Supplementary information

The tertiary structure of the human Xkr8– Basigin complex that scrambles phospholipids at plasma membranes

In the format provided by the authors and unedited

Supplementary Table 1. Primers for mutagenesis of human BSG, and human and mouse Xkr8

hBSG mutants N152Q and N186Q

	forward primer	reverse primer				
	TCCGCTAGCGCGGCCAACTCCTAAAAAACCGCCACCATG	TCTCGAATTCGTCGATCACTTGTC				
	complementary mutagenizing primers					
N152Q	CTCATG <u>CAA</u> GGCTCCGAGAGCAGGTTCTTC	<u>GGAGCCTTGCATGAG</u> GGCCTTGTCCTCAGAG				
N186Q	CGGTGC <u>CAA</u> GGCACCAGCTCCAAGGGC	<u>GGTGCCTTG</u> GCACCGGGTACTGGCCGGG				

hBSG mutants A207C and P211C

	forward primer	reverse primer					
	GTGTCGTGAGGAATTCGCCACCATGGCGGCTGCGCTGTTC	ATGGGTACATGAATTCGGAAGAGTTCCTCTGGCGGAC					
	complementary mutagenizing primers						
A207C	CACCTG <u>TGC</u> GCCCTCTGGCCCTTCCTGG	GAGGGC <u>GCA</u> CAGGTGGCTGCGCACGC					
P211C	CTCTGG <u>TGC</u> TTCCTGGGCATCGTGGCTGAGG	CAGGAA <u>GCA</u> CCAGAGGGGGGGCCAGGTG					

hBSG mutant E230C

	forward primer	reverse primer				
	CTAGACTGCCGGATCCGCCACCATGGCGGCTG	ATGGGTACATGAATTCGGAAGAGTTCC				
	complementary mutagenizing primers					
E230A	ATCTAC <u>GCG</u> AAGCGCCGGAAGCCC	<u>GCGCTTCGC</u> GTAGATGAAGATGATGGTGACCAGC				

mXkr8 mutants

	forward primer	reverse primer		
	GTGAGGAATTGGATCCATCATGC	ACAGATTCTCGAATTCGAGGACTCC		
	complementary mu	tagenizing primers		
D12A	<u>GCCTTAGCC</u> GTGGTCGTAGGCCTGGTG	GACCAC <u>GGC</u> TAAGGCCACATGGTGGTGC		
D26A	CTGCTG <u>GCT</u> CTGGTCGCTGACCTGTGG	GACCAG <u>AGC</u> CAGCAGGAAAGACAAGATACTCAC		
D30A	GTCGCT <u>GCC</u> CTGTGGGCCGTTGTCCAG	CCACAG <u>GGC</u> AGCGACCAGATCCAGCAGG		
R42A	CCTTGGC <u>GCT</u> TATCTGTGGGCCGCGCTG	AGATAAGCGCCAAGGAGCACGTACTGGAC		
W45A	TTATCTG <u>GCG</u> GCCGCGCTGGTACTGG	GCGGC <u>CGC</u> CAGATAACGGCCAAGGAGCACG		
R98A	CTGTAT <u>GCG</u> TGTTTGCACGGAATGCATCAAGG	CAAACA <u>CGC</u> ATACAGGTAGCCGAGCTGCAG		
D129A	TCCCTG <u>GCC</u> ATCAGCATGCTGAAGCTTTTCGAG	<u>GCTGATGGCCAGGGA</u> GAGAAAGTCTGCGTAG		
K134A	ATGCTG <u>GCG</u> CTTTTCGAGAGCTTCCTGGAGG	GAAAAG <u>CGC</u> CAGCATGCTGATGTCCAGGGAG		
E137A	CTTTTC <u>GCG</u> AGCTTCCTGGAGGCGACG	GAAGCT <u>CGC</u> GAAAAGCTTCAGCATGCTGATG		
E141A	TTCCTG <u>GCG</u> GCGACGCCACAGCTC	CGTCGC <u>CGC</u> CAGGAAGCTCTCGAAAAGCTTC		
Q155A	<u>TGTATTGGCGAATGG</u> CCAGGCGGAATACTACC	CCATTCGCCAATACAATTGCCAGCACCAGTGTG		
D180A	CTGCTG <u>GCT</u> TACCATCGGTCTCTGCGTACC	ATGGTA <u>AGC</u> CAGCAGTGCCCACGAGATG		
R183A	TACCAT <u>GCG</u> TCTCTGCGTACCTGTCTTCCC	CAGAGA <u>CGC</u> ATGGTAATCCAGCAGTGCCCAC		
W310A	GGCACC <u>GCG</u> CTGCCCAGTGGGATCTCATTG	<u>GGGCAGCGGGTGCC</u> GTGTGTCACCCAG		

hXkr8 mutants, R214G, R280E, R284E, and D295K					
	forward primer	reverse primer			
	AGTTAATTAAGGATCCGCCACCATGCCCTGGTCTAG	CCTTGCTCACGAATTCTCCTTTCACAGGGCTGGCG			
	complementary mut	tagenizing primers			
R214G	GTGGCCC <u>GGA</u> GTGCTGGCCGTGGCC	AGCACTCCGGGCCACAGCAGCAGC			
R280E	AGGGC <u>GAG</u> ACAAGAGGCAGAGCCATCATC	CTCTTGT <u>CTC</u> GCCCTCGGCCACGTTG			
R284E	AGAGGC <u>GAA</u> GCCATCATCCACTTCGCTTTTC	GATGGCTTCGCCTCTTGTCCGGCCCTC			
D295K	CTGAGC <u>AAG</u> AGCATCCTGCTGGTGGCTAC	GATGCT <u>CTT</u> GCTCAGCAGAAAAGCGAAGTGG			

hXkr8 mutants, T302C and T305C

	forward primer	reverse primer				
	GTGAGGAATTGGATCCGCCACCATGCCCTGGTCTAG	ACAGATTCTCGAATTCTCCTTTCACAGGGCTGGCG				
	complementary mutagenizing primers					
T302C	GTGGCT <u>TGC</u> TGGGTCACCCACTCTAGCTGG	GACCCA <u>GCA</u> AGCCACCAGCAGGATGCTGTC				
T305C	TGGGTCTGCCACTCTAGCTGGCTGCCTAGC	AGAGTG <u>GCA</u> GACCCAGGTAGCCACCAGCAG				

*Mutated residues are underlined. The first 15 nucleotides are complementary to each other between the complementary mutagenizing primers. Each mutant was prepared by PCR. Using hBSG, mXkr8 or hXkr8 cDNA as a template, PCR was carried out with the forward primer and the second mutagenizing primer for the 5' part, and with the first mutagenizing primer and the reverse primer for 3' part. The resultant PCR products for the 5' and 3' parts and linearized vector were fused by In-Fusion HD Cloning Kit (Takara).

		10	20	-01130		40	-50	-026	0	-70	080
human	MPWSSR	GALL <mark>RD</mark> LV	LGVLGTAA	FLL <mark>D</mark> LGT	LWAAVQYA	lg <mark>g</mark> ry <mark>l</mark> waa	LVLALI	G <mark>L</mark> ASVA	LQLF <mark>SWLW</mark>	LRA <mark>D</mark> PAGLH	GSQP
mouse	MPLSVH	HVAL <mark>D</mark> VV	VGLVSILS	FLL <mark>D</mark> LVA <mark>I</mark>	LWAVVQYV	LLGRY <mark>L</mark> WAA	LVLVLI	GQASVLI	LQLF <mark>SWLW</mark>	LTA <mark>D</mark> PTELH	HSQL
Chicken	MAARGPAI	RFGPW <mark>Q</mark> WLI	LAAAGAAA	AVW <mark>D</mark> AGA <mark>L</mark>	VWVAVGYA	RA <mark>G</mark> QP <mark>G</mark> CAA	LGLG <mark>L</mark> W	AAGSAA	RQAC <mark>SWLW</mark>	FRS <mark>D</mark> PSTLR	PEL
Fugu l	MRVMGQATISI	NYSWI <mark>D</mark> FV:	FSVIGVFT	FFV <mark>D</mark> WGA <mark>I</mark>	VWVATEFY	SRGDF <mark>F</mark> WFG	LLVS <mark>L</mark> M	IV <mark>L</mark> SSVL	VQMFSWFW	LKY <mark>D</mark> RELPD	VCRQSGGG
-		_			-						
		- a3a 90	1	00 -<u>a3b</u>- -	-110	120	α4a -13	0	140	a4 b	160
human	PR	CLALLHL:	LQLGYLY <mark>R</mark>	CVQ <mark>E</mark> L <mark>R</mark> QC	LLVWQQEE	PSEF <mark>D</mark> LAYA	DFLAL	ISMLRL	F <mark>E</mark> TF <mark>LE</mark> TA	PQLT <mark>L</mark> VLA <mark>I</mark>	MLQSGRAE
mouse	SRI	PFLALLHL	LQLGYLY <mark>R</mark>	CLHGMHQC	LSMCYQEM	PSEC <mark>D</mark> LAYA	DFLSL	ISML <mark>K</mark> LI	F <mark>E</mark> SF <mark>LE</mark> AT:	P <u>Q</u> LT <mark>L</mark> VLA <mark>I</mark>	VLQNGQAE
Chicken	SRI	RPLAALHL	LQLGFLY <mark>R</mark>	CLRALRL	WRLCREEA	T-EEERDHM	AFLTH <mark>E</mark>	ISMLRL	F <mark>E</mark> TF <mark>LE</mark> NA	PQLA <mark>V</mark> LLYS	VLRTNKAE
Fugu	TTVLFGDRV	QLSWL <mark>LH</mark> V	LQLGFLC <mark>R</mark>	HISAIRQ	FRVWWRQQ	EGSEYA	VYLTH <mark>E</mark>	LSML <mark>R</mark> L	I <mark>E</mark> TFS <mark>E</mark> SA	PQLT <mark>L</mark> MVH <mark>V</mark>	MLCTNRAR
	170)0	18 <mark>0</mark>	<u>190</u>		210	<mark>α6</mark>	-220	230	<mark>-07</mark> 24	0
Human	YY <mark>Q</mark> WVGICT;	SFLGIS <mark>W</mark> A	LL <mark>DYHR</mark> AL	RTCLPSKE	LL <mark>GLG<mark>S</mark>SV</mark>	IYFLWNLLI	LWP <mark>R</mark> VI	AVALFS	ALFPSY <mark>V</mark> A	LH <mark>FL</mark> GL <mark>W</mark> LV	LLL <mark>WVWLQ</mark>
mouse	YYQWFGISS	<u>s</u> flgi <u>s</u> wa:	LL <mark>D</mark> YH <mark>R</mark> SL	<mark>R</mark> TCLPSKE	RLGRS <mark>SS</mark> A	IYFLW <u>N</u> LLL	LGP <mark>R</mark> IC	AIALFS	AVFPYY <mark>V</mark> A:	LH <mark>FF</mark> SL <mark>W</mark> LV	LLFWIWLQ
Chicken	PSQGMGICT2	ALLCVTWS	LL <mark>DYHQ</mark> SL	<mark>R</mark> SFLQDKY	EMGWGSSV	IYFLWNLFI	LCP <mark>R</mark> II	ALALFA	LLWPYG <mark>V</mark> A'	VH <mark>F</mark> PLV <mark>W</mark> LA	MFIWVSLQ
Fugu	TVQ	\$ <mark>W</mark> M	VV <mark>D</mark> YH <mark>R</mark> SL	<mark>R</mark> AFLPDKA	KQGWGSSL	IYFLWNFLI	IAP <mark>R</mark> VA	ALALFA	SVVGGF <mark>V</mark> A	VH <mark>FL</mark> LL <mark>W</mark> CV	FVMWAWLQ
	250	-260- <mark>-08</mark> -	270	280	2	90 a9	300	3	10	-320 α10	330
Human	GTDFMPDPS:	SEWLY <mark>RV</mark> T	VATILYFS	WFNVAEGF	RTRG <mark>R</mark> AIIH	FAFLLS <mark>D</mark> SI	LLVAT-	WVTHSS	WLPSGIPL	QLWLPVGCG	CFF <mark>LGL</mark> AL
mouse	GTNFMPDSK	GEWLY <mark>RV</mark> T	MALILYFS	WFNVSGGF	RTRG <mark>R</mark> AVIH	LIFIF <u>S<mark>D</mark></u> SV	LVT <u>T</u> S	WVTHGT	WLPSGISL	LMWVTIGGA	CFFLGLAL
Chicken	GTDFMESPGI	PEQLY <mark>R</mark> AM	VAVILYFS	WFNVAPGF	TLY <mark>R</mark> SIIY	HSFILL <mark>D</mark> ST	'LLTLA-	WLWGHP	PEEQRPYL	IPVLCAALP	CYL <mark>LGL</mark> LL
Fugu	GTEFMDSVC	GEGLY <mark>R</mark> AT	VGIIWYFS	WFNVAEGÇ	TRG <mark>R</mark> SIIY	HSFITT <mark>D</mark> GG	ILLLT-	WWCYRD	PVQTEPYG	LALLVTLLF	SYL <mark>LGL</mark> LF
	340-		350 α11	360							
human	RLVYYHWLHI	PSCCW	KPDP <mark>D</mark> QVD	GARSLLSE	-EGYQLPQ	NRRMTHLAÇ	KFFPKA	KDEAASI	PVKG		
mouse	RVIYYLWLHI	PSCSW	DPDLVD	GTLGLLSE	HRPPKLIY	NRRATLLAE	NFFAKA	KARAVL'	TEEVQLNG	VL	
hicken	RVTYYGWLHI	NVRAQP-1	RSGGDEVD	AEGRHDGV	VEFRSISE	PSELRSVSG	PDLVNS	RLRCLA	RSHFPLSA	LAÉPRLLNG	AAAV
Fugu	KTVYYCCFH1	TMRRPPA	RESSDLPD	AEVTFRHE	SIQDGAPS	SPLLNRRMA	AHAARF	YSERRAY	VKNLGGVD	AATSSPP	

Supplementary Fig. 1. Sequence alignment of Xkr8 orthologues. Sequences of Xkr8 from humans (UniProt: Q9H6D3), mice (UniProt: Q8C0T0), chickens (Chick) (UniProt; Q49M60), and fugu (UniProt: H2TYQ9) were analyzed by the MUSCLE Program (EMBL-EBI). Numbers above the first line are the amino acid positions for hXkr8. Conserved residues are indicated in red. Eleven α -helices are shadowed and numbered. Negatively and positively charged residues in the lipid layer are highlighted in green, while the hydrophobic amino acids forming the cleft for PtdCho are highlighted in yellow.



Supplementary Fig. 2. X-ray diffraction analysis of the hBSGΔ-Fab complex. The representative X-ray diffraction pattern of a crystal of Fab14 (**a**) and the lipidated hBSGΔ-Fab complex (**b**) in buffer containing 33% PEG400. The area of high resolution was enlarged in insets.

				20 α1	40	α2
XKR8		MPWSSRGA	LLR <mark>D</mark> LVLG <mark>V</mark> LG	TAAFLL <mark>D</mark> LG	T <mark>D</mark> LWAAVQYALGO	GRY <mark>LWAAL</mark> VLA <mark>L</mark> L
XK			-MKFPASVLAS	VFLFVAETT	AALSLSSTYRSG	GDR <mark>M</mark> WQA <mark>L</mark> TLL <mark>F</mark> S
XKR2	MDRVYEIPEEPNVDPVSSLEE	DVIRGANP	RFTFPFSILFS	TFLYCGEAA	SALYMVRIYRKN:	SETYWMTYTFS <mark>F</mark> F
XKR3	METVFEEMDEESTGGVSSSKE	EIVLGQRL	HLSFPFSIIFS	TVLYCG <mark>E</mark> VA	.F <mark>GL</mark> YMFEIYRKAI	NDT <mark>FWMSFTISF</mark> I
XKR4	MAAKSDGRLK85ALCLR	LGREQRRY	SLW <mark>D</mark> CLWILAA	.VAVYFA <mark>D</mark> VG	T <mark>D</mark> VWLAVDYYLR(GQR <mark>W</mark> WFG <mark>L</mark> TLF <mark>F</mark> V
XKR5			MHARLLGLS	ALLQAAEQS	ARLYTVAYYFTT(GRL <mark>L</mark> WGW <mark>L</mark> AL- <mark>A</mark> V
XKR6	MAAKSDGGGV-101AARPE	PPPPQVER	PWL <mark>D</mark> CLWIVLA	LLVFFG <mark>D</mark> VG	T <mark>D</mark> LWLALDYYRK(GDY <mark>V</mark> YFG <mark>L</mark> TLF <mark>F</mark> V
XKR7	MAAKSDGAAA29PGVVG	AGGPGPRY	ELR <mark>D</mark> CCWVLCA	LLVFFS <mark>D</mark> GA	.T <mark>D</mark> LWLAASYYLQI	NQHTYFS <mark>L</mark> TLL <mark>F</mark> V
XKR9		МКҮ	TKQNFMMSVLG	IIIYVT <mark>D</mark> LI	V <mark>D</mark> IWVSVRFFHE(GQY <mark>V</mark> FSA <mark>L</mark> ALS <mark>F</mark> M
	60		80 α 3a		100 α3b	_
XKR8	GLASVALQLFSWLWLRADPAG	LHGS	QPPRRCLALLH	LLQLGYLYR	CVQELRQGLLVW	QQEEPS
XK	LLPCALVQLTL-LFVHRDLSR	DRP	LVL <mark>LLH</mark>	LLQLGPLFR	CFEVFCIYFQSG	NNEEPY-14-SEE
XKR2	MESSIMVQLTL-IFVHRDLAK	DKP	ISLFMH	LILLGPVIR	CLEAMIKYLTLW	KKEEQE-16-EVL
XKR3	IVGAILDQIIL-MFFNKDLRR	NKA	ALLFWH	ILLLGPIVR	CLHTIRNYHKWL	KNLKQE-11-NTM
XKR4	VLGSLSVQVFSFRWFVHDFST	EDS-72-S	FCIWLLQS <mark>LIH</mark>	ILQL <mark>G</mark> QIWR	YFHTIYLGIRSR	QSGEND
XKR5	LLPGFLVQALSYLWFRADGHP		GHCSLMMLH	LLQL <mark>G</mark> VWKR	HWDAALTSLQKE	LEAPHR
XKR6	L <mark>V</mark> PSLLVQSLSFRWFVQDYTG	GGL - 41 - R	LSVWIWQS <mark>VIH</mark>	LLQM <mark>G</mark> QVWR	YIRTMYLGIQSQI	RRKEHQ
XKR7	LLPSLVVQLLSFRWFVYDYSE	PAG-53-R	LCIWLLQT <mark>LVH</mark>	LLQL <mark>G</mark> QVWR	YLRALYLGLQSR	VRGERL
XKR9	L <mark>E</mark> GTLVAQCFSYSWFKADLKK	AG	QESQHCFL <mark>LLH</mark>	CLQGGVFTR	YWFALKRGYHAAI	FKYDSNTSN
	120 α4a	140	α <u>4</u> b	:	.60 α.5	180
XKR8	EFDLAYADFLALDISM	L <mark>R</mark> LF <mark>E</mark> TF <mark>L</mark>	<mark>E</mark> TAP <mark>Q</mark> LT <mark>L</mark> VLA	IMLQSGR-A	EYY <mark>Q</mark> WVGICT <mark>S</mark> F1	LGISWALL <mark>D</mark> YH- <mark>R</mark>
XK	IEKEVGQAEGKLITHRSAFSR	ASVIQAF <mark>L</mark>	GSAP <mark>Q</mark> LT <mark>L</mark> QLY	<mark>I</mark> SVMQQD-V	TVGRSLLMTI <mark>S</mark> LI	LSIVYGALRCNIL
XKR2	IEWEVGHSIRTLAMHRNAYKR	MSQIQAF <mark>L</mark>	GSVP <mark>Q</mark> LTYQLY	<mark>V</mark> SLISAE-V	PLGRVVLMVF <mark>S</mark> LV	/SVTYGATLCNML
XKR3	LEREIAFSIRDNFMQQKAFKY	MSVIQAF <mark>L</mark>	GSVP <mark>Q</mark> LI <mark>L</mark> QMY	<mark>I</mark> SLTIRE-W	PLNRALLMTF <mark>S</mark> LI	LSVTYGAIRCNIL
XKR4	RWRFYWKMVYEYADVSM	LHLLATF <mark>L</mark>	<mark>E</mark> SAP <mark>Q</mark> LV <mark>L</mark> QLC	IIVQTHS-L	QAL <mark>Q</mark> GFTAAASL ^v	/SLAWALASYQ- <mark>K</mark>
XKR5	GWLQLQEADLSA	L <mark>RLLE</mark> AL <mark>L</mark>	QTGPHLL <mark>L</mark> QTY	VFLASDF-T	DIVPGVSTLFSW	SSLSWALVSYT- <mark>R</mark>
XKR6	RRFYWAMMYEYADVNM	L <mark>RLLE</mark> TF <mark>L</mark>	<mark>E</mark> SAP <mark>Q</mark> LV <mark>L</mark> QLY	IMLQKNS-A	ETLPCVSSVT <mark>S</mark> LI	4SLAWVLASYH- <mark>K</mark>
XKR7	RRHFYWQMLFESADVSM	L <mark>RLLE</mark> TF <mark>L</mark>	RSAP <mark>Q</mark> LV <mark>L</mark> QLS	LLVHRGGAP	DLLPALSTSA <mark>S</mark> LV	/SLAWTLASYQ- <mark>K</mark>
XKR9	FVEEOIDLHKEVIDRVTDLSM	LRLFETYL	EGCPOLT LOLY	TILEHGO-A	NFS <mark>OYAAIMVS</mark> C	CATSWSTVDYO-V
	~					en e
	200	0	.6 220		0.7 240	
XKR8	ALRTCLPSKPLLGL-GSSVIY	o FLWNLLLL	6 220 WP <mark>R</mark> VLAVALFS	ALFPSY <mark>V</mark> AL	α7 240 H <mark>FL</mark> GL <mark>W</mark> LVLLLW	WLQGTDFM
XKR8 XK	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI	G FLWNLLLL FLWRSFEI	6 220 WP <mark>R</mark> VLAVALFS AT <mark>R</mark> VVVLVLFT	ALFPSY <mark>V</mark> AL SVLKTW <mark>V</mark> VV	α7 240 HFLGLWLVLLW	/WLQGTDFM PWILFWCSGSPFP
XKR8 XK XKR2	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI	o FLWNLLLI FLWRSFEI TIWRTLEI	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS	ALFPSY <mark>V</mark> AL SVLKTWVVV ATLKLK <mark>A</mark> VP	α7 240 H <mark>PLGLW</mark> LVLLLW ILINFFSFFLY F <mark>LV</mark> LN <mark>F</mark> LIILFE	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP
XKR8 XK XKR2 XKR3	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV	O FLWNLLL FLWRSFEI TIWRTLEI VMWRFLEV	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS IS <mark>R</mark> VVTLAFFI	ALFPSY <mark>V</mark> AL SVLKTW <mark>V</mark> VV ATLKLKAVP ASLKLKSLP	α7 240 HPIGLWLVLLW IIINFFSFFLY FLVLNFLIILFE VIIIYFVSLLA	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP
XKR8 XK XKR2 XKR3 XKR4	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ	G FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA	ALFPSY <mark>V</mark> AL SVLKTW <mark>V</mark> VV ATLKLK <mark>A</mark> VP ASLKLKSLP SVFQLY <mark>F</mark> GI	α7 240 H CLWLVLLW I LINFFSFLY F VINFLIILFE V LIYFVSLLA F VLHWCIMTFW	WLQGTDFM PWILFWCSGSPFP PWIKFWRSGAQMP PWLEFWKSGAHLP IVHCETEFC
XKR8 XK XKR2 XKR3 XKR4 XKR5	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ	0 FLWNLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY	ALFPSY <mark>V</mark> AL SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFW <mark>V</mark> FV	0.7 240 H GLWLVLLLW I INFFSFLY FUNINFLIILFE VOI IIYFVSLLA FUNHWCIMTFW	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC LVAQQSDII
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ	O FLWNLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA	ALFPSY <mark>V</mark> AI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI	A7 240 H GLWLVLLLW I INFFSFLY FUNDFLIILFE VINFLIILFE VINFLIILFE IYFVSLLA FUNDFLIILFE IYFVSLLA FUNDFLIILFE IYFVSLLA FUNDFLIIFE IYFVSLA FUNDFLIFE IYFVSLA FUNDFLIFE IYFVSLA FUNDFLIFE IYFVSLA FUNDFLIFE IYFVSLA	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC LVAQQSDII IIHGGTDFC
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ VLRDSRDDKRPLSY-KGAVAQ	C FLWNLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA	ALFPSY <mark>V</mark> AI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI	A7 240 H GLWLVLLLW I INFFSFLY FLVLNFLIILFE VLIIYFVSLLA FLVLHWCIMTFW VACAHWLVMTFW FVVHWCAMAFW F F	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC LVAQQSDII IIHGGTDFC /IQGETDFC
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ VLRDSRDDKRPLSY-KGAVAQ ALRKSLPDKKLLNGLCPKITY	C FLWNLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF	A7 240 H GLWLVLLLW I INFFSFLY FLVLNFLIILFE VII IYFVSLLA FLVLHWCIMTFW VACAHWLVMTFW FVVHWCAMAFW FLVAHWCVMTFW LOFFLWLLGIW	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC LVAQQSDII IIHGGTDFC /IQGETDFC AFKNNTQFC
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ VLRDSRDDKRPLSY-KGAVAQ ALRKSLPDKKLLNGLCPKITY 260	C FLWNLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF 280	α7 240 H GLWLVLLLW I INFFSFLY FLVLNFLIILFE VOI IYFVSLLA FLVLHWCIMTFW VACAHWLVMTFW FLVHWCAMAFW FLVHWCAMAFW FLVHWCMMFW FLWHWCAMAFW FLWHWCMMFW AHWLVMTFW	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC LVAQQSDII IHGGTDFC /IQGETDFC AFKNNTQFC 300
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ VLRDSRDDKRPLSY-KGAVAQ ALRKSLPDKKLLNGLCPKITY 260 Q 	C FLWNLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL 8 TVATILYF	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF 280 EGRT	α7 240 H GLWLVLLLW I INFFSFLY FLVLNFLIILFE VOI IYFVSLLA FLVLHWCIMTFW VACAHWLVMTFW FLVHWCAMAFW FLVHWCAMAFW FLVHWCAMAFW FLWHWCMMFW LVFFLWLLGIW α9 RGRAIIHFAFLS	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC LVAQQSDII IHGGTDFC /IQGETDFC AFKNNTQFC 300 SDSI-LLVATWVT
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR8	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ VLRDSRDDKRPLSY-KGAVAQ ALRKSLPDKKLLNGLCPKITY 260 0 CPDPSSEWLYRV ENIEKALSRVGTTIVLCFLTI	G FLWNLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL 8 TVATILYF LYTGINMF	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL SWFNVA CWSAVQLKIDS	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF EGRT PDLISKSHN	α7 240 H GLWLVLLLW I INFFSFLY F UNFLIILFE VOI IYFVSLLA F UHWCIMTFW VACAHWLVMTFW F VHWCAMAFW F VHWCAMAFW F HWLLGIW α9 RGRAIIHFAFLS	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC LVAQQSDII IHGGTDFC /IQGETDFC AFKNNTQFC 300 SDSI-LLVATWVT IENA-ILLLWYL
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XK XKR8 XK XKR2	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ VLRDSRDDKRPLSY-KGAVAQ ALRKSLPDKKLLNGLCPKITY 260 Q 	G FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL 8 TVATILYF LYTGINMF	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL SWFNVA CWSAVQLKIDS CWSALQLRLAD	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF EGRT PDLISKSHN RDLVDKGQN	α7 240 H GLWLVLLW I L INFFSFLY FULNFLIILFE VII IYFVSLLA FULHWCIMTFW VACAHWLVMTFW FVVHWCAMAFW FVAHWCVMTFW L FLWLLGIIW α9 RGRAIIHFAFLL WQLLVYYMIRF	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC LVAQQSDII IHGGTDFC VIQGETDFC AFKNNTQFC 300 SDSI-LLVATWVT IENA-ILLLWYL VENV-IMVLVFKF
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XK XKR2 XKR2 XKR3	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LIRDSRDDKKSMSY-RGAIQ VIRDSRDDKRPLSY-KGAVAQ ALRKSLPDKKLLNGLCPKITY 260 Q PDPSSEWLYR ENIEKALSRVGTTIVLCFLTI NNIEKNFSRVGTLVVLISVTU GNKENNSNMVGTVLMLFLITI	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL 8 TVATILYF LYTGINMF LYAGINFS LYAAINFS	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL SWFNVA CWSAVQLKIDS CWSALQLRLAD CWSAVKLQLSD	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF EGRT PDLISKSHN RDLVDKGQN DKIIDGRQR	a7 240 HelgLWLVLLW ILINFFSFLY FININFLIILFE VolIIYFVSLLA FININFLIILFE VolIIYFVSLLA FININFLIILFE VolIIYFVSLA FININFLIILFE VolIIYFVSLA FININF VOLIYFVSLA FININF VOLIYFV FININF VOLIYFV GRAIIHFAFLL WGHMGLHYSVRL WGHRILHYSFQF	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC LVAQQSDII IHGGTDFC VIQGETDFC AFKNNTQFC 300 SDSI-LLVATWVT IENA-ILLLWYL VENV-IMILVFKF ENV-MILVFKF
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XK XKR2 XKR8 XKR2 XKR3 XKR4	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIQ VIRDSRDDKKPLSY-KGAVAQ ALRKSLPDKKLLNGLCPKITY 260 Q PDPSSEWLYRV ENIEKALSRVGTTIVLCFLTI NNIEKNFSRVGTLVVLISVT GNKENNSNMVGTVLMLFLITU ITKWEEIVFD	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI LFYKLFTI S TVATILYF LYTGINMF LYAGINFS LYAAINFS VVGIIYIF	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL SWFNVA CWSAVQLKIDS CWSALQLRLAD CWSAVKLQLSD SWFNVK	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF 280 EGRT PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT	a7 240 HolgLWLVLLW ILINFFSFLY FUNNFLIILFE VNIIYFVSLLA FUNHWCIMTFW VALAHWLVMTFW FUNHWCAMAFW FUNHWCAMAFW FUNHWCAMAFW FUNHWCAMAFW FUNHWCAMAFW GRAIIHFAFLL WYQLLVYYMIRF WGHMGLHYSVRL WGHRILHYSFQF RCRAFIYYFVIL	WLQGTDFM PWILFWCSGSPFP PWIKFWRSGAQMP PWLEFWKSGAHLP IVHCETEFC UVAQQSDII IHGGTDFC JUQGETDFC AFKNNTQFC 300 SDSI-LLVATWVT IENA-ILLLWYL VENV-IMVLVFKF ENV-IMILVFRF LENT-ALSALWYL
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XK XKR2 XKR8 XKR2 XKR3 XKR4 XKR5	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIQ VIRDSRDDKKPLSY-KGAVAQ AIRKSLPDKKLLNGLCPKITY 260 0 260 0 260 0 260 0 260 0 260 0 0 0 0 0 0 0 0 0 0 0 0 0 0	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL 8 TVATILYF LYAGINFS LYAGINFS LYAGINFS VVGIIYIF LVGGVYIL	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWFNVA CWSAVQLKIDS CWSALQLRLAD CWSAVKLQLSD SWFNVK CYLSFW	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF 280 EGRT PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT BGRT	a7 240 HolgLWLVLLW IIINFFSFLY FUNNFLIILFE VOIIYFVSLAN FUNHWCIMTFW VOIAHWCVMTFW FUNHWCNMTFW FUNHWCNMTFW FUNHWCVMTFW FUNHWCNMTFW GRAIHFAFLLS WYQLLVYYMIRF WGHMGLHYSVRL WGHRILHYSFQF RCRLFIYYFVLL	WLQGTDFM PWILFWCSGSPFP PWIKFWRSGAQMP PWLEFWKSGAHLP IVHCETEFC IVAQQSDII IHGGTDFC VIQGETDFC AFKNNTQFC 300 SDSI-LIVATWVT ENA-ILLLWYL VENV-IMVLVFKF ENV-IMILVFRF ENT-ALSALWYL LENI-ILLLAT-
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XK XKR2 XKR8 XKR2 XKR3 XKR4 XKR5 XKR6	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ ULRDSRDDKKSMSY-RGAIIQ VLRDSRDDKKPLSY-KGAVAQ ALRKSLPDKKLLNGLCPKITY 260 0 260 0 260 0 260 0 0 0 0 0 0 0 0 0 0 0 0 0 0	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWHLFSI LFYKLFTL 8 TVATILYF LYAGINFS LYAGINFS LYAAINFS VVGIIYIF LVGAVYIL VVGIVYIF	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWHNVA CWSAVQLKIDS CWSALQLRLAD CWSAVKLQLSD SWFNVK CYLSFW	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT EGRT EGRT	a7 240 H GLWLVLLLW I LINFFSFLY F.VINFLIILFE V.I IYFVSLLA F.VLHWCIMTFW V.A.HWCVMTFW F.V.HWCAMAFW F.V.HWCMMFW F.V.HWCMMFW GRAIIHFAFLS WYQLLVYYMIRF WGHMGLHYSVRL WGHRILHYSFQF1 RCRLFIYYFVIL RNRWTFYMVML RYRMFAYYTIVL	WLQGTDFM PWILFWCSGSPFP PWIKFWRSGAQMP PWLEFWKSGAHLP IVHCETEFC VAQQSDII IHGGTDFC VIQGETDFC AFKNNTQFC 300 SDSI-LLVATWVT IENA-ILLLWYL VENV-IMVLVFKF LENV-IMILVFRF LENT-ALSALWYL LENI-ILLLAT- FENA-ALTFLWYF
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ ULRDSRDDKKSMSY-RGAIIQ VLRDSRDDKKPLSY-KGAVAQ AIRKSLPDKKLLNGLCPKITY 260 0 260 0	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL 8 TVATILYF LYAGINFS LYAGINFS VVGIYIF LVGAVYIL VVGIYIF	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL SWFNVA CWSAVQLKIDS CWSALQLRLAD CWSAVKLQLSD SWFNVK CYLSFW CWFNVK	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT EGRT EGRT EGRT	a7 240 HIGLWLVLLW IIINFFSFLY FWINFLIILFE VIIIYFVSLLA FWLHWCIMTFW FVLHWCIMTFW FVLHWCIMTFW FVLHWCIMTFW FVLHWCIMTFW FVLHWCIMTFW FVLHWCIMTFW FVLHWCIMTFW GRAIIHFAFLS WYQLLVYYMIRF WGHMGLHYSVRLY WGHRILHYSFQF1 RCRLFIYYFVIL RNRWTFYMVML RYRMFAYYTIVL'	WLQGTDFM PWILFWCSGSPFP PWIKFWRSGAQMP PWLEFWKSGAHLP IVHCETEFC VAQQSDII IHGGTDFC VIQGETDFC AFKNNTQFC 300 SDSI-LLVATWVT IENA-ILLLWYL VENV-IMVLVFKF LENT-ALSALWYL LENI-ILLLAT- FENA-ALTFLWYF LENA-ALTGFWYS
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ VLRDSRDDKKSMSY-RGAIQ ALRKSLPDKKLLNGLCPKITY 260 260 260 260 260 260 260 260	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL 8 TVATILYF LYAGINFS LYAGINFS LYAGINFS VVGIYIF LVGGVYIL VVGIYIF VVGIIYIF	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL SWFNVA CWSAVQLKIDS CWSALQLRLAD CWSAVKLQLSD SWFNVK CYLSFW CWFNVK TFFNIK	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT EGRT EGRS EQNT	a7 240 H GLWLVLLLW I INFFSFLY F VINFLIILFE FUNHCAMAFW FINFLIG FINFLIC RGRAIIHFAFLL WGHMGLHYSVRL WGHMGLHYSVRL WGHRILHYSFQFI RCRLFIYYFVILI RNRMVTFYMVML RYRMFAYYTIVL RRRMTLYHCIVL KCPMSCYYIVRV	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC VAQQSDII IIHGGTDFC VIQGETDFC AFKNNTQFC 300 SDSI-LLVATWVT IENA-ILLLWYL VENV-IMILVFKF LENT-ALSALWYL LENI-ILLLAT- FENA-ALTFLWYF LENA-ALTGFWYS LGTLGILTVFWVC
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ VLRDSRDDKKSMSY-RGAIQ ALRKSLPDKKLLNGLCPKITY 260 260 260 260 260 260 260 260	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL 8 TVATILYF LYAGINFS LYAGINFS LYAGINFS VVGIYIF VVGIYIF VVGIYIF VVGIYIF VVGIIYIF VVGILIF C10	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL SWFNVA CWSAVQLKIDS CWSALQLRLAD CWSAVKLQLSD SWFNVK CYLSFW CWFNVK CWFNVK TFFNIK 340	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT EGRT EGRS EQNT (011/00/00/00/00/00/00/00/00/00/00/00/00/	a7 240 H GLWLVLLLW I INFFSFLY F VINFLIILFE VOI IIYFVSLLAN F VLHWCIMTFW F VHWCAMAFW F VHWCAMAFW F VHWCAMAFW F VHWCAMAFW F VHWCAMAFW F VHWCAMAFW F HWCVMTFW CB FLWLLGIW CB CH WYQLLVYYMIRF CB WGHRILHYSVRL CB WGHRILHYSFQFI RCRLFIYYFVILI RNRMVTFYMVMLI RYRMFAYYTIVL' RRRMTLYHCIVLI XCPMSCYYIVRV 360 CDDOUT	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC VAQQSDII IIHGGTDFC VIQGETDFC AFKNNTQFC 300 SDSI-LLVATWVT IENA-ILLLWYL VENV-IMILVFKF LENT-ALSALWYL LENI-ILLLAT- FENA-ALTFLWYF LENA-ALTFWYF LENA-ALTGFWYS LGTLGILTVFWVC
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR7 XKR9	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ VLRDSRDDKKSMSY-RGAIQ ALRKSLPDKKLLNGLCPKITY 260 0 0 0 0 0 0 0 0 0 0 0 0 0	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL S TVATILYF LYGINMF LYAGINFS LYAAINFS VVGIIYIF VVGIYIF VVGIYIF VVGIYIF VVGIYIF VVGILIF C10 FFLGLALR	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL SWFNVA CWSAVQLKIDS CWSAVQLKIDS CWSAVQLKIDS CWSAVLQLSD SWFNVK CYLSFW CWFNVK CWFNVK TFFNIK 340 LVYYHWLHPSCC	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT EGRT EGRT EGRS EGRT EGRT EGRT EGRT 	a7 240 H GLWLVLLLW I INFFSFLY F VINFLIILFE VOI IYFVSLAN F VLHWCIMTFW F VHWCAMAFW F VHWCAMAFW F VHWCAMAFW F VHWCAMAFW F HWCVMTFW L FLWLLGITW øg RGRAIIHFAFLLGIW WGHMGLHYSVRL øg WGHRILHYSFQFI RCRLFIYYFVILI RRMTLYHCYVFVILI RRRMTLYHCIVL RRRMTLYHCIVL XCPMSCYYIVRV 360 DGARSLLSPEGYU	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC UVAQQSDII IIHGGTDFC VIQGETDFC AFKNNTQFC 300 SDSI-LLVATWVT IENA-ILLLWYL VENV-IMULVFKF ENV-IMILVFKF ENV-IMILVFKF ENT-ALSALWYL LENI-ILLLAT- FENA-ALTFLWYF ENA-ALTFWYF LENA-ALTFWYF LENA-ALTGFWYS LGTLGILTVFWVC
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR6 XKR7 XKR9 XKR8 XKR4 XKR5 XKR6 XKR7 XKR9	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ VLRDSRDDKKSMSY-RGAIQ VLRDSRDDKKLLNGLCPKITY 260 CHARGE ENIEKALSRVGTIVLCFLTY 000 ENIEKALSRVGTIVLCFLTY NNIEKNFSRVGTLVVLISVTY GNKENNSNMVGTVLMLFLITY 	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LYAGINFS LYAATILYF LYAGINFS LYAATISS VVGIIYIF LVGAVYIL VVGIVYIF VVGIYIF VVGIYIF VVGIYIF VVGILIF α10 FFLGLALR YCTAILFM	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLL SWFNVA CWSAVQLKIDS CWSALQLRLAD CWSAVKLQLSD SWFNVK CYLSFW CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT EGRT EGRT EGRT EGRT EGRT EGRT EGRT 	a7 240 H GLWLVLLLW I INFFSFLY F V.I. F V.H. GRAND V.H. 360 DGARSLLSPEGY GFQRWLRCF V.H.	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC UVAQQSDII IIHGGTDFC VIQGETDFC AFKNNTQFC 300 SDSI-LLVATWVT ENA-ILLLWYL VENV-IMVLVFKF ENV-IMVLVFKF ENT-ALSALWYL ENI-ILLLAT- FENA-ALTFLWYF ENA-ALTFWYF ENA-ALTFWYF ENA-ALTFWYF CGTLGILTVFWVC QLPQ-25END CRQQ-42END
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR2 XKR3 XKR4 XKR2 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR2 XKR8 XKR6 XKR7 XKR8 XKR8 XKR8 XKR8 XKR8 XKR8 XKR8 XKR8	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ VLRDSRDDKKSMSY-RGAIQ VLRDSRDDKKLLNGLCPKITY 260 COMMONSTRUCTIVLCFLTY	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL 8 TVATILYF LYTGINMF LYAGINFS LYAAINFS VVGIIYIF VVGIYIF VVGIYIF VVGIYIF VVGIYIF VVGIYIF VVGIYIF VVGIYIF VVGIYIF VVGIYIF VVGIXIF FFLGLALR YCTAILFM	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL SWFNVA CWSAVQLKIDS CWSAUQLRLAD CWSAVKLQLSD SWFNVK CYLSFW CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT EGRT EGRT EGRS GQNT a11 CWKPDPDQV KLFSSSVSE SLFTHNVVD	α7 240 H GLWLVLLW I INFFSFLY F VINFLIILFE V.I IYFVSLA F VLHWCIMTFW V.I IYFVSLA F VLHWCIMTFW V.V HWLVMTFW F VHWCAMAFW F AHWCVMTFW L FLWLLGITW α9 RGRAIIHFAFLI WGHRILHYSVRLW α9 WGHRLHYSVRLW RGRAIIHFAFLI WGHRLLYSVRLW α9 RRMMCLYYMIRF RCRLFIYFVILJ RNRMVTFYMVMIN RRRMTLYHCIVL RRRMTLYHCIVL RRRMTLYHCIVL 360 DGARSLLSPEGY GFQRWLRCFCWA YLHCVCCHQHPR	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC LVAQQSDII IIHGGTDFC VIQGETDFC 300 SDSI-LLVATWVT ENA-ILLLWYL VENV-IMILVFKF LENT-ALSALWYL LENI-ILLLAT- FENA-ALTFLWYF LENA-ALTFWYF LENA-ALTGFWYS LGTLGILTVFWVC 2LPQ-25END CRQQ-42END TRVE-15END
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR2 XKR2 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR2 XKR8 XKR2 XKR8 XKR2 XKR8 XKR3	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIIQ VLRDSRDDKKPLSY-KGAVAQ ALRKSLPDKKLLNGLCPKITY 260 C PDPSSEWLYRV ENIEKALSRVGTIVLCFLTI NNIEKNFSRVGTLVVLISVTI GNKENNSNMVGTVLMLFLTI 	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL 8 TVATILYF LYTGINMF LYAGINFS LYAAINFS VVGIIYIF VVGIYIF VVGIYIF VVGIYIF VVGIYIF VVGIYIF VVGIYIF VVGILIF α10 FFLGLALR YCTAILFM YLLSIGFM	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL SWFNVA CWSAVQLKIDS CWSAVQLY CWSAVQ	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF 280 EGRT PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT EGRT EGRT CWKPDPDQV KLFSSSVSE SLFTHNVVD SGKVLPGRT	α7 240 H GLWLVLLW I INFFSFLY F V.I. F INFFSFLY F V.N.FLIILFE V.I. IYFVSLA F V.HWCIMTFW V.V. IYFVSLA F V.HWCAMAFW WQHUSH CONSTRUCTION α9 RGRAIIHFAFLI WGHRGLHYSVRLW CONSTRUCTION GROW SCHINCK RRMTLYHCIVL RRRMTLYHCIVL RRRMTLYHCIVL X MGARSLLSPEGY GFQRWLRCFCWA YLHCVCCHQHPK Y ENQPEAPYYW X	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC LVAQQSDII IIHGGTDFC VIQGETDFC AFKNNTQFC 300 SDSI-LLVATWVT ENA-ILLLWYL VENV-IMILVFKF LENT-ALSALWYL LENI-ILLLAT- FENA-ALTFLWYF LENI-ILLLAT- FENA-ALTFWYF LENI-ILLAT- FENA-ALTFWYF FENA-ALTF
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR2 XKR3 XKR4 XKR2 XKR6 XKR7 XKR9 XKR8 XKR4 XKR7 XKR9 XKR8 XKR4 XKR2 XKR3 XKR4	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIIQ FMGFMKPGHLAMPW-AALFCQ LIRDSRDDKKSMSY-RGAIQ VIRDSRDDKKPLSY-KGAVAQ ALRKSLPDKKLLNGLCPKITY 260 Q PDPSSEWLYR ENIEKALSRVGTTIVLCFLT NNIEKNFSRVGTLVVLISVT GNKENNSNMVGTVLMLFLIT TKWEEIVFD MSKWEEIIFN MSKWEEIIFN TCISMEFLYR 320 HSSWLPSGIPLQLWLPVGCGC FKTDIYMYVCAPLLVLQLIG FGVKVLLNYCHSLIALQLIA FGGKTLINCCDSLIAVQLIS	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI LYKLFTL 8 TVATILYF LYAGINFS LYAGINFS LYAGINFS LYAGINFS LYAGINFS VVGIIYIF VVGIIYIF VVGIIYIF VVGILIF alo FFLGLALR YCTAILFM YLLSIGFM YLLATGFM	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWMLSVVLLL SWFNVA CWSAVQLKIDS CWSAVQLKIDS CWSAVKLQLSD SWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK LVYYHWLHPSC LVFYQFFHPCK LLFYQYLYPWQ LMYYAFFHPNG	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF 280 EGRT PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT EGRT EGRT EGRT EGRT CWKPDPDQV KLFSSSVSE SLFTHNVVD SGKVLPGRT PRFGQSPSC	a7 240 Heiglwight GLWLVLLW IIIFFSFFLY FININFLIILFE VMIIYFVSLA FININFLIILFE VMIIYFVSLA FININFLIILFE VMIIYFVSLA FININFLIILFE VMIIYFVSLA FININF VMIIYFVSLA FININF VMIIYFVSLA FININF VMINF VMINF VHWCAMAFW FININF VMINF VHWCAMAFW FININF VMINF VHWCAMAFW GRAILHFAFLL WGHRILHYSFQF RCRLFIYFVIL RRRMTLHYSFQF RRRMTLYHCIVL XCPMSCYYIVRV 360 DGARSLLSPEGY GFQRWLRCFCWAG YLHCVCCHQHPR ENQPEAPYYVN ACEDPAAAFTLF	WLQGTDFM PWILFWCSGSPFP PWIKFWRSGAQMP PWLEFWKSGAHLP IVHCETEFC UVAQQSDII IHGGTDFC JVAQTDFC JVAQTDFC AFKNNTQFC 300 SDSI-LLVATWVT IENA-ILLLWYL JENU-IMVLVFKF LENU-IMULVFKF LENU-IMILVFRF LENT-ALSALWYL LENI-ILLLAT- FENA-ALTFLWYF LENA-ALTFWYF LGTLGILTVFWVC QLPQ-25END CRQQ-42END TRVE-15END IEKT-30END PDVA-108END
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR3 XKR4 XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR7 XKR9 XKR8 XKR2 XKR3 XKR4 XKR5 XKR7 XKR9 XKR8 XKR5 XKR3 XKR4 XKR5 XKR3 XKR4 XKR5 XKR3 XKR4 XKR5 XKR3 XKR4 XKR5 XKR3 XKR4 XKR5 XKR5 XKR6 XKR7 XKR3 XKR4 XKR5 XKR5 XKR6 XKR7 XKR9 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR3 XKR4 XKR5 XKR6 XKR7 XKR3 XKR4 XKR5 XKR3 XKR4 XKR5 XKR7 XKR3 XKR4 XKR5 XKR6 XKR7 XKR7 XKR7 XKR7 XKR7 XKR7 XKR7 XKR7	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKPLSY-KGAVAQ ALRKSLPDKKLLNGLCPKITY 260 Q 	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI LYKLFTI S TVATILYF LYYGINMF LYAGINFS LYAAINFS VVGIIYIF VVGIYIF VVGIYIF VVGIYIF VVGIYIF VVGIALRFM YLATGFM FLTGVVFM FLTGVVFM	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWHNVA CWSAVQLKIDS CWSALQLRLAD CWSAVKLQLSD SWFNVK CWFNVK CWFNVK TFFNIK 340 LVYYHWLHPSC LVFYQFFHPCK LLFFQYLHPLR LLFYQYLYPWQ LMYYAFFHPNG VIYYSLLHPKS	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF 280 EGRT PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT 	a7 240 HI GLWLVLLW INFFSFLY INFFSFLY FUNNFLIILFE VN IYFVSLA FUNNFLIILFE VN IYFVSLA FUNNFUNFV FUNNFLIILFE VN IYFVSLA FUNNFLIILFE VN IYFVSLA FUNNFLIILFE VN IYFVSLA FUNNFUN IYFVSLA FUNNFUN IYFVSLA FUNNFUN FUNNFUN FUNNFUN GAGAA GRAIIHFAFLL GAGAA WGHMGLHYSVRL WGHMGLHYSVRL WGHRILHYSFQF RRMMYFYMVMI RYRMFAYTYTVI STAN RYRMFAYTYTVI STAN J360 DGARSLLSPEGY(GFQRWLRCFCWA(YLHCVCCHQHPR' ENQPEAPYYVN ACEDPAAAFTLP KSCGIAGGDKTE GAGAAFTUATO	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC IVAQQSDII IHGGTDFC JQQFTDFC AFKNNTQFC 300 SDSI-LLVATWVT ENA-ILLLWYL VENV-IMVLVFKF ENV-IMILVFRF ENT-ALSALWYL ENI-ILLLAT- FENA-ALTFLWYF ENA-ALTFLWYF LENA-ALTFLWYF LENA-ALTFLWYF LGTLGILTVFWVC QLPQ-25-END CRQQ-42-END FRVE-15-END IEKT-30-END PDVA-108-END RDS-339-END
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR7 XKR9 XKR8 XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR8 XKR6 XKR7 XKR8 XKR3 XKR4 XKR5 XKR6 XKR7 XKR8 XKR3 XKR4 XKR5 XKR6 XKR7 XKR8 XKR3 XKR4 XKR5 XKR6 XKR7 XKR8 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR7 XKR9 XKR8 XKR7 XKR9 XKR8 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XKR6 XKR7 XKR9 XKR8 XKR6 XKR7 XKR8 XKR7 XKR8 XKR7 XKR8 XKR7 XKR8 XKR7 XKR8 XKR7 XKR8 XKR7 XKR8 XKR7 XKR8 XKR7 XKR8 XKR7 XKR8 XKR7 XKR8 XKR7 XKR8 XKR7 XKR7 XKR7 XKR7 XKR7 XKR7 XKR7 XKR7	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIQ FMGFMKPGHLAMPW-AALFCQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKPLSY-KGAVAQ ALRKSLPDKKLLNGLCPKITY 260 Q 260 Q 2	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI LFYKLFTI 38 TVATILYF LYAGINFS LYAGINFS LYAGINFS LYAGINFS VVGIIYIF VVGIIYIF VVGIIYIF VVGIIYIF VVGIIYIF TLGALALR YLLSIGFM YLLATGFM FLTGVVFM FLIGSVSL	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWHNVA CWSAVQLKIDS CWSALQLRLAD CWSAVKLQLSD SWFNVK CWSAVKLQLSD SWFNVK CWFNVK CWFNVK TFFNIK 340 LVYYHWLHPSC LVYQFFHPCK LLFFQYLHPLR LLFYQYLYPWQ LMYYAFFHPNG VIYYSLLHPKS LLYYQVLYPWC	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF 280 EGRT PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT 	a7 240 HI GLWLVLLW INFFSFLY I INFFSFLY FLUNFLIILFE VN IIYFVSLA FLUNFLIILFE VN IIYFVSLA FLUNFLILFE VN IIYFVSLA FLUNFW VN IIYFVSLA FLUNFW FVLHWCIMTFW FVNHWCAMAFW FVLHWCIMTFW FVNHWCAMAFW FVNHWCAMAFW FVNHWCAMAFW FVNHWCAMAFW GPLWYLKING GRAIIHFAFLI GP WGHMGLHYSVRL G9 RGRAIIHFAFLI GP WGHMGLHYSVRL G9 RGRAIIHFAFLI G9 RGRAIIHFAFLI G9 RGRAIIHFAFLI G9 RGRAIIHFAFLI G9 RGRAILYSVR G9 RGRAILHYSVR G9 RGRAILLYSVR G9 RRMTLYHCIVI G1 XCPMSCYYIVRV 360 DGARSLLSPEGY GFQRWLRCFCWAG YLHCVCCHQHPR ENQPEAPYYVN ACEDPAAFTLP KSCGIAGGDKTEI CCAELLWGIPLE G14000000000000000000000000000000000000	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP IVHCETEFC IVAQQSDII IHGGTDFC JVAQQSDII IHGGTDFC AFKNNTQFC 300 SDSI-LIVATWVT ENA-ILLLWYL VENV-IMVLVFKF ENV-IMILVFRF ENT-ALSALWYL ENI-ILLLAT- TENA-ALTFLWYF ENA-ALTFLWYF LENA-
XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XK XKR2 XKR3 XKR4 XKR5 XKR6 XKR7 XKR9 XKR8 XK XKR2 XKR3 XKR4 XKR2 XKR3 XKR4 XKR7 XKR7 XKR8 XKR7 XKR8 XKR7 XKR7 XKR7 XKR7 XKR7 XKR7 XKR7 XKR7	200 ALRTCLPSKPLLGL-GSSVIY AIKIKYDEYEVKVKPLAYVCI AIQIKYDDYKIRLGPLEVLCI AIQISNDDTTIKLPPIEFFCV ALRDSRDDKKPISY-MAVIQ FMGFMKPGHLAMPW-AALFCQ LLRDSRDDKKSMSY-RGAIQ ULRDSRDDKKPLSY-KGAVAQ AIRKSLPDKKLLNGLCPKITY 260 260 0 260 0 260 0 260 0 260 0 260 0 260 0 260 0 260 0 260 0 260 0 260 0 260 0 260 0 0 260 0 0 260 0 0 260 0 0 260 0 0 260 0 0 260 0 0 260 0 0 260 0 0 0 0 0 0 0 0 0 0 0 0 0	C FLWNLLLL FLWRSFEI TIWRTLEI VMWRFLEV FCWHFFTI QLWRMGML VFWRLFTI VLWHLFSI LFYKLFTL 8 TVATILYF LYAGINFS LYAGINFS LYAGINFS LYAGINFS VVGIIYIF VVGIYIF VVGIYIF FFLGLALR YCTAILFM YLLATGFM FLTGVVFM FALGIFFM	6 220 WPRVLAVALFS ATRVVVLVLFT TSRLLILVLFS ISRVVTLAFFI AARVITFALFA GTRVLSLVLFY SSRVISFALFA AARGLAFALFA LSWHNVA CWSAVQLKIDS CWSALQLRLAD CWSAVKLQLSD SWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK CWFNVK LVYYWLLHPSC LVYYLLHPKS LLYYGVLHPTG CVYYCLLHPKS LLYYGVLHPTG CVYYCLLHPKS LLYYGVLMAAN	ALFPSYVAI SVLKTWVVV ATLKLKAVP ASLKLKSLP SVFQLYFGI KAYHFWVFV SIFQLYFGI SVYKLYFGI FLNVKIALF FLNVKIALF PDLISKSHN RDLVDKGQN DKIIDGRQR EGRT EGRT EGRT EGRT CWKPDPDQV KLFSSVSE SLFTHNVVD SGKVLPGRT PRFGQSPSC TDIWQGCLR PRAKILASS PMLGPQAPC	a7 240 HIGLWLVLLW IIIFFSFLY FUINFLIILFE VIIIFLIILFE VIIIFLIILFE VIIIFLIILFE VIIIFLIILFE VIIIFLIILFE VIIIFLIILFE VIIIFLIIFE VIIIFLIIFE VIIIFLIIFE VIIIFLIIFE VIIIFLIIFE VIIIFL FUNT GARMENT FUNT GRAIIHFAFLI WYQLLVYMIRF WGHMGLHYSVRL WGHMGLHYSVRL WGHRILHYSPOFI RRRMTLYHCIVI RRRMTYTYVII XCPMSCYYIVRVI 360 DGARSLLSPEGYO GFQRWLRCFCWAG YLHCVCCHQHPR' ENQPEAPYYVNI ACEDPAAAFTLPI KSCGIAGGDKTEI CCAELLWGIPLPI CIFRKASEPCGPI	WLQGTDFM WILFWCSGSPFP WIKFWRSGAQMP WLEFWKSGAHLP WLEFWKSGAHLP VHCETEFC VAQQSDII IHGGTDFC VIQGETDFC AFKNNTQFC 300 SDSI-LIVATWVT ENA-ILLLWYL VENV-IMVLVFKF ENV-IMILVFRF ENT-ALSALWYL ENI-ILLLAT- FENA-ALTFLWYF ENA-ALTFLWYF ENA-ALTGFWYS LGTLGILTVFWVC QLPQ-25-END CRQQ-42-END FRVE-15-END IEKT-30-END PDVA-108-END RRDS-339-END PDVE-114-END PADA-111-END

Supplementary Fig. 3. Alignment of amino acid sequences of the human XKR family. Amino acid sequences of XKR8 (Q9H6D3), XK (P51811), XKR2 (Q6PP77), XKR3 (Q5GH77), XKR4 (Q5GH76), XKR5 (Q6UX68), XKR6 (Q5GH73), XKR7 (Q5GH72), and XKR9 (Q5GH70) were aligned by introducing several gaps to obtain maximum homology. Amino acids that were identical among all members are shown in red, while those in the same categories (non-polar: G, A, V, I, L, P, F, W, and M;

uncharged polar: S, T, C, Y, Q, and N; charged polar: D, E, K, R, and H) are in orange. Eleven α -helices are shadowed and numbered. Hydrophobic amino acids forming the cleft carrying PtdCho are highlighted in green, while the charged amino acids that lie in the putative phospholipid path are in yellow. A pair of amino acids in XK (R222 and E327), the mutation of which was identified as missense mutations in McLeod syndrome^{34,35}, are highlighted in magenta. Numbers above the first line are the amino acid positions for human XKR8.



Supplementary Fig. 4. Representative gating strategy for flow cytometric analysis. a, Gating strategy for flow cytometric analysis of Annexin V staining of Ba/F3 transformants expressing the GFP-tagged hXkr8 (Fig. 4a,d, Fig. 5h, and Fig. 6a,b,e,f.). b, Gating strategy for flow cytometric analysis of NBD-SM incorporation by Ba/F3 transformants (Fig. 4c,d, Fig. 6d, and Extended Data Fig. 8a,b). c, Gating strategy for flow cytometric analysis of Annexin V staining of W3 transformants (Extended Data Fig. 1c).