

		10	20	30	40	50	
AKR1C2	1	MDSKYQCVKLN	DGHFMPVLG	FGTYAPAEV	PKSKALEAV	KLAIEAGFH	HIDSAHVYNNEEQ 60
		MDSK+QCVKLN	DGHFMPVLG	FGTYAP	EVP+SKALE	KLAIEAGF	HIDSAH+YNNEEQ
AKR1C3	1	MDSKHQCVKLN	DGHFMPVLG	FGTYAPPEV	PRSKALEVT	KLAIEAGFR	HIDSAHLYNNEEQ 60
AKR1C2	61	VGLAIRSKIAD	GSVKREDIF	YTSKLSNS	HRPELVRPA	LERSLKNLQ	LDYVDLYLIHFPV 120
		VGLAIRSKIAD	GSVKREDIF	YTSKLS	HRPELVRPA	LE SLK	QLDYVDLYLIH P+
AKR1C3	61	VGLAIRSKIAD	GSVKREDIF	YTSKLSW	STFHRPEL	VRPALENSL	KKQAQLDYVDLYLIHSPM 120
AKR1C2	121	SVKPGEEV	I	PKDENGKIL	FDTVDLCAT	WEAMEKCK	DAGLAKSIGVSNFNHRLLEMILNKP 180
		S+KPGEE+ P	DENGK++FD	VDLC	TWEAMEKCK	DAGLAKSIGVSNFN	R LEMILNKP
AKR1C3	121	SLKPGEE	LS	PTDENGK	VIFDIVDLC	TTWEAMEKCK	DAGLAKSIGVSNFNRRQLEMILNKP 180
AKR1C2	181	GLKYKPCVN	QVECHPYFN	RQKLLDF	CKSKDIVLV	VAYSALGSH	REEPWVDPNSPVLLEDPV 240
		GLKYKPCVN	QVECHPYFN+	KLLDF	CKSKDIVLV	VAYSALGS	R++ WVDPNSPVLLEDPV
AKR1C3	181	GLKYKPCVN	QVECHPYFN	RSKLLDF	CKSKDIVLV	VAYSALGS	QRDKRWVDPNSPVLLEDPV 240
AKR1C2	241	LCALAKKHK	RTPALIAL	RYQLQRG	VVVLAKSY	NEQRIRQ	NVQVFEFQLTSEEMKAIDGLN 300
		LCALAKKHK	RTPALIAL	RYQLQRG	VVVLAKSY	NEQRIRQ	NVQVFEFQLT+E+MKAIDGL+
AKR1C3	241	LCALAKKHK	RTPALIAL	RYQLQRG	VVVLAKSY	NEQRIRQ	NVQVFEFQLTAEDMKAIDGLD 300
AKR1C2	301	RNVRYLT	LDI	FAGPPNYP	SDEY		323
		RN+ Y	D	FA	PNYP+SDEY		
AKR1C3	301	RNLHY	FNS	DSF	AASHPNYP	SDEY	323

Supplemental. Sequence alignment of human AKR1C2 and AKR1C3 using the 'align two or more sequences' feature of protein BLAST (<https://blast.ncbi.nlm.nih.gov>). AKR1C3 shares 91% sequence similarity and 87% identity with AKR1C2. Identical residues are shown in the consensus sequence between the two compared sequences. Similar residues are marked with a '+'. Residues in contact with compound **2** in the structure of **AKR1C3·NADP+·2** are shown in bold and highlighted in yellow. Of these 11 residues, 3 residues that are different in AKR1C2 are shown in red and highlighted in yellow.