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## Entry information

Entry name	<b>A1A1_HORSE</b>
Primary accession number	<b>P18907</b>
Secondary accession numbers	None
Entered in Swiss-Prot in	Release 16, November 1990
Sequence was last modified in	Release 16, November 1990
Annotations were last modified in	Release 43, March 2004

## Name and origin of the protein

Protein name	<b>Sodium/potassium-transporting ATPase alpha-1 chain [Precursor]</b>
Synonyms	<b>EC <a href="#">3.6.3.9</a> Sodium pump 1 Na<sup>+</sup>/K<sup>+</sup> ATPase 1</b>
Gene name	<b>ATP1A1</b>
From	<a href="#">Equus caballus (Horse)</a> [TaxID: <a href="#">9796</a> ]
Taxonomy	<a href="#">Eukaryota</a> ; <a href="#">Metazoa</a> ; <a href="#">Chordata</a> ; <a href="#">Craniata</a> ; <a href="#">Vertebrata</a> ; <a href="#">Euteleostomi</a> ; <a href="#">Mammalia</a> ; <a href="#">Eutheria</a> ; <a href="#">Perissodactyla</a> ; <a href="#">Equidae</a> ; <a href="#">Equus</a> .

## References

## [1] SEQUENCE FROM NUCLEIC ACID.

MEDLINE=89290042; PubMed=2544461; [[NCBI](#), [ExPASy](#), [EBI](#), [Israel](#), [Japan](#)]  
[Kano I.](#), [Nagai F.](#), [Satoh K.](#), [Ushiyama K.](#), [Nakao T.](#), [Kano K.](#);  
 "Structure of the alpha 1 subunit of horse Na,K-ATPase gene."  
 FEBS Lett. 250:91-98(1989).

**Comments**

- **FUNCTION:** This is the catalytic component of the active enzyme, which catalyzes the hydrolysis of ATP coupled with the exchange of sodium and potassium ions across the plasma membrane. This action creates the electrochemical gradient of sodium and potassium ions, providing the energy for active transport of various nutrients.
- **CATALYTIC ACTIVITY:**  $\text{ATP} + \text{H}_2\text{O} + \text{Na}^+(\text{In}) + \text{K}^+(\text{Out}) = \text{ADP} + \text{phosphate} + \text{Na}^+(\text{Out}) + \text{K}^+(\text{In})$ .
- **SUBUNIT:** Composed of three subunits: alpha (catalytic), beta and gamma.
- **SUBCELLULAR LOCATION:** Integral membrane protein.
- **PTM:** Phosphorylation on Tyr-10 modulates pumping activity (*By similarity*).
- **SIMILARITY:** Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IIC.

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**Cross-references**

	X16773; CAA34716.1; -.	<a href="#">[EMBL / GenBank / DDBJ]</a> <a href="#">[CoDingSequence]</a>
	X16774; CAA34716.1; JOINED.	<a href="#">[EMBL / GenBank / DDBJ]</a> <a href="#">[CoDingSequence]</a>
	X16775; CAA34716.1; JOINED.	<a href="#">[EMBL / GenBank / DDBJ]</a> <a href="#">[CoDingSequence]</a>
	X16776; CAA34716.1; JOINED.	<a href="#">[EMBL / GenBank / DDBJ]</a> <a href="#">[CoDingSequence]</a>
	X16777; CAA34716.1; JOINED.	<a href="#">[EMBL / GenBank / DDBJ]</a> <a href="#">[CoDingSequence]</a>
EMBL	X16778; CAA34716.1; JOINED.	<a href="#">[EMBL / GenBank / DDBJ]</a> <a href="#">[CoDingSequence]</a>
	X16779; CAA34716.1; JOINED.	<a href="#">[EMBL / GenBank / DDBJ]</a> <a href="#">[CoDingSequence]</a>
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	X16781; CAA34716.1; JOINED.	<a href="#">[EMBL / GenBank / DDBJ]</a> <a href="#">[CoDingSequence]</a>
	X16782; CAA34716.1; JOINED.	<a href="#">[EMBL / GenBank / DDBJ]</a> <a href="#">[CoDingSequence]</a>

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 X16784; CAA34716.1; [\[EMBL / GenBank / DDBJ\]](#)  
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 X16785; CAA34716.1; [\[EMBL / GenBank / DDBJ\]](#)  
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 X16795; CAA34716.1; [\[EMBL / GenBank / DDBJ\]](#)  
 JOINED. [\[CoDingSequence\]](#)

PIR [S04630](#); S04630.

HSSP [P04191](#); 1EUL. [\[HSSP ENTRY / PDB\]](#)

[GO:0005890](#); Cellular component: sodium/potassium-exchanging ATPase complex (*inferred from sequence or structural similarity*).

[GO:0005391](#); Molecular function: sodium/potassium-exchanging ATPase activity (*inferred from sequence or structural similarity*).

[GO:0015991](#); Biological process: ATP hydrolysis coupled proton transport (*inferred from sequence or structural similarity*).

GO

[GO:0030641](#); Biological process: hydrogen ion homeostasis (*inferred from sequence or structural similarity*).

[GO:0006813](#); Biological process: potassium ion transport (*inferred from sequence or structural similarity*).

[GO:0006814](#); Biological process: sodium ion transport (*inferred from sequence or structural similarity*).

[GO:0030317](#); Biological process: sperm motility (*inferred from sequence or structural similarity*).

[IPR001757](#); ATPase\_E1-E2.

InterPro

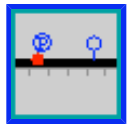
[IPR006069](#); Cation\_ATPase.

[IPR006068](#); Cation\_ATPase\_C.

	<a href="#">IPR004014</a> ; Cation_ATPase_N. <a href="#">IPR008250</a> ; E1-E2_ATPase_reg. <a href="#">IPR005834</a> ; Hydrolase. <a href="#">IPR005775</a> ; Na/K_ATPase_alph. <a href="#">Graphical view of domain structure.</a>
Pfam	<a href="#">PF00689</a> ; Cation_ATPase_C; 1. <a href="#">PF00690</a> ; Cation_ATPase_N; 1. <a href="#">PF00122</a> ; E1-E2_ATPase; 1. <a href="#">PF00702</a> ; Hydrolase; 1. <a href="#">Pfam graphical view of domain structure.</a>
PRINTS	<a href="#">PR00119</a> ; CATATPASE. <a href="#">PR00121</a> ; NAKATPASE.
TIGRFAMs	<a href="#">TIGR01106</a> ; ATPase-IIC_X-K; 1. <a href="#">TIGR01494</a> ; ATPase_P-type; 5.
PROSITE	<a href="#">PS00154</a> ; ATPASE_E1_E2; 1.
ProDom	[ <a href="#">Domain structure</a> / <a href="#">List of seq. sharing at least 1 domain</a> ]
HOVERGEN	[ <a href="#">Family</a> / <a href="#">Alignment</a> / <a href="#">Tree</a> ]
BLOCKS	<a href="#">P18907</a> .
ProtoNet	<a href="#">P18907</a> .
ProtoMap	<a href="#">P18907</a> .
PRESAGE	<a href="#">P18907</a> .
DIP	<a href="#">P18907</a> .
ModBase	<a href="#">P18907</a> .
SMR	<a href="#">P18907</a> ; 4FEB03FFB04E0216.
SWISS-2DPAGE	<a href="#">Get region on 2D PAGE.</a>

**Keywords**

[Hydrolase](#); [Sodium/potassium transport](#); [Transmembrane](#); [Phosphorylation](#); [Magnesium](#); [Metal-binding](#); [ATP-binding](#); [Multigene family](#).

**Features**

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Key	From	To	Length	Description
PROPEP	<a href="#">1</a>	<a href="#">5</a>	5	<i>By similarity.</i>
CHAIN	<a href="#">6</a>	<a href="#">1021</a>	1016	Sodium/potassium-transporting ATPase alpha-1 chain.
DOMAIN	<a href="#">6</a>	<a href="#">85</a>	80	Cytoplasmic ( <i>Potential</i> ).
TRANSMEM	<a href="#">86</a>	<a href="#">106</a>	21	<i>Potential.</i>
DOMAIN	<a href="#">107</a>	<a href="#">129</a>	23	Luminal ( <i>Potential</i> ).
TRANSMEM	<a href="#">130</a>	<a href="#">150</a>	21	<i>Potential.</i>
DOMAIN	<a href="#">151</a>	<a href="#">286</a>	136	Cytoplasmic ( <i>Potential</i> ).
TRANSMEM	<a href="#">287</a>	<a href="#">306</a>	20	<i>Potential.</i>
DOMAIN	<a href="#">307</a>	<a href="#">318</a>	12	Luminal ( <i>Potential</i> ).

TRANSMEM	<a href="#">319</a>	<a href="#">336</a>	18	<i>Potential.</i>
DOMAIN	<a href="#">337</a>	<a href="#">770</a>	434	Cytoplasmic ( <i>Potential</i> ).
TRANSMEM	<a href="#">771</a>	<a href="#">790</a>	20	<i>Potential.</i>
DOMAIN	<a href="#">791</a>	<a href="#">800</a>	10	Luminal ( <i>Potential</i> ).
TRANSMEM	<a href="#">801</a>	<a href="#">821</a>	21	<i>Potential.</i>
DOMAIN	<a href="#">822</a>	<a href="#">841</a>	20	Cytoplasmic ( <i>Potential</i> ).
TRANSMEM	<a href="#">842</a>	<a href="#">864</a>	23	<i>Potential.</i>
DOMAIN	<a href="#">865</a>	<a href="#">916</a>	52	Luminal ( <i>Potential</i> ).
TRANSMEM	<a href="#">917</a>	<a href="#">936</a>	20	<i>Potential.</i>
DOMAIN	<a href="#">937</a>	<a href="#">949</a>	13	Cytoplasmic ( <i>Potential</i> ).
TRANSMEM	<a href="#">950</a>	<a href="#">968</a>	19	<i>Potential.</i>
DOMAIN	<a href="#">969</a>	<a href="#">983</a>	15	Luminal ( <i>Potential</i> ).
TRANSMEM	<a href="#">984</a>	<a href="#">1004</a>	21	<i>Potential.</i>
DOMAIN	<a href="#">1005</a>	<a href="#">1021</a>	17	Cytoplasmic ( <i>Potential</i> ).
MOD_RES	<a href="#">10</a>	<a href="#">10</a>		PHOSPHORYLATION ( <i>BY SIMILARITY</i> ).
MOD_RES	<a href="#">16</a>	<a href="#">16</a>		PHOSPHORYLATION (BY PKC) ( <i>BY SIMILARITY</i> ).
MOD_RES	<a href="#">374</a>	<a href="#">374</a>		PHOSPHORYLATION ( <i>BY SIMILARITY</i> ).
MOD_RES	<a href="#">941</a>	<a href="#">941</a>		PHOSPHORYLATION (BY PKA) ( <i>BY SIMILARITY</i> ).
BINDING	<a href="#">80</a>	<a href="#">82</a>		BINDING OF PHOSPHOINOSITIDE-3 KINASE ( <i>BY SIMILARITY</i> ).
METAL	<a href="#">715</a>	<a href="#">715</a>		Magnesium ( <i>By similarity</i> ).
METAL	<a href="#">719</a>	<a href="#">719</a>		Magnesium ( <i>By similarity</i> ).

## Sequence information

Length: **1021 AA** [This is the length of the unprocessed precursor]      Molecular weight: **112696 Da** [This is the MW of the unprocessed precursor]      CRC64: **4FEB03FFB04E0216** [This is a checksum on the sequence]

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MGKGGGRDKY	EPAAISEHGN	KKKAKKERDM	DELKKEVSMD	DHKLSDLDELQ	RKYGTDLSRG
70	80	90	100	110	120
LTARAAEIL	ARDGPNALTP	PPTTPEWVKF	CRQLFGGFSM	LLWIGAILCF	LAYGIQAATE
130	140	150	160	170	180
EEPQNDNLYL	GVVLSAVVII	TGCFSYQEA	KSSKIMESFK	NMVPQQALVV	RNGEKMSINA
190	200	210	220	230	240
EEVVVGDIVE	VKGGDRIPAD	LRIISANGCK	VDNSSLTGES	EPQTRSPDFT	NENPLETRNI
250	260	270	280	290	300
AFFSTNCVEG	TARGIVVYTG	DRTVMGRIAT	LASGLEGGQT	PIAAEIEHFI	HIITGVAVFL
310	320	330	340	350	360

P18907 in  
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|           |           |           |           |           |           |
GVTFFILSLI LEYTWLEAVI FLIGIIVANV PEGLLATVTV CLTLTAKRMA RKNCLVKNLE
|           |           |           |           |           |           |
370         380         390         400         410         420
|           |           |           |           |           |           |
AVETLGSTST ICSDKTGTLT QNRMTVAHMW FDNQIHEADT TENQSGVSFD KTSATWLSLS
|           |           |           |           |           |           |
430         440         450         460         470         480
|           |           |           |           |           |           |
RIAGLCNRAV FQANQENIPI LKRAVAGDAS ESALLKCIEL CCGSVKEMRD RYPKIVEIPF
|           |           |           |           |           |           |
490         500         510         520         530         540
|           |           |           |           |           |           |
NSTNKYQLSI HKNPNTSEPO HLLVMKGAPD RILDRCSSIL LNGKEQPLDE ELKDAFQNAV
|           |           |           |           |           |           |
550         560         570         580         590         600
|           |           |           |           |           |           |
LELGGLGERV LGFCHLFLPD EQFPEGFQFD TDDVNFPLEN LCFVGLISMI DPPRAAVPDA
|           |           |           |           |           |           |
610         620         630         640         650         660
|           |           |           |           |           |           |
VGKCRSAGIK VIMVTGDHPI TAKAIAKGVG IISEGNETVE DIAARLNIPV SQVNPRDAKA
|           |           |           |           |           |           |
670         680         690         700         710         720
|           |           |           |           |           |           |
CVVHGSDLKD MTPEQLDDIL RHHTEIVFAR TSPQQKLIIV EGCQRQGAIV AVTGDGVNDS
|           |           |           |           |           |           |
730         740         750         760         770         780
|           |           |           |           |           |           |
PALKKADIGV AMGIAGSDVS KQAADMILLD DNFASIVTGV EEGRLIFDNL KKSIAAYTLTS
|           |           |           |           |           |           |
790         800         810         820         830         840
|           |           |           |           |           |           |
NIPEITPFLI FIIANIPLPL GTVTILCIDL GTDMVPAISL AYEQAESDIM KRQPRNPQTD
|           |           |           |           |           |           |
850         860         870         880         890         900
|           |           |           |           |           |           |
KLVNERLISM AYGQIGMIQA LGGFFTYFVI LAENGFLPIH LLGLRVDWDD RWVNDVEDSY
|           |           |           |           |           |           |
910         920         930         940         950         960
|           |           |           |           |           |           |
GQQWTYEQRK IVEFTCHTAF FVSIVVVQWA DLVICKTRRN SVFQQGMKNK ILIFGLFEET
|           |           |           |           |           |           |
970         980         990         1000        1010        1020
|           |           |           |           |           |           |
ALAAFLSYCP GMGVALRMYP LKPTWWFCAF PYSLLIFVYD EVRKLIIIRR PGGWVEKETY

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