

Anhang

A1 Genstruktur von *pld1* und *pld2* aus Schlafmohnkeimlingen

Gelb markiert, Sequenzunterschiede in der codierenden Region, die keine Änderung in der Aminosäure bewirken; violett markiert, Sequenzunterschiede in der codierenden Region, die eine Änderung in der Aminosäure bewirken; blau, Intronbereich; grün markiert, Start-Codon; rot markiert, Stopp-Codon.

mRNAp1d1	1	ATG	GCTCAGATTTCTCTCCATGGA	ACTCTACATGTTACGATCTTTGAAGCAA	AATTCAATT	60
mRNAp1d2	1	ATG	GCTCAGATTTCTCTCCATGGA	ACTCTACATGTTACGATCTTTGAAGCGA	AATTCAATT	60
gDNAp1d1	1	ATG	GCTCAGATTTCTCTCCATGGA	ACTCTACATGTTACGATCTTTGAAGCAA	AATTCAATT	60
gDNAp1d2	1	ATG	GCTCAGATTTCTCTCCATGGA	ACTCTACATGTTACGATCTTTGAAGCGA	AATTCAATT	60
mRNAp1d1	61	TCTCATCCTGATAGGAAA	ACTGGTGGTGCTCCTAAGTTC	TTTAGGAAGCTTGTGGAAAAC		120
mRNAp1d2	61	TCTCATCCTGATAGGAAA	ACTGGTGGTGCTCCTAAGTTC	TTTAGGAAGCTTGTGGAAAAC		120
gDNAp1d1	61	TCTCATCCTGATAGGAAA	ACTGGTGGTGCTCCTAAGTTC	TTTAGGAAGCTTGTGGAAAAC		120
gDNAp1d2	61	TCTCATCCTGATAGGAAA	ACTGGTGGTGCTCCTAAGTTC	TTTAGGAAGCTTGTGGAAAAC		120
mRNAp1d1	121	ATCGAGGAGACAGTTGG	ATTGGCAAAGGAGCTAGTATG	CTTTATGCCTCAGTTGATCTC		180
mRNAp1d2	121	ATCGAGGAGACAGTTGG	ATTGGCAAAGGAGCTAGTATG	CTTTATGCCTCAGTTGATCTC		180
gDNAp1d1	121	ATCGAGGAGACAGTTGG	ATTGGCAAAGGAGCTAGTATG	CTTTATGCCTCAGTTGATCTC		180
gDNAp1d2	121	ATCGAGGAGACAGTTGG	ATTGGCAAAGGAGCTAGTATG	CTTTATGCCTCAGTTGATCTC		180
mRNAp1d1	181	GATAAGGCTAGAGTTGG	AAGGACCAGAATCATAAAA	AGATGAACCTGTCAACCCTA	AGTGG	240
mRNAp1d2	181	GATAAGGCTAGAGTTGG	AAGGACCAGAATCATAAAA	AGATGAACCTGTCAACCCTA	AGTGG	240
gDNAp1d1	181	GATAAGGCTAGAGTTGG	AAGGACCAGAATCATAAAA	AGATGAACCTGTCAACCCTA	AGTGG	240
gDNAp1d2	181	GATAAGGCTAGAGTTGG	AAGGACCAGAATCATAAAA	AGATGAACCTGTCAACCCTA	AGTGG	240
mRNAp1d1	241	TAT	GAGTCTTTTCACATCTACT	GTGCCATATGGCTGCTAATG	TGCATCTTCACTGTCAA	300
mRNAp1d2	241	TAC	GAGTCTTTTCACATCTACT	GTGCCATATGGCTGCTAATG	TGCATCTTCACTGTCAA	300
gDNAp1d1	241	TAT	GAGTCTTTTCACATCTACT	GTGCCATATGGCTGCTAATG	TGCATCTTCACTGTCAA	300
gDNAp1d2	241	TAC	GAGTCTTTTCACATCTACT	GTGCCATATGGCTGCTAATG	TGCATCTTCACTGTCAA	300
mRNAp1d1	301	GATGATAATCCCAT	TGGAGCAACTCTGATTGGA	AGAGCTTATGTTCC	TATTGACAAAGTT	360
mRNAp1d2	301	GATGATAATCCCAT	TGGAGCAACTCTGATTGGA	AGAGCTTATGTTCC	TATTGACAAAGTT	360
gDNAp1d1	301	GATGATAATCCCAT	TGGAGCAACTCTGATTGGA	AGAGCTTATGTTCC	TATTGACAAAGTT	360
gDNAp1d2	301	GATGATAATCCCAT	TGGAGCAACTCTGATTGGA	AGAGCTTATGTTCC	TATTGACAAAGTT	360
mRNAp1d1	361	CTAAGTGGGGAAGA	AGTGGATGAATGGGT	CGAGGTGGTAGATC	AGGAGCGTAATCCTGTG	420
mRNAp1d2	361	CTAAGTGGGGAAGA	AGTGGATGAATGGGT	CGAGGTGGTAGATC	AGGAGCGTAATCCTGTG	420
gDNAp1d1	361	CTAAGTGGGGAAGA	AGTGGATGAATGGGT	CGAGGTGGTAGATC	AGGAGCGTAATCCTGTG	420
gDNAp1d2	361	CTAAGTGGGGAAGA	AGTGGATGAATGGGT	CGAGGTGGTAGATC	AGGAGCGTAATCCTGTG	420
mRNAp1d1	421	CAAGTGGTTGTA	AGATCCACGTGAAGCT	GCAATATTTGATGTT	GGTCAAGACAAGAAT	480
mRNAp1d2	421	CAAGTGGTTGTA	AGATCCACGTGAAGCT	GCAATATTTGATGTT	GGTCAAGACAAGAAT	480
gDNAp1d1	421	CAAGTGGTTGTA	AGATCCACGTGAAGCT	GCAATATTTGATGTT	GGTCAAGACAAGAAT	480
gDNAp1d2	421	CAAGTGGTTGTA	AGATCCACGTGAAGCT	GCAATATTTGATGTT	GGTCAAGACAAGAAT	480
mRNAp1d1	481	TGGGCTCGGGGA	AATTAGAAGCGCCAAAT	TTCTGGAGTTCCTT	ACACATTCTTCACCCAG	540
mRNAp1d2	481	TGGGCTCGGGGA	AATTAGAAGCGCCAAAT	TTCTGGAGTTCCTT	ACACATTCTTCACCCAG	540
gDNAp1d1	481	TGGGCTCGGGGA	AATTAGAAGCGCCAAAT	TTCTGGAGTTCCTT	ACACATTCTTCACCCAG	540
gDNAp1d2	481	TGGGCTCGGGGA	AATTAGAAGCGCCAAAT	TTCTGGAGTTCCTT	ACACATTCTTCACCCAG	540
mRNAp1d1	541	AGAACAGGATG	CAAAGTTTCTCTATAT	CAAGATGCTCACGT	CCCAGATAACTTTATTCC	600
mRNAp1d2	541	AGAACAGGATG	CAAAGTTTCTCTATAT	CAAGATGCTCACGT	CCCAGATAACTTTATTCC	600
gDNAp1d1	541	AGAACAGGATG	CAAAGTTTCTCTATAT	CAAGATGCTCACGT	CCCAGATAACTTTATTCC	600
gDNAp1d2	541	AGAACAGGATG	CAAAGTTTCTCTATAT	CAAGATGCTCACGT	CCCAGATAACTTTATTCC	600
mRNAp1d1	601	AAAATCCCTCT	TGCTGGAGGCAAGATTT	ACGAGCCTGCCAGAT	GTTGGGAGGATATATTT	660
mRNAp1d2	601	AAAATCCCTCT	TGCTGGAGGCAAGATTT	ACGAGCCTGCCAGAT	GTTGGGAGGATATATTT	660
gDNAp1d1	601	AAAATCCCTCT	TGCTGGAGGCAAGATTT	ACGAGCCTGCCAGAT	GTTGGGAGGATATATTT	660
gDNAp1d2	601	AAAATCCCTCT	TGCTGGAGGCAAGATTT	ACGAGCCTGCCAGAT	GTTGGGAGGATATATTT	660

mRNApld1	661	GATGCAATCAGTAATGCGAAACACATGATTTACATTACTGGGTGGTCTGTGTACACTGAA	720
mRNApld2	661	GATGCAATCAGTAATGCGAAACACATGATTTACATTACTGGATGGTCTGTGTACACTGAA	720
gDNApld1	661	GATGCAATCAGTAATGCGAAACACATGATTTACATTACTGGGTGGTCTGTGTACACTGAA	720
gDNApld2	661	GATGCAATCAGTAATGCGAAACACATGATTTACATTACTGGATGGTCTGTGTACACTGAA	720
mRNApld1	721	GTCGTTTTGATAAGGGACTCTAGAAGGCAAAAACCTGGTGGGGACATCACTCTTGGAGAG	780
mRNApld2	721	GTCGTTTTGATAAGGGACTCTAGAAGGCAAAAACCTGGTGGGGACATTACCCCTTGGAGAG	780
gDNApld1	721	GTCGTTTTGATAAGGGACTCTAGAAGGCAAAAACCTGGTGGGGACATCACTCTTGGAGAG	780
gDNApld2	721	GTCGTTTTGATAAGGGACTCTAGAAGGCAAAAACCTGGTGGGGACATTACCCCTTGGAGAG	780
mRNApld1	781	TTGCTTAAGAAAAAGGCTGATGAAGGTGTTAGGGTCCTTATGCTTGTATGGGATGACAGA	840
mRNApld2	781	TTGCTTAAGAAAAAGGCTGATGAAGGTGTTAGGGTCCTTATGCTTGTATGGGATGACAGA	840
gDNApld1	781	TTGCTTAAGAAAAAGGCTGATGAAGGTGTTAGGGTCCTTATGCTTGTATGGGATGACAGA	840
gDNApld2	781	TTGCTTAAGAAAAAGGCTGATGAAGGTGTTAGGGTCCTTATGCTTGTATGGGATGACAGA	840
mRNApld1	841	ACCTCTGTGGGTTTATTGAAAAAAGATGGATTGATGGCTACCATGACGAAGACACTTTT	900
mRNApld2	841	ACCTCCGTGGGTTTATTGAAAAAAGATGGATTGATGGCTACTCATGACGAAGACACTTTT	900
gDNApld1	841	ACCTCTGTGGGTTTATTGAAAAAAGATGGATTGATGGCTACCATGACGAAGACACTTTT	900
gDNApld2	841	ACCTCCGTGGGTTTATTGAAAAAAGATGGATTGATGGCTACTCATGACGAAGACACTTTT	900
mRNApld1	901	AATTACTTCCAAGGTACACAGGTGAACTGTGTCTTGTGTCCCCGTAATCCTGATGATGGA	960
mRNApld2	901	AATTACTTCCAAGGTACACAGGTGAACTGTGTCTTGTGTCCCCGTAACCTGATGATGGA	960
gDNApld1	901	AATTACTTCCAAGGTACACAGGTGAACTGTGTCTTGTGTCCCCGTAATCCTGATGATGGA	960
gDNApld2	901	AATTACTTCCAAGGTACACAGGTGAACTGTGTCTTGTGTCCCCGTAACCTGATGATGGA	960
mRNApld1	961	GGCAGCTTCATTCAGGATTTACAGATCTCAACTATGTTCACTCATCACCAGAAGATTGTT	1020
mRNApld2	961	GGCAGCTTTATTCAGGATTTACAGATCTCAACTATGTTCACTCATCACCAGAAGATCGTG	1020
gDNApld1	961	GGCAGCTTCATTCAGGATTTACAGATCTCAACTATGTTCACTCATCACCAGAAGATTGTT	1020
gDNApld2	961	GGCAGCTTTATTCAGGATTTACAGATCTCAACTATGTTCACTCATCACCAGAAGATCGTG	1020
mRNApld1	1021	GTCACGGATAGTGCAATGCCAGTGAAGGATCAAACAGAGGAGAATTGTGAGTTTTGTT	1080
mRNApld2	1021	GTCACGGATAGTGCAATGCCAGTGAAGGATCAAACAGAGGAGAATAGTGAGTTTTGTT	1080
gDNApld1	1021	GTCACGGATAGTGCAATGCCAGTGAAGGATCAAACAGAGGAGAATTGTGAGTTTTGTT	1080
gDNApld2	1021	GTCACGGATAGTGCAATGCCAGTGAAGGATCAAACAGAGGAGAATTGTGAGTTTTGTT	1080
mRNApld1	1081	GGGGTATTGATCTCTGCGATGGAAGATATGATACTCAGTTCATTCTCTTTTTAGAACC	1140
mRNApld2	1081	GGGGTATTGATCTCTGCGATGGAAGATATGATACTCAGTTCATTCTCTTTTTAGAACC	1140
gDNApld1	1081	GGGGTATTGATCTCTGCGATGGAAGATATGATACTCAGTTCATTCTCTTTTTAGAACC	1140
gDNApld2	1081	GGGGTATTGATCTCTGCGATGGAAGATATGATACTCAGTTCATTCTCTTTTTAGAACC	1140
mRNApld1	1141	TTGGATACTGCCCATCATGATGATTTCCATCAACCTAACTTCACTGGTGGTGAATTACT	1200
mRNApld2	1141	TTGGACACTGCTCACCATGATGATTTCCATCAACCTAACTTCACTGGTGGTGAATTACT	1200
gDNApld1	1141	TTGGATACTGCCCATCATGATGATTTCCATCAACCTAACTTCACTGGTGGTGAATTACT	1200
gDNApld2	1141	TTGGACACTGCTCACCATGATGATTTCCATCAACCTAACTTCACTGGTGGTGAATTACT	1200
mRNApld1	1201	AAAGTGGGCCAGGGAGCCTTGGCATGATATCCACTCCTGTTTAGAAGGACCCATTGCT	1260
mRNApld2	1201	AAAGTGGGCCAGGGAGCCTTGGCATGATATCCACTCCTGTTTAGAAGGACCCATTGCT	1260
gDNApld1	1201	AAAGTGGGCCAGGGAGCCTTGGCATGATATCCACTCCTGTTTAGAAGGACCCATTGCT	1260
gDNApld2	1201	AAAGTGGGCCAGGGAGCCTTGGCATGATATCCACTCCTGTTTAGAAGGACCCATTGCT	1260
mRNApld1	1261	TGGGATGTCCTTTTCAATTTTGAACAGAGGTGGAGGAAAACAGGGTGGGAAAAGACATTCTG	1320
mRNApld2	1261	TGGGATGTACTTTTCAATTTTGAACAGAGGTGGAGGAAAACAGGGTGGGAAAAGACATTCTG	1320
gDNApld1	1261	TGGGATGTCCTTTTCAATTTTGAACAGAGGTGGAGGAAAACAGGGTGGGAAAAGACATTCTG	1320
gDNApld2	1261	TGGGATGTACTTTTCAATTTTGAACAGAGGTGGAGGAAAACAGGGTGGGAAAAGACATTCTG	1320
mRNApld1	1321	GTCAACTTGAGAGAGCTTTCTGAGATTAATTATTCCTCCCTCCCCGTTACGTTCTCTGAA	1380
mRNApld2	1321	GTCAACTTGAGAGAGCTTTCTGAGATAATTATTCCTCCCTCTCCTGTACGTTCTCCGAA	1380
gDNApld1	1321	GTCAACTTGAGAGAGCTTTCTGAGATTAATTATTCCTCCCTCCCCGTTACGTTCTCTGAA	1380
gDNApld2	1321	GTCAACTTGAGAGAGCTTTCTGAGATAATTATTCCTCCCTCTCCTGTACGTTCTCCGAA	1380
mRNApld1	1381	GACCCAGAATCATGGAACGTTTCAGTTGTTTCAGATCCATTGATGGTGGGCTGCTTTTGGGA	1440
mRNApld2	1381	GACCCAGAATCATGGAACGTTTCAGTTGTTTCAGATCCATTGATGGTGGTGGCTGCTTTTGGGA	1440
gDNApld1	1381	GACCCAGAATCATGGAACGTTTCAGTTGTTTCAGATCCATTGATGGTGGGCTGCTTTTGGGA	1440
gDNApld2	1381	GACCCAGAATCATGGAACGTTTCAGTTGTTTCAGATCCATTGATGGTGGTGGCTGCTTTTGGGA	1440
mRNApld1	1441	TTCCCTGATTACCTGAGGATGCAGCCAAAGCTGGGCTTGTTAGTGGAAAAGACAACATC	1500
mRNApld2	1441	TTCCCTGATTACCTGAGGATGCAGCCAAAGCTGGGCTTGTTAGTGGAAAAGACAACATC	1500
gDNApld1	1441	TTCCCTGATTACCTGAGGATGCAGCCAAAGCTGGGCTTGTTAGTGGAAAAGACAACATC	1500
gDNApld2	1441	TTCCCTGATTACCTGAGGATGCAGCCAAAGCTGGGCTTGTTAGTGGAAAAGACAACATC	1500

mRNApld1	1501	ATCGACCGCAGCATT	CAGGATGCTTATATTAATGCCATT	CGAAGAGCAAAGGACTTCATT	1560
mRNApld2	1501	ATCGACCGCAGCATT	CAGGATGCTTATATTAATGCCATT	CGAAGAGCAAAGGACTTCATT	1560
gDNApld1	1501	ATCGACCGCAGCATT	CAGGATGCTTATATTAATGCCATT	CGAAGAGCAAAGGACTTCATT	1560
gDNApld2	1501	ATCGACCGCAGCATT	CAGGATGCTTATATTAATGCCATT	CGAAGAGCAAAGGACTTCATT	1560
mRNApld1	1561	TACATAGAAAATCAGTATTT	CCTCGGAAAGTTCATACGGTTGGAAAGCAGATGGCATTAAAG	1620	
mRNApld2	1561	TACATAGAAAATCAGTATTT	CCTCGGAAAGTTCATACGGTTGGAAAGCAGATGGCATTAAAG	1620	
gDNApld1	1561	TACATAGAAAATCAGTATTT	CCTCGGAAAGTTCATACGGTTGGAAAGCAGATGGCATTAAAG	1620	
gDNApld2	1561	TACATAGAAAATCAGTATTT	CCTCGGAAAGTTCATACGGTTGGAAAGCAGATGGCATTAAAG	1620	
mRNApld1	1621	CCTGAGGAAATAAATCGCTCTGCATCTTATTCCCAAGGAACTCTCACTAAAAATTGTTAGC	1680		
mRNApld2	1621	CCAGAGGAAATAAATGCTCTGCATCTTATTCCCAAGGAACTCTCACTAAAAATTGTTAGC	1680		
gDNApld1	1621	CCTGAGGAAATAAATCGCTCTGCATCTTATTCCCAAGGAACTCTCACTAAAAATTGTTAGC	1680		
gDNApld2	1621	CCAGAGGAAATAAATGCTCTGCATCTTATTCCCAAGGAACTCTCACTAAAAATTGTTAGC	1680		
mRNApld1	1681	AAGATTGAAGCTGGTGAGAGGTTTACTGTCTATGTCGTTGTTCCGATGTGGCCAGAGGGT	1740		
mRNApld2	1681	AAGATTATGGCTGGTGAGAGGTTTACTGTTTATGTTGTTGTTCCAATGTGGCCAGAGGGT	1740		
gDNApld1	1681	AAGATTGAAGCTGGTGAGAGGTTTACTGTCTATGTCGTTGTTCCGATGTGGCCAGAGGGT	1740		
gDNApld2	1681	AAGATTATGGCTGGTGAGAGGTTTACTGTTTATGTTGTTGTTCCAATGTGGCCAGAGGGT	1740		
mRNApld1	1741	ATCCCAGAGAGTGCATCAGTTCAGGCGATATTAGATTGGCAGAGGAGGACTTGGGACATG	1800		
mRNApld2	1741	ATCCCAGAGAGTGCATCAGTTCAGGCGATATTAGATTGGCAGAGGAGGACTTGGGACATG	1800		
gDNApld1	1741	ATCCCAGAGAGTGCATCAGTTCAGGCGATATTAGATTGGCAGAGGAGGACTTGGGACATG	1800		
gDNApld2	1741	ATCCCAGAGAGTGCATCAGTTCAGGCGATATTAGATTGGCAGAGGAGGACTTGGGACATG	1800		
mRNApld1	1801	ATGTACGCTGACATCACTCAAGCTCTTAAAGCTAAAGGGCTTGTGTGCTGACCCTAGGGAC	1860		
mRNApld2	1801	ATGTACGCTGACATCACTCAAGCTCTTAAAGCTAAAGGGATTGTAGCTGACCCTAGGGAC	1860		
gDNApld1	1801	ATGTACGCTGACATCACTCAAGCTCTTAAAGCTAAAGGGCTTGTGTGCTGACCCTAGGGAC	1860		
gDNApld2	1801	ATGTACGCTGACATCACTCAAGCTCTTAAAGCTAAAGGGATTGTAGCTGACCCTAGGGAC	1860		
mRNApld1	1861	TACTTGACATTCTTCTGTCTCGGTAATCGAGAGGTGAAGAAAGAAGGAGAGTATGTACCA	1920		
mRNApld2	1861	TATTTGACATTCTTCTGTCTCGGTAATCGAGAGGTGAAGAAAGAAGGAGAGTATGTACCA	1920		
gDNApld1	1861	TACTTGACATTCTTCTGTCTCGGTAATCGAGAGGTGAAGAAAGAAGGAGAGTATGTACCA	1920		
gDNApld2	1861	TATTTGACATTCTTCTGTCTCGGTAATCGAGAGGTGAAGAAAGAAGGAGAGTATGTACCA	1920		
mRNApld1	1921	TCAGAAACTCCAGACCCTGATACGGATTATAGTAGAGCTCAGGCGGCTCGACGATTTCATG	1980		
mRNApld2	1921	TCAGAAACTCCAGACCCTGATACAGATTATAGTAGAGCTCAGGAGGCTCGACGATTTCATG	1980		
gDNApld1	1921	TCAGAAACTCCAGACCCTGATACGGATTATAGTAGAGCTCAGGCGGCTCGACGATTTCATG	1980		
gDNApld2	1921	TCAGAAACTCCAGACCCTGATACAGATTATAGTAGAGCTCAGGAGGCTCGACGATTTCATG	1980		
mRNApld1	1981	ATCTACGTTACACCAAGATGATGAT-----	2006		
mRNApld2	1981	ATCTACGTTACACCAAGATGATGAT-----	2006		
gDNApld1	1981	ATCTACGTTACACCAAGATGATGATAGGTACGTATGACGGCTTTAGTGATTTCTTTTAT	2040		
gDNApld2	1981	ATCTACGTTACACCAAGATGATGATAGGTACGTATGACGGCTTTAGTGATTTCTTTTAT	2040		
mRNApld1	2006	-----	2006		
mRNApld2	2006	-----	2006		
gDNApld1	2041	TAGCTTGAATTAGCATTTTCTGAAATCTTTCTTCTTAGATTGGGAATATAGATTAGTGGT	2100		
gDNApld2	2041	TAGCTTGAATTAGCATCTTCTGAAATCTTTCTTCTTAGACTGGGAATATAGATTAGTGGT	2099		
mRNApld1	2006	-----	2006		
mRNApld2	2006	-----	2006		
gDNApld1	2101	TTAAATGTTAATTTACAACCTTGATCTGGTAACTCTAGACGTGCATAGTTGGTCTAAATC	2160		
gDNApld2	2100	TTAAATGTTAATTTAAAACCTTGATCTGGTAACTCTAGACGTGCATAGTTGGTCTAAATC	2159		
mRNApld1	2006	-----	2006		
mRNApld2	2006	-----	2006		
gDNApld1	2161	AGGAGTCAAGACTCCAATGTTCTTCCCAAGTCTTAACA-GTTAACATGTTTAGAAAACCTC	2219		
gDNApld2	2160	AGGAGTCATGAATCCAATTTTCTTCCCAAGTCTTAACACGTTTACTCATTTAGAAAACCC	2219		
mRNApld1	2006	-----	2006		
mRNApld2	2006	-----	2006		
gDNApld1	2220	TGTAACCTAGGTGTCAATTGCCATTGCTGAGGTGTCCCAACCCCTGCTTACATGTTAGTC	2279		
gDNApld2	2220	TGCAAACTAGGCGTCGTTGCTGTTGGTGAGGTGTCCCAACCCCTGCGTAAACATGTTAGTC	2279		
mRNApld1	2006	-----	2006		
mRNApld2	2006	-----	2006		
gDNApld1	2280	AAAAAAATGGAACCTTGCTTTGATGTTGTAGTTCAATCATGCCGAAACTAAATACTCA	2339		
gDNApld2	2280	GACAAAATGAACTTGTGCTTTGATGTTGTAGTTCAATCATGCCGAAACTAAATACTCA	2339		

mRNApld1	2006	-----AGTTGACGATGAATACATAATCATTGGATCAGC	2039
mRNApld2	2006	-----AGTTGATGATGAATACATAATCATTGGATCAGC	2039
gDNApld1	2340	TTTTGGATTATTTTGCTGCTTTTACAGTTGACGATGAATACATAATCATTGGATCAGC	2399
gDNApld2	2340	TTTTGGATTATTTTGCTGCTTTTACAGTTGATGATGAATACATAATCATTGGATCAGC	2399
mRNApld1	2040	TAACATCAATGAGAGATCAATGAATGGTGCAAGGATTCTGAAATTGCCATGGGAGGTTA	2099
mRNApld2	2040	CAACATCAACGAGAGATCAATGAATGGTGCAAGAGATTCTGAAATTGCCATGGGAGGTTA	2099
gDNApld1	2400	TAACATCAATGAGAGATCAATGAATGGTGCAAGGGATTCTGAAATTGCCATGGGAGGTTA	2459
gDNApld2	2400	CAACATCAACGAGAGATCAATGAATGGTGCAAGAATTCTGAAATTGCCATGGGAGGTTA	2459
mRNApld1	2100	CCAACCTCATCACCTAGCTCACAGAGAACCAGCAACGGGTCAAATCCACGGATTCCGTAT	2159
mRNApld2	2100	CCAACCTCATCACCTAGCTCACAGAGAACCAGCAACGGGTCAAATCCACGGATTCCGTAT	2159
gDNApld1	2460	CCAACCTCATCACCTAGCTCACAGAGAACCAGCAACGGGTCAAATCCACGGATTCCGTAT	2519
gDNApld2	2460	CCAACCTCATCACCTAGCTCACAGAGAACCAGCAACGGGTCAAATCCACGGATTCCGTAT	2519
mRNApld1	2160	GGCATTATGGTATGAACATCTTGGCATGCTCGATGAAGTTTTCTCCATCCTAACAGCGA	2219
mRNApld2	2160	GGCATTATGGTATGAACATCTTGGCATGCTGGATGAAGTTTTCTCCATCCCAACAGTGA	2219
gDNApld1	2520	GGCATTATGGTATGAACATCTTGGCATGCTCGATGAAGTTTTCTCCATCCTAACAGCGA	2579
gDNApld2	2520	GGCATTATGGTATGAACATCTTGGCATGCTGGATGAAGTTTTCTCCATCCCAACAGTGA	2579
mRNApld1	2220	GGAATGTGTGCAAAAGGTGAACAGGATCGCTGATAAAATACTGGGATCTTACTCGAGTGA	2279
mRNApld2	2220	GGAATGTGTGCAAAAGGTGAACAGGATCGCTGATAAAATACTGGGATCTGTACTCGAGCGA	2279
gDNApld1	2580	GGAATGTGTGCAAAAGGTGAACAGGATCGCTGATAAAATACTGGGATCTTACTCGAGTGA	2639
gDNApld2	2580	GGAATGTGTGCAAAAGGTGAACAGGATCGCTGATAAAATACTGGGATCTGTACTCGAGCGA	2639
mRNApld1	2280	TTCTCTTGAACGTGATCTACCTGGACACCTCCTTAGGTACCCAATTGGAATCACTGAAAA	2339
mRNApld2	2280	TTCTCTTGAACGTGATCTACCTGGACACCTCCTCAGGTACCCAATCGGAATCACTGAAAA	2339
gDNApld1	2640	TTCTCTTGAACGTGATCTACCTGGACACCTCCTTAGGTACCCAATTGGAATCACTGAAAA	2699
gDNApld2	2640	TTCTCTTGAACGTGATCTACCTGGACACCTCCTCAGGTACCCAATCGGAATCACTGAAAA	2699
mRNApld1	2400	TGGAGATGTTACTGCGTTGCCCGGTTCATGAGTTCTTCCCCGACACTAAAGCTAGAGTACT	2399
mRNApld2	2400	TGGAGATGTGACTGAGTTGCCAGGTTCATGAGTTCTTCCCCGACACTAAAGCACGTGTTCT	2399
gDNApld1	2700	TGGAGATGTTACTGCGTTGCCCGGTTCATGAGTTCTTCCCCGACACTAAAGCTAGAGTACT	2759
gDNApld2	2700	TGGAGATGTGACTGAGTTGCCAGGTTCATGAGTTCTTCCCCGACACTAAAGCACGTGTTCT	2759
mRNApld1	2400	TGGTGCAAGTCTGATTACCTTCCCTCCTATTCTCACAACATAGGTTCTATCCTTCTTTCT	2459
mRNApld2	2400	TGGTGCAAGTCCGATTACCTTCCCTCCAATTCTCACTACATAGGTTATGTACTTATATCC	2459
gDNApld1	2760	TGGTGCAAGTCTGATTACCTTCCCTCCTATTCTCACAACATAGGTTCTATCCTTCTTTCT	2819
gDNApld2	2760	TGGTGCAAGTCCGATTACCTTCCCTCCAATTCTCACTACATAGGTTATGTACTTATATCC	2819
mRNApld1	2460	CTCTACTAATCGTACTCTTATATCATACTAGTggtataatggtatgtagtataataaaaaat	2519
mRNApld2	2460	TTCTTTCTCCCGTACTCTTATATCCAATAAAAAGT-----	2493
gDNApld1	2820	CTCTACTAAT-----	2829
gDNApld2	2820	TTCTTTCTC-----	2828
mRNApld1	2520	ctcttgccTGTAACTTTGGAGTGTTTA---GGGTTTATGATCATAGATTGTTTATTTTA	2576
mRNApld2	2493	-----TGTAACTTTGGAGTGTTTAAttaGGTTTCTGATCAGAGATTGTTTATTTTA	2545
gDNApld1	2829	-----	2829
gDNApld2	2828	-----	2828
mRNApld1	2577	TAAATtctgcatgtgTGGTCACAGGTCTGTTTGCTTATAAGCTGTATTTTCTCATCTGT	2636
mRNApld2	2546	CAAAT-----TGGTCACGGTCTGTTTCGCTTATAAACTGTATTTGCTAATTTGT	2595
gDNApld1	2829	-----	2829
gDNApld2	2828	-----	2828
mRNApld1	2637	TTTAGTaatgaaattctgtgttttaaaaaaaaaaaaaaaaaaaaaa	2679
mRNApld2	2596	TTTAGT-----	2601
gDNApld1	2829	-----	2829
gDNApld2	2828	-----	2828

A2 Primärstruktur und Sekundärstrukturvorhersage für die 2 PLD-Isoenzyme aus Schlafmohn

Gelb markiert, Sequenzunterschiede; türkis markiert, Cystein-Reste; rot, HxKxxxxDxxxxxGSxN (katalytische Motive); grau markiert, Asn-Glykosylierungsstelle NFTG; PHD Sekundärstrukturvorhersage, profile network prediction Heidelberg für alle Reste mit einer durchschnittlichen Genauigkeit von > 82 %; H, Helix; E, Faltblatt; L, Loop (andere Strukturelemente); ., keine Vorhersage (Rel < 5); Rel, Wahrscheinlichkeitsfaktor (0 für gering bzw. 9 für hoch).

PHDMohn1			L	.EEE	L	.EEEEEE	.LLLLLLLLLLLLL	HHHHLLLLLLL	.EEEE			
Mohn1	1	MAQISLHGTLHVTIFEANSISHPDRKTGGAPKFFRKLVENIEETVFGKGASMLYASVDL										60			
Mohn2	1	MAQISLHGTLHVTIFEANSISHPDRKTGGAPKFFRKLVENIEETVFGKGASMLYASVDL										60			
PHDMohn2			L	.EEE	L	.EEEEEE	.LLLLLLLLLLLLL	HHHHLLLLLLL	.EEEE			
PHDMohn1		EEELLLEEE	.EEEEEEE	.LLL	.EEEEEE	.E
Mohn1	61	DKARVGRTRIIKDEPVNPKWYESFHICYAHMAANVIFTVKDDNPIGATLIGRAYVPIDK													120
Mohn2	61	DKARVGRTRIIKDEPVNPKWYESFHICYAHMAANVIFTVKDDNPIGATLIGRAYVPIDQ													120
PHDMohn2		EEELLLEEEEEEEEEE	.LLL	.EEEE		
PHDMohn1			.LLL	.HHLLLLLLLLL	.EEEEEE	.LLLLLLLLLLLL				
Mohn1	121	LSGEEVDEWEVVDQERNPVQGGCKIHVKLQYFDVGQDNWARGIRSAKFPQVPYTFFTQ													180
Mohn2	121	LSGEEVDEWEVVDERNPVQGGCKIHVKLQYFDVGQDNWARGIRSAKFPQVPYTFFTQ													180
PHDMohn2			.LLL	.HH	.ELLLLLLLLL	.EEEEEE	.LLLLLLLLLLLL			
PHDMohn1			.LLL	.EEEELLLLLLLLLLLLLLLLLLHHHHHHHHHEEE		
Mohn1	181	RTGCKVSLYQDAHVPDNFIPKIPLAGGIYEPARCWEDIFDAISNAKHMIIYITGWSVYTE													240
Mohn2	181	RTGCKVSLYQDAHVPDNFIPKIPLAGGIYEPARCWEDIFDAISNAKHMIIYITGWSVYTE													240
PHDMohn2			.LLL	.EEEELLLLLLLLLLLLLLLLLLHHHHHHHHHEEEE	
PHDMohn1			.EEEELLLLLLLLLHHHHHHHHHL	.EEEE	.LLLLL	.LL	.HHH
Mohn1	241	VVLIRDSRRQKPGGDITLGELLKKKADEGVRVLMVWDDRTSVGLLKKDGLMATHDEDTF													300
Mohn2	241	VVLIRDSRRQKPGGDITLGELLKKKADEGVRVLMVWDDRTSVGLLKKDGLMATHDEDTF													300
PHDMohn2			.EEEELLLLLLLLLHHHHHHHHHL	.EEEE	.LLLLL	.LL	.HHH
PHDMohn1			.HHLLL	.EEEELLLEEEEEEEE	.LLLLLLL	.EEEE
Mohn1	301	NYFQGTQVNCVLCPRNPDDGGSFIQDLQISTMFTHHQKIVVTDSAMPSAGSQRRIVSFV													360
Mohn2	301	NYFQGTQVNCVLCPRNPDDGGSFIQDLQISTMFTHHQKIVVTDSAMPSAGSEQRRIVSFV													360
PHDMohn2			.HHLLL	.EEEELLLEEEEEEEE	.LLLLLLL	.EEEE

PHDMohn1	LL . LLLLLLLL LLLLLLLLLLLLLLLL LL . . .
Mohn1	361 GGIDL CDGRYDTQFHSLFRTLDTAHHDDFHQP NFTGGAITKGGPREPWHDIHSC LEGPIA 420
Mohn2	361 GGIDL CDGRYDTQFHSLFRTLDTAHHDDFHQP NFTGGAITKGGPREPWHDIHSR LEGPIA 420
PHDMohn2	LL . LLLLLLLL L . LLLLLLLLLLLLLLLL LL . . .

PHDMohn1	HHHHHHHHHH . LL H LLLLLLLLLLLL . EEEEE . LLLLLL
Mohn1	421 WDLVFNFEQRWRKQGGKDILVNLRELSEIIIPSPVTFSEDPESWNVQLFRSIDGGAAFG 480
Mohn2	421 WDLVFNFEQRWRKQGGKDILVNLRELSEIIIPSPVTFSEDPESWNVQLFRSIDGGAAFG 480
PHDMohn2	HHHHHHHHHH . LL LLLLLLLLLLLL . EEEEE . LLLLLL

PHDMohn1	LLL HHHH LL HHHHHHHHH EEEEE LLLLLL
Mohn1	481 FPDSPEDAAGLVSGKDNIIDRSIQDAYINAIIRAKDFIYIENQYFLGSSYGWKA DGIK 540
Mohn2	481 FPDSPEDAAGLVSGKDNIIDRSIQDAYINAIIRAKDFIYIENQYFLGSSYGWKA EGIK 540
PHDMohn2	LLL HHHH LL HHHHHHHHH EEEEE LLLLLL

PHDMohn1	LLLLLLLLL HHHHHHHH EEEEE . LLLLLLL . HHHHHHHHHHHHHH
Mohn1	541 PEEINALHLIPKELSLKIVSKI EAGERFTVYVVVPMWPEGIPESASVQAILDWQRRTWDM 600
Mohn2	541 PEEINALHLIPKELSLKIVSKI MAGERFTVYVVVPMWPEGIPESASVQAILDWQRRTWDM 600
PHDMohn2	LLLLLLLLL HHHHHHHH EEEEE . LLLLLLL . HHHHHHHHHHHHHH

PHDMohn1	HHHHHHHHH . LLLL L LLLLLLLLLLLLLL HHHHHH . EE
Mohn1	601 MYADITQALKAKG L VADPRDYLTFF C LGNREVKKEGEYVPSETPDPD TDYSRAQA ARR FM 660
Mohn2	601 MYADITQALKAKG I VADPRDYLTFF C LGNREVKKEGEYVPSETPDPD TDYSRAQE ARR FM 660
PHDMohn2	HHHHHHHHH . LLLL L LLLLLLLLLLLLLL . HHHHHH E

PHDMohn1	EE EEE . EEEEE . L LLLL LLLLLLLLLLLL H
Mohn1	661 IYVHTKMMIVDDEYII IGSANINERSMNGARDSEIAMGGYQPHHLAHREPATQI HGFRM 720
Mohn2	661 IYVHTKMMIVDDEYII IGSANINERSMNGARDSEIAMGGYQPHHLAHREPATQI HGFRM 720
PHDMohn2	EE EEE . EEEEE . L LLLL LLLLLLLLLLLL HH

PHDMohn1	HHHHHHHHH . LLLL . HHHHHHHHHHHHHHHH . HHHH LL
Mohn1	721 ALWYEHGLMDEVFLHPNSEE CVQKVNRIADKYWDLYSSDSL ERDLP GHLLRYP I G I T E N 780
Mohn2	721 ALWYEHGLMDEVFLHPNSEE CVQKVNRIADKYWDLYSSDSL ERDLP GHLLRYP I G I T E N 780
PHDMohn2	HHHHHHHHH . LLLL . HHHHHHHHHHHHHHHH . L . HHHH L . E . LL

PHDMohn1 I.E..TTTTT.TTTTTT.E...TTTTTTTTTTTT

Mohn1 781 GDVTALPGHEFFPDTKARVLGGKSDYLPPILTT 813

Mohn2 781 GDVTELPGHEFFPDTKARVLGAKSDYLPPILTT 813

PHDMohn2 I...TTTT.T.TTTTTT.E...TTTTTTTTTTTT

A3 Multiples Alignment der Primärstrukturen der Mohn-PLD-Isoenzyme mit pflanzlichen PLDs des α -Typs mittels Clustal W

Blau, identische und ähnliche Aminosäuren; schwarz, Sequenzunterschiede; gelb markiert, Cystein-Reste; rot markiert, HxKxxxxDxxxxxxGSxN (katalytische Motive); grün, β -Faltblätter der C2-Domäne (Zheng et al., 2000); CBL, Ca^{2+} -Bindeloop; violett markiert, für Ca^{2+} -Bindung verantwortliche saure Aminosäuren; dunkelgrün markiert, mögliche PIP_2 -Bindungsmotive KxxxxRxRK bzw. RxRxxxxK. Species-Kurzformen: *Arath*, *Arabidopsis thaliana*; *Braol*, *Brassica oleracea*; *Crapl*, *Craterostigma plantagineum*; *Lyces*, *Lycopersicon esculentum*; *Nicta*, *Nicotiana tabacum*; *Orysa*, *Oryza sativa*; *Papso*, *Papaver somniferum*; *Pimbr*, *Pimpinella brachycarpa*; *Ricco*, *Ricinus communis*; *Vigun*, *Vigna unguiculata*; *Zeama*, *Zea mays*.

		$\leftarrow\beta 1\rightarrow$		CBL 1		$\leftarrow\beta 2\rightarrow$			
Arath a1	1	MAHDLHGLT	HATIYVDAL	HGG---GVMQ	G-FLGKILAN	VEETIGVGKG	ETRYLATIDL		56
Arath a2	1	MEECLLHGR	HATIYVDHL	HAE---GGRS	G-FLGSILAN	VEETIGVGKG	ETQLYATIDL		56
Braol a1	1	MAQHLLHGLT	HATIYVDL	HTG---GLRS	G-FFGKILAN	VEETIGVGKG	ETQLYATIDL		56
Braol a2	1	MAQHLLHGLT	HATIYVDAL	HTG---GLRS	AGFLGKIISN	VEETIGVGKG	ETQLYATIDL		57
Crapl a1	1	MAQILLHGLT	HVTIYVDQL	H-----SGGG	GNFFTKLKAN	IEETVGFVGK	TPKIYASIDL		55
Crapl a2	1	MARILLHGLT	HVTIYVDRL	H-----AGGG	GNIFSKLRAN	IEEKVGFVGK	TPKIYASIDL		55
Lyces a1	1	MAQIQLHGLT	HVTIYVDNL	QG----EEEG	GHFFSKIKQH	FEETVGIKKG	TPKLYATIDL		56
Nicta a	1	MAQILLHGLT	HVTIYVDNL	Q-----KEGG	GHFFSKIKEH	VEETIGVGKG	TPAIYATVDL		55
Orysa a1	1	MAQMLLHGLT	HATIFEAASL	SNPHRASGSA	PKFIRKVEG	IEDTVGVGKG	ATKVYSTIDL		60
Papso a1	1	MAQISLHGLT	HVTIFEANSI	SHDRKTGGA	PKFFRKLVEN	IEETVGFVGK	ASMLYASVDL		60
Papso a2	1	MAQISLHGLT	HVTIFEANSI	SHDRKTGGA	PKFFRKLVEN	IEETVGFVGK	ASMLYASVDL		60
Pimbr a	1	MAKTLHGLT	HVTIYVDHL	K-----AGSV	VVFSESLRRT	LRKPLVLAKG	TPKIYASIDL		55
Ricco a	1	MAQISLHGLT	HVTIYVDKL	H-----SGGG	PHFFRKLVEN	IEETVGFVGK	VSKLYATIDL		55
Vigun a	1	MAQILLHGLT	HATIYVDEL	H-----GGGG	GNFFSKLKQN	IEETVGIKKG	VTKLYATIDL		55
Zeama a	1	MAQILLHGLT	HATIFEASL	SNPHRATGGA	PKFIRKLVG	IEDTVGVGKG	ATKIYATVDL		60
		$\leftarrow\beta 3\rightarrow$		CBL 2		CBL 3			
		$\leftarrow\beta 4\rightarrow$		$\leftarrow\beta 5\rightarrow$		$\leftarrow\beta 6\rightarrow$			
Arath a1	57	QKARVGRTRK	IKNEPKNPKW	YESFQVSVVT	WLLISSLSK	DDIPIGATLI	GRAYIPVDQV		116
Arath a2	57	EKARVGRTRK	ITKEPKNPKW	FESFHICYGH	MAKHVIFTVK	DANPIGATLI	GRGYIPVEDI		116
Braol a1	57	QRARVGRTRK	IKDEAKNPKW	YESFHICYAH	LASDIIFTVK	DDNPIGATLI	GRAYVPVDQV		116
Braol a2	58	QKARVGRTRK	ITDEPKNPKW	YESFHICYAH	MASDIIFTVK	DDNPIGATLI	GRAYVPVDEV		117
Crapl a1	56	EKARVGRTRM	IEHEPNPRW	YESFHICYAH	MASNVIFTVK	DDNPIGATLI	GRAYIPVQEI		115
Crapl a2	56	EKARVGRTRM	IEHEPNPRW	YESFHICYAH	LASNIIFTVK	DDNPIGATLI	GRAYVPVDRV		115
Lyces a1	57	EKARVGRTRK	IENEPNPRW	YESFHICYAH	MASNVIFTIK	DDNPFASLI	GRAYVPVEEL		116
Nicta a	56	EKARVGRTRK	IKNEPNPRW	YESFHICYAH	MASNVIFTVK	DDNPIGATLI	GRAYVPVEEL		115
Orysa a1	61	EKARVGRTRM	ITNEPINPRW	YESFHICYAH	MASNVIFTVK	IDNPIGATNI	GRAYLPVQDL		120
Papso a1	61	DKARVGRTRI	IKDEPNPKW	YESFHICYAH	MAANVIFTVK	DDNPIGATLI	GRAYVPIDKV		120
Papso a2	61	DKARVGRTRI	IKDEPNPKW	YESFHICYAH	MAANVIFTVK	DDNPIGATLI	GRAYVPIDQV		120
Pimbr a	56	DKARVGRTRM	IENEPNPKW	NESFHICYGH	PSTNVIFTVK	DDNPIGATLI	GRAYLPVHEL		115
Ricco a	56	EKARVGRTRI	LENEQSNPRW	YESFHICYAH	QASNVIFTVK	DDNPIGATLI	GRAYVPVEEL		115
Vigun a	56	EKARVGRTRI	IENETNPKW	NESFHICYGH	LASNIIFTVK	DDNPIGATLI	GRAYVPVSEV		115
Zeama a	61	EKARVGRTRM	ISNEPNPRW	YESFHICYAH	MAADVIFTVK	IDNSIGASLI	GRAYLAVQDL		120
		$\leftarrow\beta 7\rightarrow$		$\leftarrow\beta 8\rightarrow$					
Arath a1	117	ING-EVDQWV	EILDNDRNPI	QGGSKIHVKL	QYFHVIEDRN	WNMGIKSAKF	PGVPYTFFSQ		175
Arath a2	117	LHGEEVDRWV	DILDNEKNPI	AGGSKIHVKL	QYFVVEKDKN	WNRGIKSAKF	PGVPYTFFSQ		176
Braol a1	117	IHGEEVDQWV	EILDNDRNPI	HGGSKIHVKL	QYFVVEADR	WNQGIKSAKF	PGVPYTFFSQ		176
Braol a2	118	INGEEVEKQV	EILDNDRNPI	HGESKIHVKL	QYFAVEADR	WNMGVKSASF	PGVPYTFFSQ		177
Crapl a1	116	LDGEEIDRWV	EILDNKNPI	SGESKIHVKL	QYFDVTRDLN	WNRGIKSVKY	PGVPYTFFAQ		175
Crapl a2	116	LDGEEIDRWV	ELLDNKNPI	RGESKIHVKL	QFFDVARDLN	WNRGIKSIKY	PGVPYTFFAQ		175
Lyces a1	117	LEGEEIDKWV	EIMDKEMNPI	AEGSKIHVKL	QFFDVSRDPN	WGRGIRSSRY	PGVPYTFFAQ		176
Nicta a	116	LEGEEIDKWV	EILDREMNPI	AEGSKIHVKL	QFFDVSRDPN	WGRGIRSSKY	PGVPYTFFAQ		175
Orysa a1	121	LNGEEIDRWL	DICDNNRESV	GE-SKIHVKL	QYFDVSKDRN	WARGVRSTKY	PGVPYTFFSQ		179
Papso a1	121	LSGEEVDEWV	EVVDQERNPV	QGGCKIHVKL	QYFDVGQDKN	WARGIRSAKF	PGVPYTFFTQ		180
Papso a2	121	LSGEEVDEWV	EVVDEERNPV	QGGCKIHVKL	QYFDVGQDKN	WARGIRSAKF	PGVPYTFFTQ		180
Pimbr a	116	LEGEEVDKWV	EILDEKNPI	SEGSKIHVKL	QYFDITQDRN	WAHGIRSSKF	PGVPYTFFSQ		175
Ricco a	116	LDGEEIDRWV	EILDEKNPV	HSGSKIHVKL	QYFEVTKDRN	WGQIRSSKY	PGVPYTFYSQ		175
Vigun a	116	LDGHEIDKWV	EILDTEKNPI	EGGSKIHVRL	QYFDVLKDRN	WARGIRSPKY	PGVPYTFFSQ		175
Zeama a	121	LGEEIDKWV	EISDENREPV	GD-SKIHVKL	QYFDVGKDRN	WARGVRSTKY	PGVPYTFFSQ		179

Arath a1	176	RQGCKVSLYQ	DAHIPDNFVP	RIPLAGGKNY	EPQRCWEDIF	DTISNAKHLI	YITGWSVYAE	235
Arath a2	177	RRGCKVSLYQ	DAHIPGNFVP	KIPLAGGKNY	EPHRCWEDIF	DAITNAKHLI	YITGWSVYTE	236
Braol a1	177	RQGCKVSLYQ	DAHIPDNFVP	RIPLAGGKNY	EPQRCWEDIF	DAISNAQHMI	YITGWSVYTE	236
Braol a2	178	RQGCKVSLYQ	GAHVPDNFVP	KIPLAGGKNY	EPHRCWEDIF	DAITNAKHLI	YITGWSVYTE	237
Crapl a1	176	RTGCKVSLYQ	DAHVPDSFIP	DIPLSGSNY	DPHRCWEDVF	DAISNAKHLI	YITGWSVYTE	235
Crapl a2	176	RKGCKVTLYQ	DAHIPDNFIP	EIPLSGSNY	SPHRCWEDVF	DAISNAKHLI	YITGWSVYTE	235
Lyces a1	177	RPGRVSLYQ	DAHVPDNFIP	KIPLSGGKY	EPHRCWEDIF	DAITNAKHLI	YITGWSVYTE	236
Nicta a	176	RTGCRVSLYQ	DAHVPDNFIP	KIPLSGGKY	EPHRCWEDIF	DAITNAKHLI	YITGWSVYTE	235
Orysa a1	180	RQGCKVTLYQ	DAHVPDNFIP	KIPLADGKNY	EPHRCWEDIF	DAISNAQHMI	YITGWSVYTE	239
Papso a1	181	RTGCKVSLYQ	DAHVPDNFIP	KIPLAGGKIY	EPARCWEDIF	DAISNAKHLI	YITGWSVYTE	240
Papso a2	181	RTGCKVSLYQ	DAHVPDNFIP	KIPLAGGKIY	EPARCWEDIF	DAISNAKHLI	YITGWSVYTE	240
Pimbr a	176	RPGRISLYQ	DAHVPDNFVP	KIPLSGGKFY	EPHRCWEDVF	DAITNAKHLI	YITGWSVYTE	235
Ricco a	176	RQGCKVSLYQ	DAHIPDNFVP	KIPLAGGNY	EPHRCWEDVF	DAITNAKHLI	YITGWSVYTE	235
Vigun a	176	RQGCKVSLYQ	DAHVPDNFVP	KIPLAGGKNY	EAHRCWEDIF	DAITNAKHLI	YITGWSVYTE	235
Zeama a	180	RQGCKVTLYQ	DAHVPDNFVP	RIQLADGKNY	EPHRCWEDIF	DAISNAQHMI	YITGWSVYTE	239
Arath a1	236	IALVRDSRRP	KPGGDVTIGE	LLKKKASEGV	RVLLLVWDDR	TSVDVLKKG	LMATHDEETE	295
Arath a2	237	ISLVRDSRRP	KQGGDVTIGE	LLKKKASEGV	KVILLVWDDR	TSVDLLKKG	LMATHDEETE	296
Braol a1	237	IALVRDSRRP	KPGGDVTIGE	LLKKKASEGV	RVLLLVWDDR	TSVDVLKKG	LMATHDEETE	296
Braol a2	238	ITLVRDSRRP	KPGGDMTIGE	LLKKKATEGV	RVLLLVWDDR	TSVDVLKKG	LMATHDEETE	297
Crapl a1	236	ITLIRDSRRP	KPGGDITIGE	LLKKKASEGV	NVLMVWDDR	TSVGLLKKG	LMATHDEETE	295
Crapl a2	236	IPLIRDSRRP	KPGGEITIGE	LLKKKANEGV	NVLMVWDDR	TSVGLLKKG	LMATHDEETE	295
Lyces a1	237	IALVRDSRRP	KPGGDITIGE	LLKKKASEGV	KVLMVWDDR	TSVGLLKKG	LMATHDEETE	296
Nicta a	236	ITLVRDSRRP	KPGGDITIGE	LLKKKASEGV	KVLMVWDDR	TSVGLLKKG	LMATHDEETE	295
Orysa a1	240	ITLVRDSRRP	KPGGDITIGE	LLKKKASEGV	RVLMVWDDR	TSVGLLKKG	LMATHDEETE	299
Papso a1	241	VVLIRDSRRP	KPGGDITIGE	LLKKKADEGV	RVLMVWDDR	TSVGLLKKG	LMATHDEETE	300
Papso a2	241	VVLIRDSRRP	KPGGDITIGE	LLKKKADEGV	RVLMVWDDR	TSVGLLKKG	LMATHDEETE	300
Pimbr a	236	FALIRDSRRP	KPGGDITIGE	LLKKKADEGV	RVLMVWDDR	TSVGLLKKG	LMATHDEETE	295
Ricco a	236	ISLIRDSRRP	KPGGDITIGE	LLKKKASEGV	RVLMVWDDR	TSVGLLKKG	LMATHDEETE	295
Vigun a	236	ISLIRDSRRP	KAGGDITIGE	LLKKKASEGV	RVLMVWDDR	TSVGLLKKG	LMATHDEETE	295
Zeama a	240	ITLVRDSRRP	KPGGDITIGE	LLKKKASEGV	RVLMVWDDR	TSVGLLKKG	LMATHDEETE	299
Arath a1	296	NFFRERDVHC	ILCPNPDDG	GSIVQSLQIS	TMFTHQKIV	VDSSEMPERG	G-SEMRRIVS	354
Arath a2	297	NFFRGTDVNC	ILCPNPDDG	GSIVQNLQIS	TMFTHQKIV	VDSSEMPERG	S--RSRRIVS	354
Braol a1	297	NFFRGSDVHC	ILCPNPDDG	GSIVQNLQIS	AMFTHQKIV	VDSSEMPERG	G-SQMRRIVS	355
Braol a2	298	NYFNGSEVHC	VLCPRNPDDG	GSIVQNLQIS	AMFTHQKIV	VDSSEMPERG	GGSEMRRIVS	357
Crapl a1	296	HYFQGTDVHC	VLCPRNPDDG	GSFVQDLQIS	TMFTHQKII	VDSSEMPERG	--SDKRRIVS	353
Crapl a2	296	NYFQGTDVHC	ILCPNPDDG	GSFVQDLQIS	TMFTHQKII	VDSSEMPERG	--SDKRRIVS	353
Lyces a1	297	QYFQGTDVNC	VLCPRNPDDG	GSFVQDLQIS	TMFTHQKII	VDSSEMPERG	--SEKRRIVS	354
Nicta a	296	QYFQGTDVNC	VLCPRNPDDG	GSFVQDLQIS	TMFTHQKIV	VDSSEMPERG	--SEKRRIVS	353
Orysa a1	300	NYFHGSDVNC	VLCPRNPDDG	GSIVQDLQIS	TMFTHQKIV	VDSSEMPERG	--SQRRIVS	357
Papso a1	301	NYFQGTQVNC	VLCPRNPDDG	GSFVQDLQIS	TMFTHQKIV	VDSSEMPERG	--SQRRIVS	358
Papso a2	301	NYFQGTQVNC	VLCPRNPDDG	GSFVQDLQIS	TMFTHQKIV	VDSSEMPERG	--SEKRRIVS	358
Pimbr a	296	EYFRDSDVHC	VLCPRNPDDG	GGIIQGLTIS	TIFTHQKIV	VDSSEMPERG	--SENRRIVS	353
Ricco a	296	HFFQNTDVHC	VLCPRNPDDG	GSFVQDLQIS	TMFTHQKIV	VDSSEMPERG	--SQRRIVS	353
Vigun a	296	QYFRDSDVHC	VLCPRNPDDG	GSIVQDLQIS	TMFTHQKIV	VDSSEMPERG	G--SDKRRIVS	354
Zeama a	300	NYFHGTDVNC	VLCPRNPDDG	GSFVQDLQIS	TMFTHQKIV	VDSSEMPERG	--SQRRIVS	357
Arath a1	355	FVGGIDLCDG	RYDYSVPLL	QDIGHSHDD	FHQPNFTGAA	ITKGGPREPW	HDIHSRLEGP	414
Arath a2	355	FVGGDLCDG	RYDTPFHSF	RTLDTAHDD	FHQPNFTGAA	ITKGGPREPW	HDIHCRLEGP	414
Braol a1	356	FVGGIDLCDG	RYDTPFHSF	RTLDTVHDD	FHQPNFTGAA	ITKGGPREPW	HDIHSRLEGP	415
Braol a2	358	FVGGIDLCDG	RYDTPFHSF	RTLDTVHDD	FHQPNFTGAS	ITKGGPREPW	QDIHSRLEGP	417
Crapl a1	354	FVGGIDLCDG	RYDTPFHSF	RTLDTAHDD	FHQPNFTGAA	ITKGGPREPW	HDIHSRLEGP	413
Crapl a2	354	FVGGIDLCDG	RYDTPFHSF	RTLDTAHDD	FHQPNFTGAV	IAKGGPREPW	HDIHSRLEGP	413
Lyces a1	355	FVGGIDLCDG	RYDTPFHSF	RTLDTAHDD	FHQPNFADGS	ITKGGPREPW	HDIHSRLEGP	414
Nicta a	354	FVGGIDLCDG	RYDTPFHSF	RTLDTAHDD	FHQPNFPDGA	ITKGGPREPW	HDIHSRLEGP	413
Orysa a1	358	FVGGDLCDG	RYDTQYHSF	RTLDSHDD	FHQPNFATAS	IKKGGPREPW	HDIHSRLEGP	417
Papso a1	359	FVGGIDLCDG	RYDTQFHSF	RTLDTAHDD	FHQPNFTGGA	ITKGGPREPW	HDIHSCLEGP	418
Papso a2	359	FVGGIDLCDG	RYDTQFHSF	RTLDTAHDD	FHQPNFTGGA	ITKGGPREPW	HDIHSRLEGP	418
Pimbr a	354	FVGGIDLCDG	RYDTPFHSF	RTLDTAHDD	FHQPNFEGAA	ITKGGPREPW	HDIHSRLEGP	413
Ricco a	354	FVGGDLCDG	RYDTPFHSF	RTLDSAHDD	FHQPNFAGAS	IEKGGPREPW	HDIHSRLEGP	413
Vigun a	355	FVGGDLCDG	RYDTAFHSF	RTLDTAHDD	FHQPNFPGAA	ITKGGPREPW	HDIHSRVEGP	414
Zeama a	358	FIGGIDLCDG	RYDTQYHSF	RTLDTVHDD	FHQPNFEGGS	IKKGGPREPW	HDIHSRLEGP	417

Arath a1	415	I AWDVMY NFE	Q R W S K Q G G K E	I L V K L R D L S D	I I I T P S P V M F	Q E T T M C G M S N	C L G P L M E E L L	474
Arath a2	415	I AWDVLY NFE	Q R W S R Q G G K D	I L V K M R E L G D	I I I P P S P V L F	S E D H D V W N V Q	L F R S I D G G A A	474
Braol a1	416	I AWDVLY NFE	Q R W S K Q G G K D	I L V K L R E L S D	I I I T P S P V M F	Q E D H D V W N V Q	L F R S I D G G A A	475
Braol a2	418	I AWDVLY NFE	Q R W S K Q G G K D	I L V K L R E L S D	I I I T P S P V M F	Q E D H D V W N V Q	L F R S I D G G A A	477
Crapl a1	414	I AWDVLF NFE	Q R W K K Q G G K D	V L L N L R E I D D	- I I P P T S V T Y	H D D P E T W N V Q	L F R S I D G G A A	472
Crapl a2	414	I AWDVLF NFE	Q R W K K Q A G R D	L L I N L R E I E D	- I I P P T P V T Y	D D D Q E T W N V Q	L F R S I D G G A A	472
Lyces a1	415	I AWDVLF NFE	Q R W R K Q G G K D	I L V N F R E L D D	V I I P P S P V M Y	P D D H E T W N V Q	L F R S I D G G A A	474
Nicta a	414	I AWDVLF NFE	Q R W R K Q G G K D	V L V N F R E L D D	I I I P P S P V M H	L D D S E T W N V Q	L F R S I D E G A A	473
Orysa a1	418	I AWDVLY NFE	Q R W R K Q G G K D	L L L Q L R D L S D	T I I P P S P V M F	P E D R E T W N V Q	L F R S I D G G A A	477
Papso a1	419	I AWDVLF NFE	Q R W R K Q G G K D	I L V N L R E L S E	I I I P P S P V T F	S E D P E S W N V Q	L F R S I D G G A A	478
Papso a2	419	I AWDVLF NFE	Q R W R K Q G G K D	I L V N L R E L S E	I I I P P S P V T F	S E D P E S W N V Q	L F R S I D G G A A	478
Pimbr a	414	V A W D V L F N F E	Q R W R K Q G G K D	I L L N L R E L Q D	V I I P P S P V T F	P D D D E T W N V Q	L F R S I D E G A A	473
Ricco a	414	I A W D V L F N F E	Q R W R K Q G G K D	L L I Q L R E L E D	V I I P P S P V M Y	P D D F E A W N V Q	L F R S I D G G A A	473
Vigun a	415	I A W D V L F N F E	Q R W R K Q G G K D	I L A P L R E L E D	V I I P P S P V T F	P D D H E T W N V Q	L F R S I D G G A A	474
Zeama a	418	I A W D V L Y N F E	Q R W R K Q G G K D	L L V R L R D L P D	I I I P P S P V M F	P E D R E T W N V Q	L F R S I D G G A A	477
Arath a1	475	L G F P S R L K L L	R K P G L Y S G K D	N I I D R S I Q D A	Y I H A I R R A K D	F I Y V E N Q Y F L	G S S F A W A A D G	534
Arath a2	475	A G F P D S P E A A	A E A G L V S G K D	N I I D R S I Q D A	Y I H A I R R A K D	F I Y I E N Q Y F L	G S S F A W S A D G	534
Braol a1	476	A G F P E S P E A A	A E A G L V S G K D	N I I D R S I Q D A	Y I H A I R R A K D	F I Y I E N Q Y F L	G S S F A W A A D G	535
Braol a2	478	A G F P D S P E V A	A E A G L V S G K D	N V I D R S I Q D A	Y I H A I R R A K D	F I Y I E N Q Y F L	G S S F A W A A D G	537
Crapl a1	473	F G F P D T P E E A	A K S G L V S G K D	N I I D R S I Q D A	Y I Q A I R R A K N	F I Y I E N Q Y F L	G A C F G W D S N D	532
Crapl a2	473	F G F P E T P E E A	A K A G L V S G K D	N I I D R S I Q D A	Y I Q A I R R A K N	F I Y I E N Q Y F L	G G C F G W D S N D	532
Lyces a1	475	F G F P D T P E D A	A K A G L V S G K D	N I I D R S I Q D A	Y I H A I R R A K N	F I Y I E N Q Y F L	G S C A D W Q C D D	534
Nicta a	474	F G F P E T P E D A	A K A G L V S G X D	N I I D R S I Q D A	Y I H A I R R A K N	F I Y I E N Q Y F L	G S S Y D W Q S D D	533
Orysa a1	478	F G F P D T P E E A	A K A G L V S G K D	Q I I D R S I Q D A	Y I H A I R R A K N	F I Y I E N Q Y F L	G S S Y A W K P E G	537
Papso a1	479	F G F P D S P E D A	A K A G L V S G K D	N I I D R S I Q D A	Y I N A I R R A K D	F I Y I E N Q Y F L	G S S Y G W K A D G	538
Papso a2	479	F G F P D S P E D A	A K A G L V S G K D	N I I D R S I Q D A	Y I N A I R R A K D	F I Y I E N Q Y F L	G S S Y G W K A E G	538
Pimbr a	474	F F F P Q T P E E A	A K A G L V S G K E	N I I V R S I Q D A	Y I H A I R G P K I	S F I L K I S I F L	E A L L A G I Q R I	533
Ricco a	474	F G F P E T P E D A	P E A G L V S G K D	N I I D R S I Q D A	Y I H A I R R A K N	F I Y I E N Q Y F L	G S S F G W S P D G	533
Vigun a	475	F G F P D T P E D A	A K A G L V S G K D	N I I D R S I Q D A	Y I H A I R R A K N	F I Y I E N Q Y F L	G S S F S W M N D D	534
Zeama a	478	F G F P E T P E E A	A R A G L V S G K D	Q I I D R S I Q D A	Y V N A I R R A K N	F I Y I E N Q Y F L	G S S Y G W K P E G	537
Arath a1	535	I T P E D I N A L H	L I P K E L S L K I	V S K I D Q G E K F	R V Y V V V P M W P	E G L P E S G S V Q	A I L D W Q R R T M	594
Arath a2	535	I K P E E I N A L H	L I P K E L S L K I	V S K I K A G E K F	K V Y V V V P M W P	E G I P E S G S V Q	A I L D W Q K R T M	594
Braol a1	536	I T P E D I N A L H	L I P K E L S L K I	V S K I E K G E K F	R V Y V V V P M W P	E G L P E S A S V Q	A I L D W Q R R T M	595
Braol a2	538	I T P E D I N A L H	L I P K E L S L K I	V D K I E K G E K F	R V Y V V V P M W P	E G I P E S A S V Q	A I L D W Q R R T L	597
Crapl a1	533	I K V E D V G A L H	L I P K E L S M K I	V S K I E A G E R F	T V Y I V V P M W P	E G I P E S A S V Q	A I L D W Q R R T M	592
Crapl a2	533	I K V E D V G A L H	L I P K E L S L K I	V S K I E A G E R F	A V Y V V V P M W P	E G I P E S A S V Q	A I L D W Q R R T M	592
Lyces a1	535	I K V E D I G A L H	V I P K E L A L K I	V S K I E A G E R F	T V Y V V V P M W P	E G I P E S A S V Q	A I L D W Q R R T M	594
Nicta a	534	I K V E D I G A L H	V I P K E L A L K I	V S K I E A G E R F	T V Y V V V P M W P	E G I P E S A S V Q	A I L D W Q R R T M	593
Orysa a1	538	I K P E D I G A L H	L I P K E L A L K V	V S K I E A G E R F	T V Y V V V P M W P	E G V P E S G S V Q	A I L D W Q R R T M	597
Papso a1	539	I K P E E I N A L H	L I P K E L S L K I	V S K I E A G E R F	T V Y V V V P M W P	E G I P E S A S V Q	A I L D W Q R R T W	598
Papso a2	539	I K P E E I N A L H	L I P K E L S L K I	V S K I M A G E R F	T V Y V V V P M W P	E G I P E S A S V Q	A I L D W Q R R T W	598
Pimbr a	534	L K M R T S V L C I	L I P K E L S L K I	V S K I E A G K R F	T V Y V V L P M W P	E G I P E S G S V Q	A I L D W Q R R T M	593
Ricco a	534	I K P E D I N A L H	L I P K E L S L K I	L S K I A A G E R F	T V Y I V V P M W P	E G I P E S A S V Q	A I L D W Q K R T M	593
Vigun a	535	I K R E E I G A L H	L I P K E L S L K I	V S K I E A G E R F	A V Y V V V P M W P	E G I P E S S S V Q	A I L D W Q K R T I	594
Zeama a	538	I K P E E I G A L H	L I P K E L S L K I	V S K I E A G E R F	T V Y V V V P M W P	E G V P E S A S V Q	A I L D W Q R R T M	597
Arath a1	595	E M M Y K D V I Q A	L K G L E G P - E D	P R N Y L T F F C L	G N R E V K K D G E	Y E P A E K P D P D	T D Y M R A Q E A R	653
Arath a2	595	E M M Y K D V I K A	L R E N G L E G E D	P R D Y L T F F C L	G N R E V K K D G E	Y E P S E K P E P D	T D Y I R A Q E A R	654
Braol a1	596	Q M M Y K D I V Q A	L R A Q G L E - E D	P R N Y L T F F C L	G N R E V K K E G E	Y E P A E R P D A D	S S Y M K A Q E A R	654
Braol a2	598	E M M Y K D V T Q A	L R A Q G L E - E D	P R N Y L T F F C L	G N R E V K K E G E	Y E P A E R P D P D	T D Y M R A Q E A R	656
Crapl a1	593	D M M Y K D V V Q A	L Q A K G I E - E D	P R N Y L T F F C L	G N R E V K K S G E	Y E P S E Q P E P D	S D Y L K A Q E A R	651
Crapl a2	593	D M M Y K D V V Q A	L R A K G I E - E D	P R N Y L T F F C L	G N R E V K K G G E	Y E P T E Q P E P D	S D Y L R A Q Q A R	651
Lyces a1	595	E M M Y K C I V Q A	M N A K G I E - E D	P R N Y L T F F C I	G N R E V K K S G E	Y E P S E S P E P D	S N Y M R A Q E A R	653
Nicta a	594	E M M Y K H I V Q A	L N A K G I E - E D	P R N Y L T F F C I	G N R E V K K S G A	Y E P S E T P E P D	S D Y I R A Q E A R	652
Orysa a1	598	E M M Y T D I T E A	L Q A K G I E - A N	P K D Y L T F F C L	G N R E V K Q A G E	Y Q P E Q P E A D	T D Y S R A Q E A R	656
Papso a1	599	D M M Y A D I T Q A	L K A K G L V - A D	P R D Y L T F F C L	G N R E V K K E G E	Y V P S E T P D P D	T D Y S R A Q A A R	657
Papso a2	599	D M M Y A D I T Q A	L K A K G I V - A D	P R D Y L T F F C L	G N R E V K K E G E	Y V P S E T P D P D	T D Y S R A Q E A R	657
Pimbr a	594	E M M Y K D I I Q A	L Q A N G I E - E D	P R N Y L T F F C L	G N R E V K R D G E	Y E P S E K P D P D	T D Y S R A Q E S R	652
Ricco a	594	E M M Y K D I V Q A	L K A N G I I - E D	P R N Y L T F F C L	G N R E V K K S G E	Y E P A E K P E P D	T D Y I R A Q E A R	652
Vigun a	595	E M M Y K D V V Q A	L R A K G S D - E D	P R N Y L T F F C L	G N R E V K K S G E	Y E P A E Q P E P D	S D Y Q R A Q E A R	653
Zeama a	598	E M M Y T D I A Q A	L E A N G I E - A N	P K D Y L T F F C L	G N R E V K Q E G E	Y E P E E H P E P D	T D Y I R A Q E A R	656

Arath a1	654	RFMIYVTRM	MIVDEYIII	GSANINQRSM	DGARDSEIAM	GGYQPHLSH	RQPARGQIHG	713
Arath a2	655	RFMIYVTRM	MIVDEYIII	GSANINQRSM	DGARDSEIAM	GGYQPYHLST	RQPARGQIHG	714
Braol a1	655	RFMIYVTRM	MIVDEYIII	GSANINQRSM	DGARDSEIAM	GGYQPHLSH	RQPARGQIHG	714
Braol a2	657	RFMIYVTRM	MIVDEYIIV	GSANINQRSM	DGARDSEIAM	GGYQPHLSH	RQPARGQVHG	716
Crapl a1	652	RFMIYVTRM	MIVDEYIII	GSANINQRSM	DGARDSEIAM	GAYQPYHLNT	RNRARGQIHG	711
Crapl a2	652	RFMIYVTRM	MIVDEYIII	GSANINQRSM	DGARDSEIAM	GAYQPYHLNT	RNRARGQIHG	711
Lyces a1	654	RFMIYVTRM	MIVDEYIIV	GSANINQRSM	DGARDSEIAM	GAYQPYHLAT	SKPARGQVHG	713
Nicta a	653	RFMIYVTRM	MIVDEYIIV	GSANINQRSM	DGARDSEIAM	GAYQPHLAT	REPARGQIHG	712
Orysa a1	657	RFMIYVTRM	MIVDEYIII	GSANINQRSM	DGARDSEIAM	GGYQPYHLAT	RQPARGQIHG	716
Papso a1	658	RFMIYVTRM	MIVDEYIII	GSANINERSM	NGARDSEIAM	GGYQPHLAH	REPARGQIHG	717
Papso a2	658	RFMIYVTRM	MIVDEYIII	GSANINERSM	NGARDSEIAM	GGYQPHLAH	REPARGQIHG	717
Pimbr a	653	RFMIYVTRM	MIVDEYIII	GSANINQRSM	DGAKDSEIAM	GAYQPHLAT	REPARGQIHG	712
Ricco a	653	RFMIYVTRM	MIVDEYIII	GSANINQRSM	DGARDSEIAM	GAYQPHLST	RQPARGQIHG	712
Vigun a	654	RFMIYVTRM	MIVDEYIII	GSANINQRSM	DGARDSEIAM	GGYQPYHLAN	TQPARGQVYG	713
Zeama a	657	RFMIYVTRM	MIVDEYIII	GSANINQRSM	DGARDSEIAM	GAYQPYHLAT	RQPARGQIHG	716

Arath a1	714	FRMSLWYEH	GMLDETFDLP	KLSEIEKVN	RISDKYWDFY	SSESLEHDL	GHLRLYPVIG	773
Arath a2	715	FRMSLWYEH	GMLDETFDLP	SSQECIQKN	RVADKYWDLY	SSESLEHDL	GHLRLYPVIG	774
Braol a1	715	FRMSLWYEH	GMLDETFDLP	SSVECEKVN	RISDKYWDLY	SSESLEHDL	GHLRLYPVDV	774
Braol a2	717	FRMSLWYEH	GMLDETFDLP	SSLECEKVN	RIADKYWDFY	SSESLEHDL	GHLRLYPVIG	776
Crapl a1	712	FRMALWYEH	GMLDETFLEP	DSEECVRKN	HVADKYWDLY	ASEELEKDL	GHLRLYPVIG	771
Crapl a2	712	FRMALWYEH	GMLDEAFLEP	ENECCVRKN	EIADRYWELY	ASEELENDL	GHLRLYPVEI	771
Lyces a1	714	FRMALWYEH	GMLDETFQHP	ESECCVRKN	QIADKYWDLY	SSESLEHDL	GHLRLYPVIG	773
Nicta a	713	FRMALWYEH	GMLDETFLHP	ESECCVSKN	RMADKYWDLY	SSESLEHDL	GHLRLYPVIG	772
Orysa a1	717	FRMALWYEH	GMLDDVFQRP	ESLECVQKN	RIAKEYWDMY	SSDDLQDLP	GHLRLYPVIG	776
Papso a1	718	FRMALWYEH	GMLDEVFLHP	NSECCVQKN	RIADKYWDLY	SSDSLRLDL	GHLRLYPVIG	777
Papso a2	718	FRMALWYEH	GMLDEVFLHP	NSECCVQKN	RIADKYWDLY	SSDSLRLDL	GHLRLYPVIG	777
Pimbr a	713	FRMSLWYEH	GMLDDTLALP	ESVDCVQKN	TVADKYWDLY	SSETLEHDL	GHLRLYPVIG	772
Ricco a	713	FRMSLWYEH	GMLDESFLNP	ESECCVRKN	QMAEKYWDLY	SSETLEHDL	GHLRLYPVIG	772
Vigun a	714	FRMSLWYEH	GMLHDTFQRP	ESECCVQKN	QIADKYWDLY	SSESLEHDL	GHLRLYPVIG	773
Zeama a	717	FRMSLWYEH	GMLDDVFQRP	ESVDCVQKN	EVAEKYWDLY	SSDDLQDLP	GHLRLYPVIG	776

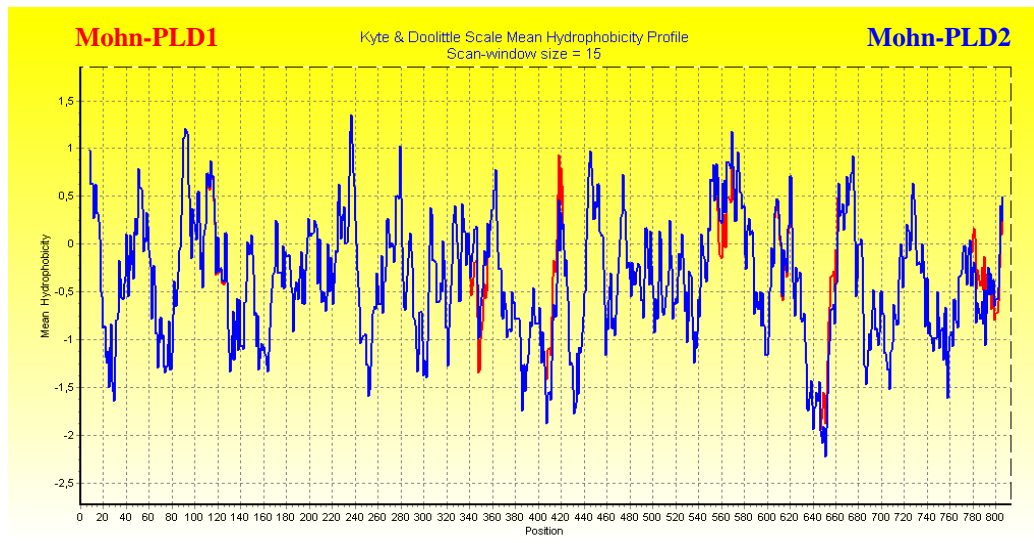
Arath a1	774	ASEGDITELP	GFEFFPDTKA	RILGTKSDYL	PPILTT	809
Arath a2	775	ASEGNITELP	GCEFFPDTKA	RILGVKSDYM	PPILTT	810
Braol a1	775	DGEGDVTEFP	GFEFFPDTKA	RILGTKSDYL	PPILTT	810
Braol a2	777	DNEGNITELP	GFEFFPDTKA	RILGNKVDYL	PPILTT	812
Crapl a1	772	SSDGEVTELP	GTEFFPDTKA	RVLGTKSDYL	PPILTT	807
Crapl a2	772	AGDGGVTELP	GAEFFPDTKA	RVLGAKSDYL	PPILTT	807
Lyces a1	774	ASEGDITELP	GHEFFPDTKA	RVLGTKSDYL	PPNLTT	809
Nicta a	773	ASEGDVTELP	GAEHFPDTKA	RVLGTKSDYL	PPILTT	808
Orysa a1	777	ASDGVVTELP	GMEYFPDTRA	RVLGAKSDYM	PPILTS	812
Papso a1	778	TENGDVTELP	GHEFFPDTKA	RVLGKSDYL	PPILTT	813
Papso a2	778	TENGDVTELP	GHEFFPDTKA	RVLGAKSDYL	PPILTT	813
Pimbr a	773	ASEGNVTELP	GTEFFPDTKA	RVLGAKSDFL	PPILTT	808
Ricco a	773	ASEGDVTELP	GTEFFPDTKA	RVLGAKSDYL	PPILTT	808
Vigun a	774	ASEGEVTELP	GFEFFPDTKA	RILGAKADYL	PPILTT	809
Zeama a	777	TADGSVTELP	GMENFPDTRA	RVLGNKSDYL	PPILTT	812

A4 Aminosäurezusammensetzung von PLD1 und PLD2 aus Schlafmohn

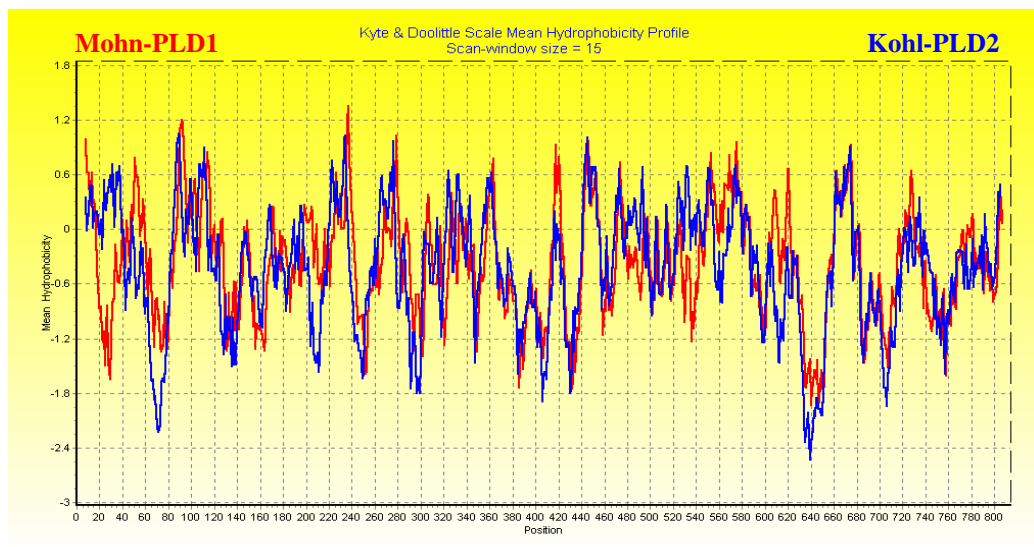
Aminosäure	Mohn-PLD1		Mohn-PLD2	
Alanin	53	(6,52 %)	53	(6,52 %)
Cystein	10	(1,23 %)	9	(1,11 %)
Asparaginsäure	64	(7,87 %)	63	(7,75 %)
Glutaminsäure	49	(6,03 %)	52	(6,40 %)
Phenylalanin	37	(4,55 %)	37	(4,55 %)
Glycin	65	(8,00 %)	64	(7,87 %)
Histidin	27	(3,32 %)	27	(3,32 %)
Isoleucin	62	(7,63 %)	63	(7,75 %)
Lysin	44	(5,41 %)	43	(5,29 %)
Leucin	55	(6,77 %)	54	(6,64 %)
Methionin	18	(2,21 %)	19	(2,34 %)
Asparagin	27	(3,32 %)	27	(3,32 %)
Prolin	45	(5,54 %)	45	(5,54 %)
Glutamin	29	(3,57 %)	28	(3,44 %)
Arginin	45	(5,54 %)	46	(5,66 %)
Serin	45	(5,54 %)	45	(5,54 %)
Threonin	39	(4,80 %)	39	(4,80 %)
Valin	54	(6,64 %)	54	(6,64 %)
Tryptophan	16	(1,97 %)	16	(1,97 %)
Tyrosin	29	(3,57 %)	29	(3,57 %)

A5 Vergleich der Hydrophobizitätsprofile

Vergleich der Hydrophobizitätsprofile der Mohn-PLD-Isoenzyme



Vergleich der Hydrophobizitätsprofile von Mohn-PLD1 und Kohl-PLD2



A6 Primärstruktur und Sekundärstrukturvorhersage von Kohl-PLD2

Türkis markiert, Cystein-Reste; rot, HxKxxxxDxxxxxxGSxN (katalytische Motive); PHD Sekundärstrukturvorhersage, profile network prediction Heidelberg für alle Reste mit einer durchschnittlichen Genauigkeit von > 82 %; H, Helix; E, Faltblatt; L, Loop (andere Strukturelemente); ., keine Vorhersage (Rel < 5); Rel, Wahrscheinlichkeitsfaktor (0 für gering bzw. 9 für hoch).

		L.....EEEEEE...LL.LLLLLL.....LLLLLLLLLLLLEEEEEE.L.	
Kohl-PLD2	1	MAQHLLHGTLHATIYEVDA LHTGGLRSAGFLGKIIISNVEETIGFGKGETQLYATIDLQKA	60
	LLLLLL.....EEE.LLLEEEEEEE.LLLLLL...EEEE...LL	
Kohl-PLD2	61	RVGRTRKITDEPKNPKWYESFHIYCAHMASDIIFTVKDDNPIGATLIGRAYVPVDEIVING	120
		LLL.....LLLLLLLLLLL.EEEEEEE...LLL.....LLLLLLLLLLL.....LLL	
Kohl-PLD2	121	EEVEKWVEILDDDRNP IHGESKIHVKLQYFAVEADRNNMVGKSAKFPVGPYTFFSQRQG	180
		L.EEEE.L.LLLLLLLLLLLLLL.LL...HHHHHHHHH.....EEEE...EEEE	
Kohl-PLD2	181	CKVSLYQGAHVDPDNFVPKIPLAGGKNYEPHRCWEDIFDAITNAKHLIYITGWSVYTEITL	240
		EE.LLLLLL...HHHHHHHHHLLL.EEEEE.LLLLLL...LL...LL...HH..	
Kohl-PLD2	241	VRDSRRPKPGDMTLGELLKKKKATEGVRVLLLWDDRTSVDVLKKGGLMATHDEDTENYF	300
		.LL.EEEE...LLLLL.....LL.EEEE.LLLLLLLLLLLL.EEEEE..	
Kohl-PLD2	301	NGSEVHCVLCPRNPDDGGSIVQNLQVSAMFTHQKIVVVDSEVPSQGGGSEMRRIMSFVG	360
		L...LLLLL.....LL.....LLLLLLLLLLLLLLLLLLLLL.....LL.H	
Kohl-PLD2	361	GIDLCDGRYDTPFHSLFRTLDTVHHDDFHQPNTGASITKGGPREPWQDIHSRLEGPIAW	420
		HHHHHHHHHH.....LLLLLLLLLLLLLLLLLLL...EEEE.LLLLLL	
Kohl-PLD2	421	DVLYNFEQRWSKQGGKILVKLRELSDIITPSPVMFQEDHDVWVWVQLFRSIDGGAAGF	480
		LLL.....LLL...HHHHHHHHHHHHH...EEE.....L.LL..	
Kohl-PLD2	481	PDSPEVAAEAGLVSGKDNVIDRSIQDAYIHAIRRAKDFIYIENQYFLGSSFAWAADGITP	540

LLLL.....HHHHHHHHHHH...LL.EEEEEELLLLLL...HHHHHHHHHHHHHHH

Kohl-PLD2 541 EDINALHLIPKELSLKIVDKIEKGEKFRVYVVVPMWPEGIPESASVQAILDWQRRTLEMM 600

HHHHHHHHH...LLLLL.....LLLLLLLLLLLLLLLLL...HH.....EE

Kohl-PLD2 601 YKDVTQALRAQGLEEDPRNYLTFFC LGNREVKKEGEYEPAERPDPDPTDYMRAQEARRFMI 660

EE...EEE..EEEEELLL...LLLLL.....LL...LLLLL...HHH

Kohl-PLD2 661 YVHKKMMIVDDEYIIVGSANINQRSMGDARDSEIAMGGYQPHLSHRQPARGQVHGFRMS 720

HHHHH.LLL.LLLLLL.HHHHHHHHHHHHHHHH...HHH.....LLL

Kohl-PLD2 721 LWYEHGLMDETFLDPSLECIKVNRIADKYWDFYSSESLEHDLPGHLLRYPISVDNEG 780

...LLLLLLLLLLLLLLLLL...LLLLLLLLLLLLL

Kohl-PLD2 781 NITELPGFEFFPDSKARILGNKVDYLPPILTT 812