

# *P. davidi* LEA-I

## LEA-1.1

MDSTND  
 SSP<sup>T</sup>LAEIAAE  
 AAHNIAEKAQN  
 VAAAARDKLAD AYEAVAE  
 YAHDGKEKAED  
 LAEAGKEKAED  
 LG<sup>E</sup>SVKESAQN AAEKVVD  
 LAHDGKEKVVD  
 LA<sup>Q</sup>AGKEKAED  
 LA<sup>Q</sup>AGKEKAQH ASDKAKD  
 LAHDGKEKAED  
 LGERAKEK<sup>S</sup>HD  
 LAEAGKEK<sup>A</sup>QR A<sup>S</sup>EKAKD  
 VAQSGKEK<sup>A</sup>HD  
 LAESGKQKANE  
 LGDRAKEK<sup>A</sup>DH ASDKAKD  
 LA<sup>Q</sup>AGKEKAHD  
 LAQAGKEKAQH ASDKAKD  
 LAQDGKEKAQE  
 LG<sup>D</sup>RS<sup>K</sup>ENAHH *ASNKAKE*  
*LANRGNEKAQE*  
*LGDHAKKASH* ASDKAKE  
 LANRGN<sup>A</sup>KAQE  
 LGDRAKEKAES NK\*

AE QD  
 L DAGKEKA ASDKAK<sup>D</sup>  
 GQ EE E  
 E E E  
 ØØ XØK KØXD  
 Q Q Q

## LEA-1.2

MDSTND  
 SSP<sup>T</sup>LAEIAAE  
 AAHNIAEKAQN  
 VAAAARDKLAD AYEAVAE  
 YAHDGKEKAED  
 LAEAGKEKAED  
 LG<sup>A</sup>SVKESAQN AAEKVVD  
 LAHDGKEKVVD  
 LA<sup>Q</sup>AGKEKAED  
 LAEAGKEK<sup>V</sup>QH ASDKAKD  
 LAHDGKEKAED  
 LGERAKEK<sup>S</sup>HD  
 LAEAGKEK<sup>A</sup>QR A<sup>T</sup>EKAKD  
 VAQSGKEK<sup>A</sup>HD  
 LAESGKQKANE  
 LGDRAKEK<sup>A</sup>DH ASDKAKD  
 LA<sup>H</sup>AGKEKAHD  
 LAQAGKEKAQH ASDKAKD  
 LAQDGKEKAQE  
 LG<sup>D</sup>RS<sup>K</sup>ENAHH ASNKAKE  
 LANRGNEKAQE  
 LGDHAKKASH ASDKAKE  
 LANRGN<sup>A</sup>KAQE  
 LGDRAKEKAES NK\*

AE QD  
 L DAGKEKA ASDKAK<sup>D</sup>  
 GQ EE E  
 E E E  
 ØØ XØK KØXD  
 Q Q Q

## LEA-1.3

MDSTND  
 SSP<sup>T</sup>LAEIAAE  
 AAHNIAEKAQN  
 VAAAARDKLAD AYEAVAE  
 YAHDGKEKAED  
 LAEAGKEKAEG  
 LG<sup>E</sup>SVKESAQN AAEKVVD  
 LAHDGKEKVVD  
 LA<sup>Q</sup>AGKEKAED  
 LAEAGKEK<sup>V</sup>QH ASDKAKD  
 LAHDGKEKAED  
 LGERAKEK<sup>S</sup>HD  
 LAEAGKEK<sup>A</sup>QR A<sup>S</sup>EKAKD  
 VAQSGKEK<sup>A</sup>HD  
 LAESGKQKANE  
 LGDRAKEK<sup>A</sup>DH ASDKAKD  
 LA<sup>H</sup>AGKEKA<sup>H</sup>D  
 LA<sup>Q</sup>AGKEKAQH ASDKAKD  
 LAQDGKEKAQE  
 LG<sup>D</sup>RS<sup>K</sup>ENAHH ASNKAKE  
 LANRGNEKAQE  
 LGDHAKKASH ASDKAKE  
 LANRGN<sup>A</sup>KAQE  
 LGDRAKEKAES NK\*

AE QD  
 L DAGKEKA ASDKAK<sup>D</sup>  
 GQ EE E  
 E E E  
 ØØ XØK KØXD  
 Q Q Q

# *P. davidi* *lea-1* cDNA sequences

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                101                                     150
LEA1.1  AAGTGTAAAA GAAAGTGCCC AAAATGCTGC TGAAAAGGTT AAAGATCTTG
LEA1.2  AAGTGTAAAA GAAAGTGCCC AAAATGCTGC TGAAAAGGTT AAAGATCTTG
LEA1.3  AAGTGTAAAA GAAAGTGCCC AAAATGCTGC TGAAAAGGTT AAAGATCTTG
        S  V  K   E  S  A  Q   N  A  A   E  K  V   K  D  L  A

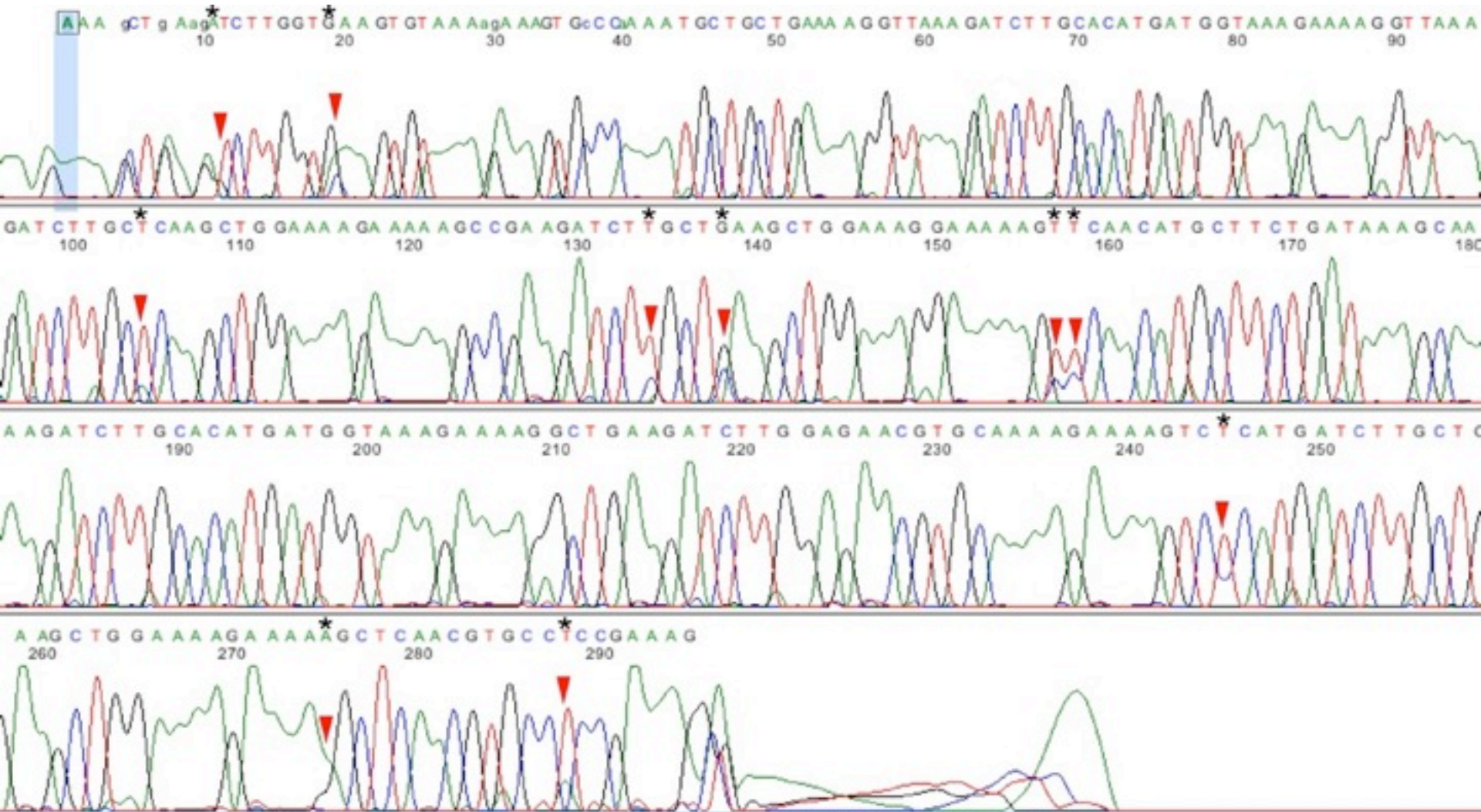
                151                                     200
LEA1.1  CACATGATGG TAAAGAAAAG GTTAAAGATC TTGCTCAAGC TGGAAAAGAA
LEA1.2  CACATGATGG TAAAGAAAAG GTTAAAGATC TTGCACAAGC TGGAAAAGAA
LEA1.3  CACATGATGG TAAAGAAAAG GTTAAAGATC TTGCTCAAGC TGGAAAAGAA
        H  D  G   K  E  K   V  K  D  L   A  Q  A   G  K  E

                201                                     250
LEA1.1  AAAGCCGAAG ATCTTGCTCA AGCTGGAAAG GAAAAAGCCC AACATGCTTC
LEA1.2  AAAGCCGAAG ATCTTGCTGA AGCTGGAAAG GAAAAAGTTC AACATGCTTC
LEA1.3  AAAGCCGAAG ATCTCGCTGA AGCTGGAAAG GAAAAAGTTC AACATGCTTC
        K  A  E  D   L  A  E   A  G  K   E  K  V  Q   H  A  S
                        (Q)                               (A)

                251                                     300
LEA1.1  TGATAAAGCA AAAGATCTTG CACATGATGG TAAAGAAAAG GCTGAAGATC
LEA1.2  TGATAAAGCA AAAGATCTTG CACATGATGG TAAAGAAAAG GCTGAAGATC
LEA1.3  TGATAAAGCA AAAGATCTTG CACATGATGG TAAAGAAAAG GCTGAAGATC
        D  K  A   K  D  L  A   H  D  G   K  E  K   A  E  D  L

                301                                     350
LEA1.1  TTGGAGAACG TGCAAAAGAA AAGTTCATG ATCTTGCTGA AGCTGGAAAA
LEA1.2  TTGGAGAACG TGCAAAAGAA AAGTCCCATG ATCTTGCTGA AGCTGGAAAA
LEA1.3  TTGGAGAACG TGCAAAAGAA AAGTTCATG ATCTTGCTGA AGCTGGAAAA
        G  E  R   A  K  E   K  S  H  D   L  A  E   A  G  K
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# *P. davidi lea-1* genome sequence



# *P. davidi lea-1* genome sequences

	101				150
LEA1.1	AAGTGTAAAA	GAAAGTGCCC	AAAATGCTGC	TGAAAAGGTT	AAAGATCTTG
LEA1.2	AAGTGTAAAA	GAAAGTGCCC	AAAATGCTGC	TGAAAAGGTT	AAAGATCTTG
LEA1.3	AAGTGTAAAA	GAAAGTGCCC	AAAATGCTGC	TGAAAAGGTT	AAAGATCTTG
<b>lea-1F</b>	<b>AAGTGTAAAA</b>	<b>GAAAGTGCCC</b>	<b>AAAATGCTGC</b>	<b>TGAAAAGGTT</b>	<b>AAAGATCTTG</b>
	151				200
LEA1.1	CACATGATGG	TAAAGAAAAG	GTTAAAGATC	TTGCTCAAGC	TGGAAAAGAA
LEA1.2	CACATGATGG	TAAAGAAAAG	GTTAAAGATC	TTGCACAAGC	TGGAAAAGAA
LEA1.3	CACATGATGG	TAAAGAAAAG	GTTAAAGATC	TTGCTCAAGC	TGGAAAAGAA
<b>lea-1F</b>	<b>CACATGATGG</b>	<b>TAAAGAAAAG</b>	<b>GTTAAAGATC</b>	<b>TTGCWCAAGC</b>	<b>TGGAAAAGAA</b>
	201				250
LEA1.1	AAAGCCGAAG	ATCTTGCTCA	AGCTGGAAAG	GAAAAAGCCC	AACATGCTTC
LEA1.2	AAAGCCGAAG	ATCTTGCTGA	AGCTGGAAAG	GAAAAAGTTC	AACATGCTTC
LEA1.3	AAAGCCGAAG	ATCTCGCTGA	AGCTGGAAAG	GAAAAAGTTC	AACATGCTTC
<b>lea-1F</b>	<b>AAAGCCGAAG</b>	<b>ATCTYGCTSA</b>	<b>AGCTGGAAAG</b>	<b>GAAAAAGYIC</b>	<b>AACATGCTTC</b>
	251				300
LEA1.1	TGATAAAGCA	AAAGATCTTG	CACATGATGG	TAAAGAAAAG	GCTGAAGATC
LEA1.2	TGATAAAGCA	AAAGATCTTG	CACATGATGG	TAAAGAAAAG	GCTGAAGATC
LEA1.3	TGATAAAGCA	AAAGATCTTG	CACATGATGG	TAAAGAAAAG	GCTGAAGATC
<b>lea-1F</b>	<b>TGATAAAGCA</b>	<b>AAAGATCTTG</b>	<b>CACATGATGG</b>	<b>TAAAGAAAAG</b>	<b>GCTGAAGATC</b>
	301				350
LEA1.1	TTGGAGAACG	TGCAAAGAA	AAGTCCATG	ATCTTGCTGA	AGCTGGAAAA
LEA1.2	TTGGAGAACG	TGCAAAGAA	AAGTCCCATG	ATCTTGCTGA	AGCTGGAAAA
LEA1.3	TTGGAGAACG	TGCAAAGAA	AAGTCCATG	ATCTTGCTGA	AGCTGGAAAA
<b>lea-1F</b>	<b>TTGGAGAACG</b>	<b>TGCAAAGAA</b>	<b>AAGTCYCATG</b>	<b>ATCTTGCTGA</b>	<b>AGCTGGAAAA</b>



# cDNA alignment (cluster 257)

*gln-5, glutamine synthetase (carbamoyl-phosphatase)*

131 140 150 160 170 180 190 200 210 220 230 240 250 260

01N16 CACRATTTGATGATGGACGACGATCTTCAAGATAGCCCTTTCCATCAGTACCAACTTGACGAGGAAATTCGACAGAACATGATCGATCAGCAATACCCCATGTAATTTATCARCAGATGAGTTTCATG  
 06E21 CACRATTTGACGATGGACGACGATCTTCAAGATAGCCCTTTCCATCAGTACCAACTTGACGAGGAAATTCGACAGAACATGATCGATCAGCAATACCCCATGTAATTTATCARCAGATGATGTTTCATG  
 13P01 CACRATTTGACGATGGACGACGATCTTCAAGATAGCCCTTTCCATCAGTACCAACTTGACGAGGAAATTCGACAGAACATGATCGATCAGCAATACCCCATGTAATTTATCARCAGATGATGTTTCATG  
 33D02 CACRATTTGACGATGGACGACGATCTTCAAGATAGCCCTTTCCATCAGTACCAACTTGACGAGGAAATTCGACAGAACATGATCGATCAGCAATACCCCATGTAATTTATCARCAGATGATGTTTCATG  
 04C02 CACRATTTGATGATGGACGACGATCTTCAAGATAGCCCTTTCCATCAGTACCAACTTGACGAGGAAATTCGACAGAACATGATCGATCAGCAATACCCCATGTAATTTATCARCAGATGAGTTTCATG  
 05F02 CACRATTTGATGATGGACGACGATCTTCAAGATAGCCCTTTCCATCAGTACCAACTTGACGAGGAAATTCGACAGAACATGATCGATCAGCAATACCCCATGTAATTTATCARCAGATGAGTTTCATG  
 14E08 CACRATTTGATGATGGACGACGATCTTCAAGATAGCCCTTTCCATCAGTACCAACTTGACGAGGAAATTCGACAGAACATGATCGATCAGCAATACCCCATGTAATTTATCARCAGATGATGTTTCATG  
 42D07 CACRATTTGACGATGGACGACGATCTTCAAGATAGCCCTTTCCATCAGTACCAACTTGACGAGGAAATTCGACAGAACATGATCGATCAGCAATACCCCATGTAATTTATCARCAGATGATGTTTCATG  
 Consensus CACRATTTGALGATGGACGACGATCTTCAAGATAGCCCTTTCCATCAGTACCAACTTGACGAGGAAATTCGACAGAACATGATCGATCAGCAATACCCCATGTAATTTATCARCAGATGALGTTTCATG

•••••

521 530 540 550 560 570 580 590 600 610 620 630 640 650

01N16 ATARTTGATCAGCCCATTTCAATTCCTTTACATATACCAATTTGAARTTCCCATTTGTGCTGGAGTTACTTCAGCATTGTACCAGCAAGCTTTAAACAGCTAATAAACATGCATTTGCATGTGCTTGTAC  
 06E21 ATARTTGATCAGCCCATTTCAATTCCTTTACATATACCAATTTGAARTTCCCATTTGTGCTGGAGTTACTTCAGCATTGTACCAGCAAGCTTTAAACAGCTAATAAACATGCATTTGCATGTGCTTGTAC  
 13P01 ATARTTGATCAGCCCATTTCAATTCCTTTACATATACCAATTTGAARTTCCCATTTGTGCTGGAGTTACTTCAGCATTGTACCAGCAAGCTTTAAACAGCTAATAAACATGCATTTGCATGTGCTTGTAC  
 33D02 ATARTTGATCAGCCCATTTCAATTCCTTTACATATACCAATTTGAARTTCCCATTTGTGCTGGAGTTACTTCAGCATTGTACCAGCAAGCTTTAAACAGCTAATAAACATGCATTTGCATGTGCTTGTAC  
 04C02 ATARTTGATCAGCCCATTTCAATTCCTTTACATATACCAATTTGAARTTCCCATTTGTGCTGGAGTTACTTCAGCATTGTACCAGCAAGCTTTAAACAGCTAATAAACATGCATTTGCATGGCTTGTAC  
 05F02 ATARTTGATCAGCCCATTTCAATTCCTTTACATATACCAATTTGAARTTCCCATTTGTGCTGGAGTTACTTCAGCATTGTACCAGCAAGCTTTAAACAGCTAATAAACATGCATTTGCATGGCTTGTAC  
 14E08 ATARTTGATCAGCCCATTTCAATTCCTTTACATATACCAATTTGAARTTCCCATTTGTGCTGGAGTTACTTCAGCATTGTACCAGCAAGCTTTAAACAGCTAATAAACATGCATTTGCATGTGCTTGTAC  
 42D07 ATARTTGATCAGCCCATTTCAATTCCTTTACATATACCAATTTGAARTTCCCATTTGTGCTGGAGTTACTTCAGCATTGTACCAGCAAGCTTTAAACAGCTAATAAACATGCATTTGCATGTGCTTGTAC  
 Consensus ATARTTGATCAGCCCATTTCAATTCCTTTACATATACCAATTTGAARTTCCCATTTGTGCTGGAGTTACTTCAGCATTGTACCAGCAAGCTTTAAACAGCTAATAAACATGCATTTGCATGTGCTTGTAC

651 660 670 680 690 700 710 720 730 740 750 760 770 780

01N16 AATTTCTCTTCCATACATTCGATCTGCAACCACCCACATAATATGGCCTTGTGGAGGTGGAGTTTATCCTTTGGCCACCAGTGGTGGAGATCCATATCCAAAAGAGATATTCCTTGTCCATA  
 06E21 AATTTCTCTTCCATACATTCGATCTGCAACCACCCACATAATATGGCCTTGTGGAGGTGGAGTTTATCCTTTGGCCACCAGTGGTGGAGATCCATATCCAAAAGAGATATTCCTTGTCCATA  
 13P01 AATTTCTCTTCCATACATTCGATCTGCAACCACCCACATAATATGGCCTTGTGGAGGTGGAGTTTATCCTTTGGCCACCAGTGGTGGAGATCCATATCCAAAAGAGATATTCCTTGTCCATA  
 33D02 AATTTCTCTTCCATACATTCGATCTGCAACCACCCACATAATATGGCCTTGTGGAGGTGGAGTTTATCCTTTGGCCACCAGTGGTGGAGATCCATATCCAAAAGAGATATTCCTTGTCCATA  
 04C02 AATTTCTCTTCCATACATTCGATCTGCAACCACCCACATAATATGGCCTTGTGGAGGTGGAGTTTATCCTTTGGCCACCAGTGGTGGAGATCCATATCCAAAAGAGATATTCCTTGTCCATA  
 05F02 AATTTCTCTTCCATACATTCGATCTGCAACCACCCACATAATATGGCCTTGTGGAGGTGGAGTTTATCCTTTGGCCACCAGTGGTGGAGATCCATATCCAAAAGAGATATTCCTTGTCCATA  
 14E08 AATTTCTCTTCCATACATTCGATCTGCAACCACCCACATAATATGGCCTTGTGGAGGTGGAGTTTATCCTTTGGCCACCAGTGGTGGAGATCCATATCCAAAAGAGATATTCCTTGTCCATA  
 42D07 AATTTCTCTTCCATACATTCGATCTGCAACCACCCACATAATATGGCCTTGTGGAGGTGGAGTTTATCCTTTGGCCACCAGTGGTGGAGATCCATATCCAAAAGAGATATTCCTTGTCCATA  
 Consensus AATTTCTCTTCCATACATTCGATCTGCAACCACCCACATAATATGGCCTTGTGGAGGTGGAGTTTATCCTTTGGCCACCAGTGGTGGAGATCCATATCCAAAAGAGATATTCCTTGTCCATA



# cDNA alignment (cluster 259)

## T25B9.9 6-phosphogluconate dehydrogenase

