



Statistics generated by:

smoensted

Sequences:

P39524, O94296, ATP8a1,

Date:

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1. Protein statistics

1.1 Sequence information

Information	P39524	O94296	ATP8a1
Sequence type	Protein	Protein	Protein
Length	1355 aa	1258 aa	1149 aa
Organism	Saccharomyces cerevisiae	Schizosaccharomyces pombe	Mus musculus
Name	P39524	O94296	ATP8a1
Description	RecName: Full=Probable phospholipid-transporting ATPase DRS2.	Probable phospholipid-transporting ATPase C887. 12.	Probable phospholipid-transporting ATPase IA (Chromaffin granule ATPase II) (ATPase class I type 8A member 1).
Modification Date	02-SEP-2008	29-APR-2008	05-FEB-2008
Weight	153,843 kDa	142,378 kDa	129,765 kDa
Isoelectric point	5,62	5,95	7,22
Aliphatic index	90,111	93,235	99,347

1.2 Half-life

Information	P39524	O94296	ATP8a1
N-terminal aa	Methionine	Methionine	Methionine
Half-life mammals	30 hours	30 hours	30 hours
Half-life yeast	>20 hours	>20 hours	>20 hours
Half-life E.Coli	>10 hours	>10 hours	>10 hours

1.3 Extinction coefficient

Conditions	P39524	O94296	ATP8a1
Non-reduced cysteines Extinction coefficient at 280nm	171 040	165 140	167 600
Non-reduced cysteines Absorption at 280nm 0.1% (=1 g/l)	1,112	1,16	1,292
Reduced cysteines Extinction coefficient at 280nm	170 260	164 000	166 280
Reduced cysteines Absorption at 280nm 0.1% (=1 g/l)	1,107	1,152	1,281

1.4 Counts of atoms

Atoms	P39524	O94296	ATP8a1
sulphur (S)	41	46	46
carbon (C)	6 938	6 449	5 868
nitrogen (N)	1 810	1 658	1 541
oxygen (O)	2 064	1 883	1 684
hydrogen (H)	10 738	10 016	9 211

1.5 Frequencies of atoms

Atoms	P39524	O94296	ATP8a1
sulphur (S)	0,002	0,002	0,003
carbon (C)	0,321	0,322	0,320
nitrogen (N)	0,084	0,083	0,084
oxygen (O)	0,096	0,094	0,092
hydrogen (H)	0,497	0,500	0,502

1.6 Counts of hydrophobic and hydrophilic residues

Type	P39524	O94296	ATP8a1
Hydrophobic (A,F,G,I,L,M, P,V,W)	642	613	571
Hydrophilic (C,N,Q,S,T,Y)	375	357	318
Other	338	288	260

1.7 Frequencies of hydrophobic and hydrophilic residues

Type	P39524	O94296	ATP8a1
Hydrophobic (A,F,G,I,L,M, P,V,W)	0,474	0,487	0,497
Hydrophil (C,N,Q,S,T,Y)	0,277	0,284	0,277
Other	0,249	0,229	0,226

1.8 Counts of charged residues

Charge type	P39524	O94296	ATP8a1
Negatively Charged (D & E)	173	143	119
Positively Charged (R & K)	138	124	117
Other	1 044	991	913

1.9 Frequencies of charged residues

Charge type	P39524	O94296	ATP8a1
Negatively Charged (D & E)	0,128	0,114	0,104
Positively Charged (R & K)	0,102	0,099	0,102
Other	0,770	0,788	0,795

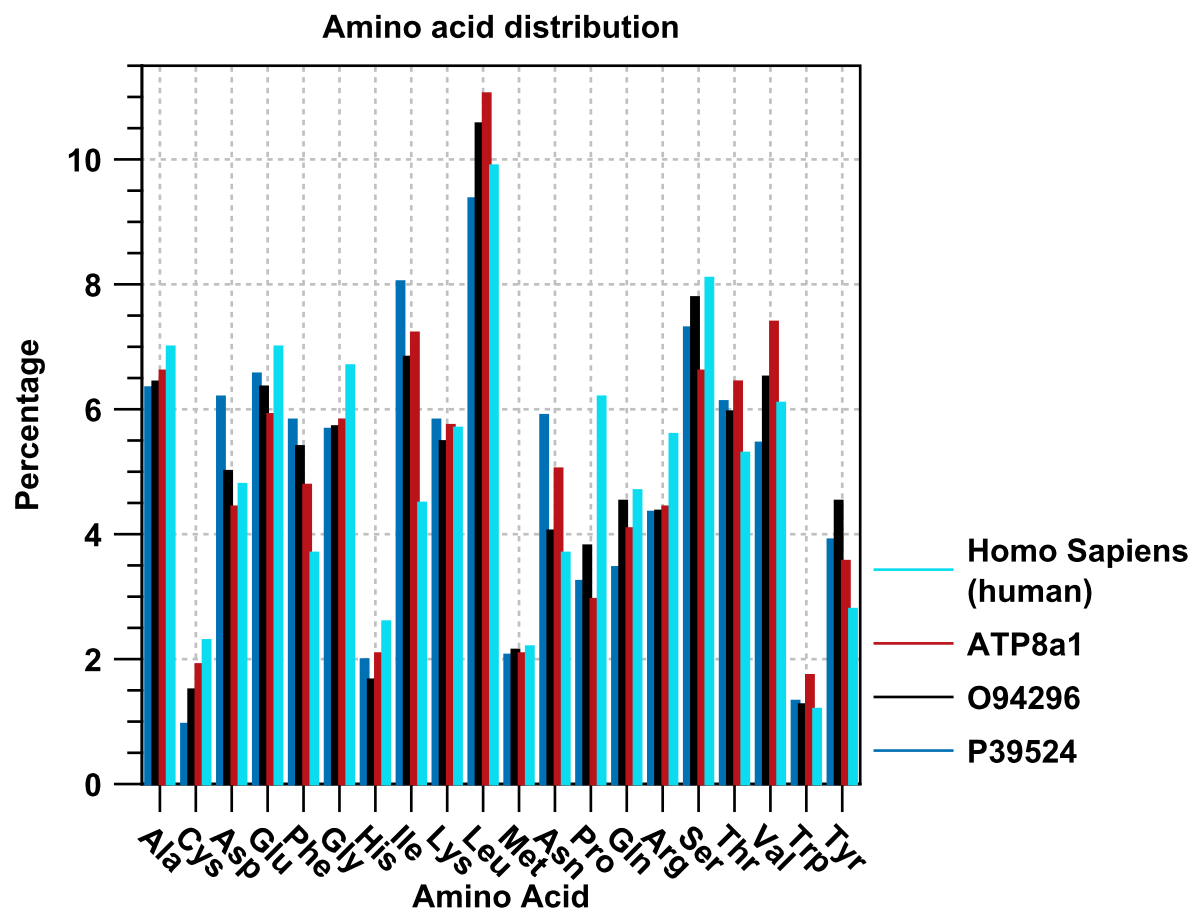
1.10 Counts of amino acids

Amino acid	P39524	O94296	ATP8a1
Alanine (A)	86	81	76
Cysteine (C)	13	19	22
Aspartic Acid (D)	84	63	51
Glutamic Acid (E)	89	80	68
Phenylalanine (F)	79	68	55
Glycine (G)	77	72	67
Histidine (H)	27	21	24
Isoleucine (I)	109	86	83
Lysine (K)	79	69	66
Leucine (L)	127	133	127
Methionine (M)	28	27	24
Asparagine (N)	80	51	58
Proline (P)	44	48	34
Glutamine (Q)	47	57	47
Arginine (R)	59	55	51
Serine (S)	99	98	76
Threonine (T)	83	75	74
Valine (V)	74	82	85
Tryptophan (W)	18	16	20
Tyrosine (Y)	53	57	41

1.11 Frequencies of amino acids

Amino acid	P39524	O94296	ATP8a1	Homo Sapiens (human)
Alanine (A)	0,063	0,064	0,066	0,070
Cysteine (C)	0,010	0,015	0,019	0,023
Aspartic Acid (D)	0,062	0,050	0,044	0,048
Glutamic Acid (E)	0,066	0,064	0,059	0,070
Phenylalanine (F)	0,058	0,054	0,048	0,037
Glycine (G)	0,057	0,057	0,058	0,067
Histidine (H)	0,020	0,017	0,021	0,026
Isoleucine (I)	0,080	0,068	0,072	0,045
Lysine (K)	0,058	0,055	0,057	0,057
Leucine (L)	0,094	0,106	0,111	0,099
Methionine (M)	0,021	0,021	0,021	0,022
Asparagine (N)	0,059	0,041	0,050	0,037
Proline (P)	0,032	0,038	0,030	0,062
Glutamine (Q)	0,035	0,045	0,041	0,047
Arginine (R)	0,044	0,044	0,044	0,056
Serine (S)	0,073	0,078	0,066	0,081
Threonine (T)	0,061	0,060	0,064	0,053
Valine (V)	0,055	0,065	0,074	0,061
Tryptophan (W)	0,013	0,013	0,017	0,012
Tyrosine (Y)	0,039	0,045	0,036	0,028

1.12 Histogram of amino acid frequencies



1.13 Counts of annotations

Feature type	P39524	O94296	ATP8a1
Active site	1	0	1
Gene	1	1	1
Metal binding site	0	0	2
Modified site	3	0	3
NP-binding	0	0	2
Protein	1	1	1
Region	24	24	24
Source	1	1	1