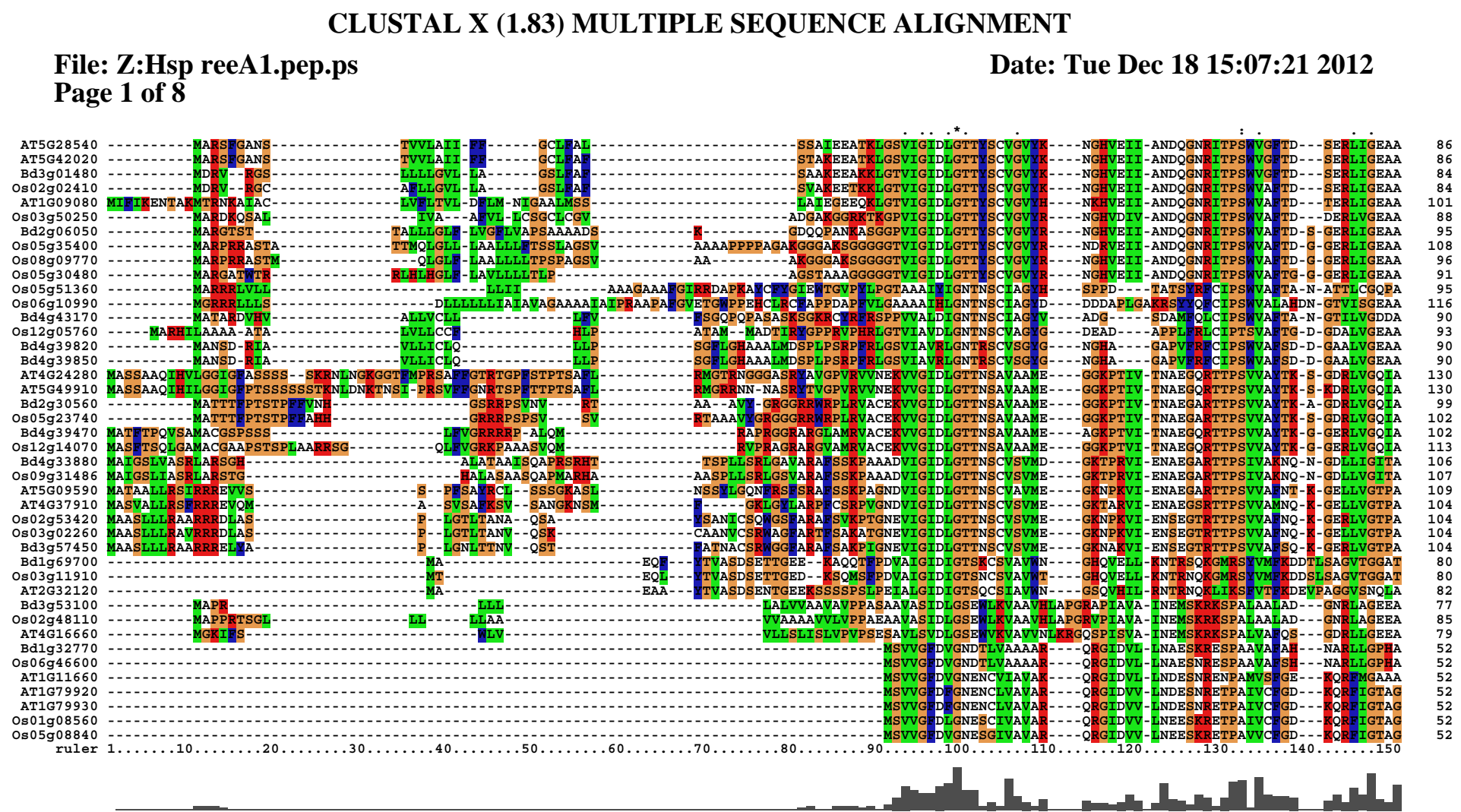


Figure S3. Clustal X (1.83) multiple sequence alignment.



CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: Z:Hsp reeA1.pep.ps
Page 2 of 8

Date: Tue Dec 18 15:07:21 2012

```

AT5G28540 KNQAA---VN-PEPTVDVKRLIGRKKED--KEVQKDRKLVVPYQIVN--K-DG-KPYIQVKI---KDGETKVSPEEISAMILTKMKETAEEAYL--GKKIKINDAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 213
AT5G42020 KNQAA---VN-PEPTVDVKRLIGRKKED--KEVQKDRKLVVPYQIVN--K-DG-KPYIQVKI---KDGETKVSPEEISAMILTKMKETAEEAYL--GKKIKINDAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 213
Bd3g01480 KNQAA---VN-PEPTVDVKRLIGRKKED--KEVQKDRKLVVPYQIVN--K-DG-KPYIQVKI---KDGENKVSPEEISAMILTKMKETAEEAYL--GKKIKINDAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 211
Os02g02410 KNQAA---VN-PEPTVDVKRLIGRKKED--KEVQKDRKLVVPYQIVN--K-DG-KPYIQVKI---KDGENKVSPEEISAMILTKMKETAEEAYL--GKKIKINDAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 211
AT1G09080 KNQAA---KN-PEPTIDPKRLIGRKKDD--PDVQDRKIFLPPYKVVN--K-DG-KPYIQVKI---K-GEKKLVSPEEISAMILTKMKETAEEAYL--GKKIKINDAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 227
Os03g50250 KNQAA---LN-PDRTIDPKRLIGRKKDD--EEVQDRKIFLPPYKVVN--K-GG-KPYVEEVV---KAGEVKVSPEEISAMILTKMKETAEEAYL--GQRVTDNAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 215
Bd2g06050 KNQAA---SN-PLRTIDAKRLIGRKKDD--AEVQKDRKLVVPYQIVN--K-RG-KPHVEVEV---KDGDVRLVSPEEISAMILTKMKETAEEAYL--GEPVTDNAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 222
Os05g35400 KNQAA---AN-PEPTIDAKRLIGRKKDD--AEVQKDRKLVVPYQIVN--R-NG-KPHVEVEV---KDGDVRLVSPEEISAMILTKMKETAEEAYL--GEPVTDNAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 235
Os08g09770 KNQAA---AN-PEPTIDAKRLIGRKKDD--AEVQKDRKLVVPYQIVN--R-NG-KPHVEVEV---KDGDVRLVSPEEISAMILTKMKETAEEAYL--GEPVTDNAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 223
Os05g30480 KNQAA---AN-PGRTVDKRLIGRKKDD--AEVQKDRKLVVPYQIVN--K-GG-KPHVEVEV---RGDDVRLVSPEEISAMILTKMKETAEEAYL--GEPVTDNAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 218
Os05g51360 VDH-----SAAISGFKRLIGRKKDD--PHAKRVQAIPYKIGE--K-IG-RCSIQVQLDD--GAKCRVDFIPEDVAGLILSHLKHAEAAH--GHRINDNAVVTTPG--HNGNQQRQVSSGSTEYGGFRVYSVVDEQVAAAA 221
Os06g10990 MNRAA---LS-PSTAVSAGFMRLLHRRVED--DVVKRETELVPYKITE--M-LG-VVSVQLDTD-----AESVDHLAGLILSHLKHAEAAH--GRHINNNAVITIPSRLSYADG-RQLVSSAAKESYSGFRVAKVVDHAAAA 242
Bd4g43170 QDAAA---VD-PASAVSAGFMRLLHRRVED--DVVKRETELVPYKITE--K-NL-YPHIKMTGILVGGTANNE--STDEVMAMVIGKLKEAAESYN--SCSRVNAVITVPP--HYVDSFWSQTE--HAGTIAGVRVARMIDEPAAAA 223
Os12g05760 MNH-----AAISGFKRLIGRKKDD--PEVRAAEHLVPYKIVD--K-CT-MAHIEVNA--GAGGAASVNASDVASVIAELKAEAAEALAGGKKVHNAVVTVP--YHSDGPPEAAH--NAARMAGLITTVRIIDEPTAAAV 219
Bd4g39820 KDAAA---AN-PQAAVGFKRLIGKTFGH--EDVQRE--SPFYKIVY--K-ET-SSTGT--G--IQVAKKQLLHVEDVAAVMVLAELKCAEAAH--GHKVHNAVITVPS--YFRDASRLAAH--DAVTSAGLEPVRIIDEPTAAAL 214
Bd4g39850 KDAAA---AN-PQAAVGFKRLIGKTFGH--EDVQRE--SPFYKIVY--K-ET-SSTGT--G--IQVAKKQLLHVEDVAAVMVLAELKCAEAAH--GHKVHNAVITVPS--YFRDASRLAAH--DAVTSAGLEPVRIIDEPTAAAL 214
AT4g24280 KRQAV---VN-PENTFFSVKRFIGRKMNE--VDEESKQVSYRVIR--DENN-NVKLECP-----AINKQFAAEETISAQVLRKLVDDASRFL--NDKVTKAVITVPA--YNDASQRTATK-DAGRIAGLEVLRRIINEPTAAAL 253
AT5G49910 KRQAV---VN-PENTFFSVKRFIGRKMNE--VDEESKQVSYRVIR--DENG-NVKLDCP-----AIGKQFAAEETISAQVLRKLVDDASRFL--NDKVTKAVITVPA--YNDASQRTATK-DAGRIAGLEVLRRIINEPTAAAL 253
Bd2g30560 KRQAV---VN-PENTFFSVKRFIGRKMNE--VDEESKQVSYRVIR--DDNG-NVKLDCP-----AIGKQFAAEETISAQVLRKLVDDASRFL--NDKVTKAVITVPA--YNDASQRTATK-DAGRIAGLEVLRRIINEPTAAAL 222
Os05g23740 KRQAV---VN-PENTFFSVKRFIGRKMNE--VDEESKQVSYRVIR--DDNG-NVKLDCP-----AIGKQFAAEETISAQVLRKLVDDASRFL--NDKVTKAVITVPA--YNDASQRTATK-DAGRIAGLEVLRRIINEPTAAAL 225
Bd4g39470 KRQAV---VN-PENTFFSVKRFIGRKMNE--VDEESKQVSYRVIR--DENG-NVKLDCP-----AIGKQFAAEETISAQVLRKLVDDASRFL--NDKVTKAVITVPA--YNDASQRTATK-DAGRIAGLEVLRRIINEPTAAAL 225
Os12g14070 KRQAV---VN-PENTFFSVKRFIGRKMNE--VDEESKQVSYRVIR--DDNG-NVKLDCP-----AIGKQFAAEETISAQVLRKLVDDASRFL--NDKVTKAVITVPA--YNDASQRTATK-DAGRIAGLEVLRRIINEPTAAAL 236
Bd4g33880 SRQAV---TN-AQNTVRSKRLIGRTD--PQTQKEMKMPYKIVR--GPNG-DAWVEM-----GGQKVSFSPQIGAVLTKMKETAEEAYL--GKTVSKAVITVPA--YNDAGRQATK-DAGRIAGLEVLRRIINEPTAAAL 229
Os09g31486 SRQAV---TN-AQNTVRSKRLIGRTD--PQTQKEMKMPYKIVR--GPNG-DAWVEM-----GGQKVSFSPQIGAVLTKMKETAEEAYL--GKTVSKAVITVPA--YNDAGRQATK-DAGRIAGLEVLRRIINEPTAAAL 230
AT5G09590 KRQAV---TN-PTNTVSGTKRLIGRKKDD--PQTQKEMKMPYKIVR--APNG-DAWVEA-----NGQKVSFSPQIGAVLTKMKETAEEAYL--GKSIVTKAVITVPA--YNDAGRQATK-DAGRIAGLEVLRRIINEPTAAAL 232
AT4G37910 KRQAV---TN-PTNTVSGTKRLIGRKKDD--PQTQKEMKMPYKIVR--APNG-DAWVEA-----NGQKVSFSPQIGAVLTKMKETAEEAYL--GKSIVTKAVITVPA--YNDAGRQATK-DAGRIAGLEVLRRIINEPTAAAL 227
Os02g53420 KRQAV---TN-PQNTFFGTKRLIGRKKDD--PQTQKEMKMPYKIVR--APNG-DAWVETT-----DGKQVSFSPQIGAVLTKMKETAEEAYL--GKTVSKAVITVPA--YNDAGRQATK-DAGRIAGLEVLRRIINEPTAAAL 228
Os03g02260 KRQAV---TN-PQNTFFGTKRLIGRKKDD--PQTQKEMKMPYKIVR--ALNG-DAWLETT-----DGKQVSFSPQIGAVLTKMKETAEEAYL--GKSIVTKAVITVPA--YNDAGRQATK-DAGRIAGLEVLRRIINEPTAAAL 228
Bd3g57450 KRQAV---TN-PQNTFFGTKRLIGRKKDD--PQTQKEMKMPYKIVR--APNG-DAWVETT-----DGKQVSFSPQIGAVLTKMKETAEEAYL--GKSIVTKAVITVPA--YNDAGRQATK-DAGRIAGLEVLRRIINEPTAAAL 228
Bd1g69700 KEHAEEDVIL-SGSAIENMKRLIGRMDTD--EVVQASKSLPFLVQT--LGIGVRPFIAALV--NNMWRSTTPEEVLAIFLLELKLALVEMH--KHPVRNAVITIPV--AFSRQQTRE--KACAMAGLHVLRMLPEPTAAL 211
Os03g11910 KEHAEEDVIL-SGSAIENMKRLIGRMDTD--EVVQASKSLPFLVQT--LGIGVRPFIAALV--NNMWRSTTPEEVLAIFLLELKLALVEMH--KHPVRNAVITIPV--AFSRQQTRE--KACAMAGLHVLRMLPEPTAAL 211
AT2G32120 KEHEEMITGAAIENMKRLVGRVDTD--FVVHASKNLPLVQT--LDIGVRPFIAALV--NNMWRSTTPEEVLAIFLLELKLALVEMH--KRPVRNAVITIPV--AFSRQQTRE--KACAMAGLHVLRMLPEPTAAL 208
Bd3g53100 AGTAA---RH-PSKVFAARMDDLKPPFY--VQSIAQSLFLPYDVFQ--DARG-AAAVRADD--G-QVTVVEEIVAMVLHVAGSLADAHV--GAPVRDAVAVVPP--YFGQAERRSLT-QAAQLAGVNVLALINEHAGAAL 201
Os02g48110 SGITA---RH-PSKVFAARMDDLKPPFY--VRSVAEALFLPYDLVP--DARG-AAAVRADD--G-QVTVVEEIVAMVLHVAGSLADAHV--GAPVRDAVAVVPP--YFGQAERRSLT-QAAQLAGVNVLALINEHAGAAL 209
AT4G16660 AGTAA---RH-PSKVFAARMDDLKPPFY--VRSVAEALFLPYDLVP--DARG-AAAVRADD--G-QVTVVEEIVAMVLHVAGSLADAHV--GAPVRDAVAVVPP--YFGQAERRSLT-QAAQLAGVNVLALINEHAGAAL 204
Bd1g32770 AGAAS---SHAPF---SSPKRLLLLAARP--ALVPRDLPLPLFPVHV--PADG-DALVHVDH--TGRRIALSPTQLLAMLGLYLQLAEADL--EAPVADCVISVPC--YFTQARRAHL-DAAAVAGLTPRLRLMHDLAATAL 177
Os06g46600 AGAAS---SHAPF---SSPKRLLLLAARP--ALVPRDLPLPLFPVHV--PADG-DALVHVDH--TGRRIALSPTQLLAMLGLYLQLAEADL--EAPVADCVISVPC--YFTQARRAHL-DAAAVAGLTPRLRLMHDLAATAL 183
AT1G16660 AASAT---MH-PKSTISQKRLIGRKKRE--PDVQNDLRLPLPFETSE--DSDG-GIQIRLRY--MGETQSFSPVQILGMLLSHLKQIAEKST--KTPVSDCVIGIPV--YFTNSQRIHL-DAAATAGLRPLRLMHDSTATAL 179
AT1G79920 AASTM---MN-PKNSISQIKRLIGRKKSD--PEVQDRKIFLPPYKVVN--K-DG-KPYIQVKI---K-GEKKLVSPEEISAMILTKMKETAEEAYL--GKKIKINDAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 213
AT1G79930 AASTM---MN-PKNSISQIKRLIGRKKSD--PEVQDRKIFLPPYKVVN--K-DG-KPYIQVKI---K-GEKKLVSPEEISAMILTKMKETAEEAYL--GKKIKINDAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 213
Os01g08560 AASST---MN-PKNSISQIKRLIGRKKSD--PEVQDRKIFLPPYKVVN--K-DG-KPYIQVKI---K-GEKKLVSPEEISAMILTKMKETAEEAYL--GKKIKINDAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 213
Os05g08840 AASST---MN-PKNSISQIKRLIGRKKSD--PEVQDRKIFLPPYKVVN--K-DG-KPYIQVKI---K-GEKKLVSPEEISAMILTKMKETAEEAYL--GKKIKINDAVVTTPA--YNDAGRQATK-DAGVIAGLNVARIIINEPTAAAI 213
ruler .....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

```



CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: Z:Hsp reeA1.pep.ps
Page 3 of 8

Date: Tue Dec 18 15:07:21 2012

```

      . . . . . : * : . . . . . : * : * : . . . . . : * : * :
AT5G28540 A G L D K K G G ----- E K N I L V D L G G G T D V S V L T I D ----- N G V E V L S T N G D T H L G G E D F D R V M E Y F I K L I K K K H - Q - K D I S K D N K A L G K L R R E C E R A K R A L S S Q H Q V R V E T E S L F D G --- V D L S E P L T R A F E E 335
AT5G42020 A G L D K K G G ----- E K N I L V D L G G G T D V S V L T I D ----- N G V E V L S T N G D T H L G G E D F D R I M E Y F I K L I K K K H - Q - K D I S K D N K A L G K L R R E C E R A K R A L S S Q H Q V R V E T E S L F D G --- V D L S E P L T R A F E E 335
Bd3g01480 A G L D K K G G ----- E K N I L V D L G G G T D V S I L T I D ----- N G V E V L A T N G D T H L G G E D F D R I M E Y F I K L I K K K Y - S - K D I S K D N R A L G K L R R E A E R A K R A L S N Q H Q V R V E T E S L F D G --- T D L S E P L T R A F E E 333
Os02g02410 A G L D K K G G ----- E K N I L V D L G G G T D V S I L T I D ----- N G V E V L A T N G D T H L G G E D F D R I M E Y F I K L I K K K Y - S - K D I S K D N R A L G K L R R E A E R A K R A L S N Q H Q V R V E T E S L F D G --- T D L S E P L T R A F E E 333
AT1G09080 A G L D K K G G ----- E S N I L V D L G G G T D V S I L T I D ----- N G V E V L S T S G D T H L G G E D F D R V M D Y F I K L V K K K Y - N - K D I S K D H K A L G K L R R E C E R A K R S L S N Q H Q V R V E T E S L F D G --- V D L S E P L T R A F E E 349
Os03g50250 A G L D R K G A ----- G - E M T N V L V D L G G G T D V S V L S I D ----- H G V E V L A T S G D T H L G G E D F D R R V M D H F I R L V K K Q H - G - R D I G G D G R A L G K L R R E C E R A K R A L S N Q H Q V R V E T E A L F V G --- V D L S E P L T R A F E E 339
Bd2g06050 A G L D N K A K ----- D A K E E R N V L V D L G G G T D V S V L T I D ----- N G V E V L A T N G D T H L G G E D F D R L M D Y L V K L V K R K H - G - K D V S H D A R A L G K L R R E C E R A K R A L S S Q H Q V R V E T E S L F D G --- V D L S E P L T R A F E E 348
Os05g35400 A G L D K K G A ----- E K N V L V D L G G G T D V S I L A I D ----- N G V E V L A T N G D T H L G G E D F D Q R L M D H V K V I R R K H - G - R D I A G D A R A L G K L R R E C E R A K R A L S N Q H Q V R V E T E S L F D G --- V D L S E P L S R A F E E 357
Os08g09770 A G L D K K G A ----- E K N V L V D L G G G T D V S I L A I D ----- N G V E V L A T N G D T H L G G E D F D Q R L M D H V K V I R R K H - G - R D I T G D A R A L G K L R R E C E R A K R A L S N Q H Q V R V E S L F D G --- V D L S E P L S R A F E E 345
Os05g30480 A G V G K E G A ----- G G K N V L V D L G G G T D V S V L A I D ----- G G V E V L A T N G D T H L G G E D F D Q R V M E H F V E L V R R K H - G - R D I A G D A R A L G K L R R E C E R A K R A L S Q H Q V R V E S L F D G --- V D L S E P L S R A F E E 341
Os05g51360 A H G L H E D R G ----- D G K V L V F H L G G R T A H A T K F V I R ----- D G T P S L I A L R H D P L G G D D F A R V D H M A D L I K D K H - G G R D V R A D A A A L R R L T A E C E R A K K A L S Q Q E T V V T M R L D D D --- D D L S E P L T R S K L E E 345
Os06g10990 A G G H T K G G ----- D R K A I L V F H L G G R T S H A T I F K I V ----- D G T A R L I A T R A H F L G G D D F A R I V D H M V E H I K E Q H - G - R D V R Q E E K A M V R L R V A C E R A K K A L S E Q Q E T L V Q M D S L L D D --- G A V S A T L T R A F E E 366
Bd4g43170 A H G L H R R I ----- R N E G V A L V L H V G G A T T A E S L M V I D ----- D G V D F L G G R H D A F L G G D D F D R R V D Y F T A L M K R K H - G - R D I S N D T Q A A K L R T A C E R A K K A L S T R E Q A E V V V E S H --- G L A E T L T R A F E E 342
Os12g05760 S H G L H H G R I ----- R D G G N V L V L H V G G G T S A A T V L T I D ----- N A V E A V A S R H D A H L G G D D F A R I A G R F S Q L I K D H - G - G G - N D D I A P A K L K S Q C E L A K R T L S S H D V A Q V N L H A T N I - A N G A S S S G S L T R A F E E 344
Bd4g39820 A H G L H E N E I ----- T K N V L V L H V G G G T A E A T V L V E E ----- D G V E A I G T W E D A H L G G D D F D R R T A N H F L Q L I R E K H - S - V D I G N D T A K L W K L R A E C E R A K K E L S D R D V A R V S V N S I V D --- G V D L F E P L T R A F E E 336
Bd4g39850 A H G L H E N E I ----- T K N V L V L H V G G G T A E A T V L V E E ----- D G V E A I G T W E D A H L G G D D F D R R T A N H F L Q L I R E K H - S - V D I G N D T A K L W K L R A E C E R A K K E L S D R D V A R V S V N S I V D --- G V D L F E P L T R A F E E 336
AT4g24280 A G G D R K A N ----- E T I L V D L G G G T D V S V L E V G ----- D G V E V L S T S G D T H L G G D D F D K R V D W I A A E F K K D E - G - I D L L D K Q A L Q R L T E A A E R A K I E L S S L T Q T N M S L P I T A T A D G P K H I E T T L T R A F E E 378
AT5G49910 A G G E R K S N ----- E T I L V D L G G G T D V S V L E V G ----- D G V E V L S T S G D T H L G G D D F D K R V D W I A S T F K K D E - G - I D L L D K Q A L Q R L T E A A E R A K I E L S S L T Q T N M S L P I T A T A D G P K H I E T T L T R A F E E 378
Bd2g30560 A G G E K K N N ----- E T I L V D L G G G T D V S V L E V G ----- D G V E V L S T S G D T H L G G D D F D K R I V D W I A G S F K K N D E - G - I D L L D K Q A L Q R L T E A A E R A K I E L S S L T Q T N I S L P I T A T A D G P K H I E T T L T R A F E E 347
Os05g23740 A G G E K K N N ----- E T I L V D L G G G T D V S V L E V G ----- D G V E V L S T S G D T H L G G D D F D K R V D W I A G N F K K N D E - G - I D L L D K Q A L Q R L T E A A E R A K I E L S S L T Q T N I S L P I T A T A D G P K H I E T T L T R A F E E 350
Bd4g39470 A G G E K K N N ----- E T I L V D L G G G T D V S V L E V G ----- D G V E V L S T S G D T H L G G D D F D K K I V D W I A S T F K K N D E - G - I D L L D K Q A L Q R L T E A A E R A K I E L S S L T Q T N I S L P I T A T A D G P K H I E T T L T R A F E E 350
Os12g14070 A G G E K K N N ----- E T I L V D L G G G T D V S V L E V G ----- D G V E V L S T S G D T H L G G D D F D K K V D W I A S N F K K D E - G - I D L L D K Q A L Q R L T E A A E R A K I E L S S L T Q T N I S L P I T A T A D G P K H I E T T L T R A F E E 361
Bd4g33880 S Y G M N N K E ----- G L I A V D L G G G T D V S I L E I S ----- N G V E V K A T N G D T F L G G E D F D A A L I D Y L S E F K K S D - N - I D L S K D K A V L Q R L R E A A E R A K V E L S S T Q T E I N L P I T A T A S G A K H I N I T L T R S K F E S 353
Os09g31486 S Y G M N N K E ----- G L I A V D L G G G T D V S I L E I S ----- N G V E V K A T N G D T F L G G E D F D G A L I D Y L S E F K K S D - N - I D L S K D K A L Q R L R E A A E R A K V E L S S T Q T E I N L P I T A T A D G A K H I N I T L T R S K F E S 354
AT5G09590 S Y G M T N K E ----- G L I A V D L G G G T D V S V L E I S ----- N G V E V K A T N G D T F L G G E D F D N A L I D F L V N E F K T T E - G - I D L A K D R I A L Q R L R E A A E R A K I E L S S T S Q T E I N L P I T A T A S G A K H I N I T L T R S R F E T 356
AT4g37910 S Y G M N N K E ----- G V I A V D L G G G T D V S I L E I S ----- S G V E V K A T N G D T F L G G E D F D N T L L E V L V N E F K R S D - N - I D L T K D N L A L Q R L R E A A E R A K I E L S S T Q T E I N L P I T A T A S G A K H I N I T L T R S K F E S 351
Os02g53420 S Y G T N N K E ----- G L I A V D L G G G T D V S I L E I S ----- N G V E V K A T N G D T F L G G E D F D N T L L E F L V S E F K R S E - A - I D L A K D R I A L Q R L R E A A E R A K I E L S S T A Q T E I N L P I T A T A S G A K H I N I T L T R S K F E S 352
Os03g02260 S Y G T N N K E ----- G L I A V D L G G G T D V S I L E I S ----- N G V E V K A T N G D T F L G G E D F D N T L L E F L V S E F K R T E - G - I D L S K D R I A L Q R L R E A A E R A K I E L S S T A Q T E I N L P I T A T A S S G A K H I N I T L T R S K F E S 352
Bd3g57450 S Y G T N N K E ----- G L I A V D L G G G T D V S I L E I S ----- N G V E V K A T N G D T F L G G E D F D N T L L E F L V S E F K R T D - A - I D L S K D R I A L Q R L R E A A E R A K I E L S S T A Q T E I N L P I T A T A S G A K H I N I T L T R S K F E S 352
Bd1g69700 L Y A Q Q Q Q L L H D N M G S G I E X I A L I N M G A G Y C D A V A S A T A ----- G G V S Q I R A L S G C T - V G G E D I L Q N V M R H L P N I D S L Y - A - G Q T M D R I K S M G L L R I A T Q D A V H K L T T Q E S T E I N V D L G G G --- Q K V S K V L G R A E F Q 340
Os03g11910 L Y A Q Q Q Q L L H D N M G S G I E X I A L I N M G A G Y C D A A V A A T A ----- G G V S Q I R A L S G S T - V G G E D I L Q N V M R H L M P D I D S L Y - A - G Q T M D R I K S I G L L R M A T Q D A I H K L A T Q E H V E I N V D L G A G --- H K V S K I L D R G E F E 340
AT2g32120 L Y A Q Q Q Q T T H D N M G S G S E R L A V I N M G A G Y C D V A V T A T A ----- G G V S Q I R A L A G S P - I G G E D I L Q N T I R H T A P P N E E ----- A S G L L R V A A Q D A I H R L T D Q E N V Q I E V D L G N G --- N K I S K V L D R I E E E 326
Bd3g53100 Q Y G I D K D F S ----- N G --- S R R V I F Y D M G S S T Y A A L V Y Y S S N A K E F G K T V S V N Q Q V K D V R R N S K L G G I E M E M R L V N Y T A D Q N K Q L G N G - D D I R Q S P K A M A K L K K Q V K R T K E I L S A N T A A P I S V E S L Y N D --- L D F R S T I T R E K F E E 339
Os02g48110 Q Y G I D K D F S ----- N E --- S R R V I F Y D M G A G S T Y A A L V Y Y S A K A K E F G K T V S V N Q Q V K D V R D S K L G G I E M E M R L V N Y T A D Q N K Q L G N G - V D I R Q S P K A M A K L K K Q V K R T K E I L S A N T A A P I S V E S L Y N D --- L D F R S T I T R E K F E E 347
AT4g16660 Q Y G I D K D I A ----- N G --- S R R V I F Y D M G S S S T Y A A L V Y Y S A N S E K E F G K T V S V N Q Q V K D V R N D L G L G G S M E M R L V E H A D E F N K Q L G N G - V D V R K S P K A M A K L K K Q V K R T K E I L S A N T A A P I S V E S L H D D --- R D F R S T I T R E K F E E 342
Bd1g32770 G Y G L R S D L ----- G V A G S P T F V A F D V G H S D T Q A T V V A I D ----- P S G M K V L S H G D A D L G G E D F D E V L E H F A E E F R D R Y - K - I D V V G N V K A S M R L R A A C E R A K K V L S A N A E A V N I E C L M E E --- K D V R G M I R R E E F E 304
Os06g46600 G Y G L R S D L ----- G G P G G P T Y A F V D V G H C D T Q V A V V A I D ----- V S G M K V L S H R D A D L G G E D F D E V L E H F A E E F R D R Y - K - I D V T G N V K A S M R L R A A C E R A K K V L S A N A E A V N I E C L M E E --- K D V R G M I R R E E F E 310
AT1G16660 G Y G I Y K T D L ----- V A N S S P T Y I V F D I G H C D T Q V C V A S E ----- S G S M R V R S H A D R N L G G G D F D E V L E N H F A E F K E K Y - N - I D V Y T N T K A C V R L R A S C E R V K K V L S A N A E A Q L N I E C L M E E --- K D V R S R I K R E E F E Q 306
AT1G79920 A G I Y K T D L ----- P E N D - Q L N V A F D I G H A S N Q V C I A G F K ----- K G Q L K I L S H A D R S L G G G D F D E V L E N H F A A K F K D E Y - K - I D V S Q N A K A S L R L R A T C E K L K K V L S A N P A P L N I E C L M A E --- K D V R G V I K R E E F E 305
AT1G79930 A G I Y K T D L ----- P E S D - Q L N V A F D I G H A S N Q V C I A G F K ----- K G Q L K I L S H A D R S L G G G D F D E V L E N H F A A K F K D E Y - K - I D V S Q N A K A S L R L R A T C E K L K K V L S A N P A P L N I E C L M D E --- K D V R G V I K R E E F E 305
Os01g08560 A G I Y K T D L ----- P E N D - Q L N V A F D V G H A S N Q V C I A G F K ----- K G Q L K I L S H A D R S L G G G D F D E V L E H F A A K F K D E Y - K - I D V V Q N A R A C I R L R V A C E K L K K V L S A N P E S P M I E C L M D E --- K D V R G I K R E E F E 305
Os05g08840 A G I Y K T D L ----- P E K E - Q L N V A F D V G H A S N Q V S I V G F K ----- K G Q L N M L S H A D R S L G G G D F D E V L E H F A E K F K D E Y - K - I D V V Q N A R A C V R L R V A C E K L K K L S A N P E A P L N I E C L M D E --- K D V R G I K R E E F E Q 305
ruler .....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

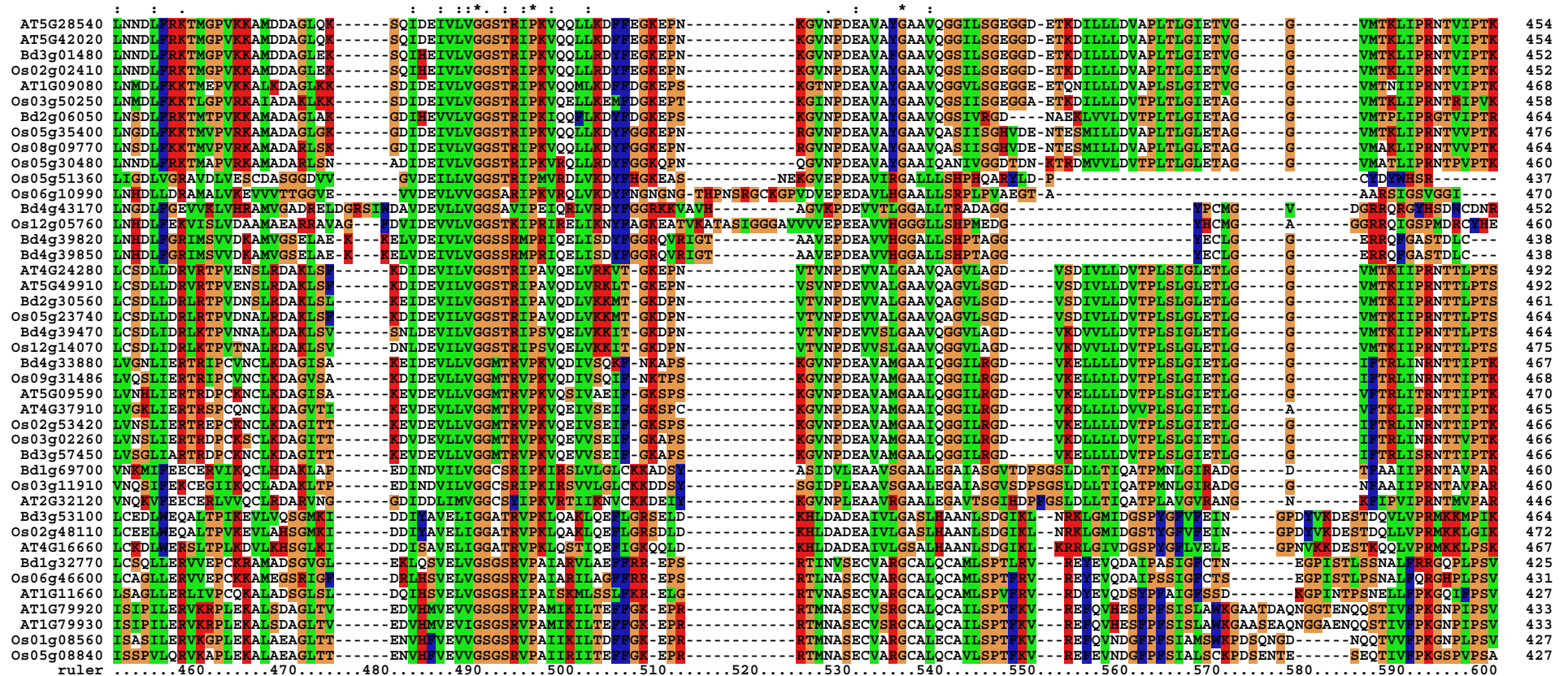
```



CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: Z:Hsp reeA1.pep.ps
Page 4 of 8

Date: Tue Dec 18 15:07:21 2012



CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: Z:Hsp reeA1.pep.ps
Page 5 of 8

Date: Tue Dec 18 15:07:21 2012

```

AT5G28540 KSVQVTTTQDQQTTSIQVFEGERSLT--KDCRLLGKFDLNGIPPAAPRG--PQIEVTEVDANGILNVAAEDKASGKSEKIT-----533
AT5G42020 KSVQVTTTQDQQTTSIQVFEGERSLT--KDCRLLGKFDLTGVPPAPRG--PQIEVTEVDANGILNVAAEDKASGKSEKIT-----533
Bd3g01480 KSVQVTTTQDQQTTSIQVFEGERSM--KDCRLLGKFDLSGIPPAAPRG--PQIEVTEVDANGILNVAAEDKGTGKSEKIT-----531
Os02g02410 KSVQVTTTQDQQTTSIQVFEGERSM--KDCRLLGKFDLSGIPPAAPRG--PQIEVTEVDANGILNVAAEDKGTGKSEKIT-----531
AT1G09080 KSVQVTTTQDQQTTSIQVFEGERSM--KDNRELGRFDLTGILPAPRGV--PQIEVTEVDANGILVAAEDKVAKTSQSIT-----547
Os03g50250 KSVQVTTTEDQQTTSIKVFEGERSLT--KDCRELGRFDLSGIAPAPRGV--PQIEVTEVDENGILHVTAEDKAAGRSKSIT-----537
Bd2g06050 KTKTFTTTQDQQTTSVVVFEGERSM--KDNKQLGKFDLTGIAPAPRG--PQIEVTEVDVNGILHVAAEDKGTGKSEKIT-----543
Os05g35400 KTVQVTTTKDRQTTVTIQVFEGERSM--RDNRLLGKFDLTGIAPAPRG--PQIAVTEVDANGILSVAAEDKATGRSEKIT-----555
Os08g09770 KTVQVTTTKDRQTTVTIQVFEGERSM--RDNRLLGRFDLAGIAPAPRG--PQIEVTEVDANGILSVAAEDKATGRSEKIT-----543
Os05g30480 KAAQLFTTKDRQTTVTIVKFEGERSM--RDNRLLGRFDLAGIAPAPRG--PQIEVTEVDADGILSVSAADKATGRSEKIT-----539
Os05g51360 -----537
Os06g10990 -----437
Bd4g43170 -----470
Os12g05760 -----454
Bd4g39820 -----461
Bd4g39850 -----438
AT4G24280 KSEVFSTAADGQTSVEINVLOGEREFV--RDNKSLSGFRLDGIPPAAPRGV--PQIEVKDIDANGILSVSAVDKGTGKKQDIT-----571
AT5G44910 KSEVFSTAADGQTSVEINVLOGEREFV--RDNKSLSGFRLDGIPPAAPRGV--PQIEVKDIDANGILSVSASDKGTGKKQDIT-----571
Bd2g30560 KSEVFSTAADGQTSVEINVLOGEREFV--RDNKSLSGFRLDGIPPAAPRGV--PQIEVKDIDANGILSVAAVDKGTGKKQDIT-----540
Os05g23740 KSEVFSTAADGQTSVEINVLOGEREFV--RDNKSLSGFRLDGIPPAAPRGV--PQIEVKDIDANGILSVSAVDKGTGKKQDIT-----543
Bd4g39470 KSEVFSTAADGQTSVEINVLOGEREFV--RDNKSLSGFRLDGIPPAAPRGV--PQIEVKDIDANGILSVAAVDKGTGKKQDIT-----543
Os12g14070 KSEVFSTAADGQTSVEINVLOGEREFV--RDNKSLSGFRLDGIPPAAPRGV--PQIEVKDIDANGILSVAAIDKGTGKKQDIT-----554
Bd4g33880 KSVTFSTAADNQTVGIRVLOGEREMA--TDNKLIGEFDLVGIPPAAPRG--PQIEVTDIDANGIVRVSAKDSTGKEQDIT-----546
Os09g31486 KSVTFSTAADNQTVGIRVLOGEREMA--TDNKLIGEFDLVGIPPAAPRG--PQIEVTDIDANGIVKVSARDKSTGKEQDIT-----547
AT5G09590 KSVTFSTAADNQTVGIRVLOGEREMA--TDNKLIGEFDLVGIPPAAPRG--PQIEVTDIDANGIVTVSARDKSTGKEQDIT-----549
AT4G37910 KSVTFSTAADNQTVGIRVLOGEREMA--ADNKVLGEFDLVGIPPAAPRG--PQIEVTDIDANGITTVSARDKATGKEQDIT-----544
Os02g53420 KSVTFSTAADNQTVGIRVLOGEREMA--TDNKLIGEFDLVGIPPAAPRG--PQIEVTDIDANGIVTVSARDKSTGKEQDIT-----545
Os03g02260 KSVTFSTAADNQTVGIRVLOGEREMA--ADNKVLGEFDLVGIPPAAPRG--PQIEVTDIDANGIVTVSARDKATGKEQDIT-----545
Bd3g57450 KSVTFSTAADNQTVGIRVLOGEREMA--TDNKLIGEFDLVGIPPAAPRG--PQIEVTDIDANGIVTVSARDKATGKEQDIT-----545
Bd1g69700 RDMLETTTHDNQTEALVAVTEGEGNQA--EENHLLGYFKITGIPAAAPKGA--VEINVCMDDIDAGNVLRVAVGVVKKPQGA--TPPFI-----541
Os03g11910 RDMLETTTHDNQTEALVAVTEGEGNQA--EENHLLGYFKITGIPAAAPKGA--VEINVCMDDIDAGNVLRVAVGVVKKPQGA--VPPFI-----541
AT2G32120 RDLFFFTTQDNQKEALITIVTEGEGTV--EENHLLGYFKLVGIPPAAPKGV--PEINVCMDDIDAGNVLRVAAVLMPGSSSPVVPVI-----528
Bd3g53100 LYRSVKHTKDDVSI---SYDKASELPPGVSSHKAQVSVISGLADASEKVGSRNLSAPIKANLHFTLSRSGITSLDRAEAVIEITEAEIIPKKNLTLLESNATDQTLSSSESGTS--DSTADSKEN--PSSGSDANNLSNTN--DEGNVDAIT-----607
Os02g48110 MFRSIRHTKDDVSI---SYDKASELPPGVSSHKAQVSVISGLADASEKVGSRNLSAPIKANLHFTLSRSGITSLDRAEAVIEITEAEIIPKKNLTLLESNATDQTLSSSESGTS--DSTADSKEN--PSSGSDANNLSNTN--DEGNVDAIT-----615
AT4G16660 MFRSVKDKDDVSI---AYESEGILPPGTTSPVAAQVSVISGLADASEKVGSRNLSAPIKANLHFTLSRSGITSLDRAEAVIEITEAEIIPKKNLTLLESNATDQTLSSSESGTS--DSTADSKEN--PSSGSDANNLSNTN--DEGNVDAIT-----608
Bd1g32770 KIITLHRNSCENLDV---FYDENELPPGT-STKIGSFQIGPFAH--TEK--SKVKVRLNLHGLISVESAVLIEDDQDNTNSS-----DSMEVDHND-----VGD-----516
Os06g46600 KVVTLHRNSKFKLDA---FYDENELPPGT-STKIGSFQIGPFAH--TEK--SKVKVRLNLHGLISVESAVLIEDDQDNTNSS-----DSMEVDHND-----VGD-----522
AT1G16660 KVVTLHRNSKFKLDA---FYDENELPPGT-STKIGSFQIGPFAH--TEK--SKVKVRLNLHGLISVESAVLIEDDQDNTNSS-----DSMEVDHND-----VGD-----530
AT1G79920 KALTFFYRSSTGTSIDV---QYSDVNDLQA---PPKISTYVTIGPQSSSKGER--AKLKVKVRLNLHGLISVESAVLIEDDQDNTNSS-----DSMEVDHND-----VGD-----571
AT1G79930 KALTFFYRSSTGTSIDV---QYSDVNDLQA---PPKISTYVTIGPQSSSKGER--AKLKVKVRLNLHGLISVESAVLIEDDQDNTNSS-----DSMEVDHND-----VGD-----571
Os01g08560 KALTFFYRSSTGTSIDV---QYSDVNDLQA---PPKISTYVTIGPQSSSKGER--AKLKVKVRLNLHGLISVESAVLIEDDQDNTNSS-----DSMEVDHND-----VGD-----566
Os05g08840 KALTFFYRSSTGTSIDV---QYSDVNDLQA---PPKISTYVTIGPQSSSKGER--AKLKVKVRLNLHGLISVESAVLIEDDQDNTNSS-----DSMEVDHND-----VGD-----565
ruler .....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750

```



CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: Z:Hsp reeA1.pep.ps
Page 6 of 8

Date: Tue Dec 18 15:07:21 2012

```

AT5G28540 -----IT-NEKGRLSQEEIDRMVKEAEFAEEDKKVKEKIDARNALETYYVNMKNQVNDKDLADKLEGDEKKEAATKEAEELDENQ---NSEEEDKLEKEVEACNPIITAVYQSSGAPGGAGGESST-- 659
AT5G42020 -----IT-NEKGRLSQEEIDRMVKEAEFAEEDKKVKEKIDARNALETYYVNMKNQVSDKDLADKLEGDEKKEAATKEAEELDENQ---NSEEEDKLEKEVEACNPIITAVYQSSGAPGGAGGESST-- 658
Bd3g01480 -----IT-NEKGRLSQEEIDRMVKEAEFAEEDKKVKEKIDARNALETYYVNMKNQVNDKDLADKLEGDEKKEAATKEAEELDENQ---NSEEEDKLEKEVEACNPIITAVYQSSGAPGGAGGESST-- 657
Os02g02410 -----IT-NEKGRLSQEEIDRMVKEAEFAEEDKKVKEKIDARNALETYYVNMKNQVNDKDLADKLEGDEKKEAATKEAEELDENQ---NSEEEDKLEKEVEACNPIITAVYQSSGAPGGAGGESST-- 657
AT1G09080 -----IT-NDKGRLTEEETEEMIREAEFAEEDKIMKEKIDARNKLETYYVNMKNQVNDKDLADKLEGDEKKEAATKEAEELDENQ---NSEEEDKLEKEVEACNPIITAVYQSSGAPGGAGGESST-- 673
Os03g50250 -----IT-NDKGRLSQEEIDRMVKEAEFAEEDRRVHERVDARNKLENYVVRMRSAVEDG-GMAGKIGDDDERMESALTEALEWLEDNDGGARTAEKEDYEKKLEVEQVCGPIIKQVYKKSQDASAGAGDDDDV-- 666
Bd2g06050 -----ITSAADRRITQEEIDRMVKEAEFAEEDKKVHERVDARNKLENYVVRMRSAVEDG-GMAGKIGDDDERMESALTEALEWLEDNDGGARTAEKEDYEKKLEVEQVCGPIIKQVYKKSQDASAGAGDDDDV-- 664
Os05g35400 -----ISGDDRKISQEEIDRMVKEAEFAEEDRRHREQVDARNKLENYVVRMRSAVEDG-GMAGKIGDDDERMESALTEALEWLEDNDGGARTAEKEDYEKKLEVEQVCGPIIKQVYKKSQDASAGAGDDDDV-- 678
Os08g09770 -----ISGDDRKISQEEIDRMVKEAEFAEEDRRHREQVDARNKLENYVVRMRSAVEDG-GMAGKIGDDDERMESALTEALEWLEDNDGGARTAEKEDYEKKLEVEQVCGPIIKQVYKKSQDASAGAGDDDDV-- 667
Os05g30480 -----ISGDDRKISQEEIDRMVKEAEFAEEDRRHREQVDARNKLENYVVRMRSAVEDG-GMAGKIGDDDERMESALTEALEWLEDNDGGARTAEKEDYEKKLEVEQVCGPIIKQVYKKSQDASAGAGDDDDV-- 660
Os05g51360 -----ISGDDRKISQEEIDRMVKEAEFAEEDRRHREQVDARNKLENYVVRMRSAVEDG-GMAGKIGDDDERMESALTEALEWLEDNDGGARTAEKEDYEKKLEVEQVCGPIIKQVYKKSQDASAGAGDDDDV-- 437
Os06g10990 -----ISGDDRKISQEEIDRMVKEAEFAEEDRRHREQVDARNKLENYVVRMRSAVEDG-GMAGKIGDDDERMESALTEALEWLEDNDGGARTAEKEDYEKKLEVEQVCGPIIKQVYKKSQDASAGAGDDDDV-- 470
Bd4g43170 -----ISGDDRKISQEEIDRMVKEAEFAEEDRRHREQVDARNKLENYVVRMRSAVEDG-GMAGKIGDDDERMESALTEALEWLEDNDGGARTAEKEDYEKKLEVEQVCGPIIKQVYKKSQDASAGAGDDDDV-- 454
Os12g05760 -----ISGDDRKISQEEIDRMVKEAEFAEEDRRHREQVDARNKLENYVVRMRSAVEDG-GMAGKIGDDDERMESALTEALEWLEDNDGGARTAEKEDYEKKLEVEQVCGPIIKQVYKKSQDASAGAGDDDDV-- 461
Bd4g39820 -----ISGDDRKISQEEIDRMVKEAEFAEEDRRHREQVDARNKLENYVVRMRSAVEDG-GMAGKIGDDDERMESALTEALEWLEDNDGGARTAEKEDYEKKLEVEQVCGPIIKQVYKKSQDASAGAGDDDDV-- 438
Bd4g39850 -----ISGDDRKISQEEIDRMVKEAEFAEEDRRHREQVDARNKLENYVVRMRSAVEDG-GMAGKIGDDDERMESALTEALEWLEDNDGGARTAEKEDYEKKLEVEQVCGPIIKQVYKKSQDASAGAGDDDDV-- 438
AT4g24280 -----IT-GASTLPKDEVDQMVEAEFAEEDKKVKEKIDARNALETYYVNMKNQVNDKDLADKLEGDEKKEAATKEAEELDENQ---NSEEEDKLEKEVEACNPIITAVYQSSGAPGGAGGESST-- 692
AT5G49910 -----IT-GASTLPKDEVDQMVEAEFAEEDKKVKEKIDARNALETYYVNMKNQVNDKDLADKLEGDEKKEAATKEAEELDENQ---NSEEEDKLEKEVEACNPIITAVYQSSGAPGGAGGESST-- 692
Bd2g30560 -----IT-GASTLPKDEVDQMVEAEFAEEDKKVKEKIDARNALETYYVNMKNQVNDKDLADKLEGDEKKEAATKEAEELDENQ---NSEEEDKLEKEVEACNPIITAVYQSSGAPGGAGGESST-- 661
Os05g23740 -----IT-GASTLPKDEVDQMVEAEFAEEDKKVKEKIDARNALETYYVNMKNQVNDKDLADKLEGDEKKEAATKEAEELDENQ---NSEEEDKLEKEVEACNPIITAVYQSSGAPGGAGGESST-- 664
Bd4g39470 -----IT-GASTLPKDEVDQMVEAEFAEEDKKVKEKIDARNALETYYVNMKNQVNDKDLADKLEGDEKKEAATKEAEELDENQ---NSEEEDKLEKEVEACNPIITAVYQSSGAPGGAGGESST-- 662
Os12g14070 -----IT-GASTLPKDEVDQMVEAEFAEEDKKVKEKIDARNALETYYVNMKNQVNDKDLADKLEGDEKKEAATKEAEELDENQ---NSEEEDKLEKEVEACNPIITAVYQSSGAPGGAGGESST-- 673
Bd4g33880 -----IK-SSGGLSESDIEKMVREAEELHSQKQDQERKSLDLKNSADTTIYSIEKSLG--EYKDKVPSEITTEVESASDLRAAMAGDD--LDNKKQKLEAANAVSKIGEHMQGGGGGDTLRLKLN-- 661
Os09g31486 -----IK-SSGGLSESDIEKMVREAEELHSQKQDQERKSLDLKNSADTTIYSIEKSLG--EYKDKVPSEITTEVESASDLRAAMAGDD--LDNKKQKLEAANAVSKIGEHMQGGGGGDTLRLKLN-- 662
AT5G09590 -----IR-SSGGLSESDIEKMVREAEELHSQKQDQERKSLDLKNSADTTIYSIEKSLG--EYKDKVPSEITTEVESASDLRAAMAGDD--LDNKKQKLEAANAVSKIGEHMQGGGGGDTLRLKLN-- 664
AT4G37910 -----IR-SSGGLSESDIEKMVREAEELHSQKQDQERKSLDLKNSADTTIYSIEKSLG--EYKDKVPSEITTEVESASDLRAAMAGDD--LDNKKQKLEAANAVSKIGEHMQGGGGGDTLRLKLN-- 660
Os02g53420 -----IR-SSGGLSESDIEKMVREAEELHSQKQDQERKSLDLKNSADTTIYSIEKSLG--EYKDKVPSEITTEVESASDLRAAMAGDD--LDNKKQKLEAANAVSKIGEHMQGGGGGDTLRLKLN-- 659
Os03g02260 -----IR-SSGGLSESDIEKMVREAEELHSQKQDQERKSLDLKNSADTTIYSIEKSLG--EYKDKVPSEITTEVESASDLRAAMAGDD--LDNKKQKLEAANAVSKIGEHMQGGGGGDTLRLKLN-- 656
Bd3g57450 -----IR-SSGGLSESDIEKMVREAEELHSQKQDQERKSLDLKNSADTTIYSIEKSLG--EYKDKVPSEITTEVESASDLRAAMAGDD--LDNKKQKLEAANAVSKIGEHMQGGGGGDTLRLKLN-- 661
Bd1g69700 -----EVRMPTLDDGHGCGQALAKMGGSTLDTATIPKKLHP--EYKDKVPSEITTEVESASDLRAAMAGDD--LDNKKQKLEAANAVSKIGEHMQGGGGGDTLRLKLN-- 578
Os03g11910 -----EVRMPTLDDGHGCGQALAKMGGSTLDTATIPKKLHP--EYKDKVPSEITTEVESASDLRAAMAGDD--LDNKKQKLEAANAVSKIGEHMQGGGGGDTLRLKLN-- 578
AT2G32120 -----EVRMPTLDDGHGCGQALAKMGGSTLDTATIPKKLHP--EYKDKVPSEITTEVESASDLRAAMAGDD--LDNKKQKLEAANAVSKIGEHMQGGGGGDTLRLKLN-- 563
Bd3g53100 EKVLKKRTFRVPLKVVEKTAGAGSILSKELYSEAKNRLEVLDDKDAERRRTAELKNNLESYIYSMEKLEENTDILAVSTEQERESAEKLENEVDWLYMDG---EQAQANETQERLDQLKAIGDPIILRLSELKARPAACGSA---- 747
Os02g48110 EKVLKKRTFRVPLKVVEKMAGAGSILSKELYSEAKNRLEVLDDKDAERRRTAELKNNLESYIYSMEKLEENTDILAVSTEQERESAEKLENEVDWLYMDG---EQAQANETQERLDQLKAIGDPIILRLSELKARPAACGSA---- 756
AT4G16660 EKVLKKRTFRVPLKVVEKTAGAGSILSKELYSEAKNRLEVLDDKDAERRRTAELKNNLESYIYSMEKLEENTDILAVSTEQERESAEKLENEVDWLYMDG---EQAQANETQERLDQLKAIGDPIILRLSELKARPAACGSA---- 748
Bd1g32770 KSRNERPQRODLQIGSIYGA---MSKQELLEAEQEQEQLAQDKLMERTKERRKNALESYVVDIRNKLESE--RYRSPATDSEEREESVNLQOTEEWLYEEDG---DDETEAVYNSKLEELKRLVDPIENRCDDDEVRTQTTREI-- 652
Os06g46600 QVDSRSERLQPLPIVQSIYGA---MSKQELLEAEQEQEQLAQDKLMERTKERRKNALESYVVDIRNKLESE--RYRSPATDSEEREESVNLQOTEEWLYEEDG---DDETEAVYNSKLEELKRLVDPIENRCDDDEVRTQTTREI-- 658
AT1G16660 LGNEPKAIAKMEIPVANVSGA---LTKDELSEAKQRENSLVEQDLKMEESTKDKKNALESYVVDIRNKLESE--RYRSPATDSEEREESVNLQOTEEWLYEEDG---DDETEAVYNSKLEELKRLVDPIENRCDDDEVRTQTTREI-- 666
AT1G79920 AKAPKKKVKKTNVPLSELVYGA---LKTVEVEKAVEKEFEMALQDRVMEETKDRKNALESYVVDIRNKLESE--RYRSPATDSEEREESVNLQOTEEWLYEEDG---DDETEAVYNSKLEELKRLVDPIENRCDDDEVRTQTTREI-- 707
AT1G79930 AKAPKKKVKKTNVPLSELVYGA---LKTVEVEKAVEKEFEMALQDRVMEETKDRKNALESYVVDIRNKLESE--RYRSPATDSEEREESVNLQOTEEWLYEEDG---DDETEAVYNSKLEELKRLVDPIENRCDDDEVRTQTTREI-- 707
Os01g08560 VEPKSKKVKKTNVPLSELVYGA---LKTVEVEKAVEKEFEMALQDRVMEETKDRKNALESYVVDIRNKLESE--RYRSPATDSEEREESVNLQOTEEWLYEEDG---DDETEAVYNSKLEELKRLVDPIENRCDDDEVRTQTTREI-- 702
Os05g08840 VEPLIKNVKKIDVPVSGLVYGA---LGSEELVRASENEFEMALQDRVMEETKDRKNALESYVVDIRNKLESE--RYRSPATDSEEREESVNLQOTEEWLYEEDG---DDETEAVYNSKLEELKRLVDPIENRCDDDEVRTQTTREI-- 701
ruler .....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900

```

CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: Z:Hsp reeA1.pep.ps
Page 7 of 8

Date: Tue Dec 18 15:07:21 2012

```

AT5G28540 -----EEEDESHDEL-----669
AT5G42020 -----EEEDESHDEL-----668
Bd3g01480 -----D--DEEHDEL-----665
Os02g02410 -----V--DDEEHDEL-----665
AT1G09080 -----E-----F-----675
Os03g50250 -----NEL-----669
Bd2g06050 -----E--DDHDEL-----671
Os05g35400 -----DD--EDDHDEL-----687
Os08g09770 -----DD--EDDHDEL-----676
Os05g30480 -----GG--DDDDEL-----669
Os05g51360 -----GG--DDDDEL-----437
Os06g10990 -----GG--DDDDEL-----470
Bd4g43170 -----GG--DDDDEL-----454
Os12g05760 -----GG--DDDDEL-----461
Bd4g39820 -----GG--DDDDEL-----438
Bd4g39850 -----GG--DDDDEL-----438
AT4G24280 ASSGDSSSSKGGDGDVIDADFTDSQ-----718
AT5G49910 SSDTSSSAKGGDNGGDVIDADFTDSN-----718
Bd2g30560 DS--G-PSEKPGDDGDVIDADFTDSK-----684
Os05g23740 GSAGF-SEKPGGEGGDVIDADFTDSQ-----689
Bd4g39470 PTPGAGPTGSSGNDGDVIDADFTDSN-----688
Os12g14070 AGPT--SSGKGPNDDGDVIDADFTDSN-----698
Bd4g33880 -----TRT--PRKLRCRNN--LQAPTFFLCVPSVGS-----689
Os09g31486 -----SSSGGQTPAEAEQDAAKEAKM-----684
AT5G09590 -----SEGGSDQAPEAEEEVKK-----682
AT4G37910 -----EGT--SGTEQTPAEAEESGSRK-----682
Os02g53420 -----GGSQGGGQAPEAEEEVKK-----679
Os03g02260 -----AGSQGGGQAPEAEEEVKK-----676
Bd3g57450 -----EGSQGGGQAPEAEEEVKK-----681
Bd1g69700 -----EGSQGGGQAPEAEEEVKK-----578
Os03g11910 -----EGSQGGGQAPEAEEEVKK-----578
AT2G32120 -----EGSQGGGQAPEAEEEVKK-----563
Bd3g53100 -----RLYLTEIQKIVKNWETNKPWLPKKRVDEVVSEADKIRTWLDEXEALQKSTTLVSTPAFTSEEVVQKVLDLQDKVSSVNRIPKPKPKIEKKPPTTEESANK-----EKT-----ASSESTSSSESEST863
Os02g48110 -----RLYLAEIQKIVKNWDSNKPWLPKKRVDEVVSEAEKVKTWLEKEEALQKSTPVYSPPAFTSEEVVQKVLDLQDKVSSVNRIPKPKPKIEKKPPTTEESANK-----EKT-----DSSESESKAEEST872
AT4G16660 -----RKLYLTELKEIKEETNKTNLPEKIDEVSKAEKVKSMLDKNVAEQKETSLSKSPVFTSTEVYAKVTLQDKVTKVKNKIPKPKPKIEKVTKTENTTKEE-----EQS-----KGSDEAAKEEESH864
Bd1g32770 -----LKCIVDHRMAAK-----SLSAPEEAVDNECAKVEQNLREGLEQLQESLPKNDVPVLWSPEIKRKEEELDMYLELPLRLLETLMLSSFTKMGVSLRRFA-----747
Os06g46600 -----LKEILDHKTAAK-----SLPTPEQEAVDSECTRAEQMLRERSQLQESLPKNVDPALWSHEIKKKEHELDMPYRNIVRYKGSPPADSSGGSDHMTTDRD-----753
AT1G11660 -----LKTIANRMAAE-----SLPPPRKNAVLDECHKAERWLEHXTTEQESLPKDANPELQSAETRRKADALNATCKYIGKSNSPPAKPEHNGSVGSRKSDDMELD-----763
AT1G79920 -----GYCINSYREAAVSNDPKFDHIELAEKQKVLNECVAEAEANLREKQQQQDTLPKYATPALLSADVKSAAEALDKFCRPIMTKPKPAANAFAAPQAKGGEQA-----DEGKS-----EPEQPAS817
AT1G79930 -----GYCINSYREAAVSNDPKFDHIELAEKQKVLNECVAEAEANLREKQQQQDTLPKYATPALLSADVKSAAEALDKFCRPIMTKPKPAANAFAAPQAKGGEQA-----DEGKS-----EPEQPAS817
Os01g08560 -----AYCINSYRDAALSKDPKFDHIEEEKQKVINQCSAEAEVWLRKKLQQQDALPKHANPVLLSSDLKKKAETVDRFCRPIIMMKPKBPAPKQTPPF-QTPPTETFPAGGAQTPEQQPQGAEEAGEASE---GG--ASEST830
Os05g08840 -----VHCINGKEVALSNSQAQDHIDMSEKQKVLDECSEAEIWLIEKQQQDALPKHADPVLLISDMKKKAELDRSCRPIMSKPKFPAPKQTPPPPTTPPTESPTTPEFQTPEQQQSNAGAGEAEPTSEGGAQDQEP836
ruler .....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050

```

CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

File: Z:Hsp reeA1.pep.ps
Page 8 of 8

Date: Tue Dec 18 15:07:21 2012

```
AT5G28540 ----- 669
AT5G42020 ----- 668
Bd3g01480 ----- 665
Os02g02410 ----- 665
AT1G09080 ----- 675
Os03g50250 ----- 669
Bd2g06050 ----- 671
Os05g35400 ----- 687
Os08g09770 ----- 676
Os05g30480 ----- 669
Os05g51360 ----- 437
Os06g10990 ----- 470
Bd4g43170 ----- 454
Os12g05760 ----- 461
Bd4g39820 ----- 438
Bd4g39850 ----- 438
AT4G24280 ----- 718
AT5G49910 ----- 718
Bd2g30560 ----- 684
Os05g23740 ----- 689
Bd4g39470 ----- 688
Os12g14070 ----- 698
Bd4g33880 ----- 689
Os09g31486 ----- 684
AT5G09590 ----- 682
AT4G37910 ----- 682
Os02g53420 ----- 679
Os03g02260 ----- 676
Bd3g57450 ----- 681
Bd1g69700 ----- 578
Os03g11910 ----- 578
AT2G32120 ----- 563
Bd3g53100 DTSSSDAPE-----KTDDSEPEANDEL 886
Os02g48110 ETSSSAAPESQSSEPKTDDSEPEANDEL 902
AT4G16660 DEL----- 867
Bd1g32770 ----- 747
Os06g46600 ----- 753
AT1G11660 ----- 763
AT1G79920 AEAMETENPAEGST----- 831
AT1G79930 AEPMETENPAEGST----- 831
Os01g08560 GEQMETDKPEGTEA----- 845
Os05g08840 AEQMDTDKPDG----- 847
ruler .....1060.....1070.....1080
```
