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          *           20           *           40           *           60
Col-0 : MKKQYLKSGSGT--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 58
Bay-0 : MKKQYLKSGSGT--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 57
Bil-5 : MKKQYLKSGSGT--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 58
Br-0 : MKKQYLKSGSGT--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 58
Ct-1 : MKKQYLKSGSGT--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 58
Cvi-0 : MKKQYLKSGSGT--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 58
Ei-2 : MKKQYLKSGSGT--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 58
Est-1 : MKKQYLKSGSGT--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 58
Kas-1 : MKKQYLKSGSGT--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 58
Lp2-2 : MKKQYLKSGSGT--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 58
Nd-1 : MKKQYLKSGSGT--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 58
Zdr-1 : MKKQYLKSGSGT--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 58
Alyrata : MKKQYLKSGSGSRTRKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 60
Brapa : MKKQYLKSGSGR--RKEKDKAKRWFLDNGSIFTELVELVADONGKSIPIRSFSPEQILKATN : 58

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          *           80           *           100          *           120
Col-0 : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 118
Bay-0 : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 117
Bil-5 : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 118
Br-0 : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 118
Ct-1 : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 118
Cvi-0 : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 118
Ei-2 : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 118
Est-1 : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 118
Kas-1 : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 118
Lp2-2 : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 118
Nd-1 : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 118
Zdr-1 : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 118
Alyrata : NFDSSCFVSDVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 120
Brapa : NFDSSCFISEDAVYKWKYRGEIEDRSYMIKRFSEDEITGKRHRVKEVYNDIVLSARMSNHS : 116

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GxGxxG

VAVK

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          *           140          *           160          *           180
Col-0 : NFLQLLGCCLFPPFPVLVFEFAEHGAMNQRGGVIVNGEESLLPWSVRLKIGKEIANAVTY : 178
Bay-0 : NFLQLLGCCLFPPFPVLVFEFAEHGAMNQRGGVIVNGEESLLPWSVRLKIGKEIANAVTY : 177
Bil-5 : NFLQLLGCCLFPPFPVLVFEFAEHGAMNQRGGVIVNGEESLLPWSVRLKIGKEIANAVTY : 178
Br-0 : NFLQLLGCCLFPPFPVLVFEFAEHGAMNQRGGVIVNGEESLLPWSVRLKIGKEIANAVTY : 178
Ct-1 : NFLQLLGCCLFPPFPVLVFEFAEHGAMNQRGGVIVNGEESLLPWSVRLKIGKEIANAVTY : 178
Cvi-0 : NFLQLLGCCLFPPFPVLVFEFAEHGAMNQRGGVIVNGEESLLPWSVRLKIGKEIANAVTY : 178
Ei-2 : NFLQLLGCCLFPPFPVLVFEFAEHGAMNQRGGVIVNGEESLLPWSVRLKIGKEIANAVTY : 178
Est-1 : NFLQLLGCCLFPPFPVLVFEFAEHGAMNQRGGVIVNGEESLLPWSVRLKIGKEIANAVTY : 178
Kas-1 : NFLQLLGCCLFPPFPVLVFEFAEHGAMNQRGGVIVNGEESLLPWSVRLKIGKEIANAVTY : 178
Lp2-2 : NFLQLLGCCLFPPFPVLVFEFAEHGAMNQRGGVIVNGEESLLPWSVRLKIGKEIANAVTY : 178
Nd-1 : NFLQLLGCCLFPPFPVLVFEFAEHGAMNQRGGVIVNGEESLLPWSVRLKIGKEIANAVTY : 178
Zdr-1 : NFLQLLGCCLFPPFPVLVFEFAEHGAMNQRGGVIVNGEESLLPWSVRLKIGKEIANAVTY : 178
Alyrata : NFLQLLGCCLFPPFPVLVFEFAEYGAALNQRGGVIVNGEESLLPWSVRLKIGKEIANAVSY : 180
Brapa : NFLQLLGCCLFPPFPVLVFEFAAGNGLNERGGIVNGEESLLPWSVRLKIGKEIANAVTY : 176

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          *           200           *           220           *           240
Col-0 : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYIDPL : 238
Bay-0 : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYIDPL : 237
Bil-5 : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYIDPL : 238
Br-0 : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYIDPL : 238
Ct-1 : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYIDPL : 238
Cvi-0 : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYIDPL : 238
Ei-2 : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYIDPL : 238
Est-1 : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYIDPL : 238
Kas-1 : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYIDPL : 238
Lp2-2 : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYIDPL : 238
Nd-1 : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYIDPL : 238
Zdr-1 : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYIDPL : 238
Alyrata : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYLDPL : 240
Brapa : LHIAFPKIIHRDVKPMHVFLDKNWTAKLSDLSEFSISLPEGKSRIEAEWVLGTFGYLDPL : 236

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HRD

DFG

APE

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*           260           *           280           *           300
Col-0 : YHKTCFVTEYTDVYSFGICLLVLIITGKPAIMTISDGDLOGILSLVRELCENGKLDEVIDP : 298
Bay-0 : YHKTCFVTEYTDVYSFGICLLVLIITGKPAIMTISDGDLOGILSLVRELCENGKLDEVIDP : 297
Bil-5 : YHKTCFVTEYTDVYSFGICLLVLIITGKPAIMTISDGDLOGILSLVRELCENGKLDEVIDP : 298
Br-0   : YHKTCFVTEYTDVYSFGICLLVLIITGKPAIMTISDGDLOGILSLVRELCENGKLDEVIDP : 298
Ct-1   : YHKTCFVTEYTDVYSFGICLLVLIITGKPAIMTISDGDLOGILSLVRELCENGKLDEVIDP : 298
Cvi-0  : YHKTCFVTEYTDVYSFGICLLVLIITGKPAIMTISDGDLOGILSLVRELCENGKLDEVIDP : 298
Ei-2   : YHKTCFVTEYTDVYSFGICLLVLIITGKPAIMTISDGDLOGILSLVRELCENGKLDEVIDP : 298
Est-1  : YHKTCFVTEYTDVYSFGICLLVLIITGKPAIMTISDGDLOGILSLVRELCENGKLDEVIDP : 298
Kas-1  : YHKTCFVTEYTDVYSFGICLLVLIITGKPAIMTISDGDLOGILSLVRELCENGKLDEVIDP : 298
Lp2-2  : YHKTCFVTEYTDVYSFGICLLVLIITGKPAIMTISDGDLOGILSLVRELCENGKLDEVIDP : 298
Nd-1   : YHKTCFVTEYTDVYSFGICLLVLIITGKPAIMTISDGDLOGILSLVRELCENGKLDEVIDP : 298
Zdr-1  : YHKTCFVTEYTDVYSFGICLLVLIITGKPAIMTISDGDLOGILSLVRELCENGKLDEVIDP : 298
Alyrata : YHKTSFVTEYTDVYSFGICLLVILTGKPAIITISDGDLOGILSYVRLCENGKLDEVIDP : 300
Brapa  : YHATSFVTEYTDVYSFGICLLVLVTGKPSVVIITSDGDPQGILSYVVGLWENGLKVNVEVIDP : 296

*           320           *           340           *
Col-0 : RLMKDITSGQRLOVEACVVLALRCCCKERDEDRPKMIQVAKELKQIEASLKNSS : 351
Bay-0 : RLMKDITSGQRLOVEACVVLALRCCCKERDEDRPKMIQVAKELKQIEASLKNSS : 350
Bil-5 : RLMKDITSGQRLOVEACVVLALRCCCKERDEDRPKMIQVAKELKQIEASLKNSS : 351
Br-0   : RLMKDITSGQRLOVEACVVLALRCCCKERDEDRPKMIQVAKELKQIEASLKNSS : 351
Ct-1   : RLMKDITSGQRLOVEACVVLALRCCCKERDEDRPKMIQVAKELKQIEASLKNSS : 351
Cvi-0  : RLMKDITSGQRLOVEACVVLALRCCCKERDEDRPKMIQVAKELKQIEASLKNSS : 351
Ei-2   : RLMKDITSGQRLOVEACVVLALRCCCKERDEDRPKMIQVAKELKQIEASLKNSS : 351
Est-1  : RLMKDITSGQRLOVEACVVLALRCCCKERDEDRPKMIQVAKELKQIEASLKNSS : 351
Kas-1  : RLMKDITSGQRLOVEACVVLALRCCCKERDEDRPKMIQVAKELKQIEASLKNSS : 351
Lp2-2  : RLMKDITSGQRLOVEACVVLALRCCCKERDEDRPKMIQVAKELKQIEASLKNSS : 351
Nd-1   : RLMKDITSGQRLOVEACVVLALRCCCKERDEDRPKMIQVAKELKQIEASLKNSS : 351
Zdr-1  : RLMKDITSGQRLOVEACVVLALRCCCKERDEDRPKMIQVAKELKQIEASLKNSS : 351
Alyrata : RLMKDITSGQRLOVEACVVLALRCCCKERDEYRPKVIQVAKELKRIEASLRNSS : 353
Brapa  : MIAKDITSGQKSQVEMCVGLALRCCCEARDEYRPKMIQVAKELKLIETLRDTS : 349

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Figure S12. Alignment of the 12 different *RKS1* protein sequences from *A. thaliana* and putative *RKS1* orthologous from *Arabidopsis lyrata* and *Brassica rapa* subsp. *pekinensis*. The major domains in the kinase catalytic core of kinase proteins described in Figure S6 are underlined in red. Numbering corresponds to the amino acid sequence. Every tenth residue in *RKS1* is marked by *. *A. lyrata* NCBI Reference Sequence: XM_002878122.1. *Brassica rapa* subsp. *pekinensis* Sequence ID: [gb|AC232509.1](https://www.ncbi.nlm.nih.gov/nuccore/gb|AC232509.1)