

**Table S2 Tryptic peptides of *Ap*CatSper 1-4,  $\beta$ ,  $\delta$ , and  $\gamma$  identified by mass spectrometry in immunoprecipitates obtained with anti-*Ap*CatSper 2 and 3 antibodies.**

Protein	Peptide sequence	anti- <i>Ap</i> CatSper 2		anti- <i>Ap</i> CatSper 3	
		XCorr	PEP ( $\times 10^{-5}$ )	XCorr	PEP ( $\times 10^{-5}$ )
<i>Ap</i> CatSper 1	HLQGTGPVGAQDAALQK	4.67	2.8	4.77	3.3
	RQTLVGPQDILPSHLK	3.32	264.3	3.51	1,580.0
	QTLVGPQDILPSHLK	2.78	1,814.0		
	TLLDDYYDEDEYTR	4.25	38.8	4.25	5.1
	LLAAIEQNAHIM(ox)R	3.05	338.0	2.88	86.8
	EEDEEEEEELQAR	3.40	23.5	3.77	8,256.0
	AAEDALFDDGHTKPIDTK	3.40	1,374.0	2.66	339.8
	GNSANYLLSLSYHR	3.22	3,423.0		
<i>Ap</i> CatSper 2	VVHDNLQMLVNSPSETVWPR	4.91	3.8		
	VVHDNLQM(ox)LVNSPSETVWPR	3.65	2,890.0		
	YFQLMEALQENLQER	4.88	3.0		
	YFQLM(ox)EALQENLQER	4.54	3.2		
	MTSGIFDELAPLAEIFR	3.02	1,105.0		
	M(ox)TSGIFDELAPLAEIFR	4.70	3.0		
	VDLTYQDSFR	3.39	1,801.0	2.36	5,457.0
	HGSSLTGLDGVK	3.38	1,900.0	2.69	7,826.0
	TVGSSDALFR	2.33	1,575.0	1.64	14,310.0
	MM(ox)LDNPHGLVK	2.50	4,635.0		
	M(ox)M(ox)LDNPHGLVK	2.95	1,125.0	3.04	6,046.0
	FNEELER	2.64	5,156.0	1.98	21,570.0
NELFLEVK	2.61	8,295.0			
<i>Ap</i> CatSper 3	WIRPDFEFHR	3.74	475.2		
	M(ox)SSESLPLSTR	2.63	6,853.0	2.55	3,115.0
	LQQLHFEMVNLAM(ox)ALEK	4.59	35.5	3.49	144.8
	LQQLHFEM(ox)VNLAM(ox)ALEK	3.68	5.8	4.71	1.8
	QSDVIIDDEGEM(ox)KR	3.09	2,090.0	2.67	27,260.0
<i>Ap</i> CatSper 4	KGDILSNLLELEQR	4.07	19,170.0	4.01	290.5
	LFTFDPSAVQR	2.80	12,710.0	2.80	2,293.0
	GITAEIEGFHDITK	4.04	191.5		
	LVDSIWR	3.17	3,740.0	2.61	7,816.0
	EVPIITSVDDVM(ox)AK	2.83	12,690.0	3.35	699.4
NSSLSPSAQALIK			2.42	11,070.0	
Predicted Protein	Peptide sequence	anti- <i>Ap</i> CatSper 2		anti- <i>Ap</i> CatSper 3	
		XCorr	PEP ( $\times 10^{-5}$ )	XCorr	PEP ( $\times 10^{-5}$ )
<i>Ap</i> CatSper $\beta$	EVVSIQVPHR			2.95	60,520.0
	EVVSIQVPHREPIQILR	2.74	586.0	2.74	66,930.0
	TFTFGADSWNVDLGHWK	2.71	968.8	1.63	70,060.0
	YDVGYYR	2.21	73,780.0		
	ELLSFSVTNPSLLDVQVAR	4.78	70.7		
	NTYTENVYPHLVIR	4.31	317.9	3.94	1,775.0
	NIYNADPSQPR	3.60	545.5	3.25	5,952.0
	LHFVYDPLVTAEFLHGSPK	3.24	1,614.0	4.07	1,139.0
	RLHFVYDPLVTAEFLHGSPK			4.05	4,164.0
	LNDHYDASK	2.74	8,540.0		
	LGISPLTK	2.44	3,679.0	2.47	63,560.0
	FLILSSK	1.51	17,270.0		
SIQESSHPVDSAITVEHIAATR			4.81	5,635.0	
<i>Ap</i> CatSper $\delta$	TSLLTGAAVGHGLSR	3.56		3.78	48,510.0
	LPYQVM(ox)NAGSNRR	3.25	11,320.0	2.63	58,220.0
	LPYQVMNAGSNRR	1.95	4,419.0	2.69	463.9
	TPQSWVEMLGR	2.23	13,200.0	2.63	61,980.0
	ILQFPH		5,770.0	1.89	25,020.0
	WSASLFPEDIGQTALR			1.94	28,690.0
	HTETTFSSLPLITLQEK			2.91	10,520.0
<i>Ap</i> CatSper $\gamma$	LDVVQSVFPYVVEPIVNNR	4.65	42,510.0	4.41	234.0
	ENELAADTHDPFLQWHR	3.70	50,630.0		
	EGLDHRPIGESTTSTYIER	3.64	275.6	3.65	1,399.0
	SVSGSILHSSLSK	3.06	6,942.0	3.52	1,805.0
	YSLAAPQLTDGSLGHSEK	2.93	61,740.0		
	SSALMSAGSYPK			3.36	2,058.0
	SSALM(ox)SAGSYPK	2.86	578.6	2.84	248.9
	FIAFDGYSR	2.55	1,827.0	1.97	5,283.0
	ISNLHHR	2.51	72,890.0		
	DTTFVLLTR	2.43	6,191.0	2.25	7,796.0
	AIHFETPGK	1.77	73,980.0		
	VQTTGIGTLDTAWK	3.29	939.7		

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