

CLUSTAL W (1.83) multiple sequence alignment

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Q7M4E1_HOMAM      -DLVGPSGIVRKDGRNVQFTQEEADNYFNVVKGPSGIVRKDGNNIQFTAQEAARQ---- 54
Q7M4E2_HOMAM      -DLVGPSGIVRTDGRNVQFTQEEADNYFNVVKGPSGIVRKDGNNIQFTAQEAARQ---- 54
PpCUT5            SAQVGQSGIVSPDGNNIQFT--HDFAHSIVLSGPGSIVTSDGKNLQLTGGQAALHAASP 80
P81580|CUPC1_CANPG --QVGYSGIVSPDGNNIQFT--HDFAHSIVLKGPSGIVTSDGKNLQLTAGQASLQAAAP 55
Q7M4E3_HOMAM      --QVGSGIVSPTGANTQFS--HEFAANIVLIGPSGIVTANGENRQLTAGEAQLHAG-- 53
Q7M4E4_HOMAM      --QVGYSGIVSPTGANTQFS--HEFAANIVLIGPSGIVTANGENRQLTAGEAQLHAG-- 53
P81581|CUPC2_CANPG --NYGESGIVYPDGRVLQFT--RAEADNIAEIGEAGVVMHDGTHVQFDRDMAAHHAGTP 55
P81582|CUPC3_CANPG --NYGESGIVYPDGRVLQFT--RAEADNIAEIGEAGVVMHDGTHVQFDRDMAAHHAGTP 55
PpCUT2            SAQYGQSGIVNPDGTLRQFT--REEADNVATIGESGVVFKDGSHLQFNMDFAALHNNLP 88
Q7M492_HOMAM      --QFGTSGIVYPDGINRQLT--QAEADNIVLIGPAGVVTKDGKNIQLNDQGVPTHRI-- 53
PpCUT4            -----
Q7M4E0_HOMAM      AGNIGYSGIVRTDGTIEAFP--GDFSHDIVLIGPSGIVTKSGKNVQLDRNLHRT----- 60
PpCUT7            FSPCLSLSDPQRRWSLRNRESCRKCSIHSRDGRQVRGWSLRHCDQERQKHPSSTTKGF-- 139
PpCUT10           -----
P81585|CUPC6_CANPG -----
PpCUT8            SAQVGYSGIVSPDGNNVQFT--RDFAYGIVLVGPSGIVTKDGNNLQLTGGQAALHAASP 79
PpCUT9            -----FVYGIVLVGPSGIVTKDGNNLQLTGGQAALHAASP 35
Q7M4A1_HOMAM      -ALIGPSGAILDDGTQVQFS---KAGVTVLLEGPSGYVFDGTLVQKKS----- 45
Q7M4A2_HOMAM      -ALFGPSGAILDDGTQVQFS---KAGVTVLLEGPSGYVFDGTLVQKKS----- 45
PpCUT3            -----
P81588|CUC10_CANPG KATVGESGIITPGRLIQLP---HGVSIILEGPSAALLSNGDFVTYESS----- 50
PpCUT1            SAQYGESGIVNPDGTLRQFT--REEADNVATIGESGVVFKDGSHLQFNMDFAALHNNLP 78
Q7M494_HOMAM      PPLVGASGIITPSGRLIQLP---AGVTVASAGPSGAVLSNGDNIQYV----- 46
Q7M493_HOMAM      -HVIGDSGIITNDGRPFHLP---AGVSULLQGPSGIVLSNGQNIQLRN----- 44
PpCUT6            HAQFGETGIVMPDGNVQFT--HDQAENILLIGPSGAITADGKHVQLDRDGLPATRTRK 90
P81586|CUPC7_CANPG VLLKGPSGVLFDGQKRLP---PGVEIVLLTESGAVLSNGENVQF----- 44
P81587|CUPC8_CANPG VLLEGPSGVLFDGQKKYLP---PGVKIVLLSKAGAVLSNGDNVQF----- 44
P81590|CUPC9_CANPG VLLEGPSGVLFDGQKKYLP---PGVKIVLLTESGAVLSNGDNVQF----- 44
PpCUT12           NAKFKGKHGIVMPDGNNVQFT--HDQAENILLIGPSGIITADGKHLQLDADGLP----- 83
PpCUT13           PGRHGGRGNSIKQWYQRRVAITAGDCSGSSHQGVLDQFTLATMKFLVVLCLMAVGANAK 65
PpCUT11           DAQVGYSGFVSLDGTNVRT--NDFAHGMCLLD--LLDSKGGSNLQLTGARLPSTLLSQ 83

Q7M4E1_HOMAM      -----
Q7M4E2_HOMAM      -----
PpCUT5            PAPQPVPQLVISRSVVGPSGIVSPAGNVQFTHEMVDDN-VLVGPSGIVTKSGQNIQFND 141
P81580|CUPC1_CANPG PPLPVSHYVASQQSVVGPSGIVSPAGNVQFSHEF-ADNVVLVGPSGIVTKDGNNLQLRA 114
Q7M4E3_HOMAM      AHPVPVPHYVAQNIFYGPGSGYITPTGQNVQYTHEQAANIVLTGPSGIVSRDGNQIQLP- 111
Q7M4E4_HOMAM      AHPVPVPHYVAQNIFYGPGSGYITPTGQNVQYTHEQAANIILTGPSGIVSRDGNQIQLP- 111
P81581|CUPC2_CANPG PQPMPVREMLAQP--YGYSGIMKPDGNNRQFTAESDNLVLVGPSGAVTADGKNVQFTD 112
P81582|CUPC3_CANPG PQPMPERVTLQDS--YGYSGIIMPDGNNRQFTAESDNLVLVGPSGAVTADGKNVQFTD 112
PpCUT2            GPDKPTEE-VTFGP--YSYHGIIPDGNNVQFTPDQHSNNVLVGPSGAVTADGKNVQFGQ 144
Q7M492_HOMAM      -----
PpCUT4            -----VVEELITLGSHEDLVEEGAVELWQQPAPSV 30
Q7M4E0_HOMAM      -----
PpCUT7            LRTKRSAGYVLPKGNMGYSGIVRTDGTFEQFSQDFAHNILFLGPSGIVTKDGKNIQLTS 198
PpCUT10           -----
P81585|CUPC6_CANPG -----
PpCUT8            PAPQPVSQVLVLRVSVVGPSGIVSPAGNVQFTQEMVD-DNLVLVGPSGIVTKSGKNIQFND 137
PpCUT9            PAPQPVSQLLLTRSVVGPSGIVSPAGNVQFTQEMVD-DNLVLVGPSGIVTKSGKNIQFND 93
Q7M4A1_HOMAM      -----
Q7M4A2_HOMAM      -----
PpCUT3            -----
P81588|CUC10_CANPG -----
PpCUT1            GPDKPTEE---VTFGPYGYHGIIPDGNNVQFTPDQHSNNVLVGPSGAVTADGKNVQFGQ 154
Q7M494_HOMAM      -----
Q7M493_HOMAM      -----
PpCUT6            -----AVLL---EGPSGVLFDGQKRLHPPGVEI--VLMSEAGAVLSNGDNVQFRK 136
P81586|CUPC7_CANPG -----
P81587|CUPC8_CANPG -----
P81590|CUPC9_CANPG -----
PpCUT12           -----ANRAKRAVLLEGPSVLFEDGQKRLSGGVRIVEITET--GAVLSNGDNVQFKL 135
PpCUT13           -----
PpCUT11           DLQPGLRWSVAGSLAPEKSVRPEMSVPSRNGRQVRVGPWHWTRA----- 127

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Q7M4E1_HOMAM	-----	
Q7M4E2_HOMAM	-----	
PpCUT5	GLPRTKRSAGYVLPAGNLGHS	198
P81580 CUPC1_CANPG		
Q7M4E3_HOMAM	-----	
Q7M4E4_HOMAM	-----	
P81581 CUPC2_CANPG	AGLPT-----	117
P81582 CUPC3_CANPG	DGLPT-----	117
PpCUT2	EGFPL----RRKRAVALEGPSGVQFDDGQLRHL	199
Q7M492_HOMAM		
PpCUT4	-LKRDTVTTGFTRPKIGSIGFS	88
Q7M4E0_HOMAM	-----	
PpCUT7	-DLHRV-----KRSLVGPSGMILEDGTPVQFKTPFTTILRD	248
PpCUT10	SDLHRV-----KRSLVGPSGMILEDGTPVQFKTPFATVLLD	63
P81585 CUPC6_CANPG	-----ALVGPSGMILADGTPVQFPAHAKPVLT-	42
PpCUT8	QGLPRT-----KRSLVGPSGMILEDGTPVQFKTPFTTVLLD	192
PpCUT9	QGLPRT-----KRSLVGPSGMILEDGTPVQFKTPFTTVLLD	148
Q7M4A1_HOMAM	-----	
Q7M4A2_HOMAM	-----	
PpCUT3	-----	
P81588 CUC10_CANPG		
PpCUT1	EGLPLRR----KREVTLEGPSGVQFADGQLRHL	
Q7M494_HOMAM	-----	
Q7M493_HOMAM	-----	
PpCUT6	-----KRDVLLGPSGVLFKDGQKRHLPPGVEIV--	186
P81586 CUPC7_CANPG	-----	
P81587 CUPC8_CANPG	-----	
P81590 CUPC9_CANPG	-----	
PpCUT12	KNCCFPFFYATEGLLDYITN-KQLEQLPPFVTVINN	175
PpCUT13	-----FGKHGIVMPDGNNVQFTHDQAE	107
PpCUT11	-----	
Q7M4E1_HOMAM	-----	
Q7M4E2_HOMAM	-----	
PpCUT5	-----TADLHRVKRDLKGPSGMILKDGTQVQF	256
P81580 CUPC1_CANPG	-----	
PpCUT2	-----RKKRDVALQGPSGVQFADGQLRHL	257
Q7M492_HOMAM		
PpCUT4	SPGKGLVSLDAAASSPMGASFPSQRNSWTT	89
Q7M4E0_HOMAM	-----	
PpCUT7	-----RFKRSFVGPFMITADGTPIQFP-AHAE	302
PpCUT10	-----RPKRSLVGPSGMITADGTPIQFP-AHAE	104
P81585 CUPC6_CANPG	H-----	43
PpCUT8	-----RLKRSLVGLSGMILEDGTPVQFKTPFASILL	240
PpCUT9	-----RPKRSLVGPSGMIAADGTPIQFP-AHAK	195
PpCUT3	-----LFSWRRLIQLP--HDVYVVLEGPSAALL	38
P81588 CUC10_CANPG	-----	
PpCUT1	-----RKKREAPSKAVVGDSGIITPGGFQFQLP	258
Q7M494_HOMAM	-----	
Q7M493_HOMAM	-----	
PpCUT6	----RKKRSSPLIDSIKGPSGYITPTGQLFLQPP	236
P81586 CUPC7_CANPG	-----	
P81587 CUPC8_CANPG	-----	
P81590 CUPC9_CANPG	-----	
PpCUT12	GTLLSDEMSPCLTSVNVFNSRSLIYLYSAPTSTEGS	221
PpCUT13	DADGLPANRAKRAVLLEGPSSVLFEDGQKRSL	165
PpCUT11	-----	

GPSGIV shading denotes cuticle_1 domain
----- gaps assist with alignment