

## Sequence alignment between *Ailuropoda melanoleuca* P2X7 (AmP2X7) and *Homo sapiens* P2X7 (HsP2X7) using BLAST

RID: P9XTZYJU114

Job Title:tr|G1M6C4|G1M6C4\_AILME ATP receptor OS=Ailuropoda...

Program: BLASTP

**Query:** tr|G1M6C4|G1M6C4\_AILME ATP receptor OS=Ailuropoda melanoleuca OX=9646

GN=P2RX7 PE=1 SV=2 ID: lcl|Query\_50083(amino acid) Length: 606

**Subject:**sp|Q99572|P2RX7\_HUMAN P2X purinoceptor 7 OS=Homo sapiens OX=9606 GN=P2RX7

PE=1 SV=4 ID: lcl|Query\_50085(amino acid) Length: 595

Sequences producing significant alignments:

							Scientific
Common	Max	Total	Query	E	Per.	Acc.	
Description							Name
Name	Taxid	Score	Score	cover	Value	Ident	Len
							Accession
sp Q99572 P2RX7_HUMAN P2X purinoceptor 7 OS=Homo sapiens OX=96...							
0	1060	1060	98%	0.0	84.71	595	Query_50085
Alignments:							
>sp Q99572 P2RX7_HUMAN P2X purinoceptor 7 OS=Homo sapiens OX=9606 GN=P2RX7 PE=1 SV=4							
Sequence ID: Query_50085 Length: 595							
Range 1: 1 to 595							
Score:1060 bits(2742), Expect:0.0,							
Method:Compositional matrix adjust.,							
Identities:504/595(85%), Positives:545/595(91%), Gaps:1/595(0%)							
Query	1	MPACCSWKDV	FQYETNKVLR	IQSTNYGTIKWIFHVLVFSYISFALISDKRYQKKEPLISS	60		
		MPACCS	DVFQYETNKV	RIQS NYGTIKW FHV++FSY+ FAL+SDK YQ+KEP+ISS			
Sbjct	1	MPACCSCSDV	FQYETNKVTRI	QSMNYGTIKWFFHVIIIFSVCFALVSDKLYQRKEPVISS	60		
Query	61	VHTKVKGIAE	VEKAEILENGM	KKMVSGVFDTADYTFPLQGNSFFVMTNFIKTEGQQQGLCP	120		
		VHTKVKGIAE	VEK EI+ENG+KK+V	VEDTADYTFPLQGNSFFVMTNF+KTEGQ+Q LCP			
Sbjct	61	VHTKVKGIAE	VEKKEIIVENG	VKKLVHVSVEDTADYTFPLQGNSFFVMTNFIKTEGQEQLCP	120		
Query	121	DFPTRRTICSS	DRGCKKGRMDP	QSKGIQTGRVCVYKERLKTCEVSAWCPIEEVEDAPRPA	180		
		++PTRRT+CSS	DRGCKKG MDP	QSKGIQTGRVCVY+ KTCEVSAWCPIE VE+APRPA			
Sbjct	121	EYPTRRTLCS	SDRGCKKGWMDP	QSKGIQTGRVCVYEGNQKTCEVSAWCPIEAVEEAPRPA	180		
Query	181	LLNSAENFTV	LIKNNIDFPGH	NYTTRNILPGVNITCTFHKTQNPQCPIFRLGDIFQETGD	240		
		LLNSAENFTV	LIKNNIDFPGH	NYTTRNILPG+NITCTFHKTQNPQCPIFRLGDIF+ETGD			
Sbjct	181	LLNSAENFTV	LIKNNIDFPGH	NYTTRNILPGLNITCTFHKTQNPQCPIFRLGDIFRETGD	240		
Query	241	NFSDVAIQGG	IMGIEIYWDCN	LDGWFFHCRPKYSFRRLDDKTNTNESLYPGYNFRYAKYYK	300		
		NFSDVAIQGG	IMGIEIYWDCN	LDWFHCRPKYSFRRLDDKTN SLYPGYNFRYAKYYK			
Sbjct	241	NFSDVAIQGG	IMGIEIYWDCN	LDLRFHCRPKYSFRRLDDKTNTNVS LYPGYNFRYAKYYK	300		
Query	301	ENNVEKRTL	IKVFGIRFDIL	VFGTGGKFNVIQLAVYIGSVISYFGLATVFIDILINTYSS	360		
		ENNVEKRTL	IKVFGIRFDIL	VFGTGGKF++IQL VYIGS +SYFGLA VFID LI+TYSS			
Sbjct	301	ENNVEKRTL	IKVFGIRFDIL	VFGTGGKFDIIQLVVYIGSTLSYFGLAAVFIDFLIDTYSS	360		
Query	361	KCCRSRIYPC	FKCCEYCAVNE	YYYRKKKSEPIAEPKPTLKYVSFVDETHIRMVDQQLLGKS	420		
		CCRS IYP KCC+	C VNEYYYRKK E I	EPKPTLKYVSFVDE+HIRMV+QQLLG+S			
Sbjct	361	NCCRSHIYP	WCKCCQPCVV	NEYYYRKKCESIVEPKPTLKYVSFVDESHIRMVNQQLLGRS	420		
Query	421	LQNVKGEKV	QRPVDFDLSR	LSLSCDPTPIPGQPEEMQLFSEEVT	480		
		LQ+VKG++V	RP++DFTDLSR	L+L D PIPGQPEE+QL +E TPRS +SP WCQCG			
Sbjct	421	LQDVKGQEV	PRPAMDFTDLSR	LPLALHDTPIPGQPEEIQLLRKEATPRS	480		
Query	481	HCLPSQLPES	HRCLEELCCR	KKAGACITTSEPFRKLVLRSQVLQFLLLYQEPLLVDGNS	540		
		CLPSQLPES	HRCLEELCCR	KK GACITTSE FRKLVLRS VLQFLLLYQEPLL LD +S			
Sbjct	481	SCLPSQLPES	HRCLEELCCR	KKPGACITTSELFRKLVLRSRHLQFLLLYQEPLLALDVS	540		
Query	541	S-SRLRHCA	YRCYTTWRF	GSPDLADFAILPSCCRWRIRREFPKSEGQYTG	595		
		+ SRLRHCA	YRCY TWRFGS	D+ADFAILPSCCRWRIR+EFPKSEGQY+GF+SPY			
Sbjct	541	TNSRLRHCA	YRCYATWRF	GSDMADFAILPSCCRWRIRKEFPKSEGQYSGFKSPY	595		

Residues highlighted in yellow form the allosteric binding site that accommodates JNJ-47965567.