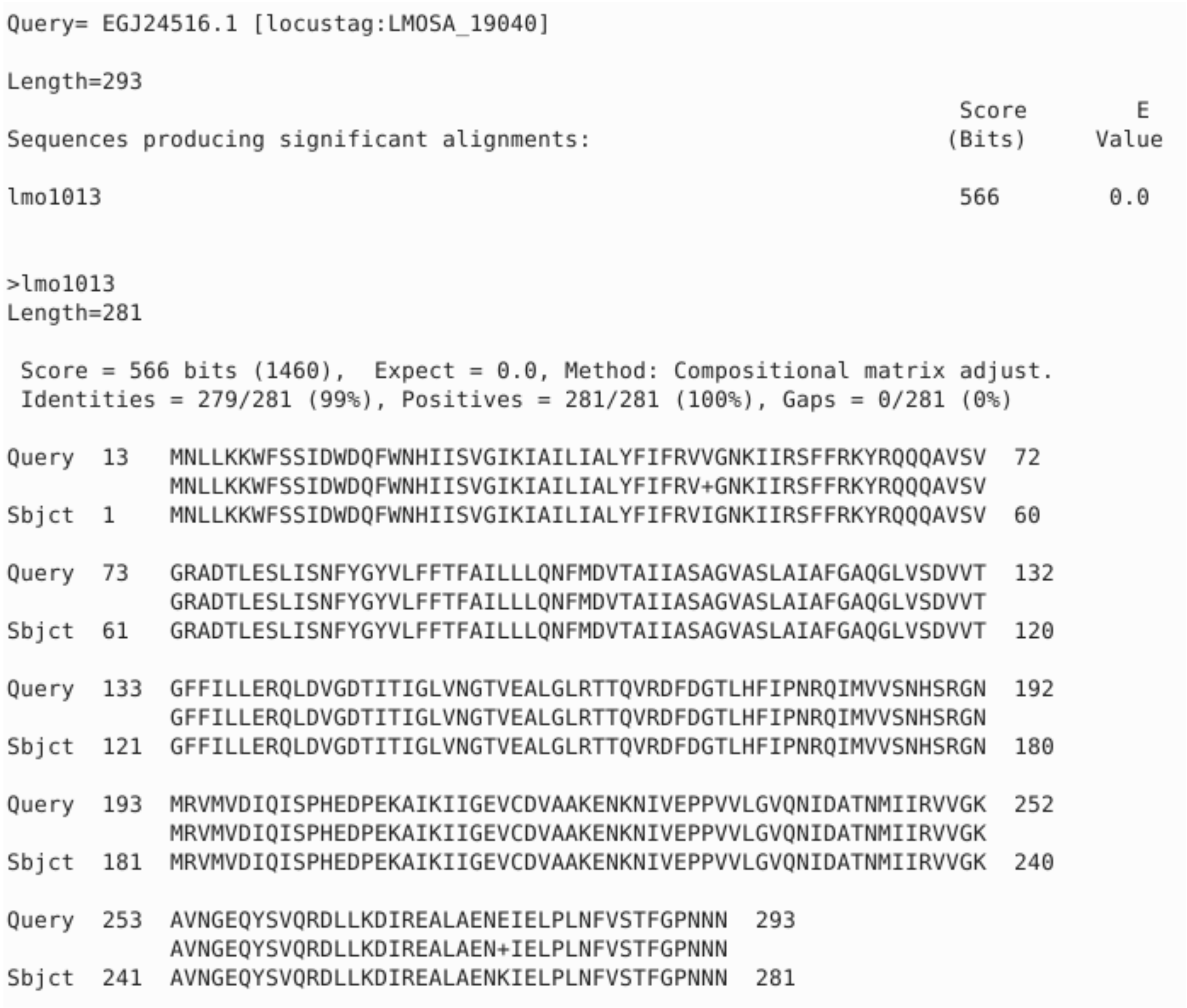
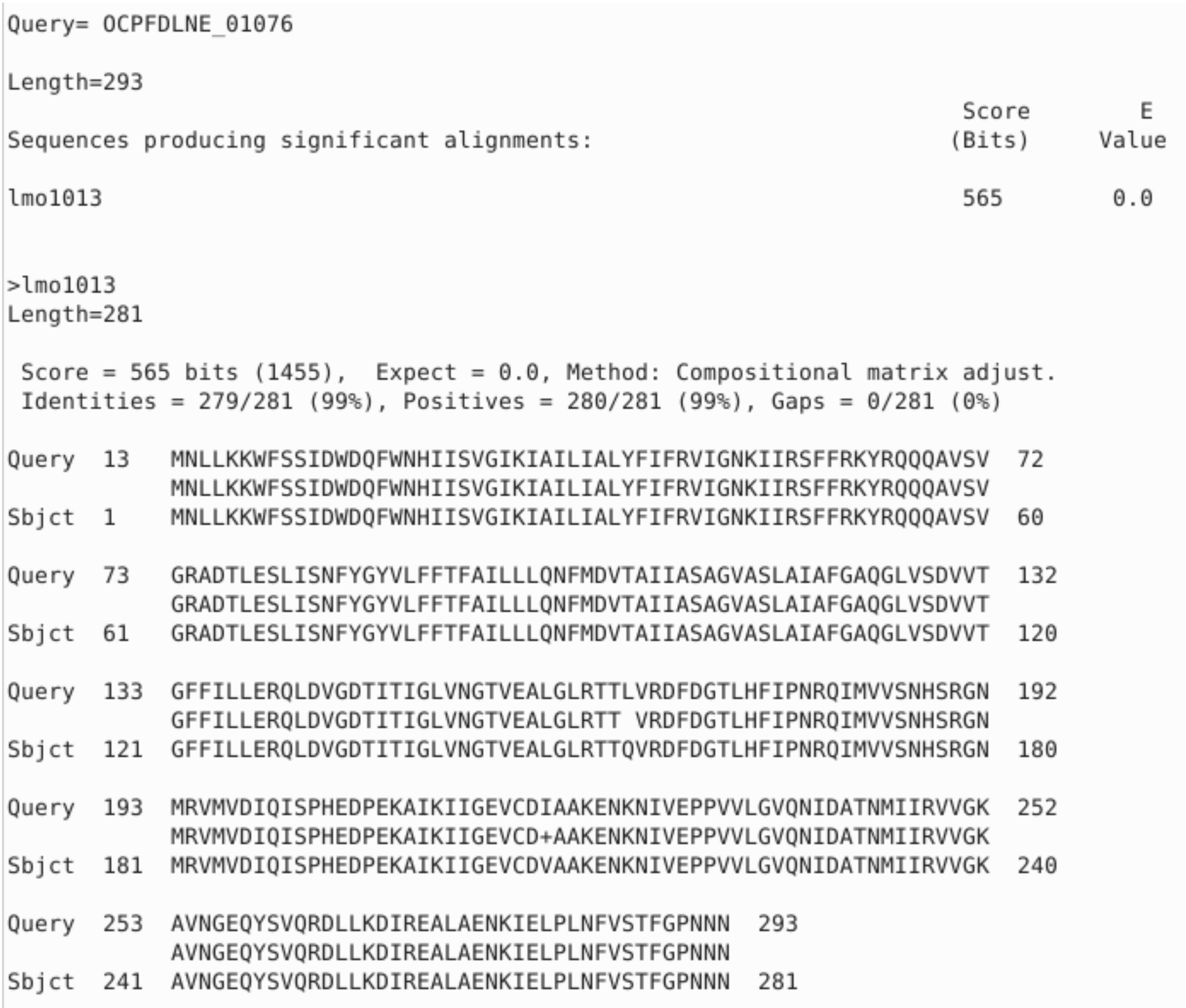
lmo1013 vs LMOSA_19040 (ScottA) BLASTP alignment



```
Query= EGJ24516.1 [locustag:LMOSA_19040]

Length=293
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

lmo1013                                                                566    0.0


>lmo1013
Length=281

 Score = 566 bits (1460),  Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 279/281 (99%), Positives = 281/281 (100%), Gaps = 0/281 (0%)

Query  13   MNLLKKWFSSIDWDQFWNHIISVGIKIAILIALYFIFRVVGNKIIRSFFRKYRQQQAVSV  72
            MNLLKKWFSSIDWDQFWNHIISVGIKIAILIALYFIFRV+GNKIIRSFFRKYRQQQAVSV
Sbjct  1    MNLLKKWFSSIDWDQFWNHIISVGIKIAILIALYFIFRVIGNKIIRSFFRKYRQQQAVSV  60

Query  73   GRADTLESLISNFYGYVLFFTFAILLLQNFMDVTAIIASAGVASLAIAFGAQGLVSDVVT  132
            GRADTLESLISNFYGYVLFFTFAILLLQNFMDVTAIIASAGVASLAIAFGAQGLVSDVVT
Sbjct  61   GRADTLESLISNFYGYVLFFTFAILLLQNFMDVTAIIASAGVASLAIAFGAQGLVSDVVT  120

Query  133  GFFILLERQLDVGDTITIGLVNGTVEALGLRTTQVRDFDGTLHFIPNRQIMVVSNHSRGN  192
            GFFILLERQLDVGDTITIGLVNGTVEALGLRTTQVRDFDGTLHFIPNRQIMVVSNHSRGN
Sbjct  121  GFFILLERQLDVGDTITIGLVNGTVEALGLRTTQVRDFDGTLHFIPNRQIMVVSNHSRGN  180

Query  193  MRVMVDIQISPHEDPEKAIKIIGEVCDVAAKENKNIVEPPVVLGVQNIDATNMIIRVVGK  252
            MRVMVDIQISPHEDPEKAIKIIGEVCDVAAKENKNIVEPPVVLGVQNIDATNMIIRVVGK
Sbjct  181  MRVMVDIQISPHEDPEKAIKIIGEVCDVAAKENKNIVEPPVVLGVQNIDATNMIIRVVGK  240

Query  253  AVNGEQYSVQRDLLKDIREALAENEIELPLNFVSTFGPNNN  293
            AVNGEQYSVQRDLLKDIREALAEN+IELPLNFVSTFGPNNN
Sbjct  241  AVNGEQYSVQRDLLKDIREALAENKIELPLNFVSTFGPNNN  281
```

lmo1013 vs OCPFDLNE_01076 (RO15) BLASTP alignment



```
Query= OCPFDLNE_01076

Length=293
                                                                      Score     E
Sequences producing significant alignments:                          (Bits)  Value

lmo1013                                                                565    0.0


>lmo1013
Length=281

 Score = 565 bits (1455),  Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 279/281 (99%), Positives = 280/281 (99%), Gaps = 0/281 (0%)

Query  13   MNLLKKWFSSIDWDQFWNHIISVGIKIAILIALYFIFRVIGNKIIRSFFRKYRQQQAVSV  72
            MNLLKKWFSSIDWDQFWNHIISVGIKIAILIALYFIFRVIGNKIIRSFFRKYRQQQAVSV
Sbjct  1    MNLLKKWFSSIDWDQFWNHIISVGIKIAILIALYFIFRVIGNKIIRSFFRKYRQQQAVSV  60

Query  73   GRADTLESLISNFYGYVLFFTFAILLLQNFMDVTAIIASAGVASLAIAFGAQGLVSDVVT  132
            GRADTLESLISNFYGYVLFFTFAILLLQNFMDVTAIIASAGVASLAIAFGAQGLVSDVVT
Sbjct  61   GRADTLESLISNFYGYVLFFTFAILLLQNFMDVTAIIASAGVASLAIAFGAQGLVSDVVT  120

Query  133  GFFILLERQLDVGDTITIGLVNGTVEALGLRTTLVRDFDGTLHFIPNRQIMVVSNHSRGN  192
            GFFILLERQLDVGDTITIGLVNGTVEALGLRTT VRDFDGTLHFIPNRQIMVVSNHSRGN
Sbjct  121  GFFILLERQLDVGDTITIGLVNGTVEALGLRTTQVRDFDGTLHFIPNRQIMVVSNHSRGN  180

Query  193  MRVMVDIQISPHEDPEKAIKIIGEVCDIAAKENKNIVEPPVVLGVQNIDATNMIIRVVGK  252
            MRVMVDIQISPHEDPEKAIKIIGEVCD+AAKENKNIVEPPVVLGVQNIDATNMIIRVVGK
Sbjct  181  MRVMVDIQISPHEDPEKAIKIIGEVCDVAAKENKNIVEPPVVLGVQNIDATNMIIRVVGK  240

Query  253  AVNGEQYSVQRDLLKDIREALAENKIELPLNFVSTFGPNNN  293
            AVNGEQYSVQRDLLKDIREALAENKIELPLNFVSTFGPNNN
Sbjct  241  AVNGEQYSVQRDLLKDIREALAENKIELPLNFVSTFGPNNN  281
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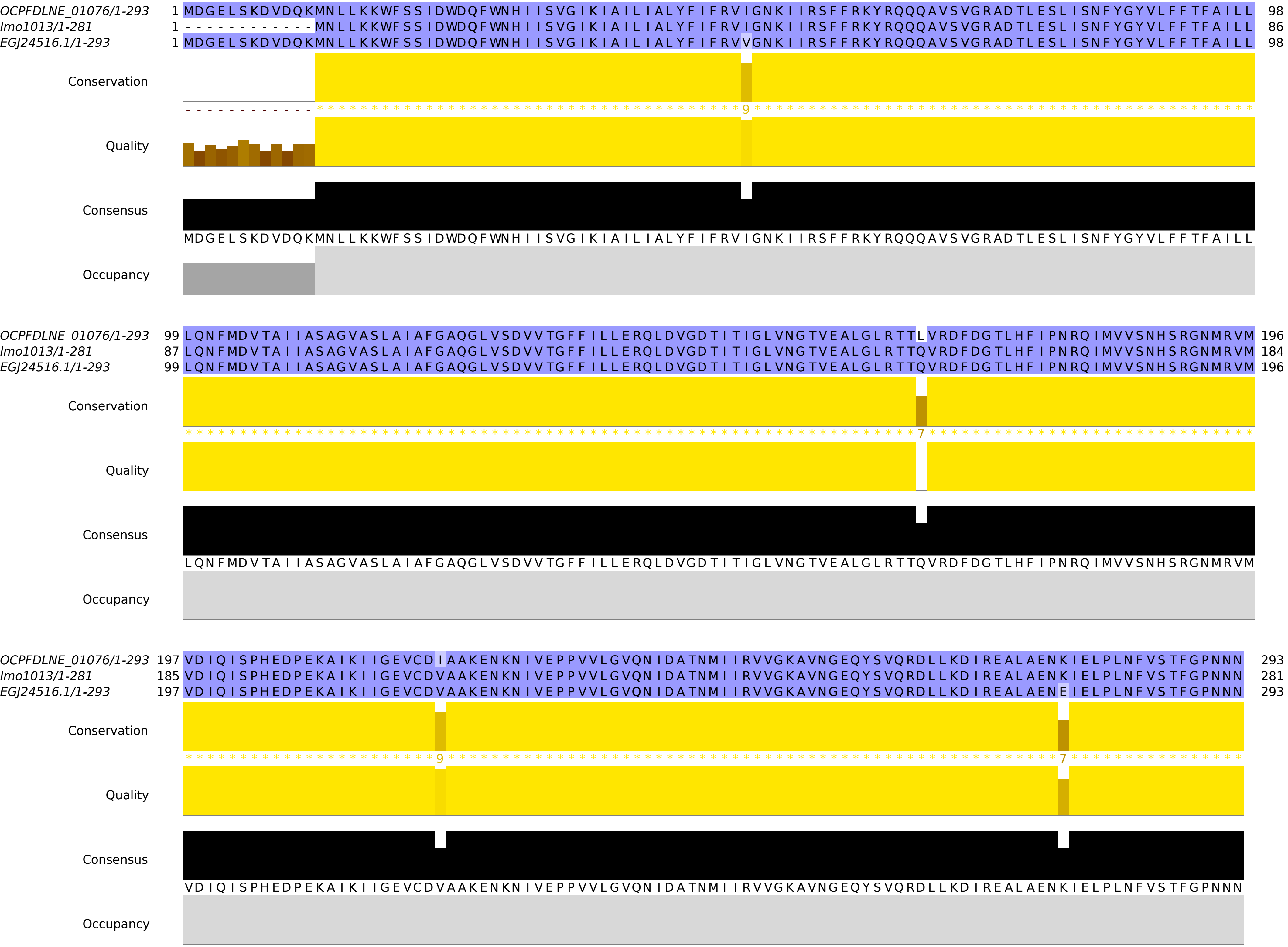
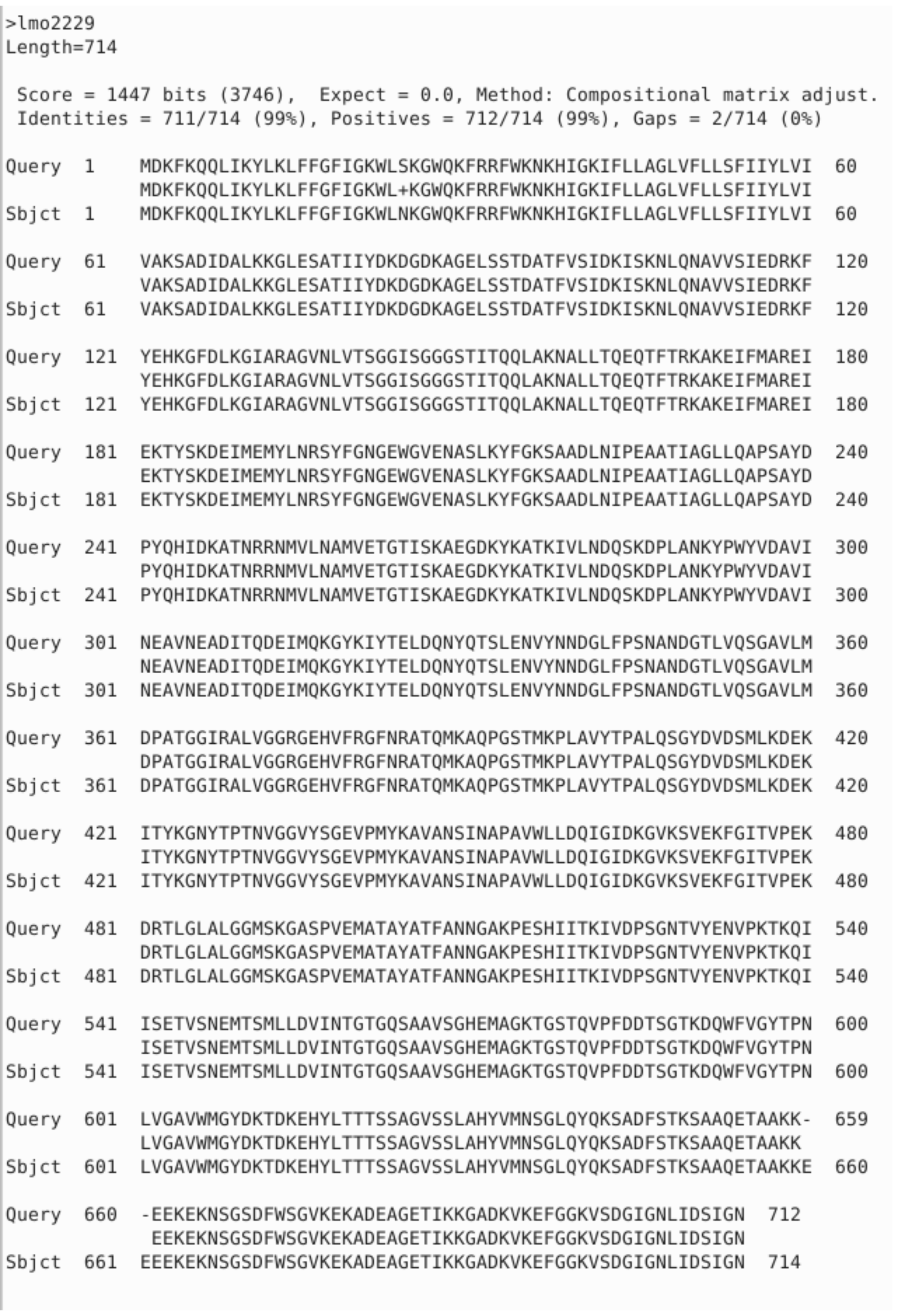

OCPFDLNE_01076/1-293 1 MDGELSKDVDQKMNLLKKWFSSIDWDQFWNHIISVGIKIAILIALYFIFRVIGNKIIRSFFRKYRQQQAVSVGRADTLESLISNFYGYVLFFTFAILL 98
lmo1013/1-281 1 ------------MNLLKKWFSSIDWDQFWNHIISVGIKIAILIALYFIFRVIGNKIIRSFFRKYRQQQAVSVGRADTLESLISNFYGYVLFFTFAILL 86
EGJ24516.1/1-293 1 MDGELSKDVDQKMNLLKKWFSSIDWDQFWNHIISVGIKIAILIALYFIFRVVGNKIIRSFFRKYRQQQAVSVGRADTLESLISNFYGYVLFFTFAILL 98
Conservation
9
Quality
Consensus
MDGELSKDVDQKMNLLKKWFSSIDWDQFWNHIISVGIKIAILIALYFIFRVIGNKIIRSFFRKYRQQQAVSVGRADTLESLISNFYGYVLFFTFAILL
Occupancy
OCPFDLNE_01076/1-293 99 LQNFMDVTAIIASAGVASLAIAFGAQGLVSDVVTGFFILLERQLDVGDTITIGLVNGTVEALGLRTTLVRDFDGTLHFIPNRQIMVVSNHSRGNMRVM 196
lmo1013/1-281 87 LQNFMDVTAIIASAGVASLAIAFGAQGLVSDVVTGFFILLERQLDVGDTITIGLVNGTVEALGLRTTQVRDFDGTLHFIPNRQIMVVSNHSRGNMRVM 184
EGJ24516.1/1-293 99 LQNFMDVTAIIASAGVASLAIAFGAQGLVSDVVTGFFILLERQLDVGDTITIGLVNGTVEALGLRTTQVRDFDGTLHFIPNRQIMVVSNHSRGNMRVM 196
Conservation
7
Quality
Consensus
LQNFMDVTAIIASAGVASLAIAFGAQGLVSDVVTGFFILLERQLDVGDTITIGLVNGTVEALGLRTTQVRDFDGTLHFIPNRQIMVVSNHSRGNMRVM
Occupancy
OCPFDLNE_01076/1-293 197 VDIQISPHEDPEKAIKIIGEVCDIAAKENKNIVEPPVVLGVQNIDATNMIIRVVGKAVNGEQYSVQRDLLKDIREALAENKIELPLNFVSTFGPNNN 293
lmo1013/1-281 185 VDIQISPHEDPEKAIKIIGEVCDVAAKENKNIVEPPVVLGVQNIDATNMIIRVVGKAVNGEQYSVQRDLLKDIREALAENKIELPLNFVSTFGPNNN 281
EGJ24516.1/1-293 197 VDIQISPHEDPEKAIKIIGEVCDVAAKENKNIVEPPVVLGVQNIDATNMIIRVVGKAVNGEQYSVQRDLLKDIREALAENEIELPLNFVSTFGPNNN 293
Conservation
9
7
Quality
Consensus
VDIQISPHEDPEKAIKIIGEVCDVAAKENKNIVEPPVVLGVQNIDATNMIIRVVGKAVNGEQYSVQRDLLKDIREALAENKIELPLNFVSTFGPNNN
Occupancy

***lmo2229* vs LMOSA_2530 (ScottA) BLASTP alignment**



```
>lmo2229
Length=714

 Score = 1447 bits (3746),  Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 711/714 (99%), Positives = 712/714 (99%), Gaps = 2/714 (0%)

Query  1    MDKFKQQLIKYLKLFFGFIGKWLSKGWQKFRRFWKNKHIGKIFLLAGLVFLLSFIIYLVI  60
            MDKFKQQLIKYLKLFFGFIGKWL+KGWQKFRRFWKNKHIGKIFLLAGLVFLLSFIIYLVI
Sbjct  1    MDKFKQQLIKYLKLFFGFIGKWLNKGWQKFRRFWKNKHIGKIFLLAGLVFLLSFIIYLVI  60

Query  61   VAKSADIDALKKGLESATIIYDKDGDKAGELSSTDATFVSIDKISKNLQNAVVSIEDRKF  120
            VAKSADIDALKKGLESATIIYDKDGDKAGELSSTDATFVSIDKISKNLQNAVVSIEDRKF
Sbjct  61   VAKSADIDALKKGLESATIIYDKDGDKAGELSSTDATFVSIDKISKNLQNAVVSIEDRKF  120

Query  121  YEHKGFDLKGIARAGVNLVTSGGISGGGSTITQQLAKNALLTQEQTFTRKAKEIFMAREI  180
            YEHKGFDLKGIARAGVNLVTSGGISGGGSTITQQLAKNALLTQEQTFTRKAKEIFMAREI
Sbjct  121  YEHKGFDLKGIARAGVNLVTSGGISGGGSTITQQLAKNALLTQEQTFTRKAKEIFMAREI  180

Query  181  EKTYSKDEIMEMYLNRSYFGNGEWGVENASLKYFGKSAADLNIPEAATIAGLLQAPSAYD  240
            EKTYSKDEIMEMYLNRSYFGNGEWGVENASLKYFGKSAADLNIPEAATIAGLLQAPSAYD
Sbjct  181  EKTYSKDEIMEMYLNRSYFGNGEWGVENASLKYFGKSAADLNIPEAATIAGLLQAPSAYD  240

Query  241  PYQHIDKATNRRNMVLNAMVETGTISKAEGDKYKATKIVLNDQSKDPLANKYPWYVDAVI  300
            PYQHIDKATNRRNMVLNAMVETGTISKAEGDKYKATKIVLNDQSKDPLANKYPWYVDAVI
Sbjct  241  PYQHIDKATNRRNMVLNAMVETGTISKAEGDKYKATKIVLNDQSKDPLANKYPWYVDAVI  300

Query  301  NEAVNEADITQDEIMQKGYKIYTELDQNYQTSLENVYNNDGLFPSNANDGTLVQSGAVLM  360
            NEAVNEADITQDEIMQKGYKIYTELDQNYQTSLENVYNNDGLFPSNANDGTLVQSGAVLM
Sbjct  301  NEAVNEADITQDEIMQKGYKIYTELDQNYQTSLENVYNNDGLFPSNANDGTLVQSGAVLM  360

Query  361  DPATGGIRALVGGRGEHVFRGFNRATQMKAQPGSTMKPLAVYTPALQSGYDVDSMLKDEK  420
            DPATGGIRALVGGRGEHVFRGFNRATQMKAQPGSTMKPLAVYTPALQSGYDVDSMLKDEK
Sbjct  361  DPATGGIRALVGGRGEHVFRGFNRATQMKAQPGSTMKPLAVYTPALQSGYDVDSMLKDEK  420

Query  421  ITYKGNYTPTNVGGVYSGEVPMYKAVANSINAPAVWLLDQIGIDKGVKSVEKFGITVPEK  480
            ITYKGNYTPTNVGGVYSGEVPMYKAVANSINAPAVWLLDQIGIDKGVKSVEKFGITVPEK
Sbjct  421  ITYKGNYTPTNVGGVYSGEVPMYKAVANSINAPAVWLLDQIGIDKGVKSVEKFGITVPEK  480

Query  481  DRTLGLALGGMSKGASPVEMATAYATFANNGAKPESHIITKIVDPSGNTVYENVPKTKQI  540
            DRTLGLALGGMSKGASPVEMATAYATFANNGAKPESHIITKIVDPSGNTVYENVPKTKQI
Sbjct  481  DRTLGLALGGMSKGASPVEMATAYATFANNGAKPESHIITKIVDPSGNTVYENVPKTKQI  540

Query  541  ISETVSNEMTSMLLDVINTGTGQSAAVSGHEMAGKTGSTQVPFDDTSGTKDQWFVGYTPN  600
            ISETVSNEMTSMLLDVINTGTGQSAAVSGHEMAGKTGSTQVPFDDTSGTKDQWFVGYTPN
Sbjct  541  ISETVSNEMTSMLLDVINTGTGQSAAVSGHEMAGKTGSTQVPFDDTSGTKDQWFVGYTPN  600

Query  601  LVGAVWMGYDKTDKEHYLTTTSSAGVSSLAHYVMNSGLQYQKSADFSTKSAAQETAAKK-  659
            LVGAVWMGYDKTDKEHYLTTTSSAGVSSLAHYVMNSGLQYQKSADFSTKSAAQETAAKK
Sbjct  601  LVGAVWMGYDKTDKEHYLTTTSSAGVSSLAHYVMNSGLQYQKSADFSTKSAAQETAAKKE  660

Query  660  -EEKEKNSGSDFWSGVKEKADEAGETIKKGADKVKEFGGKVSDGIGNLIDSIGN  712
             EEKEKNSGSDFWSGVKEKADEAGETIKKGADKVKEFGGKVSDGIGNLIDSIGN
Sbjct  661  EEEKEKNSGSDFWSGVKEKADEAGETIKKGADKVKEFGGKVSDGIGNLIDSIGN  714
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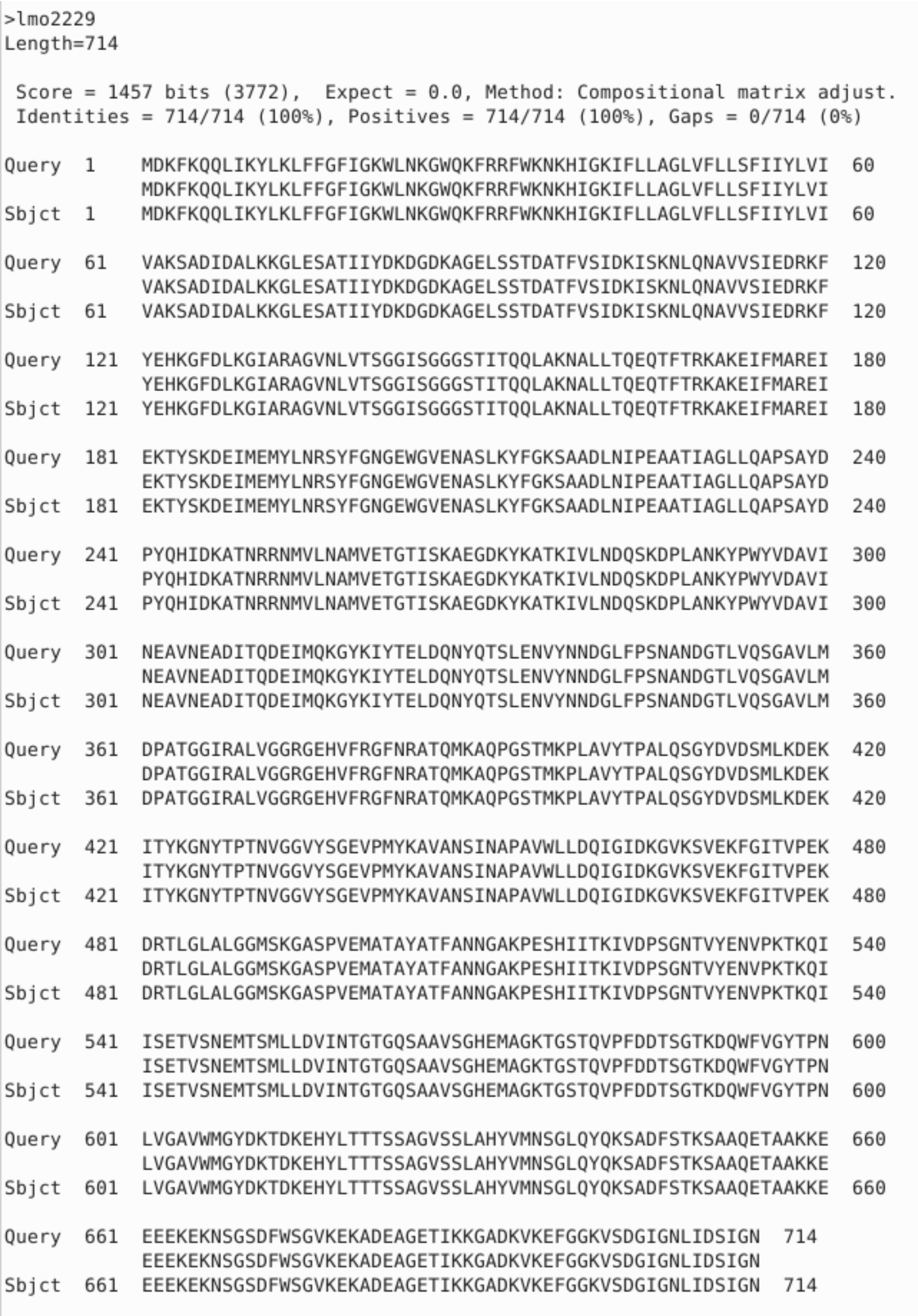
***lmo2229* vs OCPFDLNE_02389 (RO15) BLASTP alignment**



```
>lmo2229
Length=714

 Score = 1457 bits (3772),  Expect = 0.0, Method: Compositional matrix adjust.
 Identities = 714/714 (100%), Positives = 714/714 (100%), Gaps = 0/714 (0%)

Query  1    MDKFKQQLIKYLKLFFGFIGKWLNKGWQKFRRFWKNKHIGKIFLLAGLVFLLSFIIYLVI  60
            MDKFKQQLIKYLKLFFGFIGKWLNKGWQKFRRFWKNKHIGKIFLLAGLVFLLSFIIYLVI
Sbjct  1    MDKFKQQLIKYLKLFFGFIGKWLNKGWQKFRRFWKNKHIGKIFLLAGLVFLLSFIIYLVI  60

Query  61   VAKSADIDALKKGLESATIIYDKDGDKAGELSSTDATFVSIDKISKNLQNAVVSIEDRKF  120
            VAKSADIDALKKGLESATIIYDKDGDKAGELSSTDATFVSIDKISKNLQNAVVSIEDRKF
Sbjct  61   VAKSADIDALKKGLESATIIYDKDGDKAGELSSTDATFVSIDKISKNLQNAVVSIEDRKF  120

Query  121  YEHKGFDLKGIARAGVNLVTSGGISGGGSTITQQLAKNALLTQEQTFTRKAKEIFMAREI  180
            YEHKGFDLKGIARAGVNLVTSGGISGGGSTITQQLAKNALLTQEQTFTRKAKEIFMAREI
Sbjct  121  YEHKGFDLKGIARAGVNLVTSGGISGGGSTITQQLAKNALLTQEQTFTRKAKEIFMAREI  180

Query  181  EKTYSKDEIMEMYLNRSYFGNGEWGVENASLKYFGKSAADLNIPEAATIAGLLQAPSAYD  240
            EKTYSKDEIMEMYLNRSYFGNGEWGVENASLKYFGKSAADLNIPEAATIAGLLQAPSAYD
Sbjct  181  EKTYSKDEIMEMYLNRSYFGNGEWGVENASLKYFGKSAADLNIPEAATIAGLLQAPSAYD  240

Query  241  PYQHIDKATNRRNMVLNAMVETGTISKAEGDKYKATKIVLNDQSKDPLANKYPWYVDAVI  300
            PYQHIDKATNRRNMVLNAMVETGTISKAEGDKYKATKIVLNDQSKDPLANKYPWYVDAVI
Sbjct  241  PYQHIDKATNRRNMVLNAMVETGTISKAEGDKYKATKIVLNDQSKDPLANKYPWYVDAVI  300

Query  301  NEAVNEADITQDEIMQKGYKIYTELDQNYQTSLENVYNNDGLFPSNANDGTLVQSGAVLM  360
            NEAVNEADITQDEIMQKGYKIYTELDQNYQTSLENVYNNDGLFPSNANDGTLVQSGAVLM
Sbjct  301  NEAVNEADITQDEIMQKGYKIYTELDQNYQTSLENVYNNDGLFPSNANDGTLVQSGAVLM  360

Query  361  DPATGGIRALVGGRGEHVFRGFNRATQMKAQPGSTMKPLAVYTPALQSGYDVDSMLKDEK  420
            DPATGGIRALVGGRGEHVFRGFNRATQMKAQPGSTMKPLAVYTPALQSGYDVDSMLKDEK
Sbjct  361  DPATGGIRALVGGRGEHVFRGFNRATQMKAQPGSTMKPLAVYTPALQSGYDVDSMLKDEK  420

Query  421  ITYKGNYTPTNVGGVYSGEVPMYKAVANSINAPAVWLLDQIGIDKGVKSVEKFGITVPEK  480
            ITYKGNYTPTNVGGVYSGEVPMYKAVANSINAPAVWLLDQIGIDKGVKSVEKFGITVPEK
Sbjct  421  ITYKGNYTPTNVGGVYSGEVPMYKAVANSINAPAVWLLDQIGIDKGVKSVEKFGITVPEK  480

Query  481  DRTLGLALGGMSKGASPVEMATAYATFANNGAKPESHIITKIVDPSGNTVYENVPKTKQI  540
            DRTLGLALGGMSKGASPVEMATAYATFANNGAKPESHIITKIVDPSGNTVYENVPKTKQI
Sbjct  481  DRTLGLALGGMSKGASPVEMATAYATFANNGAKPESHIITKIVDPSGNTVYENVPKTKQI  540

Query  541  ISETVSNEMTSMLLDVINTGTGQSAAVSGHEMAGKTGSTQVPFDDTSGTKDQWFVGYTPN  600
            ISETVSNEMTSMLLDVINTGTGQSAAVSGHEMAGKTGSTQVPFDDTSGTKDQWFVGYTPN
Sbjct  541  ISETVSNEMTSMLLDVINTGTGQSAAVSGHEMAGKTGSTQVPFDDTSGTKDQWFVGYTPN  600

Query  601  LVGAVWMGYDKTDKEHYLTTTSSAGVSSLAHYVMNSGLQYQKSADFSTKSAAQETAAKKE  660
            LVGAVWMGYDKTDKEHYLTTTSSAGVSSLAHYVMNSGLQYQKSADFSTKSAAQETAAKKE
Sbjct  601  LVGAVWMGYDKTDKEHYLTTTSSAGVSSLAHYVMNSGLQYQKSADFSTKSAAQETAAKKE  660

Query  661  EEEKEKNSGSDFWSGVKEKADEAGETIKKGADKVKEFGGKVSDGIGNLIDSIGN  714
            EEEKEKNSGSDFWSGVKEKADEAGETIKKGADKVKEFGGKVSDGIGNLIDSIGN
Sbjct  661  EEEKEKNSGSDFWSGVKEKADEAGETIKKGADKVKEFGGKVSDGIGNLIDSIGN  714
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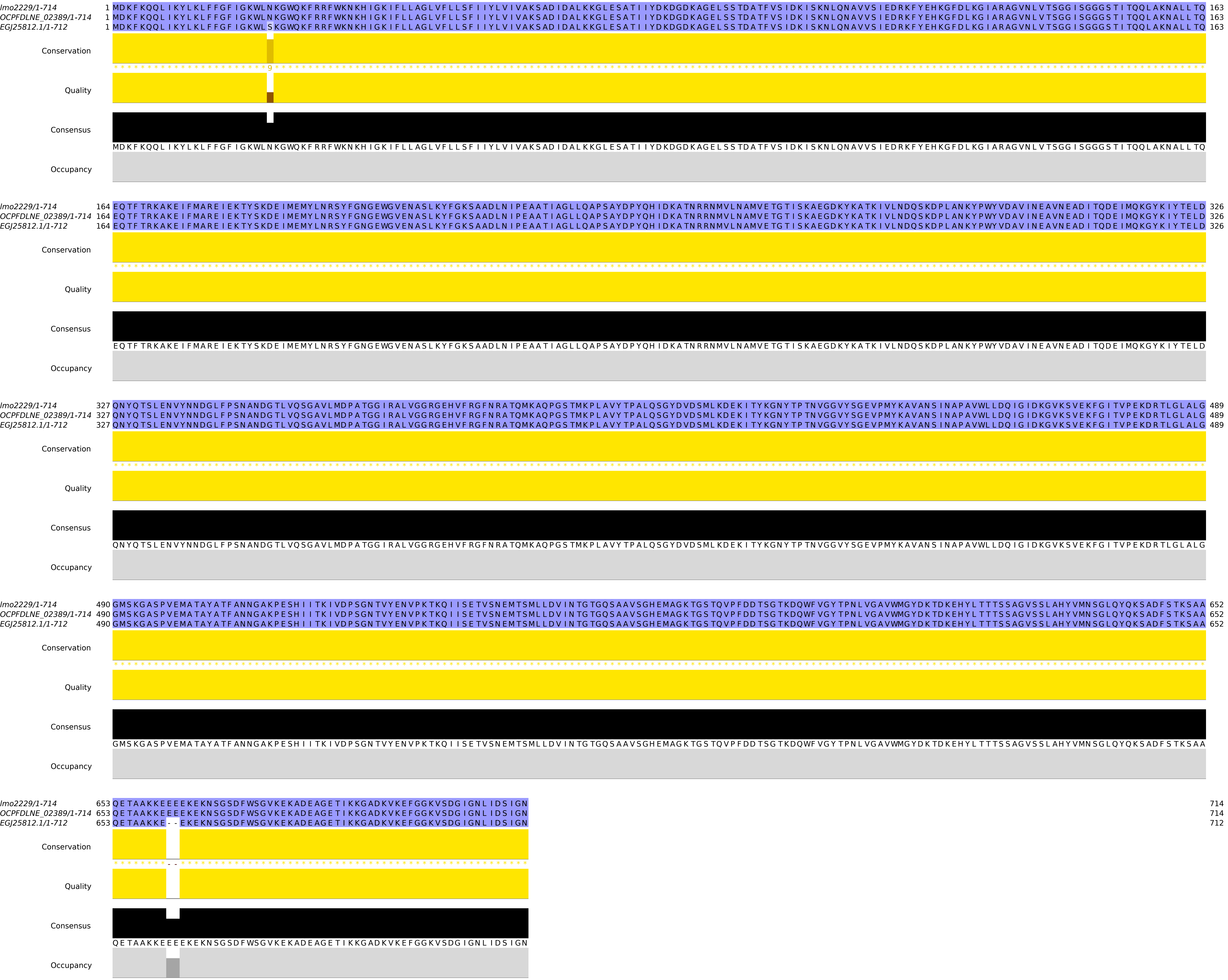

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lmo2229/1-714          1 MDKFKQQLIKYLKLFFGFIGKWLNKGWQKFRRFWKNKHIGKIFLLAGLVFLLSFIIYLVIVAKSADIDALKKGLESATIIYDKDGDKAGELSSTDATFVSIDKISKNLQNAVVSIEDRKFYEHKGFDLKGIARAGVNLVTSGGISGGGSTITQQLAKNALLTQ 163
OCPFDLNE_02389/1-714   1 MDKFKQQLIKYLKLFFGFIGKWLNKGWQKFRRFWKNKHIGKIFLLAGLVFLLSFIIYLVIVAKSADIDALKKGLESATIIYDKDGDKAGELSSTDATFVSIDKISKNLQNAVVSIEDRKFYEHKGFDLKGIARAGVNLVTSGGISGGGSTITQQLAKNALLTQ 163
EGJ25812.1/1-712       1 MDKFKQQLIKYLKLFFGFIGKWLSKGWQKFRRFWKNKHIGKIFLLAGLVFLLSFIIYLVIVAKSADIDALKKGLESATIIYDKDGDKAGELSSTDATFVSIDKISKNLQNAVVSIEDRKFYEHKGFDLKGIARAGVNLVTSGGISGGGSTITQQLAKNALLTQ 163
Conservation
                         ***********************9*******************************************************************************************************************************************
Quality
Consensus
                         MDKFKQQLIKYLKLFFGFIGKWLNKGWQKFRRFWKNKHIGKIFLLAGLVFLLSFIIYLVIVAKSADIDALKKGLESATIIYDKDGDKAGELSSTDATFVSIDKISKNLQNAVVSIEDRKFYEHKGFDLKGIARAGVNLVTSGGISGGGSTITQQLAKNALLTQ
Occupancy

lmo2229/1-714        164 EQTFTRKAKEIFMAREIEKTYSKDEIMEMYLNRSYFGNGEWGVENASLKYFGKSAADLNIPEAATIAGLLQAPSAYDPYQHIDKATNRRNMVLNAMVETGTISKAEGDKYKATKIVLNDQSKDPLANKYPWYVDAVINEAVNEADITQDEIMQKGYKIYTELD 326
OCPFDLNE_02389/1-714 164 EQTFTRKAKEIFMAREIEKTYSKDEIMEMYLNRSYFGNGEWGVENASLKYFGKSAADLNIPEAATIAGLLQAPSAYDPYQHIDKATNRRNMVLNAMVETGTISKAEGDKYKATKIVLNDQSKDPLANKYPWYVDAVINEAVNEADITQDEIMQKGYKIYTELD 326
EGJ25812.1/1-712     164 EQTFTRKAKEIFMAREIEKTYSKDEIMEMYLNRSYFGNGEWGVENASLKYFGKSAADLNIPEAATIAGLLQAPSAYDPYQHIDKATNRRNMVLNAMVETGTISKAEGDKYKATKIVLNDQSKDPLANKYPWYVDAVINEAVNEADITQDEIMQKGYKIYTELD 326
Conservation
                         *******************************************************************************************************************************************************************
Quality
Consensus
                         EQTFTRKAKEIFMAREIEKTYSKDEIMEMYLNRSYFGNGEWGVENASLKYFGKSAADLNIPEAATIAGLLQAPSAYDPYQHIDKATNRRNMVLNAMVETGTISKAEGDKYKATKIVLNDQSKDPLANKYPWYVDAVINEAVNEADITQDEIMQKGYKIYTELD
Occupancy

lmo2229/1-714        327 QNYQTSLENVYNNDGLFPSNANDGTLVQSGAVLMDPATGGIRALVGGRGEHVFRGFNRATQMKAQPGSTMKPLAVYTPALQSGYDVDSMLKDEKITYKGNYTPTNVGGVYSGEVPMYKAVANSINAPAVWLLDQIGIDKGVKSVEKFGITVPEKDRTLGLALG 489
OCPFDLNE_02389/1-714 327 QNYQTSLENVYNNDGLFPSNANDGTLVQSGAVLMDPATGGIRALVGGRGEHVFRGFNRATQMKAQPGSTMKPLAVYTPALQSGYDVDSMLKDEKITYKGNYTPTNVGGVYSGEVPMYKAVANSINAPAVWLLDQIGIDKGVKSVEKFGITVPEKDRTLGLALG 489
EGJ25812.1/1-712     327 QNYQTSLENVYNNDGLFPSNANDGTLVQSGAVLMDPATGGIRALVGGRGEHVFRGFNRATQMKAQPGSTMKPLAVYTPALQSGYDVDSMLKDEKITYKGNYTPTNVGGVYSGEVPMYKAVANSINAPAVWLLDQIGIDKGVKSVEKFGITVPEKDRTLGLALG 489
Conservation
                         *******************************************************************************************************************************************************************
Quality
Consensus
                         QNYQTSLENVYNNDGLFPSNANDGTLVQSGAVLMDPATGGIRALVGGRGEHVFRGFNRATQMKAQPGSTMKPLAVYTPALQSGYDVDSMLKDEKITYKGNYTPTNVGGVYSGEVPMYKAVANSINAPAVWLLDQIGIDKGVKSVEKFGITVPEKDRTLGLALG
Occupancy

lmo2229/1-714        490 GMSKGASPVEMATAYATFANNGAKPESHIITKIVDPSGNTVYENVPKTKQIISETVSNEMTSMLLDVINTGTGQSAAVSGHEMAGKTGSTQVPFDDTSGTKDQWFVGYTPNLVGAVWMGYDKTDKEHYLTTTSSAGVSSLAHYVMNSGLQYQKSADFSTKSAA 652
OCPFDLNE_02389/1-714 490 GMSKGASPVEMATAYATFANNGAKPESHIITKIVDPSGNTVYENVPKTKQIISETVSNEMTSMLLDVINTGTGQSAAVSGHEMAGKTGSTQVPFDDTSGTKDQWFVGYTPNLVGAVWMGYDKTDKEHYLTTTSSAGVSSLAHYVMNSGLQYQKSADFSTKSAA 652
EGJ25812.1/1-712     490 GMSKGASPVEMATAYATFANNGAKPESHIITKIVDPSGNTVYENVPKTKQIISETVSNEMTSMLLDVINTGTGQSAAVSGHEMAGKTGSTQVPFDDTSGTKDQWFVGYTPNLVGAVWMGYDKTDKEHYLTTTSSAGVSSLAHYVMNSGLQYQKSADFSTKSAA 652
Conservation
                         *******************************************************************************************************************************************************************
Quality
Consensus
                         GMSKGASPVEMATAYATFANNGAKPESHIITKIVDPSGNTVYENVPKTKQIISETVSNEMTSMLLDVINTGTGQSAAVSGHEMAGKTGSTQVPFDDTSGTKDQWFVGYTPNLVGAVWMGYDKTDKEHYLTTTSSAGVSSLAHYVMNSGLQYQKSADFSTKSAA
Occupancy

lmo2229/1-714        653 QETAAKKEEEEKEKNSGSDFWSGVKEKADEAGETIKKGADKVKEFGGKVSDGIGNLIDSIGN 714
OCPFDLNE_02389/1-714 653 QETAAKKEEEEKEKNSGSDFWSGVKEKADEAGETIKKGADKVKEFGGKVSDGIGNLIDSIGN 714
EGJ25812.1/1-712     653 QETAAKKE--EKEKNSGSDFWSGVKEKADEAGETIKKGADKVKEFGGKVSDGIGNLIDSIGN 712
Conservation
                         ********--****************************************************
Quality
Consensus
                         QETAAKKEEEEKEKNSGSDFWSGVKEKADEAGETIKKGADKVKEFGGKVSDGIGNLIDSIGN
Occupancy
```