Template Alignment: KSI_99_7058_ins, KSI_99_7427_ins, KSI_99_8...

template sequence KSI_99_6816_ins

aligned sequence KSI_99_7058_ins

aligned sequence KSI_99_7427_ins

aligned sequence KSI_99_8610_ins

aligned sequence KSI_99_8941_ins

TTAACTTTAAGAAGGAGATATACATATGCACCATCATCATCATCACGAAAATTTGTACTTCCAGGGAATGCTGACCGAGGAGGAGCTGACCGCTCTCGTT

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        M   L   T   E   E   E   L   T   A   L   V
68-445
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aligned sequence KSI_99_9867_ins
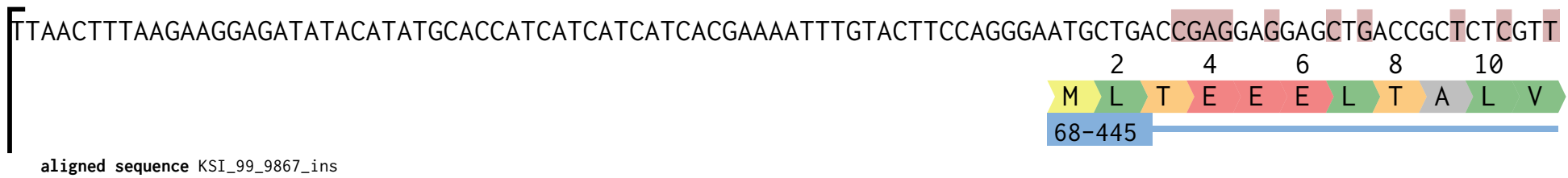
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12   14   16   18   20   22   24   26   28   30   32   34   36   38   40   42   44

E E Y L A L L N A K D L D G L V A M F A P D A V V E I P V G S E P

68-445

template sequence KSI_99_6816_ins

GAGCGCTATCTGGCAGCCTTAAATGCAAAGGACCTTGATGGATTAGTCGCAATGTTCGCGCCTGATGCCGTTTTAGAAATTCCTGTTGGTAGCGAGCCAC

26   28   30   32   34   36   38   40   42   44   46   48   50   52   54   56   58

E R Y L A A L N A K D L D G L V A M F A P D A V L E I P V G S E P

26-445

aligned sequence KSI_99_7058_ins

GAACGTTATCTGGCAGCCCTGAATGCCAAGGACCTGGATGGTCTGGTTGCAATGTTCGCCCCCGATGCCGTACTGGAAATTCCGGTAGGTAGCGAACCCA

12   14   16   18   20   22   24   26   28   30   32   34   36   38   40   42   44

E R Y L A A L N A K D L D G L V A M F A P D A V L E I P V G S E P

68-445

aligned sequence KSI_99_7427_ins

GAACGTTACCTCGCAGCGTTAAACGCCAAAGATCTTGACGGTCTCGTAGCTATGTGGGCGCCGGATGCGGTGCTGGAAATCCCAGTTGGTAGCGAACCCA

12   14   16   18   20   22   24   26   28   30   32   34   36   38   40   42   44

E R Y L A A L N A K D L D G L V A M W A P D A V L E I P V G S E P

68-445

aligned sequence KSI_99_8610_ins

AATACGTATCTGGCAGCGCTGAATGCAAAGGATCTCGATGGCCTGGTCGCAATGTTCGCCCCCGGATGCGGTGCTGGAGATCCCGGTGGGCAGTGAACCAA

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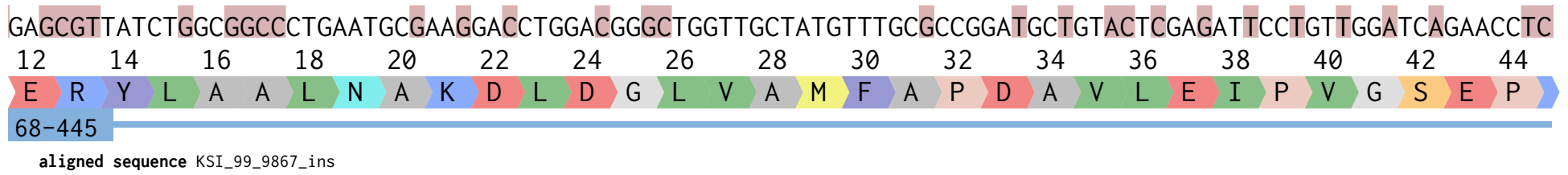N T Y L A A L N A K D L D G L V A M F A P D A V L E I P V G S E P

68-445

aligned sequence KSI_99_8941_ins

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12   14   16   18   20   22   24   26   28   30   32   34   36   38   40   42   44

E R Y L A A L N A K D L D G L V A M F A P D A V L E I P V G S E P

68-445

aligned sequence KSI_99_9867_ins

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46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78

K V G R E A I R A W Y E E W L K V D F T I T L L N P F D I D G N T V

68–445

template sequence KSI_99_6816_ins

GTGTGGGGCGCGAGGCCATTCGGGCCTGGTATGAAGAATGGCTGAAAGTAGATTTCACTATAACGTTGCTGAATCCCTTCGATATTGACGGAAATACAGT

60 62 64 66 68 70 72 74 76 78 80 82 84 86 88 90 92

R V G R E A I R A W Y E E W L K V D F T I T L L N P F D I D G N T V

26–445

aligned sequence KSI_99_7058_ins

GAGTTGGGCGCGAGGCTATCCGGGCGTGGTACGAAGAGTGGCTGAAGGTTGATTTTACCATTACGTTACTGAATCCGTTTGATATCGATGGCAATACAGT

46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78

R V G R E A I R A W Y E E W L K V D F T I T L L N P F D I D G N T V

68–445

aligned sequence KSI_99_7427_ins

GAGTTGGGCGGGAAGCGATTCGTGCGTGGTACGAAGAATGGTTGAAAGTTGATTTTACAATAACTCTCCTCAACCCTTTCGATATTGATGGCAACACTGT

46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78

R V G R E A I R A W Y E E W L K V D F T I T L L N P F D I D G N T V

68–445

aligned sequence KSI_99_8610_ins

AAGTGGGTCGTGAGGCTATACGAGCATGGTACGAAGAATGGCTGAAAGTCGACTTTAAGATAACGCTGCTCAATCCATTTGATATTGATGGCAATACCGT

46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78

K V G R E A I R A W Y E E W L K V D F K I T L L N P F D I D G N T V

68–445

aligned sequence KSI_99_8941_ins

GAGTTGGACGTGAAGCGATTAGAGCATGGTTCGAAGAATGGCTGAAAGTCGATTTCAAAATAACCCTCCTGAACCCATTCGATATAGACGGCAATACTGT

46   48   50   52   54   56   58   60   62   64   66   68   70   72   74   76   78

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68-445
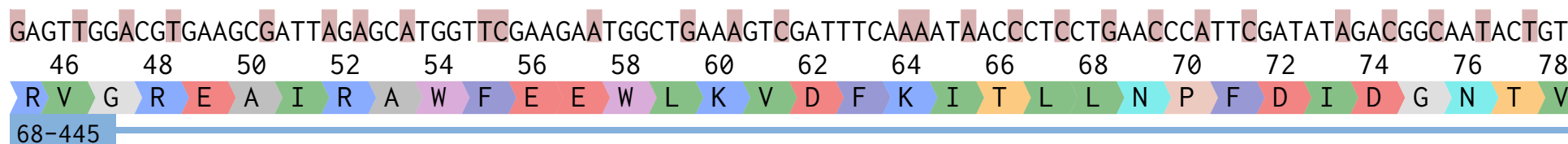
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T F D V E V T F T L D G K K F S Y K S T D R I E W N D E G K I K R

68-445

template sequence KSI_99_6816_ins

AACTTTTGATGTTGAAGTAACATTTACAAAAGATGGCAAGAAGTTCACATACAAGTCAACTGATACAATCGAATGGAACGACGAAGGCAAAATTGTCCGT

94 96 98 100 102 104 106 108 110 112 114 116 118 120 122 124

T F D V E V T F T K D G K K F T Y K S T D T I E W N D E G K I V R

26-445

aligned sequence KSI_99_7058_ins

CACGTTTGACGTAGAAGTAACGTTTACAAAGGATGGCAAGAAATTTACGATAAAGAGTACTGACACTATCGAATGGAATGATGAAGGGAAGATCGTGCGC

80 82 84 86 88 90 92 94 96 98 100 102 104 106 108 110

T F D V E V T F T K D G K K F T I K S T D T I E W N D E G K I V R

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aligned sequence KSI_99_7427_ins

TACATTTGATGTGGAAGTGACCTTTACGAAAGATGGTAAAAAATTTACCTATAAAGTACGGACACCATAGAATTTAACGACGAGGGAAAGATAGTCCGT

80 82 84 86 88 90 92 94 96 98 100 102 104 106 108 110

T F D V E V T F T K D G K K F T Y K S T D T I E F N D E G K I V R

68-445

aligned sequence KSI_99_8610_ins

AACATTTGACGTAGAGGTCGAATTCACCAAAGATGGTAAAAAATTCTCGTATAAGTCAACTGATACGATCGAGTGGAACGATGAAGGCAAAATTAAACGG

80 82 84 86 88 90 92 94 96 98 100 102 104 106 108 110

T F D V E V E F T K D G K K F S Y K S T D T I E W N D E G K I K R

68-445

aligned sequence KSI_99_8941_ins

TACATTTGATGTAGAGGTGACCTTCACAAAGGATGGTAAGAAGTTCAGCTACAAGTCCCGCGATACGATAGAATGGAACGATGAGGGCCTTATTAAACGC

80   82   84   86   88   90   92   94   96   98   100   102   104   106   108   110

T F D V E V T F T K D G K K F S Y K S R D T I E W N D E G L I K R

68-445
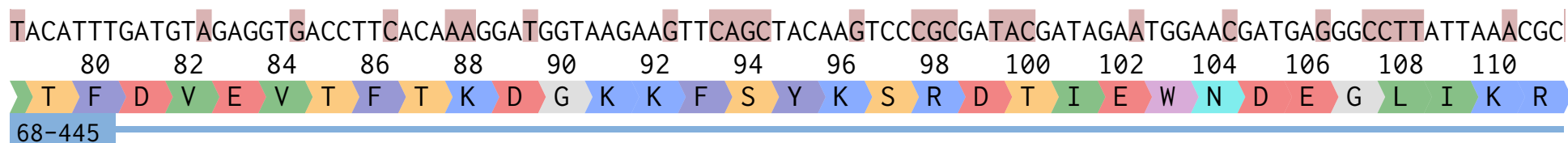
aligned sequence KSI_99_9867_ins

CTGGAGGTTGAGTTTGATCTTTCAACCTGGAAAGTGTCGGAGtga
112   114   116   118   120   122   124   126

L E V E F D L S T W K V S E *

68-445

template sequence KSI_99_6816_ins

CTTACCGTCGAGTATGATCTGTCCACCTGGAAGGTTCTGGAAtga
126   128   130   132   134   136   138   140

L T V E Y D L S T W K V L E *

26-445

aligned sequence KSI_99_7058_ins

TTGACCGTAGAGTATGACCTCTCCACCTGGAAGGTGCTGGAGtga
112   114   116   118   120   122   124   126

L T V E Y D L S T W K V L E *

68-445

aligned sequence KSI_99_7427_ins

GTTACCGTAGAGTACGATCTGTCTACTTGGAAAGTGCTGGAGtga
112   114   116   118   120   122   124   126

V T V E Y D L S T W K V L E *

68-445

aligned sequence KSI_99_8610_ins

TTTGAGGTAGAATACGATCTGTCCACCTTCAAGGAGCTGGAAtga
112   114   116   118   120   122   124   126

F E V E Y D L S T F K E L E *

68-445

aligned sequence KSI_99_8941_ins

CTTACGGTCGAATATGATCTGTCTACCTGGAAGGAATTAGAGtga

112   114   116   118   120   122   124   126

L T V E Y D L S T W K E L E *

68-445

aligned sequence KSI_99_9867_ins