

MATLAB multiple sequence alignment

lcl NM_198436.2	ITELANALSYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTLCTGLDYL	296
lcl XM_01514873	ITELANALSYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTLCTGLDYL	296
lcl NM_001038082	ITELANALSYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTLCTGLDYL	296
lcl NM_00114250	ITELANALSYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTLCTGLDYL	296
lcl XM_00563519	ITELADALSYCHSKRVIHRDIKPENLLGSAGELKIADFGWSVHAPSSRRRTLCTGLDYL	297

1c1 XM_00398335	ITELADALSYCHSKRVIHRDIKPENLLLSGAGELKIADFGWSVHAPSSRRRTL	CGTLDYL	297
1c1 XM_00567303	ITELANALSYCHSKRVIHRDTPENLLLSGAGELKIADFGWSVHAPSSRRRTL	CGTLDYL	296
1c1 XM_00148927	ITELANALAYCHSKRVIHRDIKPENLLLSGAGELKIADFGWSVHAPSSRRRTL	CGTLDYL	296
1c1 XM_00443024	ITELANALAYCHSKRVIHRDTPENLLLSGAGELKIADFGWSVHAPSSRRRTL	CGTLDYL	297
1c1 XM_00827414	ITELANALLYCHSKRVIHRDIKPENLLLSGAGELKIADFGWSVHAPSSRRRTL	CGTLDYL	295
1c1 XM_01452869	ITELTNALSYCHSKRVIHRDTPENLLLSGTGELKIADFGWSVHAPSSRRRTL	CGTLDYL	296
1c1 XM_00468690	ITELADALSYCHSKRVIHRDIKPENLLLSGAGELKIADFGWSVHAPSSRRRTL	CGTLDYL	297
1c1 XM_00341990	ITELADALSYCHSKRVIHRDTPENLLLSGTGELKIADFGWSVHAPSSRRRTL	CGTLDYL	298
1c1 XM_00432103	ITELANALSYCHSKRVIHRDIKPENLLLSGSGELKIADFGWSVHAPSSRRRTL	CGTLDYL	296

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lclNM_198436.2 RDLISRLKHNPSQRPMLREVL EHPWITANSKKPSNQNKESASKQS*-- 404
lclNM_01514873 RDLISRLKHNPSQRPMLREVL EHPWITANSKKPSNQNRYN*----- 399
lclNM_00103802 RDLISRLKHNPSQRPRTLKEVLEHPWITANSKPPSSQKKKESASKQS*-- 400
lclNM_00114250 RDLISRLKHNPSQRPRTLKEVLEHPWITANSKPPSSQKKKESASKQS*-- 403
lclXM_00563519 RDLISRLKHNPSQRPRTLKDVL EHPWIMANSKKPSSSQKNKDSTSKQS* 406
lclXM_00398335 RDLISRLKHNPSQRPRTLKEVLEHPWITANSKKPSGSKSKESTGKQS* 406
lclXM_00567303 RDLISRLKHNPSHRPTLKEVLEHPWITANSKPASSHKKESSTKQP*-- 403
lclXM_00148927 RDLISRLKHNPSQRPRTLKEVLEHPWITANSKKPSNSQKSKESTSKQP* 405
lclXM_00443024 RDLISRLKHNPSQRPRTLKEVLEHPWITANASKKPSNSQKSKESTSKQS* 406
lclXM_00827416 KDFISRLKHNPSHRPTLAEVLEHPWIAKSSKPPSSCPDKKESASKQS*-- 403
lclXM_01452869 RDLISRLMHNNQRLTLKEVLEHPWITANSKKPSSSQKKKESASKQS* 405
lclXM_00468690 RDLISRLKHNPSQRPRTLKEVLEHPWITANSKKPPSSQKNKESSTSKQS* 406
lclXM_00341990 RDLVSRLLKHNPSQRLTLKEVLEHPWITANSKKPPSSQNKESSTSKQS*-- 406
lclXM_00432103 RDLISRLKHNPSQRPRTLKEVLEHPWITANSKPPSSQKKESASKQS*-- 403
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