

Science-II
Biology
Tutorial Assignment - 2

Gowlapalli Rohit

2021101113

Q1] Protein

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#
# Percent Identity Matrix - created by Clustal2.1
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1: YP_009047204.1	100.00	30.63	32.53	32.32	32.10	32.29
2: YP_009824990.1	30.63	100.00	34.68	34.00	33.72	33.89
3: NP_828851.1	32.53	34.68	100.00	76.82	77.22	77.68
4: QLR06869.1	32.32	34.00	76.82	100.00	90.59	89.64
5: YP_009724390.1	32.10	33.72	77.22	90.59	100.00	97.71
6: QHR63300.2	32.29	33.89	77.68	89.64	97.71	100.00

Closest relatives:

- NP_828851.1 is the closest relative of YP_009047204.1
- NP_828851.1 is the closest relative of YP_009824990.1
- QHR63300.2 is the closest relative of NP_828851.1
- YP_009724390.1 is the closest relative of QLR06869.1
- QHR63300.2 is the closest relative of YP_009724390.1
- YP_009724390.1 is the closest relative of QHR63300.2

CLUSTAL O(1.2.4) multiple sequence alignment

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YP_009047204.1
MIHSVFLLMFLLTPTESYVDVGPDSVKSACIEVDIQQTFFDKTW-PRPIDVSKADGIIYP 59
YP_009824990.1
-MVVLLEFVMFSLVVA-----DRPNCYLPQYSYTISPATITNTSYFNVNPISIVVP 49
NP_828851.1
--MFIFLLFLTLTSGS-----DLDRCTTFDDVQAPNY-----TQHTSSMRGVYYP 43
QLR06869.1
-MLFFFFLHFALVNS-----QCVNLTGRAAIQP-----SFTNSSQRGVYYP 40
YP_009724390.1
--MFVFLVLLPLVSS-----QCVNLTTRTQLPP-----AYTNSFTRGVYYP 39
QHR63300.2
--MFVFLVLLPLVSS-----QCVNLTTRTQLPP-----AYTNSSTRGVYYP 39
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YP_009047204.1
 QGR^TYSN^IT^ITYQGLFPYQGDHGD^MYVYSAGHATGTT^PQKLFVANYSQ^DVK^QFANGFV^VR 119
 YP_009824990.1
 EFSVARTNLVVR^QRLQVAAYD-----FTKIPIT-PPHRSIFN----NTYFRVGDGILVN 98
 NP_828851.1
 DEIFRSD^TLYLTQDLFLPFYS--NVTGFHTIN-----HTFG----NPVIPFKDGIYFA 90
 QLR06869.1
 DTIFRSNTLVLSQGYFLPFYS--NVSWYYALT^KTN-SAEKRVD----NPVLDFK^DGIYFA 93
 YP_009724390.1
 DKVFRSSVLHSTQDLFLPFFS--NVTWEHAIHVSGTNGTKRFD----NPVLPFNDGVYFA 93
 QHR63300.2
 DKVFRSSVLH^LTQDLFLPFFS--NVTWEHAIHVSGTNGIKRFD----NPVLPFNDGVYFA 93
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YP_009047204.1
 IGAANSTGT^VIISPST-SATIR^KIYPAFMLGSSVGN-----FSDG^KMGRFF-----N 166
 YP_009824990.1
 THMYH^R---TNIATNLGSSFYGCQEPFGAAFGNTFVNEPITLVMFYAGNVGSWSSLVTQ^Q 155
 NP_828851.1
 ATE-----KS-----NVVRGWVFGSTMN^KKSQ-----SVIIINN 119
 QLR06869.1
 ATE-----KS-----NIVRGWIFGTTL^DNTSQ-----SLLIVNN 122
 YP_009724390.1
 STE-----KS-----NIIRGWIFGTTL^DSKTQ-----SLLIVNN 122
 QHR63300.2
 STE-----KS-----NIIRGWIFGTTL^DSKTQ-----SLLIVNN 122
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YP_009047204.1
 HTLVLLP^DGCGTLL--RAFYCILEPRSGNHCPAGNSYTSFATYHTPAT^DCS^DGNYN^RNAS 224
 YP_009824990.1
 QANITIVSCDNATLCANPFFLRWGP-----GVIRSFT 187
 NP_828851.1
 STNVVIR-ACNFELCDNPFFAVSKP-----MGT---- 146
 QLR06869.1
 ATNVI^IK-VCNFQFCYDPYLSGY^YH-----N-NKTWS 152
 YP_009724390.1
 ATNVV^IK-VCEFQFCNDPFLGV^YYH-----KNNKSWM 153
 QHR63300.2
 ATNVV^IK-VCEFQFCNDPFLGV^YYH-----KNNKSWM 153
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YP_009047204.1
 LNSF^KEYFN^LRNCTFMYTYNITEDEILEWFGITQTAQ^G----VHLFSS^RYVDLYGGNMF- 279

YP_009824990.1
 I-----SNAFQCHGNYTFYDTKL--VNFTVSTAR----YNLAFTFADGDIFMY--YAAL 233
 NP_828851.1
 QTHTMIFDNAFNCTFEYISDAF-S--LDVSEKSGNFKHLREFVFKNKDGFYVYKGYQPI 203
 QLR06869.1
 TREFAVYSSYANCTFEYVSKSF-M--LDIAGKSGLFDTLREFVFVNVDGYFKIYSKYTPV 209
 YP_009724390.1
 ESEFRVYSSANNCTFEYVSQPF-L--MDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPI 210
 QHR63300.2
 ESEFRVYSSANNCTFEYVSQPF-L--MDLEGKQGNFKNLREFVFKNIDGYFKIYSKHTPI 210
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YP_009047204.1
 -QFATLP-VYDTIKYYSIIPHSI-----RSIQSDRKAW----AAFYVYKL 318
 YP_009824990.1
 GDSLNLPTAY-PLQPYLRIPAGFKPDVVQFFQAITRPN--GESAEVACASSTVSWYVSRL 290
 NP_828851.1
 DVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFS-----PAQDIWGTSAAYFVGYL 257
 QLR06869.1
 NVNSNLPIGFSALEPLVEIPAGINITKFRLLTIHRGDPMP---NNGWTVFSAAYYVGYL 266
 YP_009724390.1
 NLVRDLPPQGFSALEPLVDLPIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYL 270
 QHR63300.2
 NLVRDLPPGFSALEPLVDLPIGINITRFQTLALHRSYLT PGDSSSGWTAGAAAYYVGYL 270
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YP_009047204.1
 QPLTFLLDFSVDGYIRRAIDCGFNDLSQLHCSYESFDVESGVYSVSSFEAKPSGSVVEQA 378
 YP_009824990.1
 YYKELLVGYSYSSIVNVSFCSSDAESELQCLLGT FAPANGVYSLSNFRSSPTDNV-RIT 349
 NP_828851.1
 KPTTFMLKYDENGITDAVDCSQNPLAELKCSVKSF EIDKGIYQTSNFRVVP SGDVVRFP 317
 QLR06869.1
 APRTFMLNYNENGTITDAVDCALDPLSEAKCTLKSLTVEKGIYQTSNFRVQPTESIVRFP 326
 YP_009724390.1
 QPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF TVEKGIYQTSNFRVQPTESIVRFP 330
 QHR63300.2
 QPRTFLLKYNENGTITDAVDCALDPLSETKCTLKSF TVEKGIYQTSNFRVQPTDSIVRFP 330
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YP_009047204.1
 E-GVECDFESPL-LSGTPPQVYNFKRLVFTNCNYNLT KLLSLFSVNDFTCSQISPAAIASN 436
 YP_009824990.1
 NSASSCSVPYS-VLSRPPLPFVWKRYAISNCKFDFQALLSHLPTFQLRCFGISPTKLATM 408

NP_828851.1
NITNLCPFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLNDL 377
QLR06869.1
NITNLCPFGEVFNATTFASVYAWNKKRISNCVADYSVLYNSTSFSTFKCYGVSPTKLNDL 386
YP_009724390.1
NITNLCPFGEVFNATRFASVYAWNKKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDL 390
QHR63300.2
NITNLCPFGEVFNATTFASVYAWNKKRISNCVADYSVLYNSTSFSTFKCYGVSPTKLNDL 390
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YP_009047204.1
CYSSLILDYFSYPLSMKSDLSVSSAGPISQFNYKQSFNSPTCLILATVPHNLTTITKPLK 496
YP_009824990.1
CFGTVTLIDIMLVNVTHYNNLLNDVPDDFSLYNYQLPRNFYGLHSYYLPNDTA----- 461
NP_828851.1
CFSNVYADSFVVKGDDVRQIAPGQTGVADYNYKLPDDFMGCVLAWNTRNIDATSTGNYN 437
QLR06869.1
CFTNVYADSFVVRGDEVQRQIAPGQTGRIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYN 446
YP_009724390.1
CFTNVYADSFVIRGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYN 450
QHR63300.2
CFTNVYADSFVITGDEVQRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSKHIDAKEGGNFN 450
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YP_009047204.1
YSYINKCS-RLLSDDRTEV-----PQLV--NANQYSPCVSIVPS-TVWEDGDYYRKQL 545
YP_009824990.1
FSYTVASRIRYPSWVHSITPGGRQPVGPFLDSLQSSSKPCTGS----- 504
NP_828851.1
YKYRYLRHGKLRPFERDIS-----NVPFSPDGKPCPT-PALNCYW----- 476
QLR06869.1
YLYRLFRKSNLKPFERDIS-----TEIYQAGSTPCNGVEGFNCYF----- 486
YP_009724390.1
YLYRLFRKSNLKPFERDIS-----TEIYQAGSTPCNGVEGFNCYF----- 490
QHR63300.2
YLYRLFRKANLKPFERDIS-----TEIYQAGSKPCNGQTGLNCYY----- 490
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YP_009047204.1
SPLEGGGWLVASGSTVAMTEQLQMFGGITVQYGTDTNSVCPKLEFANDTKIASQLGNCVE 605
YP_009824990.1
-----CLGLAVI----SLSIASANKLVCPVGN----DTDIVPDTCVN 538
NP_828851.1
-PLNDYGFYTTTGIGYQPYRVVVL----SFELLNAPATVCGPKL----STDLIKNCQCVN 526
QLR06869.1
-PLQSYGFHP TNGVGYQPYRVVVL----SFELLNAPATVCGPKQ----STNLVKNKCVN 536

YP_009724390.1
 -PLQSYGFQPTNGVGYQPYRVVVL----SFELLHAPATVCGPKK-----STNLVKNKCVN 540
 QHR63300.2
 -PLYRYGFYPTDGVGHQPYRVVVL----SFELLNAPATVCGPKK-----STNLVKNKCVN 540
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YP_009047204.1
 YSLYGVSGRGVFQNCTAVGVRQQRFVYDAYQNL-VGYYSDDGNYYCLRACVSPVSVIYD 664
 YP_009824990.1
 YNIYGYQGTGVISRSNYTLPSSKVFSLSSSGE--LTVFAVGSSFYQLSPCAFAPISAAFY 596
 NP_828851.1
 FNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPFAFGGVSVITP 586
 QLR06869.1
 FNFNGLTGTGVLTESSKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITP 596
 YP_009724390.1
 FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITP 600
 QHR63300.2
 FNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEILDITPCSFGGVSVITP 600
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YP_009047204.1
 KE--TKTHATLFGSVACEHISSTMSQYSRSTRSMLKRRDSTYGPLQTPVGCVLGLVNS-S 721
 YP_009824990.1
 ---KGYTTSLLFNNLPSCSNRHRAV-VEP--VSAYWRRSVADNNTFDTTAGCIFNAYNLTS 650
 NP_828851.1
 GTNASSEVAVLYQDVNCTDVSTAIHADQ--LTPAWRIYSTGNNVFQQTQAGCLIGAEHVD 644
 QLR06869.1
 GTNTSNQVAVLYQDVNCTEVPVAIHADQ--LTPTWRVYSTGSNVFQTRAGCLIGAEHVNN 654
 YP_009724390.1
 GTNTSNQVAVLYQDVNCTEVPVAIHADQ--LTPTWRVYSTGSNVFQTRAGCLIGAEHVNN 658
 QHR63300.2
 GTNASNQVAVLYQDVNCTEVPVAIHADQ--LTPTWRVYSTGSNVFQTRAGCLIGAEHVNN 658
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YP_009047204.1
 LFVEDCKLPLGQSLCALPDTPTLTTPRSVRSVPGEMRLASIAFNHPIQV-DQLNSSYFKL 780
 YP_009824990.1
 IVVNQCDLPIGDSYCLQPSLIKFFE-AT-----LSLVTYNP-LADSLTPITPVYQV 699
 NP_828851.1
 --SYECDIPIGAGICASYHTVSL-----LRSTSQ---KSIVAYTMSLGADSSIAYSNNNTI 694
 QLR06869.1
 --TYECDIPIGAGICASYQTQTN-----RSVSS---QAI IAYTMSLGAENSVAYANN SI 704
 YP_009724390.1
 --SYECDIPIGAGICASYQTQTN SP-RRARSVAS---QSIIAYTMSLGAENSVAYSNN SI 712

QHR63300.2

--SYECDIPIGAGICASYQTQTN-----RSVAS---QSIIAYTMSLGAENSVAYSNNNSI 708

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YP_009047204.1

SIPTNFSFGVTQEYIQTTIQKVTVDCKQYVCNGFQKCEQLLREYGFCSKINQALHGANL 840

YP_009824990.1

SVPTNFTLVASTEYIQTYASKISIDCAKYLCDSSQCRTVLLQYGTFCNDVNVALTRVFT 759

NP_828851.1

AIPTNFSISITTEVMPVSMKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAA 754

QLR06869.1

AIPTNFTISVTTEILPVSMKTSVDCTMYICGDSIECSNLLLQYGSFCTQLNRALTGIAV 764

YP_009724390.1

AIPTNFTISVTTEILPVSMKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAV 772

QHR63300.2

AIPTNFTISVTTEILPVSMKTSVDCTMYICGDSTECNLLLQYGSFCTQLNRALTGIAV 768

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YP_009047204.1

RQDDSVRNLFASVKSSQSSPIIPGFGGDFNLTLEPVSI STGSRSAIEDLLFDKVTI 900

YP_009824990.1

LLDNLSLVDTFSSLKSTA-PVQLAYTGDFNFTSLVGCIGTDCDSKSHRSALSDLLFSKVS 818

NP_828851.1

EQDRNTREVFAQVKQMYKTPTLK YFGGFNFSQIL----PDPLKPTKRSFIEDLLFNKVTL 810

QLR06869.1

EQDKNTQEVFAQVKQIYKTPIKDFGGFNFSQIL----PDPSKPSKRSFIEDLLFNKVTL 820

YP_009724390.1

EQDKNTQEVFAQVKQIYKTPIKDFGGFNFSQIL----PDPSKPSKRSFIEDLLFNKVTL 828

QHR63300.2

EQDKNTQEVFAQVKQIYKTPIKDFGGFNFSQIL----PDPSKPSKRSFIEDLLFNKVTL 824

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YP_009047204.1

ADPGYMQGYDDCMQOG-PASARDLICAQYVAGYKVLPLMDVNMEAAYTSSLLGSIAGVG 959

YP_009824990.1

ADPGFMQSYQQCLDAQWGGNIRDLLCTQT FNGISVLPPIVSPSMQALYTTALVGGIAASG 878

NP_828851.1

ADAGFMKQYGECLGDI---NARDLICAQKFNGLTVLPPLLTDDEMIAAYTAALVSGTATAG 867

QLR06869.1

ADAGFIKQYGDCLGDI---AARDLICAQKFNGLTVLPPLLTDDEMIAQYTSALLAGTITSG 877

YP_009724390.1

ADAGFIKQYGDCLGDI---AARDLICAQKFNGLTVLPPLLTDDEMIAQYTSALLAGTITSG 885

QHR63300.2

ADAGFIKQYGDCLGDI---AARDLICAQKFNGLTVLPPLLTDDEMIAQYTSALLAGTITSG 881

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YP_009047204.1
WTAGLSSFAAIPFAQSIFYRLNGVGITQQVLSENQKLIANKFNQALGAMQTGFTTTNEAF 1019
YP_009824990.1
FTFGVSSAAVIPFATQLQFRLNGLGVTTNVLMENQQLIANAFNKALVSIQEGFTATNQAL 938
NP_828851.1
WTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTAL 927
QLR06869.1
WTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNKAISQIQDSLSSTASAL 937
YP_009724390.1
WTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNKAISQIQDSLSSTASAL 945
QHR63300.2
WTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNKAISQIQDSLSSTASAL 941
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YP_009047204.1
QKVQDAVNNAQALSKLASELSNTFGAISASIGDIIQRLDVLEQDAQIDRLINGRLTTLN 1079
YP_009824990.1
NKIQTVVNNNALQLQVLVQQLGNTFGAISASVNEIFSRDLLEANAQVDR LISGRMVVLN 998
NP_828851.1
GKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQ 987
QLR06869.1
GKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQ 997
YP_009724390.1
GKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQ 1005
QHR63300.2
GKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQ 1001
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YP_009047204.1
AFVAQQLVRSSESAALSAQLAKDKVNECVKAQSKRSGFCGQGTHIVSFVVNAPNGLYFMHV 1139
YP_009824990.1
TYVTQQLLIQASELRSQAELAKQKMSQSLRNDFCGNGTHVLSIPQLAPNGMLFIHY 1058
NP_828851.1
TYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHV 1047
QLR06869.1
TYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHV 1057
YP_009724390.1
TYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHV 1065
QHR63300.2
TYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHV 1061
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YP_009047204.1
 GYYPSNHI^EVVSAYGLCD^AANPTNCIAPVNGYFIKTNNT^RIVDEWSYTGSSFYAPEPITS 1199
 YP_009824990.1
 SYQPT^KYAQVYT^TAGLCFNGT⁻--GFVPRDGLFVRENNE⁻--SQVWYFT^KASFYNPVNLSY 1113
 NP_828851.1
 TYVPSQ^ERNFTTAPAICHEGK⁻--AYFPREGV^FVFN⁻----GTSWFITQ^RNFFSPQIITT 1099
 QLR06869.1
 TYVPSQ^EKNFTTTAPAICHEGK⁻--AHFPREGV^FVSN⁻----GTHWFTQ^RNFYEPQIITT 1109
 YP_009724390.1
 TYVPAQ^EKNFTTAPAICH^DGK⁻--AHFPREGV^FVSN⁻----GTHWFTQ^RNFYEPQIITT 1117
 QHR63300.2
 TYVPAQ^EKNFTTAPAICH^DGK⁻--AHFPREGV^FVSN⁻----GTHWFTQ^RNFYEPQIITT 1113
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YP_009047204.1
 LNT^KYVAPQ⁻VTYQNISTNLPPPLLGNSTGID^FQDELDEFK^NVSTSI^PNFGSLTQINTT 1258
 YP_009824990.1
 ENTHLLDTCGVNYTTVNNSVLNPIE⁻--PPNYNFQEEFDK^YFKNQSSQFNITFDSSQFNVS 1171
 NP_828851.1
 DNTFVSGNCDV^VIGIINNTVYDPLQ⁻--PELDSFKEELDK^YFKNHTSPDV^DLDISGINAS 1157
 QLR06869.1
 DNTFVSGSCD^VIGIVNNTVYDPLQ⁻--PELDSFKEELDK^YFKNHTSPDV^DLDISGINAS 1167
 YP_009724390.1
 DNTFVSGNCDV^VIGIVNNTVYDPLQ⁻--PELDSFKEELDK^YFKNHTSPDV^DLDISGINAS 1175
 QHR63300.2
 DNTFVSGSCD^VIGIVNNTVYDPLQ⁻--PELDSFKEELDK^YFKNHTSPDV^DLDISGINAS 1171
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YP_009047204.1
 LLDLT^YEMLSLQ^QVVKALNESYIDL^KEIGNYTYYN^KWPWYIWLGFIAGLVALALCVFFIL 1318
 YP_009824990.1
 IVNLNEQMAALDSV^VKSLNESFIDL^KKLGVYTQQPNTPWYAWLGMIAGLVGLALAVFMLC 1231
 NP_828851.1
 VVNIQ^KEIDRLNEVAKNLNESLIDLQELG^KYEQYIKWPWYVWLGFIAGLIAIVMTILLC 1217
 QLR06869.1
 VVNIQ^KEIDRLNEVAKNLNESLIDLQELG^KYEQYIKWPWYIWLGFIAGLIAIIMVTIMLC 1227
 YP_009724390.1
 VVNIQ^KEIDRLNEVAKNLNESLIDLQELG^KYEQYIKWPWYIWLGFIAGLIAIVMTIMLC 1235
 QHR63300.2
 VVNIQ^KEIDRLNEVAKNLNESLIDLQELG^KYEQYIKWPWYIWLGFIAGLIAIIMVTIMLC 1231
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YP_009047204.1 CCTGCGTNC^MGKLKCN^RCCDRYEEYDLEPH^KVHVH⁻---- 1353

YP_009824990.1	CMTNCCSGFRGICSCKQCQYD-DYADVYPVVRVSGKRTV	1269
NP_828851.1	CMTSCCSCCLKGACSCGSCCKF-DEDDSEPVKGVKLHYT	1255
QLR06869.1	CMTSCCSCCLKGCCSCGSCCKF-DEDDSEPVKGVKLHYT	1265
YP_009724390.1	CMTSCCSCCLKGCCSCGSCCKF-DEDDSEPVKGVKLHYT	1273
QHR63300.2	CMTSCCSCCLKGCCSCGSCCKF-DEDDSEPVKGVKLHYT	1269
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Nucleotide

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# Percent Identity Matrix - created by Clustal2.1
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1: NC_019843.3_21456-25517	100.00	44.16	45.49	45.55	46.19	45.96
2: NC_048212.1_20814-24623	44.16	100.00	47.18	46.94	47.71	47.12
3: NC_004718.3_21492-25259	45.49	47.18	100.00	73.12	73.35	73.26
4: MT799526.1	45.55	46.94	73.12	100.00	84.14	83.39
5: NC_045512.2_21563-25384	46.19	47.71	73.35	84.14	100.00	93.12
6: MN996532.1_21545-25354	45.96	47.12	73.26	83.39	93.12	100.00

Closest relatives:

- NC_045512.2_21563-25384 is the closest relative of NC_019843.3_21456-25517
- NC_045512.2_21563-25384 is the closest relative of NC_048212.1_20814-24623
- NC_045512.2_21563-25384 is the closest relative of NC_004718.3_21492-25259
- NC_045512.2_21563-25384 is the closest relative of MT799526.1
- MN996532.1_21545-25354 is the closest relative of NC_045512.2_21563-25384
- NC_045512.2_21563-25384 is the closest relative of MN996532.1_21545-25354

CLUSTAL O(1.2.4) multiple sequence alignment

NC_019843.3:21456-25517
 ATGATACACTCAGTGTCTTCTACTGATGTTCTTGTTAACACCTACAGAAAGTTACGTTGAT 60

NC_048212.1:20814-24623
 ATGGTCGT---CTTATTGTTTCGTGATGTTTAGTTTAGTGGTAGCTGACAGGCCTAATTGT 57
 NC_004718.3:21492-25259
 ---ATGTT---TAT-----TTTCTTATTATTTCTTACTCTCACTAGTGGTAGT 42
 MT799526.1
 ATGTTGTT---TTT-----CTTCTTTTTACACTTTGCC-----TTAGT 35
 NC_045512.2:21563-25384
 ---ATGTT---TGT-----TTTCTTGTTTTATTGCCA-----CTAGT 32
 MN996532.1:21545-25354
 ---ATGTT---TGT-----TTTCTTGTTTTATTGCCA-----CTAGT 32
 * * ** *

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NC_019843.3:21456-25517
 GTAGGGCCAGATTCTGTTAAGTCTGCTTGTAATTGAGGTTGATATACAACAGACTTTCTTT 120
 NC_048212.1:20814-24623
 TATTTCCTCA-----GTATTCTTAC----- 78
 NC_004718.3:21492-25259
 GACCTTGACCG-----GTGCAC---C----- 60
 MT799526.1
 AAATTC--ACA-----ATGTGT---T----- 51
 NC_045512.2:21563-25384
 CTCTAG--TCA-----GTGTGT---T----- 48
 MN996532.1:21545-25354
 TTCTAG--TCA-----GTGTGT---T----- 48
 *

NC_019843.3:21456-25517
 GATAAACTTGGCCTAGGCCAATTGATGTTTCTAAGGCTGACGGTATTATATACCCTCAA 180
 NC_048212.1:20814-24623
 -----ACTATTTACACGCAACCATCACTAACACCTCCTATT---TTAATGTCAATCC 128
 NC_004718.3:21492-25259
 -----ACTTTTGATGATGTTCAAGCTCCTAATTACACTCAACATACTTCATCTATGAGG 114
 MT799526.1
 -----AATTTAACAGGTAGAGCTGCTATCCAGCCTTCATTCACCAATTCCTCTCAAAGA 105
 NC_045512.2:21563-25384
 -----AATCTTACAACCAGAACTCAATTACCCCCTGCATACACTAATTCTTTACACGT 102
 MN996532.1:21545-25354
 -----AATCTAACAACCTAGAAGTACAGTTACCTCCTGCATACACCAACTCATCCACCCGT 102
 * *

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NC_019843.3:21456-25517
 GGCCGTACATATTCTAACAATAACTATCACTTATCAAGG----TCTTTTCCCTATCAGGG 236
 NC_048212.1:20814-24623
 CATTTCCAATTGTTGTCCCGAGTTTTCAAGTTGCGCGCACCAACCTTGTTGTGCGCCAGCG 188

NC_004718.3:21492-25259

GGGGTTTACTATCCTGATGAAATTTTATGATCAGACAC----TCTTTATTTAACTCAGGA 170

MT799526.1

GGTGTTTATTATCCTGACACCATATTTAGATCAAACAC----ACTTGTGTGAGTCAGGG 161

NC_045512.2:21563-25384

GGTGTTTATTACCCCTGACAAAGTTTTTCAGATCCTCAGT----TTTACATTCAACTCAGGA 158

MN996532.1:21545-25354

GGTGTCTATTACCCCTGACAAAGTTTTTCAGATCTTCAGT----TTTACATTAACTCAGGA 158

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NC_019843.3:21456-25517

AGACCATGGTGATATGTATGTTTA-----CTCTGCAGGACATGCTACAGGCAC 284

NC_048212.1:20814-24623

TTTACAAGTTGCTGCTT--ATGATTTTACTAAGATACCCATTACACC----- 233

NC_004718.3:21492-25259

TTTATTTCTTCCATTTTATTCTAATGTTACAGGGTTTCA----- 209

MT799526.1

TTACTTTTTACCTTTTTATTCTAATGTTAGCTGGTATTATGCATTGAC---AAAACTAA 218

NC_045512.2:21563-25384

CTTGTTCTTACCTTTCTTTTCCAATGTTACTTGGTTCATGCTATACATGTCTCTGGGAC 218

MN996532.1:21545-25354

TTTGTTTTTACCTTTCTTCTCCAATGTGACCTGGTTCATGCTATACATGTTTCAGGGAC 218

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NC_019843.3:21456-25517

AACTCCACAAAAGTTGTTTGTAGCTAACTATTCTCAGGACGTCAAACAGTTTGCTAATGG 344

NC_048212.1:20814-24623

GCCACACCGTAGTATTTT-----TAATAA 257

NC_004718.3:21492-25259

TACTATTAATCATACGTT-----TGGCAA 233

MT799526.1

CAGTGCTGAAAAGAGAGT-----TGATAA 242

NC_045512.2:21563-25384

CAATGGTACTAAGAGGTT-----TGATAA 242

MN996532.1:21545-25354

CAATGGTATTAAAAGGTT-----TGATAA 242

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NC_019843.3:21456-25517

GTTTGTCTGTCGGTATAGGAGCAGCTGCCAATTCCACTGGCACTGTTATTATTAGCCCATC 404

NC_048212.1:20814-24623

CACTTATTTTCGTGTAGGCGATGGTATTTTAGTGAATACTCACAT----- 302

NC_004718.3:21492-25259

CCCTGTCATACCTTTTAAAGGATGGTATTTATTTTGCTGCCACAGA----- 278

MT799526.1
 CCCTGTTTTGGATTTCAAAGACGGTATTTACTTTGCTGCAACTGA----- 287
 NC_045512.2:21563-25384
 CCCTGTCCCTACCATTTAATGATGGTGTATTTTGGCTTCCACTGA----- 287
 MN996532.1:21545-25354
 CCCAGTTCTGCCATTC AACGATGGCGTCTATTTTGGCTTCCACTGA----- 287
 * * * * *

NC_019843.3:21456-25517
 TACCAAGCGCTACTATACGAAAAATTTACCCTGCTTTTATGCTGGGTTCTTCAGTTGGTAA 464
 NC_048212.1:20814-24623
 -----GTATCACAGAACTAACATAGCTACCAACTTAGGTAGCTCCTTCTATGG 350
 NC_004718.3:21492-25259
 -----GAAATCAAATGTTGTCCGTGGTTGGGTTTTTGGTTCTACC----ATGA 322
 MT799526.1
 -----AAAATCTAACATTGTCAGAGGTTGGATCTTTGGAACGACT----CTTG 331
 NC_045512.2:21563-25384
 -----GAAGTCTAACATAATAAGAGGCTGGATTTTTGGTACTACT----TTAG 331
 MN996532.1:21545-25354
 -----GAAGTCTAATATAATAAGAGGATGGATTTTTGGTACTACC----TTAG 331
 * * * * *

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NC_019843.3:21456-25517
 TTTCTCAGATGGTAAAATGGGCCGCTTCTTCAATCATACTCTAGTTCTTTTGC----- 517
 NC_048212.1:20814-24623
 TT----GTCAAGAGCCTTTTGGTGC-----AGCCTTTGGCAACACTTTTGTTAATGAA 399
 NC_004718.3:21492-25259
 AC----AACAAATCAGTCGGTGATTATTATTAACAATTCTACTAATGTTGTTATACGA 378
 MT799526.1
 AC----AACACATCAGTCACCTTTTGATAGTTAACACGCAACTAATGTTATCATCAA 387
 NC_045512.2:21563-25384
 AT----TCGAAGACCCAGTCCCTACTTATTGTTAATAACGCTACTAATGTTGTTATTAAA 387
 MN996532.1:21545-25354
 AT----TCGAAGACCCAGTCTCTACTTATTGTTAATAACGCTACTAATGTTGTTATTAAA 387
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NC_019843.3:21456-25517
 -----CCGATGGATGTGGCACTTTACTTAGAGCTTTTATTGTATTCTA 561
 NC_048212.1:20814-24623
 CCCATAACTTTAGTTATGTTTTATGCAGGCAATGTTGGTAGTTGGTCTAGTCTTGTTACT 459
 NC_004718.3:21492-25259
 GCATGTAACTT---TGAATTGTGTGACAAACCCTTTCTTTGCTGTTTCTAAACCCATGGGT 435
 MT799526.1
 GTTTGTAAATT---CCAGTTTTGTTATGACCCTTACCTTAGTGGTTATTATCATAACAAT 444

NC_045512.2:21563-25384

GTCTGTGAATT---TCAATTTTGTAAATGATCCATTTTGGGTGTTTATTACCACAAAAAC 444

MN996532.1:21545-25354

GTCTGTGAATT---TCAATTTTGTAAATGATCCATTTTGGGTGTTTATTACCACAAAAAC 444

* *

NC_019843.3:21456-25517

GAGCCTCGCTCTGGAAATCATTGTCCTGCTGGCAAT---TCCTATACTTCTTTTGCCACT 618

NC_048212.1:20814-24623

CAGCAGCAAGCTAACATCACCATAGTGTCTTGTGATAACGCCACTTTGTGTGCTAACCCC 519

NC_004718.3:21492-25259

A---CACAGACACATAC-----TATGATATTCGATAATGCATTTAATTGCACT 480

MT799526.1

-----AAACGTGGAGCACGAGAGAGTTTGCTGTTTATTCCTCTTATGCCAATTGCACT 498

NC_045512.2:21563-25384

A---ACAAAAGTTGGATGGAAGTGAGTTCAGAGTTTATTCTAGTGCGAATAATTGCACT 501

MN996532.1:21545-25354

A---ACAAAAGTTGGATGGAAGTGAGTTCAGAGTTTACTCTAGTGCGAATAATTGCACT 501

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NC_019843.3:21456-25517

TATCACACTCCTGCAACAGATTGTTCTGATGGCAATTACAATCGTA-ATGCCAGTCTGAA 677

NC_048212.1:20814-24623

TTCTT-----TCTAAG--ATGGGGTCCAGGTGTCATACGCAGTTTTAC 560

NC_004718.3:21492-25259

TTCGAGTACATA-TCTGATGCCTTTTCGCTTGATGTTTCAGAAAAGTCAGGTAATTTTAA 539

MT799526.1

TTTGAATATGTC-TCTAAGTCTTTTATGCTAGATATAGCTGGCAAAAGTGGCTTATTGA 557

NC_045512.2:21563-25384

TTTGAATATGTC-TCTCAGCCTTTTCTTATGGACCTTGAAGGAAAACAGGGTAATTTCAA 560

MN996532.1:21545-25354

TTTGAATATGTC-TCTCAGCCTTTTCTTATGGACCTTGAAGGAAAACAGGGTAATTTCAA 560

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NC_019843.3:21456-25517

CTCTTTTAAAGGAGTATTTTAAATTTACGTAACCTGCACCTTTATGTACACTTATAACATTAC 737

NC_048212.1:20814-24623

TATAAGTAATGCATTTTCAGTGTGATGGTAATTATACATTTTATGACACT----- 609

NC_004718.3:21492-25259

ACACTTACGAGAGTTTGTGTTTAAAAATAAG----- 571

MT799526.1

CACATTAAGAGAGTTTGTGTTTCCGAAATGTCG----- 589

NC_045512.2:21563-25384

AAATCTTAGGGAATTTGTGTTTAAAGATATTG----- 592

MN996532.1:21545-25354

AAATCTTAGGGAATTCGTGTTTAAGAAATTG----- 592

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NC_019843.3:21456-25517

CGAAGATGAGATT-TTAGAGTGGTTTGGCATTACACAACTGCTCAAG-GTGTTACCTC 795

NC_048212.1:20814-24623

-AAACTTGTTAATTTTACTGTTTCCACTGCTCGCTATAATTTAGCTTTTACTTTTGCAGA 668

NC_004718.3:21492-25259

-----ATGGGTTTCTCTATGTTTATAAGGGCTATCAACCT-----AT---AGATGTAGT 617

MT799526.1

-----ACGGATATTTCAAGATTTACTCAAAATACACACCT-----GT---TAATGTAAA 635

NC_045512.2:21563-25384

-----ATGGTTATTTTAAAATATATTCTAAGCACACGCCT-----AT---TAATTTAGT 638

MN996532.1:21545-25354

-----ATGGTTATTTTCAAATATATTCTAAACATACGCCT-----AT---TAATTTAGT 638

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NC_019843.3:21456-25517

TTCTCATCTCGGTATGTTGATTTGTACGGCGGCAATATGTTTCAATTTGCCACCTTGCCCT 855

NC_048212.1:20814-24623

TGGTGACATTTTATGTACTATGCTGCACTGGGTGATTCTTTGAATTTACCTACTGCTTA 728

NC_004718.3:21492-25259

TCGTGATCTACCTTCTGGTTTTAACACTTTGAAACCTATTTTTAAGTTGCCTCTTGGTAT 677

MT799526.1

TAGTAATTTACCTATAGGTTTTTCAGCACTTGAACTCTTGTTGAAATTCAGCTGGCAT 695

NC_045512.2:21563-25384

GCGTGATCTCCCTCAGGGTTTTTCGGCTTTAGAACCATTGGTAGATTTGCCAATAGGTAT 698

MN996532.1:21545-25354

GCGTGATCTTCCCCCTGGTTTTTCAGCTTTAGAACCATTGGTAGATCTGCCAATAGGTAT 698

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NC_019843.3:21456-25517

GTTTATGATACTATTAAGTATTATTCTATCATTCCTCA----- 893

NC_048212.1:20814-24623

CCCGCTGCAGCCATATTTACGTATACCTGCTGGTTTTAAACCAGATGTTGTACAGTTTTT 788

NC_004718.3:21492-25259

TAACATTACAAATTTTAGAGCCATTCTTACAGCCTTTT----- 715

MT799526.1

AAATATTAATAAATTTAGAACTCCTCACTATACATA----- 733

NC_045512.2:21563-25384

TAACATCACTAGGTTTCAAACCTTACTTGCTTTACATA----- 736

MN996532.1:21545-25354

TAACATCACTAGGTTTCAAACCTTACTTGCTTTACATA----- 736

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NC_019843.3:21456-25517

--CA-----GTATT---CGTTCTATCCAAAGTGATAGAAAAGCTTGGGC 932

NC_048212.1:20814-24623

CCAGGCCATAACACGCCCCAATGGTGAAAAGTGCTGAAGTTGCTTGCTTCTAGCACCGT 848

NC_004718.3:21492-25259

-CA-----CCTGCTCAAGACATTTGGGGCACGTCAGCTGC 749

MT799526.1

-GAGGAGACCCCA-----TGCCTA-----ATAATGGCTGGACAGTCTTTTCAGC 776

NC_045512.2:21563-25384

-GAAGTTATTGTA-----CTCCTGGTGATTCTTCTTCAGGTTGGACAGCTGGTGCTGC 788

MN996532.1:21545-25354

-GAAGCTATTGTA-----CTCCTGGTGATTCTTCTTCAGGTTGGACAGCTGGTGCTGC 788

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NC_019843.3:21456-25517

TGCCTTCTACGTATATAAACTTCAACCGTTAACTTTCCTGTTGGAATTTTCTGTTGATGG 992

NC_048212.1:20814-24623

TTCTTGGTATGTGTCGCGGTTGTATTATAAAGAGCTACTGGTTGGTTATGATTCTTACAG 908

NC_004718.3:21492-25259

AGCCTATTTTGTGGCTATTTAAAGCCAACTACATTTATGCTCAAGTATGATGAAAATGG 809

MT799526.1

TGCTTATTACGTGGGCTATTTAGCTCCACGTACATTTATGTTAAATTATAATGAAAATGG 836

NC_045512.2:21563-25384

AGCTTATTATGTGGGTTATCTTCAACCTAGGACTTTTCTATTAAAATATAATGAAAATGG 848

MN996532.1:21545-25354

AGCTTATTATGTGGGTTATCTTCAACCAAGGACTTTTCTACTAAAATATAATGAGAATGG 848

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NC_019843.3:21456-25517

TTATATACGCAGAGCTATAGACTGTGGTTTTAATGATTTGTCACAACTCCACTGCTCATA 1052

NC_048212.1:20814-24623

TAGTATCGTTAATGTTAGTTTTTGTCTTCAGATGCTGAAAGTGAGTTGCAGTGCTTGTT 968

NC_004718.3:21492-25259

TACAATCACAGATGCTGTTGATTGTCTCAAAATCCACTTGCTGAACTCAAATGCTCTGT 869

MT799526.1

TACAATAACAGATGCTGTTGATTGTGCCCTAGATCCTCTATCTGAGGCTAAATGCACATT 896

NC_045512.2:21563-25384

AACCATTAACAGATGCTGTAGACTGTGCACTTGACCCCTCTCTCAGAAACAAAGTGTACGTT 908

MN996532.1:21545-25354

AACCATTAACAGATGCTGTAGACTGTGCACTTGACCCCTCTTTCAGAAACAAAGTGTACGTT 908

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NC_019843.3:21456-25517

TGAATCCTTCGATGTTGAATCTGGAGTTTATTCAGTTTCGTCTTTCGAAGCAAAACCTTC 1112

NC_048212.1:20814-24623
GGGTACATTTGCGCCAGCTAATGGTGTATTCCTCAGTAATTTTCGTAGTAGTCCAC 1028
NC_004718.3:21492-25259
TAAGAGCTTTGAGATTGACAAAGGAATTTACCAGACCTCTAATTTACGGGTGTTCCCTC 929
MT799526.1
AAATCCTTAACGTGTGAAAAGGAATCTATCAGACTTCTAACTTTAGAGTTCAACCAAC 956
NC_045512.2:21563-25384
GAAATCCTTCACTGTAGAAAAGGAATCTATCAAACTTCTAACTTTAGAGTCCAACCAAC 968
MN996532.1:21545-25354
AAATCCTTCACTGTGTGAAAAGGAATTTATCAAACTTCTAACTTTAGAGTCCAACCAAC 968

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NC_019843.3:21456-25517
TGGCTCAGTTGTGGAACAGGCTGAAGGTGTTGAATGTGAT--TTTTCACCTCTTCTGTC 1169
NC_048212.1:20814-24623
TGACAAATGTACGTATCATAACAGTGCTTCTTCTGTAGTGTACCTTATTCTGTTTTGAG 1088
NC_004718.3:21492-25259
AGGAGATGTTGTGAGATTCCCTAATATTACAACTTGTGTCCTTTTGGAGAGGTTTTTAA 989
MT799526.1
TGAATCTATAGTTAGGTTTCCAAATATTACAACTTATGCCCTTTTGGTGAAAGTTTTCAA 1016
NC_045512.2:21563-25384
AGAATCTATTGTTAGATTTCCTAATATTACAACTTGTGCCCTTTTGGTGAAAGTTTTTAA 1028
MN996532.1:21545-25354
AGATTCTATTGTTAGATTCCCAAATATTACAACTTATGTCCTTTTGGTGAAAGTTTTTAA 1028

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NC_019843.3:21456-25517
TGG---CACACCTCCTCAGGTTTATAATTTCAAGCGTTTGGTTTTTACCAATTGCAATTA 1226
NC_048212.1:20814-24623
TCGGCCACCTTTACC-----TTTGTATGGAAGCGTTATGCCATTTCCAATTGTAAGTT 1142
NC_004718.3:21492-25259
TGCTACTAAATTCCCTTCTGTCTATGCATGGGAGAGAAAAAAATTTCTAATTGTGTTGC 1049
MT799526.1
TGCAACCACTTTTGCATCTGTTTATGCTTGGAATAGAAAGAGAATCAGTAACTGTGTTGC 1076
NC_045512.2:21563-25384
CGCCACCAGATTGTCATCTGTTTATGCTTGGAACAGGAAGAGAATCAGCAACTGTGTTGC 1088
MN996532.1:21545-25354
CGCCACCACATTCGCATCAGTTTATGCTTGGAACAGAAAGAGAATTAGCAACTGTGTTGC 1088

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NC_019843.3:21456-25517
TAATCTTACCAATTGCTTTTCTGTTTCTGTGAATGATTTTACTTGTAGTCAAATATC 1286
NC_048212.1:20814-24623
TGATTTTCAGGCATTGCTTAGCCATTTGCCTACATTTCAACTTCGCTGTTTGGCATATC 1202

NC_004718.3:21492-25259
 TGATTACTCTGTGCTCTACAACTCAACATTTTTTTTCAACCTTTAAGTGCTATGGCGTTTC 1109
 MT799526.1
 TGATTACTCTGTTCTTTACAACTCCACTTCTTTCTCAACATTCAAATGTTATGGAGTTTC 1136
 NC_045512.2:21563-25384
 TGATTATTCTGTCCTATATAATTCCGCATCATTTTCCACTTTTAAGTGTTATGGAGTGTC 1148
 MN996532.1:21545-25354
 TGATTACTCTGTCCTATATAATTCCACTTCATTTTCTACCTTTAAATGTTATGGAGTGTC 1148

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NC_019843.3:21456-25517
 TCCAGCAGCAATTGCTAGCAACTGTTATTCTTCACTGATTTTGGATTACTTTTCATACCC 1346
 NC_048212.1:20814-24623
 GCCTACTAAGCTTGCCACTATGTGTTTTGGCACTGTCACCTTTAGACATTATGTTGGTTAA 1262
 NC_004718.3:21492-25259
 TGCCACTAAGTTGAATGATCTTTGCTTCTCCAATGTCTATGCAGATTCTTTTGTAGTCAA 1169
 MT799526.1
 ACCAACCAAAATAAATGATCTCTGCTTTACTAACGTTTATGCAGACTCATTTGTAGTTAG 1196
 NC_045512.2:21563-25384
 TCCTACTAAATTAATGATCTCTGCTTTACTAATGTCTATGCAGATTCAATTGTAAATTAG 1208
 MN996532.1:21545-25354
 TCCTACTAAATTAATGATCTCTGCTTTACTAATGTTTATGCAGACTCATTTGTGATTAC 1208

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NC_019843.3:21456-25517
 ACTTAGTATGAAATCCGATCTCAGTGTTAGTTCCTGCTGGTCCAATATCCCAGTTTAATTA 1406
 NC_048212.1:20814-24623
 TGTTACTCATTACAATAACCTCCTTAATGATGTTTCCTGATGATTTTAGCCTTTATAATTA 1322
 NC_004718.3:21492-25259
 GGGAGATGATGTAAGACAAATAGCGCCAGGACAAACTGGTGTTATTGCTGATTATAATTA 1229
 MT799526.1
 AGGTGATGAAGTCAGACAAATTGCTCCAGGACAAACAGGAAGAATTGCTGACTATAATTA 1256
 NC_045512.2:21563-25384
 AGGTGATGAAGTCAGACAAATCGCTCCAGGGCAAACAGGAAGATTGCTGATTATAATTA 1268
 MN996532.1:21545-25354
 AGGTGATGAAGTCAGACAAATTGCGCCAGGACAAACTGGAAGATTGCTGACTACAATTA 1268

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NC_019843.3:21456-25517
 TAAACAGTCCTTTTCTAATCCACATGTTTGATTTTAGCGACTGTTCCCTCATAACCTTAC 1466
 NC_048212.1:20814-24623
 TCAATTACCGCGTAATTTCTACGGTTGTTGTCAT---AGTTATTATTTACCTAATG---A 1376
 NC_004718.3:21492-25259
 TAAATTGCCAGATGATTTTCATGGGTTGTGTCCTT---GCTTGAATACTAGGAACATTGA 1286

MT799526.1

TAAACTCCCTGATGATTTACAGGTTGTGTAATA---GCTTGGAAATTCTAACCAACCTTGA 1313

NC_045512.2:21563-25384

TAAATTACCAAGATGATTTTACAGGCTGCGTTATA---GCTTGGAAATTCTAACCAATCTTGA 1325

MN996532.1:21545-25354

TAAACTACCAGATGATTTTACTGGTTGTGTTATA---GCTTGGAAATTCTAAGCATATTGA 1325

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NC_019843.3:21456-25517

TACTATTACTAAGCCTCTTAAGTACAGCTATATTAACAAGTGCTCTCGTCTTCTTTCTGA 1526

NC_048212.1:20814-24623

CACTGCA-----TTTAGTTATACTGTA-----GC 1400

NC_004718.3:21492-25259

TGCTACT---TCAACTGGTAATTATAATTATAAATATAGGTATCTTA-----GA 1332

MT799526.1

TTCTAAG---GTTGGTGGTAATTATAAACTACCTTTATAGATTGTTTA-----GA 1359

NC_045512.2:21563-25384

TTCTAAG---GTTGGTGGTAATTATAATTACCTGTATAGATTGTTTA-----GG 1371

MN996532.1:21545-25354

TGCAAAA---GAGGGCGGTAATTTTAACTATCTTTACCGTCTCTTTA-----GA 1371

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NC_019843.3:21456-25517

TGATCGTACTGAAGTACCTCAGTTAGTGAAACGCTAATCAATACTCACCCCTGTGTATCCAT 1586

NC_048212.1:20814-24623

TTCGCGCATACGTTACCCT----TCTTGG-----GTGCATTC 1433

NC_004718.3:21492-25259

CATGGCAAGCTTAGGCCCT----TTGAGAGAGACATATCTAATGTGCCTTCTCCCTGA 1388

MT799526.1

AAGTCCAACTCAAACCTT----TTGAACGAGACATTTCTACAGAAATATACCAAGCTGG 1415

NC_045512.2:21563-25384

AAGTCTAATCTCAAACCTT----TTGAGAGAGATATTTCAACTGAAATCTATCAGGCCGG 1427

MN996532.1:21545-25354

AAAGCTAATCTTAAACCTT----TTGAGAGGGATATCTCAACTGAAATTTACCAAGCAGG 1427

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NC_019843.3:21456-25517

TGTCCCATCCACTGTGTGGGAACGGTGATTATTATAGGAAACAACCTATCTCCACTTGA 1646

NC_048212.1:20814-24623

TATCACACCTGGTGGTAGACAACCCG---TTGGCCCTTTCTTA-----GA 1475

NC_004718.3:21492-25259

TGGCAAAACCTTGCACCC---ACCTGCTCTTAATTGTTATTGG-----CCATTAAA 1436

MT799526.1

TAGTACACCCCTGCAATGGGGTTGAAGGTTTTAACTGTTACTTT-----CCTCTACA 1466

NC_045512.2:21563-25384

TAGCACACCTTGTAAATGGTGGTTGAAGGTTTTAATTGTTACTTT-----CCTTTACA 1478

MN996532.1:21545-25354

CAGCAAAACCTTGTAAATGGTCAAACCTGGTCTAAATTGCTACTAC-----CCACTTTA 1478

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NC_019843.3:21456-25517

AGGTGGTGGCTGGCTTGTGCTAGTGGCTCAACTGTTGCCATGACTGAGCAATTACAG-- 1704

NC_048212.1:20814-24623

T-----TCC-TTACAAAGTTCC-----AGCAAGCCTTGTACCGGATCATGTTT 1517

NC_004718.3:21492-25259

TGATTATGGTTTTTACACCACT-----ACTGGCATTGGCTACCAACCTTA--- 1481

MT799526.1

ATCTTATGGTTTCCACCCTACT-----AATGGTGTGGTTACCAACCTTA--- 1511

NC_045512.2:21563-25384

ATCATATGGTTTCCAACCCACT-----AATGGTGTGGTTACCAACCATTA--- 1523

MN996532.1:21545-25354

TAGATATGGAATTTACCCCTACT-----GATGGTGTGGTCAACCAACCTTA--- 1523

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NC_019843.3:21456-25517

ATGGGCTTTGGTATTACAGTTCAATATGGTACAGACACC-AATAGTGTGTTGCCCCAAGCT 1763

NC_048212.1:20814-24623

AGGTTTAGCCGTTATTTCTTTAAGTATAGCCTCGGCAAACAAATTAGTTTGTCCAG---- 1573

NC_004718.3:21492-25259

CAGAGTTGTAGTACTTTCTTTTGAACCTTTTAAATGCACCGGCCACGGTTTGTGGAC---- 1537

MT799526.1

TAGAGTAGTAGTATTGTCAATTTGAACTTTTAAATGCACCTGCTACTGTTGTGGAC---- 1567

NC_045512.2:21563-25384

CAGAGTAGTAGTACTTTCTTTTGAACCTTCTACATGCACCAGCAACTGTTTGTGGAC---- 1579

MN996532.1:21545-25354

TAGGGTAGTAGTACTTTCTTTTGAACCTTCTAAATGCACCAGCAACTGTTTGTGGAC---- 1579

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NC_019843.3:21456-25517

TGAATTTGCTAATGACACAAAAATTGCCTCTCAATTAGGCAATTGCGTGGAATATTCCTT 1823

NC_048212.1:20814-24623

-----TAGGCAATGACACAGATATTGTGCCTGACACTTGTGTCAACTACAATAT 1622

NC_004718.3:21492-25259

-----CAAAATTATCCACTGACCTTATTAAGAACCAGTGTGTCAATTTTAATTT 1586

MT799526.1

-----CTAAACAGTCCACTAACCTAGTTAAAAACAAATGTGTCAACTTCAATTT 1616

NC_045512.2:21563-25384

-----CTAAAAAGTCTACTAATTTGGTTAAAAACAAATGTGTCAATTTCAACTT 1628

MN996532.1:21545-25354

-----CTAAGAAGTCTACTAACTTGGTTAAAAATAAATGTGTCAAATTTCAACTT 1628

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NC_019843.3:21456-25517

CTATGGTGTTCGGGCCGTGGTGTTCAGAAATTGCACAGCTGTAGGTGTTTCGACAGCA 1883

NC_048212.1:20814-24623

TTATGGTTATCAAGGCAGTGGTGTATTAGTAGGTCAAATTACACTTTGCCCTCTTCTAA 1682

NC_004718.3:21492-25259

TAATGGACTCACTGGTACTGGTGTGTTAACTCCTTCTTCAAGAGATTTCACCATTTC 1646

MT799526.1

TAATGGTCTAACAGGCACAGGTGTTCTTACAGAGTCTAGCAAAAAGTTTTGCCTTTCCA 1676

NC_045512.2:21563-25384

CAATGGTTTAAACAGGCACAGGTGTTCTTACTGAGTCTAACAAAAAGTTTCTGCCTTTCCA 1688

MN996532.1:21545-25354

TAATGGTTTAACTGGCACAGGTGTCCTCACAGAGTCTAATAAAAAGTTTCTACCTTTCCA 1688

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NC_019843.3:21456-25517

GCGCTTTGTTTATGA-----TGCGTACCAGAATTTAGTTGGCTATTATT---CTGATGA 1934

NC_048212.1:20814-24623

GGTTTTCTCGCTTAGTTCCTTCTGGTGAAGTTGACTGTCTTTGCAGTTG-----GTTCTTC 1736

NC_004718.3:21492-25259

ACAATTTGGCCGTGATGTTTCTGATTTCACTGATTCCGTTTCGAGATCCTAAACATCTGA 1706

MT799526.1

ACAATTTGGCAGAGATATTGCCGACACTACTGATGCTGTCCGTGATCCACAGACACTTGA 1736

NC_045512.2:21563-25384

ACAATTTGGCAGAGACATTGCTGACACTACTGATGCTGTCCGTGATCCACAGACACTTGA 1748

MN996532.1:21545-25354

ACAATTTGGTAGAGACATTGCAGACACTACTGATGCCGTCCGTGATCCACAGACACTTGA 1748

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NC_019843.3:21456-25517

TGGCAACTACTACTGTTTGCCTGCTTGTGTTAGTGTTTCCTGTTTCTGTCATCTATGATAA 1994

NC_048212.1:20814-24623

TTTTTACCAGCTATCTCCGTGTGCATTGCTCCTATATCTGCAG-----CTTTTTTA 1787

NC_004718.3:21492-25259

AATATTAGACATTTACCTTGCGCTTTTGGGGGTGTAAGTGTAATTACACCTGGAACAAA 1766

MT799526.1

AATTCCTTGATATCACACCGTGTCTTTTGGTGGTGTGTCAGTGTTATAACACCAGGAACAAA 1796

NC_045512.2:21563-25384

GATTCTTGACATTACACCATGTTCTTTTGGTGGTGTGTCAGTGTTATAACACCAGGAACAAA 1808

MN996532.1:21545-25354

GATTCTTGACATTACACCATGTTCTTTTGGTGGTGTGTCAGTGTTATAACACCCTGGAACAAA 1808

NC_019843.3:21456-25517
 AGAAACTAAACCCACGCTACTCTATTTGGTAGTGTTGCATGTGAACACATTTCTTCTAC 2054
 NC_048212.1:20814-24623
 TAAGGGTTACACTACTTCTTTGTTGTTTAAATAACCTTCCTTGTTCCAACCGGCATCGTGC 1847
 NC_004718.3:21492-25259
 TGCTTCATCTGAAGTTGCTGTTCTATATCAAGATGTTAACTGCACATGATGTTTCTACAGC 1826
 MT799526.1
 CACTTCTAACCAAGTGGCTGTTCTTTATCAGGATGTTAACTGCACATGAAGTCCCTGTTGC 1856
 NC_045512.2:21563-25384
 TACTTCTAACCAAGTTGCTGTTCTTTATCAGGATGTTAACTGCACAGAAGTCCCTGTTGC 1868
 MN996532.1:21545-25354
 TGCCTCTAACCAAGTTGCTGTTCTTTATCAGGATGTTAACTGCACAGAAGTCCCTGTTGC 1868
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 NC_019843.3:21456-25517
 CATGTCTCAATACTCCCGTTCTACGCGATCAATGCTTAAACGGCGAGATTCTACATATGG 2114
 NC_048212.1:20814-24623
 AGT---CGTGGAACTGTAGTGCTTATTGGCGTCG-----TAGTGTTGCAGACAATAA 1898
 NC_004718.3:21492-25259
 AATTCATGCAGATCAACTCACACCAGCTTGGCGCAT-----ATATTCTACTGGAACAA 1880
 MT799526.1
 TATTCATGCAGATCAATTAAACCAACCTGGCGTGT-----TACTCTACAGGTTCAA 1910
 NC_045512.2:21563-25384
 TATTCATGCAGATCAACTTACTCCTACTTGGCGTGT-----TTATTCTACAGGTTCTAA 1922
 MN996532.1:21545-25354
 TATCCATGCAGACCAACTTACTCCCACTTGGCGTGT-----TACTCCACAGGTTCTAA 1922
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 NC_019843.3:21456-25517
 CCCCCTTCAGACACCTGTTGTTGTGTCCTAGGACTTGTTAATTCCTCTT---TGTTTCGT 2171
 NC_048212.1:20814-24623
 CACGTTTGACACAACTGCTGGGTGCATTTTTAATGCGTATAATTTAACTAGCATTTGTAGT 1958
 NC_004718.3:21492-25259
 TGTATTCCAGACTCAAGCAGGCTGTCTTATAGGAGCTGAGCATGTCGA-----CACTTC 1934
 MT799526.1
 TGTTTTTCAAACGCGTGCAGGCTGTTTAAATAGGGGCTGAACATGTTAA-----CAACAC 1964
 NC_045512.2:21563-25384
 TGTTTTTCAAACACGTGCAGGCTGTTTAAATAGGGGCTGAACATGTCAA-----CAACTC 1976
 MN996532.1:21545-25354
 TGTTTTTCAAACACGTGCAGGTTGTTTAAATAGGGGCTGAACATGTCAA-----TAACTC 1976
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NC_019843.3:21456-25517
AGAGGACTGCAAGTTGCCTCTTGGTCAATCTCTCTGTGCTCTTCCTGACACACCTAGTAC 2231
NC_048212.1:20814-24623
TAATCAGTGTGATTTACCTATTGGTGATAGTTATTGTTA-----CAACCATC-C---C 2008
NC_004718.3:21492-25259
TTATGAGTGCGACATTCCTATTGGAGCTGGCATTGTGCTAGTTACCATACAGTTT---C 1991
MT799526.1
TTACGAGTGTGACATACCAATTGGTGCAGGAATATGTGCCAGTTATCAGACTCAAA---C 2021
NC_045512.2:21563-25384
ATATGAGTGTGACATACCCATTGGTGCAGGTATATGCGCTAGTTATCAGACTCAGA---C 2033
MN996532.1:21545-25354
GTATGAGTGTGACATACCTATTGGTGCAGGAATATGCGCCAGTTATCAGACTCAAA---C 2033
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NC_019843.3:21456-25517
TCTCACACCTCGCAGTGTGCGCTCTGTTCCAGGTGAAATGCGCTTGGCATCCATTGCTTT 2291
NC_048212.1:20814-24623
TTATTAAGG-----GTTTTGAAGCCACATTATCATTGGTTACGTACAACCCATT 2057
NC_004718.3:21492-25259
TTTATTACG-----TAGTACTAGCCAAAAATCTATTGTGGCTTATACTATGTC 2039
MT799526.1
TAATTCACG-----TAGTGTTCAGTCAAGCTATTATTGCCTACACTATGTC 2069
NC_045512.2:21563-25384
TAATTCTCCTCGGCGGGCACGTAGTGTAGCTAGTCAATCCATCATTGCCTACACTATGTC 2093
MN996532.1:21545-25354
TAATTCAC-----GTAGTGTGGCCAGTCAATCTATTATTGCCTACACTATGTC 2081
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NC_019843.3:21456-25517
TAATCATCCTATTCAGGTTGATCAACTTAATAGTAGTTATTTTAAATTAAGTATACCCAC 2351
NC_048212.1:20814-24623
GGCT-----GAT---TCTTTAACACCTATCACACCGGTTTATCAAGTTTCAGTGCCTAC 2108
NC_004718.3:21492-25259
TTTA-----GGTGCT-GATAGTTCAATTGCTTACTCTAATAACACCATTGCTATACCTAC 2093
MT799526.1
ACTT-----GGTGCA-GAAAATTCAGTTGCTTATGCTAATAACTCTATTGCCATACCTAC 2123
NC_045512.2:21563-25384
ACTT-----GGTGCA-GAAAATTCAGTTGCTTACTCTAATAACTCTATTGCCATACCCAC 2147
MN996532.1:21545-25354
ACTT-----GGTGCA-GAAAATTCAGTTGCTTATTCTAATAACTCTATTGCCATACCTAC 2135
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NC_019843.3:21456-25517
TAATTTTTCCTTTGGTGTGACTCAGGAGTACATTCAGACAACCATTAGAAAATTACTGT 2411

NC_048212.1:20814-24623
CAATTTTACTTTGGTAGCTTCTACTGAATATATTCAAACCTTATGCATCAAAAATTTCTAT 2168
NC_004718.3:21492-25259
TAACTTTTCAAATTAGCATTACTACAGAAGTAATGCCTGTTTCTATGGCTAAAACCTCCGT 2153
MT799526.1
AAATTTTACTATTAGTGTGACCACTGAAATTCTACCAGTGTCTATGACAAAGACATCAGT 2183
NC_045512.2:21563-25384
AAATTTTACTATTAGTGTACCACAGAAATTCTACCAGTGTCTATGACCAAGACATCAGT 2207
MN996532.1:21545-25354
AAATTTTACTATTAGTGTGACCACTGAAATTCTACCTGTGTCTATGACAAAGACATCGGT 2195
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NC_019843.3:21456-25517
TGATTGTAAACAGTACGTTTGCAATGGTTTCCAGAAGTGTGAGCAATTACTGCGCGAGTA 2471
NC_048212.1:20814-24623
TGATTGTGCTAAGTATTTATGTGGTGATTCTTCACAGTGCAGAACGGTGTGTTGCAGTA 2228
NC_004718.3:21492-25259
AGATTGTAATATGTACATCTGCGGAGATTCTACTGAATGTGCTAATTTGCTTCTCCAATA 2213
MT799526.1
AGATTGTACAAATGTACATTTGTGGTGACTCAATAGAGTGCAGCAACCTTTTGCTCCAATA 2243
NC_045512.2:21563-25384
AGATTGTACAAATGTACATTTGTGGTGATTCAACTGAATGCAGCAATCTTTTGTTGCAATA 2267
MN996532.1:21545-25354
AGACTGTACAAATGTATATTTGTGGTGATTCAACTGAGTGCAGCAACCTTTTGTTGCAATA 2255
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NC_019843.3:21456-25517
TGGCCAGTTTTGTTCCAAAATAAACCAGGCTCTCCATGGTGCCAATTTACGCCAGGATGA 2531
NC_048212.1:20814-24623
CGGCACATTTTGTAAATGATGTTAATGTTGCTTTAACGAGGGTTTTTACGTTGCTTGACAA 2288
NC_004718.3:21492-25259
TGGTAGCTTTTGCACACAATAAATCGTGCACTCTCAGGTATTGCTGCTGAACAGGATCG 2273
MT799526.1
TGGTAGTTTTTGCACACAACCTTAATCGTGCTTTAACTGGAATTGCTGTTGAACAAGACAA 2303
NC_045512.2:21563-25384
TGGCAGTTTTTGTACACAATTAACCGTGCTTTAACTGGAATAGCTGTTGAACAAGACAA 2327
MN996532.1:21545-25354
TGGTAGTTTTTGCACACAATTAATCGTGCTTTAACTGGAATAGCTGTTGAACAGGACAA 2315
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NC_019843.3:21456-25517
TTCTGTACGTAAATTTGTTTGCGAGCGTGAAGAAGCTCTCAATCATCTCCTATCA-TACCAG 2590
NC_048212.1:20814-24623
TTCACGTTGATACGTTTTTCATCCTTGA----AGTCCACAGCACCAAGTTCAGTTAGCTT 2344

NC_004718.3:21492-25259
CAACACACGTGAAGTGTTCGCTCAAGTCAAACAAATGTACAAAACCCCACTT-TGAAAT 2332
MT799526.1
AAACACACAGGAAGTTTTTGCACAAGTTAAACAAATTTACAAGACACCACCAA-TAAAGG 2362
NC_045512.2:21563-25384
AAACACCCAAAGAGTTTTTGCACAAGTCAAACAAATTTACAAAACACCACCAA-TTAAAG 2386
MN996532.1:21545-25354
AAATACTCAAGAAGTTTTTGTCTCAAGTTAAACAAATTTATAAGACACCACCAA-TTAAAG 2374

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NC_019843.3:21456-25517
GTTTTGGAGGTGACTTTAATTTGACACTTC---TAGAACCTGTTTCTATATCTACTGGCA 2647
NC_048212.1:20814-24623
ATACG---GGTGATTTTAATTTTCACATCGTTAGTGGGCTGTATTGGTACTGATTGTGATT 2401
NC_004718.3:21492-25259
ATTTT---GGTGGTTTTAATTTTTTCACAAATATTA-----CCTGACCCTCTAA 2377
MT799526.1
ATTTT---GGTGGTTTCAACTTTTCTCAAAATATTA-----CCAGATCCATCAA 2407
NC_045512.2:21563-25384
ATTTT---GGTGGTTTTAATTTTTTCACAAATATTA-----CCAGATCCATCAA 2431
MN996532.1:21545-25354
ATTTT---GGTGGTTTCAATTTTTTCACAAATATTA-----CCAGATCCATCAA 2419

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NC_019843.3:21456-25517
GTCGTAGTGCACGTAGTGCTATTGAGGATTTGCTATTGACAAAGTCACTATAGCTGATC 2707
NC_048212.1:20814-24623
CTAAGTCACATAGGTCCGCTTTGTCAGATCTATTGTTTAGTAAGGTTAGTGTGCTGACC 2461
NC_004718.3:21492-25259
AGCCAACTAAGAGGTCTTTTATTGAGGACTTGCTCTTTAATAAGGTGACACTCGCTGATG 2437
MT799526.1
AACCAAGCAAGAGGTCATTTATTGAAGATTTACTCTTCAACAAAGTGACACTTGCTGATG 2467
NC_045512.2:21563-25384
AACCAAGCAAGAGGTCATTTATTGAAGATCTACTTTTCAACAAAGTGACACTTGCTGATG 2491
MN996532.1:21545-25354
AACCAAGCAAGAGGTCATTTATTGAGGATTTACTTTTCAATAAAGTGACACTTGCTGATG 2479

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NC_019843.3:21456-25517
CTGGTTATATGCAAGGTTACGATGATTGCAT---GCAGCAAGGTCCAGCATCAGCTCGTG 2764
NC_048212.1:20814-24623
CAGGTTTCATGCAATCTTACCAACAATGTTTGGATGCACAGTGGGGTGGAATATACGTG 2521
NC_004718.3:21492-25259
CTGGCTTCATGAAGCAATA-----TGGCGAATGCCTAGGTGATATTAAATGCTAGAG 2488

MT799526.1
CTGGCTTCATCAACAATA-----TGGTGATTGCCTTGGTGATATTGCCGCTAGAG 2518
NC_045512.2:21563-25384
CTGGCTTCATCAACAATA-----TGGTGATTGCCTTGGTGATATTGCTGCTAGAG 2542
MN996532.1:21545-25354
CTGGCTTCATCAACAATA-----TGGTGATTGCCTTGGTGATATTGCTGCTAGGG 2530
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NC_019843.3:21456-25517
ATCTTATTTGTGCTCAATATGTGGCTGGTTACAAAGTATTACCTCCTCTTATGGATGTTA 2824
NC_048212.1:20814-24623
ATTTGCTTTGTACTCAGACGTTCAATGGCATCTCAGTATTGCCACCCATTGTATCTCCTT 2581
NC_004718.3:21492-25259
ATCTCATTTGTGCGCAGAAGTTCAATGGACTTACAGTGTTCGCCACCTCTGCTCACTGATG 2548
MT799526.1
ATCTTATTTGTGCACAAAAGTTTAAATGGCCTTACTGTTCTGCCACCTTTGCTCACAGATG 2578
NC_045512.2:21563-25384
ACCTCATTTGTGCACAAAAGTTTAAACGGCCTTACTGTTTTGCCACCTTTGCTCACAGATG 2602
MN996532.1:21545-25354
ATCTTATTTGTGCTCAAAAAGTTCAATGGCCTTACTGTTCTGCCACCTTTGCTCACAGATG 2590
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NC_019843.3:21456-25517
ATATGGAAGCCGCGTATACTTCATCTTTGCTTGGCAGCATAGCAGGTGTTGGCTGGACTG 2884
NC_048212.1:20814-24623
CCATGCAGGCTCTCTATACGACCGCCTTAGTCGGTGGCATTGCAGCCTCTGGTTTTACTT 2641
NC_004718.3:21492-25259
ATATGATTGCTGCCTACACTGCTGCTCTAGTTAGTGGTACTGCCACTGCTGGATGGACAT 2608
MT799526.1
AAATGATTGCTCAATACACCTCTGCACTACTTGCAGGGACAATCACATCAGGTTGGACCT 2638
NC_045512.2:21563-25384
AAATGATTGCTCAATACACTTCTGCACTGTTAGCGGGTACAATCACTTCTGGTTGGACCT 2662
MN996532.1:21545-25354
AAATGATCGCTCAATACACTTCTGCACTATTAGCAGGTACAATCACTTCTGGTTGGACTT 2650
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NC_019843.3:21456-25517
CTGGCTTATCCTCCTTTGCTGCTATTCCATTTGCACAGAGTATCTTTTATAGGTTAAACG 2944
NC_048212.1:20814-24623
TTGGTGTGTCATCTGCTGCTGTAATTCCTTTTGCCACACAGTTGCAGTTCAGACTTAATG 2701
NC_004718.3:21492-25259
TTGGTGCTGGCGCTGCTCTTCAAATACCTTTTGCTATGCAAAATGGCATATAGGTTCAATG 2668
MT799526.1
TTGGTGCTGGTGCAGCATTACAGATACCAATTTGCTATGCAAAATGGCTTATAGGTTTAATG 2698

NC_045512.2:21563-25384
 TTGGTGCAGGTGCTGCATTACAAATACCATTTGCTATGCAAAATGGCTTATAGGTTTAATG 2722
 MN996532.1:21545-25354
 TTGGTGCAGGTGCTGCTTTACAAATACCATTTGCCATGCAAAATGGCTTATAGGTTTAATG 2710
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NC_019843.3:21456-25517
 GTGTTGGCATTACTCAACAGGTTCTTTTCAGAGAACC AAAAGCTTATTGCCAATAAGTTTA 3004
 NC_048212.1:20814-24623
 GGTTAGGTGTGACCACTAATGTTTTAATGGAGAATCAACAATTGATAGCTAATGCTTTTA 2761
 NC_004718.3:21492-25259
 GCATTGGAGTTACCCAAAATGTTCTCTATGAGAACC AAAACAAATCGCCAACCAATTTA 2728
 MT799526.1
 GTATTGGAGTTACACAAAATGTTCTCTACGAGAACC AAAAATAATTGCAAAACCAATTCA 2758
 NC_045512.2:21563-25384
 GTATTGGAGTTACACAGAATGTTCTCTATGAGAACC AAAAATTGATTGCCAACCAATTTA 2782
 MN996532.1:21545-25354
 GTATTGGAGTTACACAGAATGTTCTCTATGAGAACC AAAAATTGATTGCCAACCAGTTTA 2770
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NC_019843.3:21456-25517
 ATCAGGCTCTGGGAGCTATGCAAAACAGGCTTCACTACAATAATGAAGCTTTTCAGAAGG 3064
 NC_048212.1:20814-24623
 ATAAGGCTCTTGTTTCGATACAGGAAGGGTTTACAGCCACTAATCAGGCTCTAAACAAAA 2821
 NC_004718.3:21492-25259
 ACAAGGCGATTAGTCAAATTCAAGAATCACTTACAACAACATCAACTGCATTGGGCAAGC 2788
 MT799526.1
 ACAGTGCAATTGGCAAAATTCAAGATTCACTTTCTACTGCAAGTGCACTTGGAAAAAC 2818
 NC_045512.2:21563-25384
 ATAGTGCTATTGGCAAAATTCAAGACTCACTTTCTTCCACAGCAAGTGCACTTGGAAAAAC 2842
 MN996532.1:21545-25354
 ATAGTGCTATTGGCAAAATTCAAGACTCACTTTCTTCTACAGCAAGTGCACTTGGAAAAAC 2830
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NC_019843.3:21456-25517
 TTCAGGATGCTGTGAACAACAATGCACAGGCTCTATCCAAATTAGCTAGCGAGCTATCTA 3124
 NC_048212.1:20814-24623
 TCCAAACTGTTGTCAATAACAATGCCTTGCAATTGCAAGTGTTAGTGCAGCAGTTGGGTA 2881
 NC_004718.3:21492-25259
 TGCAAGACGTTGTTAACCAGAATGCTCAAGCATTA AACACACTTGTTAAACAACCTTAGCT 2848
 MT799526.1
 TTCAAGATGTTGTCAACC AAAATGCACAGGCTTTAAACACACTTGTTAAACAACCTCAGCT 2878
 NC_045512.2:21563-25384
 TTCAAGATGTGGTCAACC AAAATGCACAAGCTTTAAACACGCTTGTTAAACAACCTTAGCT 2902

MN996532.1:21545-25354

TTCAAGATGTTGTCACCCAAAATGCACAAGCTTTAAACACGCTTGTTAAACAACCTTAGCT 2890

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NC_019843.3:21456-25517

ATACTTTTGGTGCTATTTCCGCCTCTATTGGAGACATCATACAACGTCTTGATGTTCTCG 3184

NC_048212.1:20814-24623

ATACATTTGGTGCTATATCAGCATCTGTTAATGAAATTTTATAGCCGTCTCGACTTGTTGG 2941

NC_004718.3:21492-25259

CTAATTTTGGTGCAATTTCAAGTGTGCTAAATGATATCCTTTTCGCGACTTGATAAAGTCG 2908

MT799526.1

CTAATTTTGGAGCCATTTTCAGTGTGTTAAATGACATTCTTTACGTCTTGACAAAGTTG 2938

NC_045512.2:21563-25384

CCAATTTTGGTGCAATTTCAAGTGTTTTAAATGATATCCTTTTCAGTCTTGACAAAGTTG 2962

MN996532.1:21545-25354

CCAATTTTGGAGCTATTTCTAGCGTGTAAATGATATCCTTTTCAGTCTCGACAAAGTTG 2950

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NC_019843.3:21456-25517

AACAGGACGCCCAAATAGACAGACTTATTAATGGCCGTTTGACAACACTAAATGCTTTTG 3244

NC_048212.1:20814-24623

AGGCTAATGCCGAAGTTGATAGGCTGATTTCTGGTCGTATGGTTGTACTTAACACATATG 3001

NC_004718.3:21492-25259

AGGCGGAGGTACAAATTGACAGGTTAATTACAGGCAGACTTCAAAGCCTTCAAACCTATG 2968

MT799526.1

AGGCTGAAGTCCAAATTGACAGGTTGATCACTGGCAGATTACAAAGTTTGCAGACATACG 2998

NC_045512.2:21563-25384

AGGCTGAAGTGCAAATTGATAGGTTGATCACAGGCAGACTTCAAAGTTTGCAGACATATG 3022

MN996532.1:21545-25354

AGGCTGAAGTGCAGATTGACAGGTTGATCACAGGCAGACTTCAAAGCTTGCAGACATATG 3010

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NC_019843.3:21456-25517

TTGCACAGCAGCTTGTTTCGTTCCGAATCAGCTGCTCTTTCCGCTCAATTGGCTAAAGATA 3304

NC_048212.1:20814-24623

TGACTCAGTTGCTTATTCAAGCTTCTGAACTTCGGTCTCAGGCGGAATTGGCTAAGCAA 3061

NC_004718.3:21492-25259

TAAACACAACAACTAATCAGGGCTGCTGAAATCAGGGCTTCTGCTAATCTTGCTGCTACTA 3028

MT799526.1

TGACTCAACAACCTAATTAGAGCCGCAGAAATTAGAGCTTCTGCTAATCTTGCCGCAACTA 3058

NC_045512.2:21563-25384

TGACTCAACAATTAATTAGAGCTGCAGAAATCAGAGCTTCTGCTAATCTTGCTGCTACTA 3082

MN996532.1:21545-25354

TGACTCAACAATTAATTAGAGCTGCAGAAATCAGAGCTTCTGCCAATCTTGCTGCTACTA 3070

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NC_019843.3:21456-25517
AAGTCAATGAGTGTGTCAAGGCACAATCCAAAGCGTTCTGGATTTTGCGGTCAAGGCACAC 3364

NC_048212.1:20814-24623
AGATGTCCGAATGTGTTAAGTCTCAATCTTTGCGTAATGACTTCTGTGGTAACGGGACTC 3121

NC_004718.3:21492-25259
AAATGTCTGAGTGTGTTCTTGGACAATCAAAAAGAGTTGACTTTTGTGGAAGGGCTACC 3088

MT799526.1
AGATGTCTGAAATGTGTTCTTGGACAATCTAAAAGAGTTGACTTTTGTGGTAAAGGCTACC 3118

NC_045512.2:21563-25384
AAATGTCTGAGTGTGTACTTGGACAATCAAAAAGAGTTGATTTTTGTGGAAGGGCTATC 3142

MN996532.1:21545-25354
AAATGTCTGAGTGTGTACTCGGACAATCAAAAAGAGTTGATTTTTGTGGAAGGGCTATC 3130

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NC_019843.3:21456-25517
ATATAGTGCCTTTGTTGTAATGCCCTTAATGGCCTTTACTTCATGCATGTTGGTTATT 3424

NC_048212.1:20814-24623
ATGTTCTTAGCATACCTCAGTTAGCTCCTAATGGCATGCTGTTTCATACATTATAGTTATC 3181

NC_004718.3:21492-25259
ACCTTATGTCCTTCCCAAGCAGCCCCGCATGGTGTGTCTTCCTACATGTCACGTATG 3148

MT799526.1
ACCTTATGTCCTTTTCCGCAGTCAGCACCTCATGGTGTAGTCTTTTTGCATGTGACTTATG 3178

NC_045512.2:21563-25384
ATCTTATGTCCTTCCCTCAGTCAGCACCTCATGGTGTAGTCTTCTTGCATGTGACTTATG 3202

MN996532.1:21545-25354
ATCTTATGTCCTTCCCTCAGTCAGCACCTCATGGTGTAGTCTTCTTGCATGTGACATATG 3190

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NC_019843.3:21456-25517
ACCCTAGCAACCACATTGAGGTTGTTTCTGCTTATGGTCTTTGCGATGCAGCTAACCCCTA 3484

NC_048212.1:20814-24623
AACCTACTAAGTATGCACAGGTGTATACCACGGCGGGCCTATGCTTCAATGGTACAGGCT 3241

NC_004718.3:21492-25259
TGCCATCCCAAGGAGAGGAACCTCACACAGCGCCAGCAATTTGTCATGAAGGCAAAGCAT 3208

MT799526.1
TTCCATCTCAAGAAAAGAATTTTACTACTACCCCTGCCATTTGTCATGAAGGAAAAGCAC 3238

NC_045512.2:21563-25384
TCCCTGCACAAGAAAAGAAGTTTCAAACTGCTCCTGCCATTTGTCATGATGGAAAAGCAC 3262

MN996532.1:21545-25354
TCCCTGCACAAGAAAAGAAGTTTCAAACTGCTCCTGCCATTTGTCATGATGGAAAAGCAC 3250

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NC_019843.3:21456-25517
CTAATTGTATAGCCCCTGTTAATGGCTACTTTATTAAACTAATAACACTAGGATTGTTG 3544
NC_048212.1:20814-24623
TTGTTTCCTAGGGATGGTTTGTGTCAGGGAAAACA-----ATGAATCC-----C 3286
NC_004718.3:21492-25259
ACTTCCTCGTGAAGGTGTTTTGTGTTTAAATGGCA-----CTTCT----- 3249
MT799526.1
ACTTCCTCGTGAAGGTGTTTTCGTTTCAAACGGCA-----CGCAC----- 3279
NC_045512.2:21563-25384
ACTTCCTCGTGAAGGTGTCCTTTGTTTCAAATGGCA-----CACAC----- 3303
MN996532.1:21545-25354
ACTTTCACGTGAAGGTGTTTTCGTTTCAAATGGCA-----CACAC----- 3291
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NC_019843.3:21456-25517
ATGAGTGGTCATATACTGGCTCGTCCTTCTATGCACCTGAGCCCATTACCTCCCTTAATA 3604
NC_048212.1:20814-24623
AAGTTTGGTATTTTACTAAGGCAAGTTTTTACAATCCTGTGAACCTGTCTTATGAGAACA 3346
NC_004718.3:21492-25259
-----TGGTTTATTACACAGAGGAACCTCTTTTCTCCACAAATAATTACTACAGACAATA 3304
MT799526.1
-----TGGTTTGTAAACACAAAGGAATTTCTATGAACCACAAATTATTACCACGGACAATA 3334
NC_045512.2:21563-25384
-----TGGTTTGTAAACACAAAGGAATTTTATGAACCACAAATCATTACTACAGACAACA 3358
MN996532.1:21545-25354
-----TGGTTTGTAAACACAAAGGAATTTTATGAACCACAAATTATTACAACAGACAACA 3346
**** ** ** * **
* * ** *

NC_019843.3:21456-25517
CTAAGTATG-TTGCACCACAGGTGACATACCAAAACATTTCTACTAACCTCCCTCCTCCT 3663
NC_048212.1:20814-24623
CTCATTTATTAGACACTTGTGGTGTAAATTACACTACAGTC---AATAATAGTGTGTTG 3402
NC_004718.3:21492-25259
CATTTGTCTCAGGAAATTGTGATGTGCTTATTGGCATCATT---AACAAACAGTTTAT 3360
MT799526.1
CTTTTGTCTCTGGTAGCTGTGATGTTGTGATTGGAATTGTC---AACAAACAGTTTAT 3390
NC_045512.2:21563-25384
CATTTGTGTCTGGTAACTGTGATGTTGTAAATAGGAATTGTC---AACAAACAGTTTAT 3414
MN996532.1:21545-25354
CATTTGTCTCTGGTAGCTGTGATGTTGTAAATAGGAATTGTC---AACAAACAGTTTAT 3402
* * * ** *

NC_019843.3:21456-25517
CTTCTCGGCAAATCCACCGGATTGACTTCCAAGATGAGTTGGATGAGTTTTTCAAAAT 3723

NC_048212.1:20814-24623
AACCCAAATTGAACCTCCTAATTATAATTTTCAGGAAGAGTTTCGATAAGTATTTCAAGAAC 3462
NC_004718.3:21492-25259
GATCCTCTGCAACCTGAGCTTGACTCATTCAAAAGAGCTGGACAAGTACTTCAAAAAT 3420
MT799526.1
GATCCTTTGCAACCAGAACTTGATTCAATCAAGGAGGAGTTGGACAAATATTTTAAAAAT 3450
NC_045512.2:21563-25384
GATCCTTTGCAACCTGAATTAGACTCATTCAAGGAGGAGTTAGATAAATATTTTAAGAAT 3474
MN996532.1:21545-25354
GATCCTTTGCAACCAGAACTTGATTCAATCAAGGAGGAGTTGGATAAATACTTTAAAAAT 3462
* * * * *
* * ** ** **

NC_019843.3:21456-25517
GTTAGCACCAGTATACCTAATTTTGGTTCCTAACACAGATTAATACTACATTACTCGAT 3783
NC_048212.1:20814-24623
CAGTCTTCTCAGTTTAAATATCACTTTTGATTCTTCTCAGTTTAAATGTTTCTATTGTTAAT 3522
NC_004718.3:21492-25259
CATACATCACCAAGATGTTGATCTTGGCGACATTTTCAGGCATTAACGCTTCTGTCGTCAAC 3480
MT799526.1
CATACATCACCAAGATGTTGATTTAGGTGACATTTCTGGCATCAACGCTTCAGTTGTCAAC 3510
NC_045512.2:21563-25384
CATACATCACCAAGATGTTGATTTAGGTGACATCTCTGGCATTAATGCTTCAGTTGTAAAC 3534
MN996532.1:21545-25354
CATACATCACCTGATGTAGATTTAGGTGACATTTCTGGCATTAATGCTTCAGTTGTCAAT 3522
* * * * *
* * * * *

NC_019843.3:21456-25517
CTTACCTACGAGATGTTGTCTCTTCAACAAGTTGTTAAAGCCCTTAATGAGTCTTACATA 3843
NC_048212.1:20814-24623
TTGAATGAACAGATGGCTGCTTTAGATTCAAGTCGTTAAGAGTCTCAATGAATCTTTCATT 3582
NC_004718.3:21492-25259
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MT799526.1
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NC_045512.2:21563-25384
ATTCAAAAAGAAATTGACCGCCTCAATGAGGTTGCCAAGAATTTAAATGAATCTCTCATC 3594
MN996532.1:21545-25354
ATTCAAAAAGAAATTGACCGCCTCAATGAGGTTGCCAAAAATCTAAATGAATCTCTCATC 3582
* * * * *
***** ** ***

NC_019843.3:21456-25517
GACCTTAAAGAGCTTGGCAATTATACTTATTACAACAAATGGCCGTGGTACATTTGGCTT 3903
NC_048212.1:20814-24623
GACCTCAAGAAGCTAGGTGTGTACACGCAGCAACCAACACACCCTGGTATGCGTGGTTA 3642

NC_004718.3:21492-25259
GACCTTCAAGAAATTGGGAAAATATGAGCAATATATTAAATGGCCTTGGTATGTTTGGCTC 3600
MT799526.1
GACCTCCAAGAACTTGGAAAGTATGAGCAGTATATAAAATGGCCATGGTATATTGGCTA 3630
NC_045512.2:21563-25384
GATCTCCAAGAACTTGGAAAGTATGAGCAGTATATAAAATGGCCATGGTACATTGGCTA 3654
MN996532.1:21545-25354
GATCTCCAAGAACTTGGAAAGTATGAACAGTATATAAAATGGCCATGGTACATTGGCTA 3642
** ** * * * ** ** * * ** **

***** *** *

NC_019843.3:21456-25517
GGTTTCATTGCTGGGCTTGTTGCCTTAGCTCTATGCGTCTTCTTCATACTGTGCTGCACT 3963
NC_048212.1:20814-24623
GGTATGATTGCAGGTTTAGTTGGACTCGCCTTAGCTGTTTTTATGCTTTGTTGCATGACC 3702
NC_004718.3:21492-25259
GGCTTCATTGCTGGACTAATTGCCATCGTCAATGGTTACAATCTTGCTTTGTTGCATGACT 3660
MT799526.1
GGATTTATTGCAGGCTTGATAGCTATAATCATGGTTACAATCATGTTATGCTGTATGACC 3690
NC_045512.2:21563-25384
GGTTTTATAGCTGGCTTGATTGCCATAGTAATGGTGACAATTATGCTTTGCTGTATGACC 3714
MN996532.1:21545-25354
GGTTTTATAGCTGGCTTGATTGCCATAATAATGGTCACGATTATGCTTTGCTGTATGACC 3702
** * ** ** ** * * * * *

* ** **

NC_019843.3:21456-25517
GGTTGTGGCACAACTGTATGGGAAAACTTAAGTGTAATCGTTGTTGTGATAGATACGAG 4023
NC_048212.1:20814-24623
AACTGCTGCAGTGGATTAGGGGCATATGCTCTTGTAAGCAATGCCAGTA---TGATGAT 3759
NC_004718.3:21492-25259
AGTTGTTGCAAGTTGCCTCAAGGGTGCATGCTCTTGTTGGTTCTTGCTGCAA---GTTTGAT 3717
MT799526.1
AGTTGCTGCAGTTGTCTCAAGGGCTGTTGTTCTTGTTGGCTCCTGCTGTAA---ATTGAT 3747
NC_045512.2:21563-25384
AGTTGCTGTAGTTGTCTCAAGGGCTGTTGTTCTTGTTGGATCCTGCTGCAA---ATTGAT 3771
MN996532.1:21545-25354
AGTTGCTGCAGTTGTCTCAAGGGCTGTTGTTCTTGCGGATCTTGCTGCAA---ATTGAT 3759
** * * * *** ** **

* **

NC_019843.3:21456-25517
GAATACGACCTCGAGCCGCATAAGGTTCAATGTTCACTAA----- 4062
NC_048212.1:20814-24623
TATGCTGACGTTTACCCAGCTGTTCCAGTTAGTGGTAAACGAACAGTATGA 3810
NC_004718.3:21492-25259
GAGGATGACTCTGAGCCAGTTCTCAAGGGTGTCAAATTACATTACACATAA 3768

MT799526.1
GAAGACGACTCTGAGCCAGTACTCAAAGGAGTCAAATTACATTACACATAA 3798
NC_045512.2:21563-25384
GAAGACGACTCTGAGCCAGTGCTCAAAGGAGTCAAATTACATTACACATAA 3822
MN996532.1:21545-25354
GAAGACGACTCTGAGCCAGTGCTCAAAGGAGTCAAATTACATTACACATAA 3810
* *** * **

a]

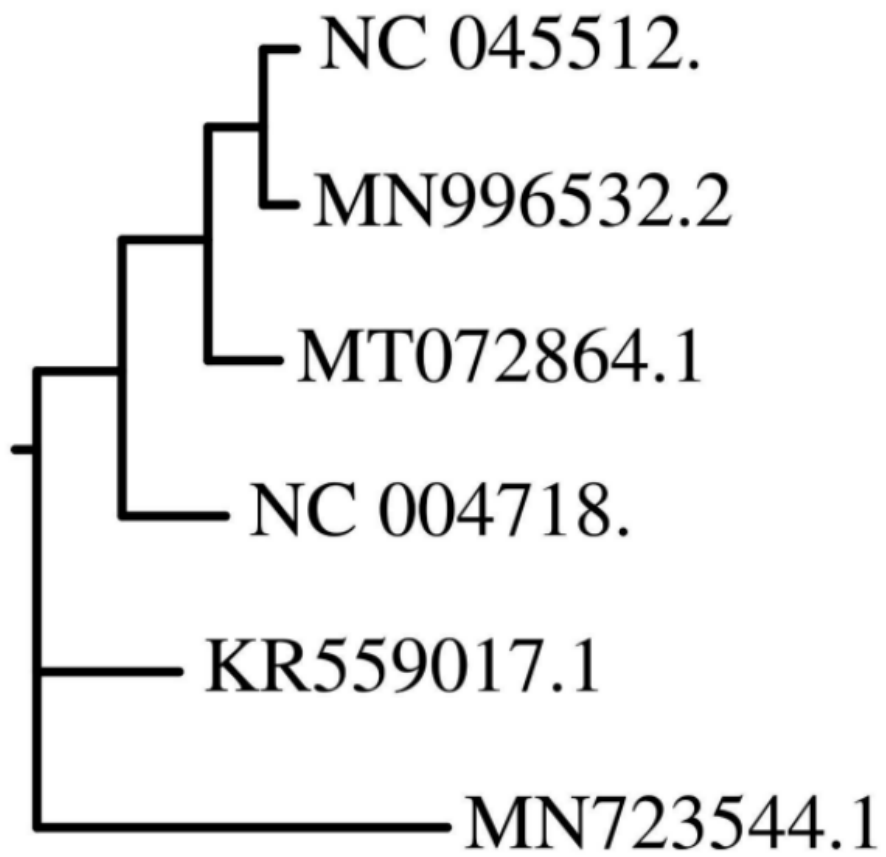
It can be observed that the spike glycoprotein found in bats and SARS-cov2 display a protein sequence similarity of 97.71 percent and a genome sequence similarity of 93.12 percent. This suggests that they are highly related to each other and may be considered as the closest relatives within their genetic lineage. The closest relatives are bat spike glycoprotein and SARS-CoV-2 protein.

b]

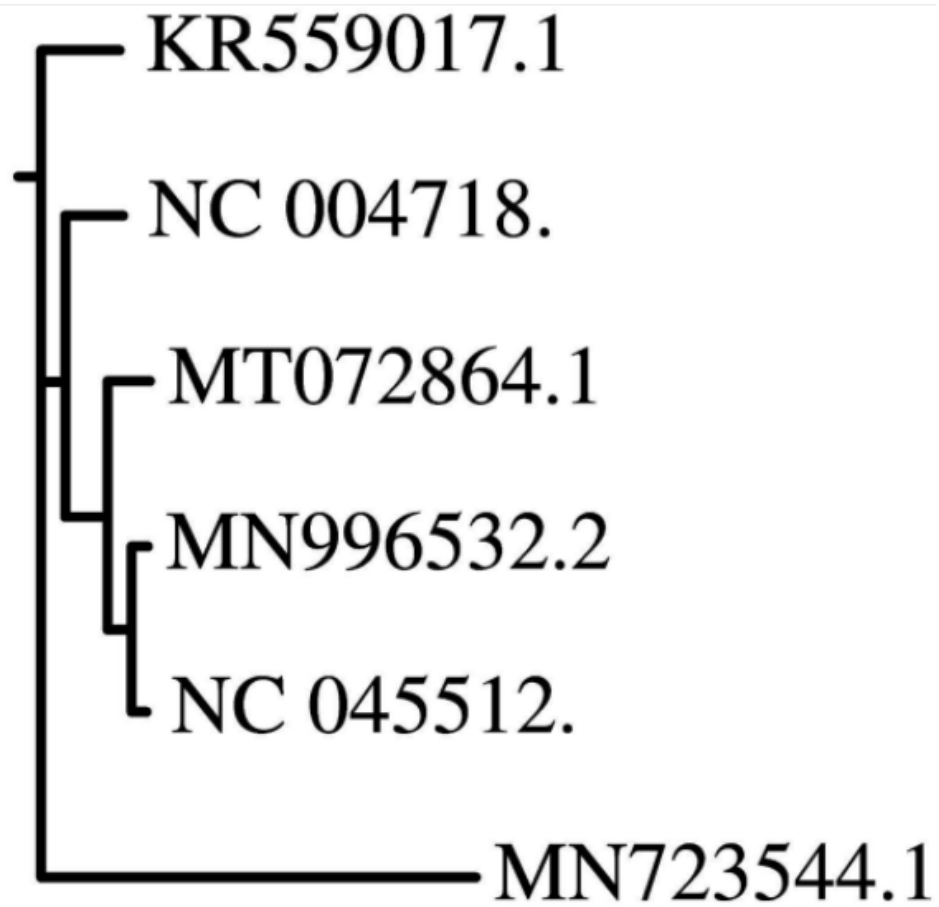
It is evident from the findings that the origin of SARS-2 can be traced back to bats. Additionally, for MERS COVID, there is a likelihood that it could be the ancestor due to its low similarity with other spike glycoproteins.

Q2]

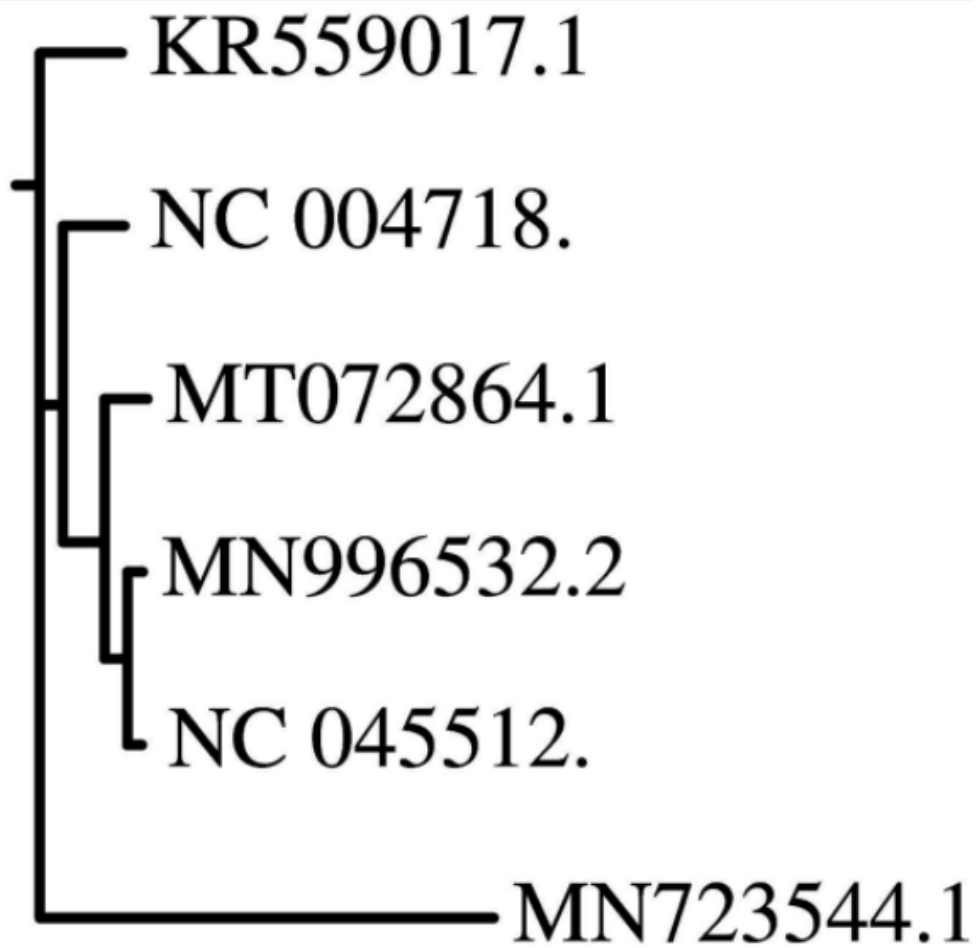
Plot file dnapars with bootstrapping



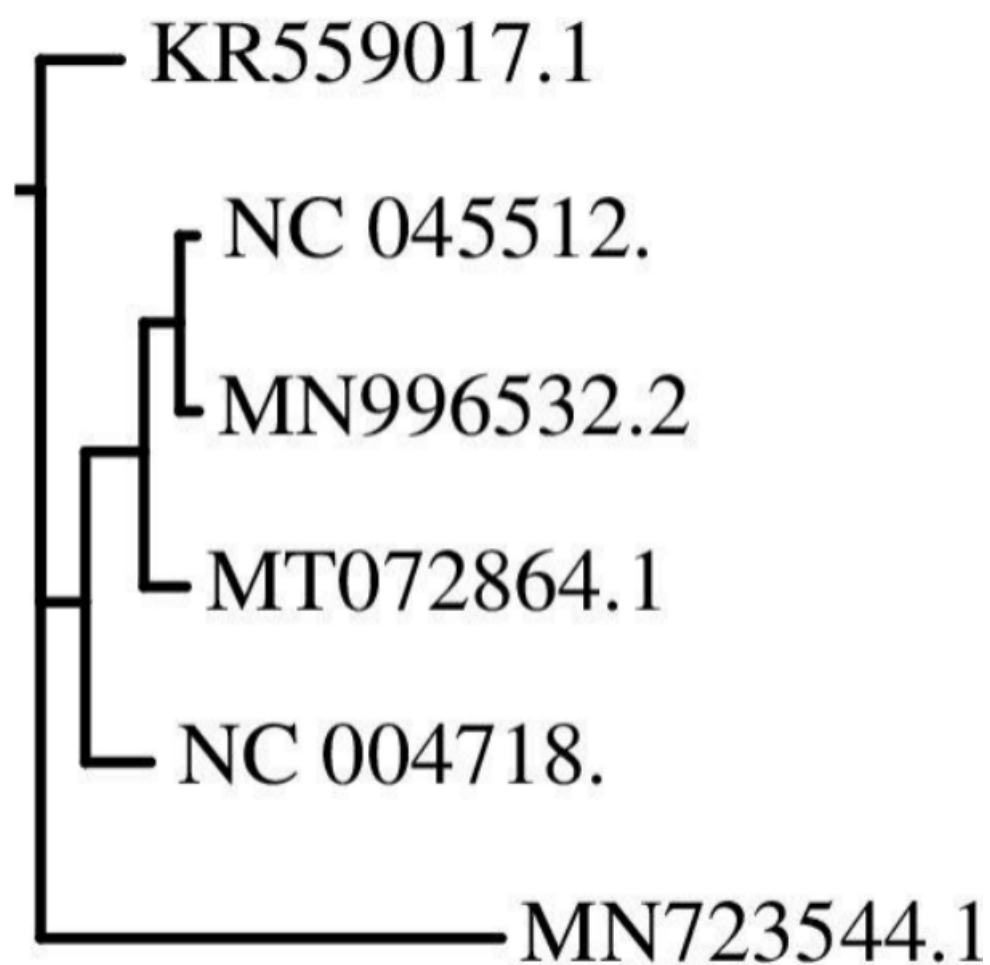
Plot file for dnadist with bootstrapping



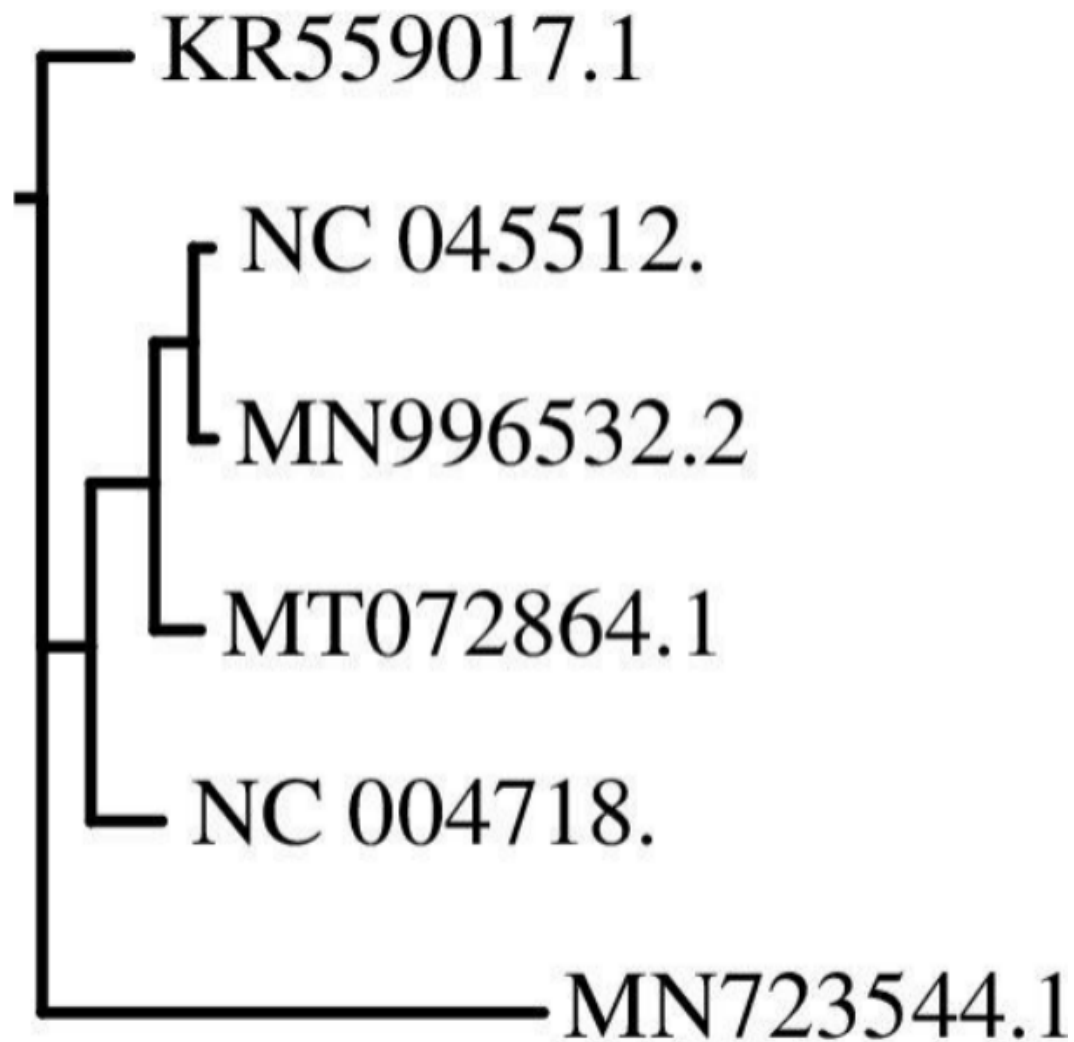
Plot file for dnadist without bootstrapping



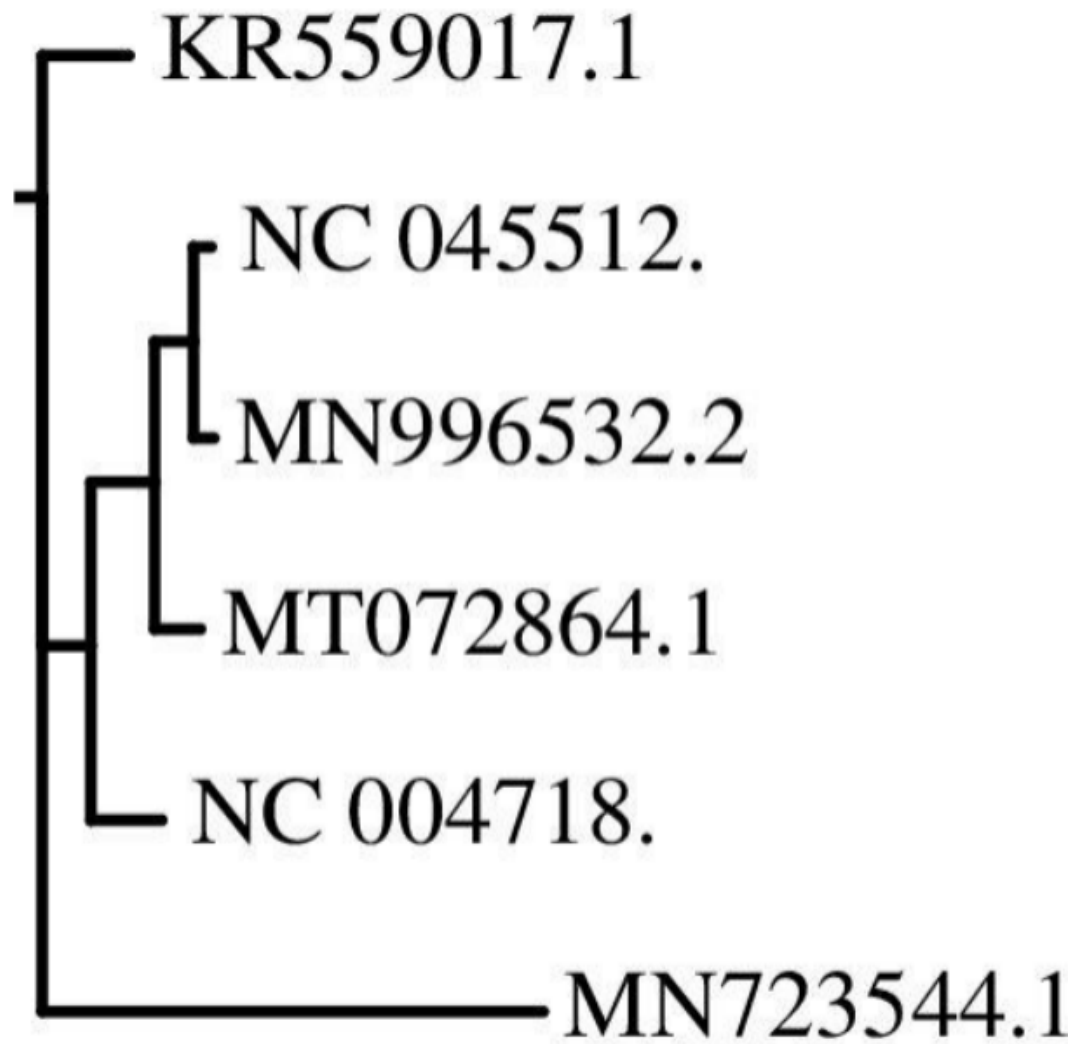
Plot file for dnaml with bootstrapping



Plot file for dnaml without bootstrapping



Plot file for dnapars without bootstrapping



a]

The phylogenetic trees generated by different methods are not in agreement with each other in terms of their topology. This means that they don't exhibit the same branch structures and relationships as those depicted in the images or reference trees.

b]

It appears from the images above that there is no significant difference between the trees generated with and without bootstrapping. Bootstrapping is a statistical technique that involves creating multiple resampled datasets from an original dataset. This process can be used to estimate standard errors, confidence intervals, and conduct hypothesis testing.

c]

The analysis conducted in 1b suggests that MERS cov is the ancestor of all the other species examined. Furthermore, it can be observed that the spike glycoprotein from Bat coronavirus RaTG13 (MN996532.2) is the origin of SARS Cov2 (NC 045512).

Q3]

Result for blastn search

Sequence-1

Sequences producing significant alignments

Download ▾

Select columns ▾

Show 100 ▾

?

☒ select all 100 sequences selected

GenBank

Graphics

Distance tree of results

MSA Viewer

	Description ▾	Scientific Name ▾	Max Score ▾	Total Score ▾	Query Cover ▾	E value ▾	Per. Ident ▾	Acc. Len ▾	Accession
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8691	8691	100%	0.0	100.00%	20021703	LR782543.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana chromosome 2	Arabidopsis thaliana	8691	8691	100%	0.0	100.00%	22468181	CP116281.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8691	8691	100%	0.0	100.00%	23012915	OX298803.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana chromosome 2	Arabidopsis thaliana	8691	8691	100%	0.0	100.00%	22868883	CP087127.2
<input checked="" type="checkbox"/>	Arabidopsis thaliana isolate t2t_salk_col chromosome 2	Arabidopsis thaliana	8691	8691	100%	0.0	100.00%	22217084	CP096025.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana chromosome 2	Arabidopsis thaliana	8691	8691	100%	0.0	100.00%	19698289	CP002685.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana chromosome 2 clone MSF3 map CIC06E08 complete sequence	Arabidopsis thaliana	8691	8691	100%	0.0	100.00%	88413	AC005724.3
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8685	8685	100%	0.0	99.98%	19416174	LR699771.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8685	8685	100%	0.0	99.98%	19252707	LR215053.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8685	8685	100%	0.0	99.98%	21328600	OX291572.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana ecotype 9412 chromosome 2 sequence	Arabidopsis thaliana	8685	8685	100%	0.0	99.98%	20497022	CP086735.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8685	8685	100%	0.0	99.98%	19454276	LR797793.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8674	8674	100%	0.0	99.94%	21027966	OX461156.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8608	8608	100%	0.0	99.72%	23046220	OX461161.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8602	8602	100%	0.0	99.70%	22870034	OX461151.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana ecotype 1254 chromosome 2 sequence	Arabidopsis thaliana	8602	8602	100%	0.0	99.70%	20533974	CP086755.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana ecotype 5856 chromosome 2 sequence	Arabidopsis thaliana	8602	8602	100%	0.0	99.70%	20220154	CP086750.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8600	8600	100%	0.0	99.70%	19229142	LR699756.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8597	8597	100%	0.0	99.68%	22850951	OX461176.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8591	8591	100%	0.0	99.66%	22206001	OX461146.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8591	8591	100%	0.0	99.66%	22107386	OX298798.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana ecotype Ga-O PHYB gene complete sequence	Arabidopsis thaliana	8591	8591	100%	0.0	99.66%	5730	GQ177627.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana ecotype Wt-5 PHYB gene complete sequence	Arabidopsis thaliana	8586	8586	100%	0.0	99.64%	5731	GQ177637.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8558	8558	100%	0.0	99.53%	23999900	OX291701.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8554	8554	99%	0.0	99.53%	21980435	OX461206.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8554	8554	99%	0.0	99.53%	22160010	OX461171.1
<input checked="" type="checkbox"/>	Arabidopsis thaliana genome assembly chromosome: 2	Arabidopsis thaliana	8554	8554	99%	0.0	99.53%	22939165	OX291792.1

The sequence of Arabidopsis thaliana (LR782543.1) is the most closely related sequence. However, it is important to note that this is a chromosome sequence, not a genome sequence. Therefore, it is not the correct answer

Sequence-2

Sequences producing significant alignments									
Download Select columns Show 100 ?									
<input checked="" type="checkbox"/> select all 100 sequences selected									
Description		Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Tomato spotted wilt virus intergenic region isolate TSWV-IT-CE genomic RNA	Tomato spotted ...	483	483	100%	9e-132	100.00%	261	AJ309924.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate T1012 segment M complete sequence	Tomato spotted ...	470	470	100%	7e-128	99.23%	4762	ON840011.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate 104DOT22S segment M complete sequence	Tomato spotted ...	464	464	100%	3e-126	98.85%	4762	OQ534350.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate 102SEC22S segment M complete sequence	Tomato spotted ...	464	464	100%	3e-126	98.85%	4762	OQ534347.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate 71SET22S segment M complete sequence	Tomato spotted ...	464	464	100%	3e-126	98.85%	4762	OQ534344.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate 106DOT22S segment M complete sequence	Tomato spotted ...	464	464	100%	3e-126	98.85%	4762	OQ534341.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate 108DOT22S segment M complete sequence	Tomato spotted ...	464	464	100%	3e-126	98.85%	4762	OQ507128.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate 107DOT22S segment M complete sequence	Tomato spotted ...	464	464	100%	3e-126	98.85%	4762	OQ507125.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate 105DOT22S segment M complete sequence	Tomato spotted ...	464	464	100%	3e-126	98.85%	4762	OQ507122.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate 86DOW22S segment M complete sequence	Tomato spotted ...	464	464	100%	3e-126	98.85%	4762	OQ507119.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate 85DOP22S segment M complete sequence	Tomato spotted ...	464	464	100%	3e-126	98.85%	4762	OQ507116.1
<input checked="" type="checkbox"/>	Tomato spotted wilt virus isolate intergenic region isolate TSWV-IT-TO	Tomato spotted ...	464	464	100%	3e-126	98.85%	260	AJ428574.1
<input checked="" type="checkbox"/>	Tomato spotted wilt virus RNA segment M complete sequence	Tomato spotted ...	448	448	100%	3e-121	97.36%	4768	AB190818.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate P349 nonstructural protein (NSm) gene complete cds	Tomato spotted ...	446	892	100%	1e-120	97.70%	1564	OM867574.1
<input checked="" type="checkbox"/>	Tomato spotted wilt virus isolate p331 putative movement protein gene partial cds	Tomato spotted ...	440	440	100%	6e-119	97.32%	876	KM213986.1
<input checked="" type="checkbox"/>	Tomato spotted wilt virus intergenic region isolate TSWV-IT-MA genomic RNA	Tomato spotted ...	433	433	99%	1e-116	96.58%	263	AJ309923.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate 15-4 segment M complete sequence	Tomato spotted ...	429	429	99%	1e-115	96.23%	4767	KU179610.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate 104DOT22S segment M complete sequence	Tomato spotted ...	429	429	100%	1e-115	96.21%	4766	OQ269471.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate TUR20SW segment M complete sequence	Tomato spotted ...	429	429	100%	1e-115	96.21%	4765	OL471962.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate TUR20ST3 segment M complete sequence	Tomato spotted ...	429	429	100%	1e-115	96.21%	4765	OL471959.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate TUR20ST2 segment M complete sequence	Tomato spotted ...	429	429	100%	1e-115	96.21%	4766	OL471956.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate TUR20ST1 segment M complete sequence	Tomato spotted ...	429	429	100%	1e-115	96.21%	4766	OL471953.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate PLE20ST3 segment M complete sequence	Tomato spotted ...	429	429	100%	1e-115	96.21%	4766	OL471950.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate PLE20ST2 segment M complete sequence	Tomato spotted ...	429	429	100%	1e-115	96.21%	4766	OL471947.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate 15-1 segment M complete sequence	Tomato spotted ...	425	425	100%	2e-114	95.86%	4767	KU179608.1
<input checked="" type="checkbox"/>	Tomato spotted wilt virus segment M complete sequence	Tomato spotted ...	425	425	99%	2e-114	96.18%	4765	KT160281.1
<input checked="" type="checkbox"/>	Tomato spotted wilt orthotospovirus isolate T1107 segment M complete sequence	Tomato spotted ...	425	425	99%	2e-114	96.18%	4763	ON840008.1
<input checked="" type="checkbox"/>	Tomato spotted wilt virus isolate CG 1 segment M complete sequence	Tomato spotted ...	425	425	100%	2e-114	96.18%	4767	M564752.1

The intergenic region of Tomato spotted wilt virus from isolate TSWV-IT-CE (AJ309924.1) is the most closely related sequence. This region contains genomic RNA, as indicated in the above image. Therefore, this is a protein coding sequence and the closest related organisms are shown in the image. The gene name for this sequence is "Tomato spotted wilt virus intergenic region, isolate TSWV-IT-CE, genomic RNA" and it

belongs to the organism known as Tomato spotted wilt orthotospovirus.