VAMATSQEASLHANMK	3.95	2.06	
	WSASLFPEDIGQTALR	3.42	0.026	
	FAEFIVWGPR	1.80	1,286.0	
<i>ApCatSper <math>\delta</math></i>	DGADYLAADIFIQELIPGISGDFAFVTTQGR	2.88	1,269.0	12.9
	TSLLTGAAGVGHGLSR	3.69	0.037	
	TPQSWVEMLGR	2.97	3.98	
	LPYQVMNAGSNRR	2.03	55.93	
	ILQFPH	1.49	20,590.0	
	LRPSEGWDHMMR	3.49	2.41	
<i>ApCatSper <math>\gamma</math></i>	KLRPSEGWDHMMR	2.81	2,830.0	9.1
	EGLDHRPIGESTTSTYIER	3.05	63.45	
	DPHGDPSWYDISLHSR	3.02	140	
	SLMAYQAIVHLLLER	2.77	31.42	
	YNRQDMFGAR	2.47	951.2	
	AIHFETPGK	2.37	1,073.0	
	ISNLHHR	2.38	2,636.0	
	EKYSLAAPQLTDGSLGHSEK	1.75	2,525.0	

*XCorr*, cross-correlation value; *Probabilities* and *PEP* (Posterior Error Probability) values were derived by mass spectrometric analysis of tryptic peptides by the Proteome Discoverer (PD) software version 1.2 and 1.4, respectively.