

Sequence alignment results of SLC7A11 proteins in different species based on clustalw tool

Header line description

A:Sequence number B:Accession number(NP/XP) C:Amino acid number

D:Species E:Amino acid sequence

Underlined: Amino acid sequence of human-derived SLC7A11 protein

Yellow marker: 7 lysine sites susceptible to ubiquitination

A	B	C	D
Sequence 1:	NP_055146.1	501 aa	human
Sequence 2:	NP_036120.1	502 aa	house mouse
Sequence 3:	NP_001101143.2	502 aa	Norway rat
Sequence 4:	XP_009289503.1	498 aa	zebrafish
Sequence 5:	NP_001239111.1	491 aa	sheep
Sequence 6:	XP_021385250.1	503 aa	Bengalese finch
Sequence 7:	XP_024833346.1	503 aa	cattle
Sequence 8:	XP_002932094.2	500 aa	tropical clawed frog
Sequence 9:	XP_008265658.1	502 aa	rabbit
Sequence 10:	NP_001253220.1	501 aa	Rhesus monkey
Sequence 11:	NP_001288791.1	527 aa	dog
Sequence 12:	XP_001136486.1	501 aa	chimpanzee
Sequence 13:	XP_426289.3	501 aa	chicken
Sequence 14:	XP_035310922.1	502 aa	Chinese hamster
Sequence 15:	XP_005607903.1	503 aa	horse
Sequence 16:	XP_020957246.1	502 aa	pig
Sequence 17:	XP_044286854.1	503 aa	Komodo dragon
Sequence 18:	XP_039607615.1	498 aa	gray bichir
Sequence 19:	XP_044911795.1	489 aa	domestic cat
Sequence 20:	NP_001305270.1	503 aa	alpaca

B	E
NP_036120.1	MVRKPVVATISKGGYLQGNMSGRLPSMGDQEPGQEKVVLKKKITLLRGVSIIGTVIGS
NP_001101143.2	MVRKPVVATISKGGYLQGNVSGRLPSVGDQEPGHEKVVLKKKITLLRGVSIIGTVIGS
XP_035310922.1	MVRKPVVTTISKGGYLQGNVSGRLPSMGDQEAPGQEKVVLKKKITLLRGVSIIGTVIGS
<u>NP_055146.1</u>	<u>MVRKPVVSTISKGGYLQGNVNGRLPSLGNKEPPGQEKVQLKRVKVTLLRGVSIIGTIIGA</u>
XP_001136486.1	MVRKPVVSTISKGGYLQGNVNGRLPSLGNKEPPGQEKVQLKRVKVTLLRGVSIIGTIIGA
NP_001253220.1	MVRKPVVSTISKGGYLQGNVNRRLPSLGNKEPPGQEKVQLKRVKVTLLRGVSIIGTIIGA
NP_001288791.1	MVRKPVVSTISSGGYLQGNVNGKLPGLGKKEPPGQEKVVLKKKITLVRGISIIGTIIGA
XP_044911795.1	MVRKPVVSTISSGGYLQGNVNGKLPGLGKKEPPGQEKVVLKKKITLVRGISIIGTIIGA
XP_005607903.1	MVRKPVVSTISNGGYLQGNVNGRLPSLGSKEPPEQEKVVLKKKITLVRGISIIGTIIGA
NP_001239111.1	MVRKPVVSTISNGAYLQGSVNGRLPAPGGKKEPPGQEKVVLKKKITLVRGISIIGTIIGA
XP_024833346.1	MVRKPVVSTISSGAYLQGSVNGRLPALGGREPPGQEKVVLKKKITLVRGISIIGTIIGA
XP_020957246.1	MVRKPVVSTISNGGYLQGNVHRRRLPSLGGREPPGQEKVVLKKKITLVRGISIIGTIIGA
NP_001305270.1	MVRKPVVSTISNGGYLQGNVHGRLPSLGSKEPPGQERVVLKKKITLVRGISIIGTIIGA
XP_008265658.1	MVRKPVVSTISKRSYLQGNVNGRLPSMGKKEPPGQEKVVLKKKITLVRGISIIGTIIGA
XP_021385250.1	MFRKAAVPTVSNQSYLQGRANGKLSMDSGQPAREGKVVVLKKKVTLLRGVSIIGTIIGA
XP_426289.3	MVRKAAVTVPNGSYLQGPNGRLPSMDSRQPQE--KVVVLKKKVTLLRGVSIIGTIIGA

NP_036120.1 STSVSWSARIQIFLTFCKLTAILIIIVPGVIQLIKGQTHHFKDAFSGRDTSLMGLPLAFY
NP_001101143.2 STSVSWSARIQIFLTFCKLTAILIIIVPGVIQLIKGQTHHFKDAFSGRDTNLMGLPLAFY
XP_035310922.1 SMSVSWASARIQIFLTFCKLTAILIIIVPGVIQLIKGHTQHFKDAFSGRDANLMGLPLAFY
NP_055146.1 SMSVSWASARIQIFLTFCKLTAILIIIVPGVMQLIKGQTONFKDAFSGRDSSITRLPLAFY
XP_001136486.1 SMSVSWASARIQIFLTFCKLTAILIIIVPGVMQLIKGQTONFKDAFSGRDSSITRLPLAFY
NP_001253220.1 SMSVSWASARIQIFLTFCKLTAILIIIVPGVMQLIKGQTONFKDAFSGRDSSITRLPLAFY
NP_001288791.1 SMSVSWASARIQIFLTFCKLTAILIIIVPGVMQLIKGQTONFKDAFSGRANIMGLPLAFY
XP_044911795.1 SMSVSWASARIQIFLTFCKLTAILIIIVPGVMQLIKGQTONFKDAFSGRDASIMGLPLAFY
XP_005607903.1 SMSVSWASARIQIFLTFCKLTAIVIIIVPGVMQLIKGQTONFKDAFSGRDANIMGLPLAFY
NP_001239111.1 SMSVSWASARIQIFLTFCKLTAILIIIVPGVMQLIKGKHSILKMPFQEMQVLWGCHWLF
XP_024833346.1 SMSVSWASARIQIFLTFCKLTAILIIIVPGVMQLIKGQTONFKDAFSGRDASIMGLPLAFY
XP_020957246.1 SMSVSWASARIQIFLTFCKLTAILIIIVPGVIQLIKGQTONFKDAFSGRNEIMGLPLAFY
NP_001305270.1 SMSVSWASARIQIFLTFCKLTAILIIIVPGVMQLIKGQTONFKDAFSGRDASIMGLPLAFY
XP_008265658.1 SMSVSWASARIQIFLTFCKLTAILIIIVPGVMQLIKGQTONFKDAFSGRDASVMGLPLAFY
XP_021385250.1 STSVSWSARIQMFLTFCKLVAILIIIVPGVIQLIKGETQHFKNAFAGNDASIMGLPLAFY
XP_426289.3 STSVSWSARIQIFLTFCKLVAILIIIVPGVIQLIKGETQHFKNAFSGNDASIMGLPLAFY
XP_044286854.1 SMSVSWSTRIQIFLTFCKLIAILIIIVPGVMQLIKGENQHFKDAFVGNAASVKGLPLAFY
XP_002932094.2 SVSVSWSARIQIFLTFCKLIAILIIIVPGVLQLIKGETQONFKDAFIGKDVSMGLPLAFY
XP_009289503.1 SMSVSWTARLQIFLTFCKLIAIAIIIVPGLYQLFKGETKNFENAFEVNTAQLTGLPLAFY
XP_039607615.1 SMSVSWASARIQIFLTFCKLLAMLIIIVPGLFQLFKGETQONFHNAFGVNEVPVMGLPLAFY
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NP_036120.1 YGMAYAGWFYLNFTITEVDNPEKTIPLAICISMAIITVGYVLTNAVYFTTISAEELLQS
NP_001101143.2 YGMAYAGWFYLNFTITEVDNPEKTIPLAICISMAIITVGYVLTNAVYFTTISAEELLQS
XP_035310922.1 YGMAYAGWFYLNFTITEVENPEKNIPLAICISMAIITVGYVLTNAVYFTTISAEELLS
NP_055146.1 YGMAYAGWFYLVNFTITEVENPEKTIPLAICISMAIIVTIGYVLTNAVYFTTINAEELLS
XP_001136486.1 YGMAYAGWFYLVNFTITEVENPEKTIPLAICISMAIIVTIGYVLTNAVYFTTINAEELLS
NP_001253220.1 YGMAYAGWFYLVNFTITEVENPEKTIPLAICISMAIIVTIGYVLTNAVYFTTINAEELLS
NP_001288791.1 YGMAYAGWFYLVNFTITEVENPEKTIPLAICISMAIIVTIGYVLTNAVYFTTISAEELLS
XP_044911795.1 YGMAYAGWFYLVNFTITEVENPEKTIPLAICISMAIIVTIGYVLTNAVYFTTISAEELLS
XP_005607903.1 YGMAYAGWFYLVNFTITEVENPEKTIPLAICISMAIIVTIGYVLTNAVYFTTISAEELLS
NP_001239111.1 MECMRTPAGFYLVNFTITEVENPEKTIPLAICISMTVVTVGYVLTNAVYFTTISAEELMS
XP_024833346.1 YGMAYAGWFYLVNFTITEVENPEKTIPLAICISMAIIVTIGYVLTNAVYFTTISAEELMS
XP_020957246.1 YGMAYAGWFYLVNFTITEVENPEKTIPLAICISMAIIVTIGYVLTNAVYFTTISAEELLS
NP_001305270.1 YGMAYAGWFYLVNFTITEVENPEKTIPLAICISMAIIVTIGYVLTNAVYFTTISAEELLS
XP_008265658.1 YGMAYAGWFYLVNFTITEVENPERTVPLAICISMAIIVTIGYVLTNAVYFTTISAEELLS
XP_021385250.1 SGMAYAGWFYLVNFTITEVENPEKNIPLAICISMAIIVTIGYVLTNAVYFTTISAGELLS
XP_426289.3 SGMAYAGWFYLVNFTITEVENPEKNIPLAICISMAIIVTIGYVLTNAVYFTTISAGELLS
XP_044286854.1 SGMAYAGWFYLVNFTITEVENPERNVPLAICTSMVIVTVGYVLTNAVYFTTISPEELMS
XP_002932094.2 SGMAYAGWFYLVNFTITEVENPEKNVPLAICISMAIIVTIGYVLTNAVYFTTISAEELVLS
XP_009289503.1 SGMAYAGWFYLVNFTITEVENPERTVPLAICISMAIIVMICYTLTNVAYYTVMSADELLAS
XP_039607615.1 SGMAYAGWFYLVNFTITEVENPEKTVPLAICISMAIIVTFSYVLINVAAYAVLTADEMPLAS
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NP_036120.1 SAVAVTFSERLLGKFLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGHLPEILSMIHV
NP_001101143.2 SAVAVTFSERLLGKFLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGHLPEILSMIHV
XP_035310922.1 NAVAVTFSERLLGNFLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGHLPEILSMIHV
NP_055146.1 NAVAVTFSERLLGNFLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGHLPEILSMIHV
XP_001136486.1 NAVAVTFSERLLGNFLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGHLPEILSMIHV
NP_001253220.1 NAVAVTFSERLLGNFLAVPIFVALSCFGSMNGGVFAVSRLFYVASREGHLPEILSMIHV

NP_001305270.1	FKVPLFIPALFSFTCLFMVALSLYSDPFSTGIGFIITLTGVPAYYLFIIWDKKPKWFRRM
XP_008265658.1	FKVPLFIPALFSFTCFMVALSLYSDPFSTGIGFVITLSGVPAYYLFIIWDKKPKWFRRM
XP_021385250.1	FKVPLFIPALFSFTCLFMVALSLYSDPVNTGIGFAITLTGIPAYYFFIVWDNKPWFRRKL
XP_426289.3	FKVPLFIPALFSFTCLFMVALSLYSDPVNTGIGFAITLTGVPAYYLFIVWDKKPKWFRKL
XP_044286854.1	FKVPLFIPALFSFTCLFMVLSLYADPVNTGIGFAITLTGVPAYYLFIIWDKKPTWFRRF
XP_002932094.2	FKVPIFIPALFSFTCLFMVALSLYSDPINTGIGFAITLTGVPAYYLFIVWDNKPWFRTF
XP_009289503.1	FKVPIFIPAVFSFTCFMVFSLYSDPINTGIGFAISLTGIPAYYIFIHSCRKPKWFQKF
XP_039607615.1	FKVPLFIPALFCFSCFLMVGLSLYSDPINTGIGFGITLTGIPAYYIFIVWNKKPKIIQKF

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NP_036120.1	SDRITRTLQIILEVVPEDSKEL-----
NP_001101143.2	SDRITRTLQIILEVVPEDSKEL-----
XP_035310922.1	SERITRTLQIILEVVPEDSKEL-----
<u>NP_055146.1</u>	<u>SEKITRTLQIILEVVPEDDKL-----</u>
XP_001136486.1	SEKITRTLQIILEVVPEDDKL-----
NP_001253220.1	SERITRTLQIILEVVPEDDKL-----
NP_001288791.1	SGKTFTQFWDLLRDRVIENPVYGYTQPHHTHTHPLMFNNVSKATAH
XP_044911795.1	SERTTSNDP-----
XP_005607903.1	SDRITRTLQIILEVVPEDCHKL-----
NP_001239111.1	SDITRTLQIILEVVPEDCHKL-----
XP_024833346.1	SDMITRTLQIILEVVPEDCHKL-----
XP_020957246.1	SDRITRTLQIILEVVPEDCHK-----
NP_001305270.1	SDKITRTLQIILEVVPEDCQKL-----
XP_008265658.1	SDTITRTLQIILEVVPEDCRK-----
XP_021385250.1	LGRVTTTLQILLEVIPAEDQKS-----
XP_426289.3	LDTVTEALQILLEVVPSEEDQKS-----
XP_044286854.1	LGRITSMQLIILEVVPAAENPRS-----
XP_002932094.2	TDRTTLMQLIILEVAPTDKNIS-----
XP_009289503.1	SDSMNRSQILLEVVPAAEH-----
XP_039607615.1	TDSTRTLQIILEVVSPE-----