Chain A, Human N-Acetyltransferase 2

Sequence ID: 2PFR_A **Length:** 294 **Number of Matches:** 1

e 1 more title(s)

Range 1: 6 to 294 GenPept Graphics Next Match Previous Match

Related Information

Structure - 3D structure displays

Identical Proteins - Identical proteins to 2PFR_A

Score	Expect	Method	Identities	Positives	Gaps
601 bits (1549)	0.0	Compositional matrix adjust.	289/289 (100%)	289/289 (100%)	0/289 (0%)

```
Query  2    DIEAYFERIGYKNSRNKLDLETLTDILEHQIRAVPFENLNMHCGQAMELGLEAIFDHIVR  61
            DIEAYFERIGYKNSRNKLDLETLTDILEHQIRAVPFENLNMHCGQAMELGLEAIFDHIVR
Sbjct  6    DIEAYFERIGYKNSRNKLDLETLTDILEHQIRAVPFENLNMHCGQAMELGLEAIFDHIVR  65

Query  62   RNRGGWCLQVNQLLYWALTTIGFQTTMLGGYFYIPPVNKYSTGMVHLLLQVTIDGRNYIV  121
            RNRGGWCLQVNQLLYWALTTIGFQTTMLGGYFYIPPVNKYSTGMVHLLLQVTIDGRNYIV
Sbjct  66   RNRGGWCLQVNQLLYWALTTIGFQTTMLGGYFYIPPVNKYSTGMVHLLLQVTIDGRNYIV  125

Query  122  DAGSGSSSQMWQPLELISGKDQPQVPCIFCLTEERGIWYLDQIRREQYITNKEFLNSHLL  181
            DAGSGSSSQMWQPLELISGKDQPQVPCIFCLTEERGIWYLDQIRREQYITNKEFLNSHLL
Sbjct  126  DAGSGSSSQMWQPLELISGKDQPQVPCIFCLTEERGIWYLDQIRREQYITNKEFLNSHLL  185

Query  182  PKKKHQKIYLFTLEPRTIEDFESMNTYLQTSPTSSFITTSFCSLQTPEGVYCLVGFILTY  241
            PKKKHQKIYLFTLEPRTIEDFESMNTYLQTSPTSSFITTSFCSLQTPEGVYCLVGFILTY
Sbjct  186  PKKKHQKIYLFTLEPRTIEDFESMNTYLQTSPTSSFITTSFCSLQTPEGVYCLVGFILTY  245

Query  242  RKFNYKDNTDLVEFKTLTEEEVEEVLKNIFKISLGRNLVPKPGDGSLTI  290
            RKFNYKDNTDLVEFKTLTEEEVEEVLKNIFKISLGRNLVPKPGDGSLTI
Sbjct  246  RKFNYKDNTDLVEFKTLTEEEVEEVLKNIFKISLGRNLVPKPGDGSLTI  294
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Supplementary Figure S2. pBLAST results showing maximum identity between template 2PFR and the target WT-human-NAT2 sequence P11245. WT: wild type; NAT2: *N*-acetyl transferase 2.