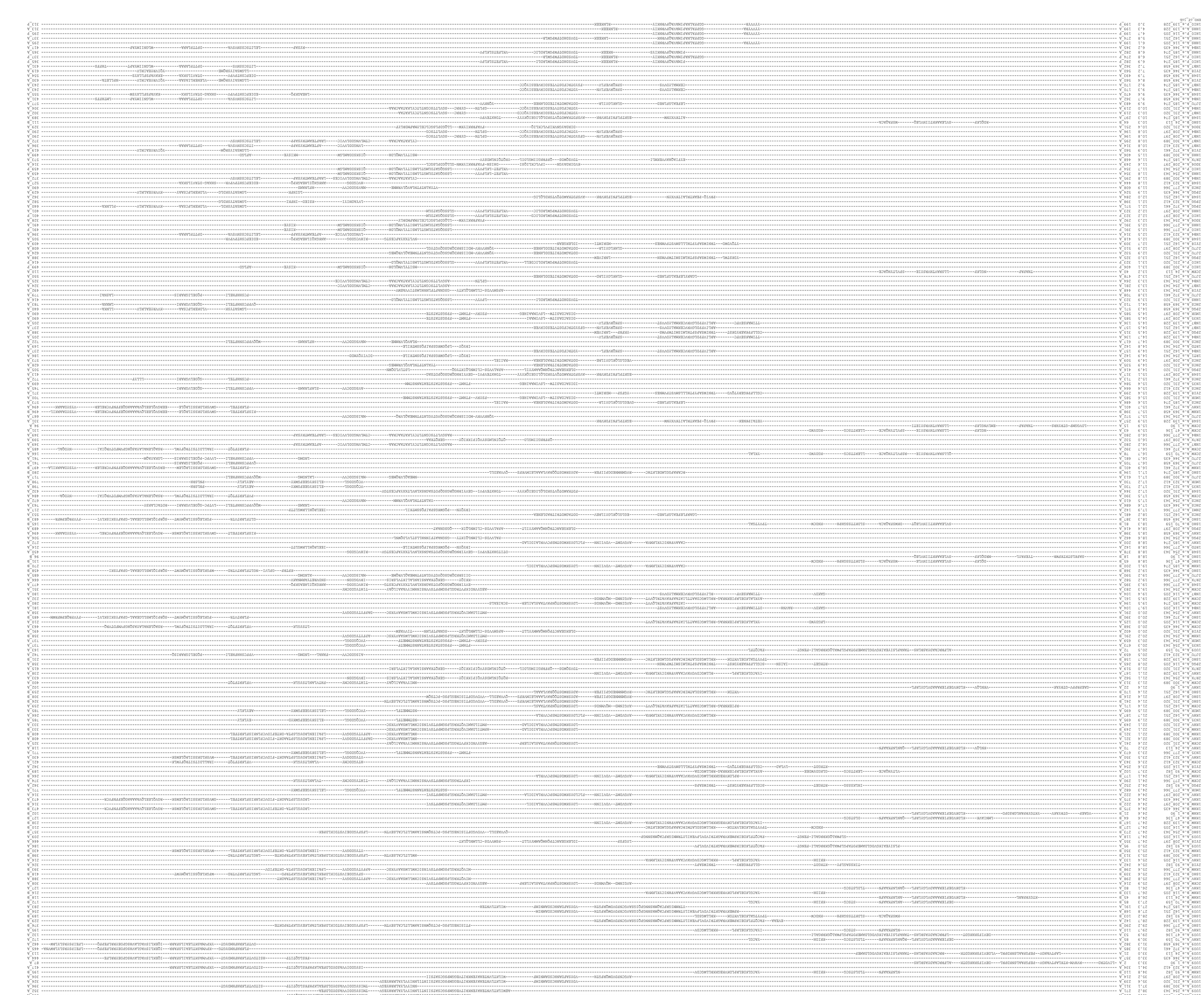

```
Residue numbering: 1_A - 461_A Selected range: 1_A - 461_A
Refname              100.0    1_A GEIQWMRPSKEVGYPIINAPSKTKLEPSAFHYVFEGVKEPAVLTKNDPRLKTDFEEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMSLDINTEQMXLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVITGSAVGXDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHLYKNKTYXVKGGMPSGXSGTSIFNSMINNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAKIRSVPIGRALDLPEYSTLYDRWLDSF 461_A
3OL7_A.s_346_435     100.0  346_A ---SGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAK--- 435_A
3OL7_A.s_323_412     100.0  323_A ---MIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQD--- 412_A
3OL7_A.s_300_389     100.0  300_A ---INNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIH--- 389_A
3OL7_A.s_1_90        100.0    1_A GEIQWMRPSKEVGYPIINAPSKTKLEPSAFHYVFEGVKEPAVLTKNDPRLKTDFEEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMSLDI--- 90_A
3OL7_A.s_116_205     100.0  116_A ---AGYPYVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVI--- 205_A
3OL6_A.s_346_435     100.0  346_A ---SGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAK--- 435_A
3OL6_A.s_323_412     100.0  323_A ---MIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQD--- 412_A
3OL6_A.s_300_389     100.0  300_A ---INNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIH--- 389_A
3OL6_A.s_1_90        100.0    1_A GEIQWMRPSKEVGYPIINAPSKTKLEPSAFHYVFEGVKEPAVLTKNDPRLKTDFEEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMSLDI--- 90_A
3OL6_A.s_116_205     100.0  116_A ---AGYPYVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVI--- 205_A
1RA6_A.s_93_182      100.0   93_A ---EQMXLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLN--- 182_A
1RA6_A.s_70_159      100.0   70_A ---VDEYMKEAVDHYAGQLMSLDINTEQMXLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVK--- 159_A
1RA6_A.s_47_136      100.0   47_A ---DPRLKTDFEEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMSLDINTEQMXLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTR--- 136_A
1RA6_A.s_372_461     100.0  372_A ---TFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAKIRSVPIGRALDLPEYSTLYDRWLDSF 461_A
1RA6_A.s_369_458     100.0  369_A ---ENVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAKIRSVPIGRALDLPEYSTLYDRWL--- 458_A
1RA6_A.s_346_435     100.0  346_A ---SGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAK--- 435_A
1RA6_A.s_323_412     100.0  323_A ---MIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQD--- 412_A
1RA6_A.s_300_389     100.0  300_A ---INNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIH--- 389_A
1RA6_A.s_277_366     100.0  277_A ---NKTYXVKGGMPSGXSGTSIFNSMINNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETV--- 366_A
1RA6_A.s_254_343     100.0  254_A ---EKIGFGDRVDYIDYLNHSHHLYKNKTYXVKGGMPSGXSGTSIFNSMINNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLL--- 343_A
1RA6_A.s_24_113      100.0   24_A ---KLEPSAFHYVFEGVKEPAVLTKNDPRLKTDFEEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMSLDINTEQMXLEDAMYGTDGLEALDLS--- 113_A
1RA6_A.s_231_320     100.0  231_A ---AFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHLYKNKTYXVKGGMPSGXSGTSIFNSMINNLIIRTLLLKTYKGIDLDH--- 320_A
1RA6_A.s_208_297     100.0  208_A ---SAVGXDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHLYKNKTYXVKGGMPSGXSGTSIFN--- 297_A
1RA6_A.s_1_90        100.0    1_A GEIQWMRPSKEVGYPIINAPSKTKLEPSAFHYVFEGVKEPAVLTKNDPRLKTDFEEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMSLDI--- 90_A
1RA6_A.s_185_274     100.0  185_A ---VAMRMAFGNLYAAFHKNPGVITGSAVGXDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHL--- 274_A
1RA6_A.s_162_251     100.0  162_A ---LRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVITGSAVGXDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKM--- 251_A
1RA6_A.s_139_228     100.0  139_A ---KEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVITGSAVGXDPDLFWSKIPVLMEEK--- 228_A
1RA6_A.s_116_205     100.0  116_A ---AGYPYVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVI--- 205_A
3OL7_A.s_93_182       98.9   93_A ---EQMCLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLN--- 182_A
3OL7_A.s_70_159       98.9   70_A ---VDEYMKEAVDHYAGQLMSLDINTEQMCLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVK--- 159_A
3OL7_A.s_47_136       98.9   47_A ---DPRLKTDFEEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMSLDINTEQMCLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTR--- 136_A
3OL7_A.s_372_461      98.9  372_A ---TFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAKIRSVPIGRALDLPEYSTLYRRWLDSF 461_A
3OL7_A.s_369_458      98.9  369_A ---ENVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAKIRSVPIGRALDLPEYSTLYRRWL--- 458_A
3OL7_A.s_24_113       98.9   24_A ---KLEPSAFHYVFEGVKEPAVLTKNDPRLKTDFEEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMSLDINTEQMCLEDAMYGTDGLEALDLS--- 113_A
3OL7_A.s_185_274      98.9  185_A ---VAMRMAFGNLYAAFHKNPGVITGSAVGCDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHL--- 274_A
3OL7_A.s_162_251      98.9  162_A ---LRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVITGSAVGCDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKM--- 251_A
3OL7_A.s_139_228      98.9  139_A ---KEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVITGSAVGCDPDLFWSKIPVLMEEK--- 228_A
3OL6_A.s_93_182       98.9   93_A ---EQMCLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLN--- 182_A
3OL6_A.s_70_159       98.9   70_A ---VDEYMKEAVDHYAGQLMSLDINTEQMCLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVK--- 159_A
3OL6_A.s_47_136       98.9   47_A ---DPRLKTDFEEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMSLDINTEQMCLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTR--- 136_A
3OL6_A.s_372_461      98.9  372_A ---TFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAKIRSVPIGRALDLPEYSTLYRRWLDSF 461_A
3OL6_A.s_369_458      98.9  369_A ---ENVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAKIRSVPIGRALDLPEYSTLYRRWL--- 458_A
3OL6_A.s_24_113       98.9   24_A ---KLEPSAFHYVFEGVKEPAVLTKNDPRLKTDFEEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMSLDINTEQMCLEDAMYGTDGLEALDLS--- 113_A
3OL6_A.s_185_274      98.9  185_A ---VAMRMAFGNLYAAFHKNPGVITGSAVGCDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHL--- 274_A
3OL6_A.s_162_251      98.9  162_A ---LRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVITGSAVGCDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKM--- 251_A
3OL6_A.s_139_228      98.9  139_A ---KEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVITGSAVGCDPDLFWSKIPVLMEEK--- 228_A
3OL7_A.s_277_366      97.8  277_A ---NKTYCVKGGMPSGCSGTSIFNSMINNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETV--- 366_A
3OL7_A.s_254_343      97.8  254_A ---EKIGFGDRVDYIDYLNHSHHLYKNKTYCVKGGMPSGCSGTSIFNSMINNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLL--- 343_A
3OL7_A.s_231_320      97.8  231_A ---AFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHLYKNKTYCVKGGMPSGCSGTSIFNSMINNLIIRTLLLKTYKGIDLDH--- 320_A
3OL6_A.s_277_366      97.8  277_A ---NKTYCVKGGMPSGCSGTSIFNSMINNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETV--- 366_A
3OL6_A.s_254_343      97.8  254_A ---EKIGFGDRVDYIDYLNHSHHLYKNKTYCVKGGMPSGCSGTSIFNSMINNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLL--- 343_A
3OL6_A.s_231_320      97.8  231_A ---AFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHLYKNKTYCVKGGMPSGCSGTSIFNSMINNLIIRTLLLKTYKGIDLDH--- 320_A
3OL7_A.s_208_297      96.7  208_A ---SAVGCDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHLYKNKTYCVKGGMPSGCSGTSIFN--- 297_A
3OL6_A.s_208_297      96.7  208_A ---SAVGCDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHLYKNKTYCVKGGMPSGCSGTSIFN--- 297_A
3DDK_A.s_372_461      80.0  373_A ---TFLKRYFRADEQYPFLVHPVMPMKDIHESIRWTKDPKNTQDHVRSLCLLAWHNGEHEYEEFIRKIRSVPVGRCLTLPAFSTLRRKWLDSF 462_A
3DDK_A.s_323_412      80.0  324_A ---MIAYGDDVIASYPWPIDASLLAEAGKGYGLIMTPADKGECFNEVTWTNVTFLKRYFRADEQYPFLVHPVMPMKDIHESIRWTKDPKNTQD--- 413_A
3DDK_A.s_369_458      78.9  370_A ---TNVTFLKRYFRADEQYPFLVHPVMPMKDIHESIRWTKDPKNTQDHVRSLCLLAWHNGEHEYEEFIRKIRSVPVGRCLTLPAFSTLRRKWL--- 459_A
3DDK_A.s_346_435      78.9  347_A ---AGKGYGLIMTPADKGECFNEVTWTNVTFLKRYFRADEQYPFLVHPVMPMKDIHESIRWTKDPKNTQDHVRSLCLLAWHNGEHEYEEFIRK--- 436_A
3DDK_A.s_47_136       77.8   48_A ---PRLKANFEEAIFSKYIGNVN-HVDEYMLEAVDHYAGQLATLDISTEPMKLEDAVYGTEGLEALDLTTSAGYPYVALGIKKRDILSKKT--- 135_A
3DDK_A.s_24_113       76.7   25_A ---LEPSVFHQVFEGNKEPAVLRSGDPRLKANFEEAIFSKYIGNVN-HVDEYMLEAVDHYAGQLATLDISTEPMKLEDAVYGTEGLEALDL--- 112_A
3DDK_A.s_162_251      76.7  163_A ---RSIEKVAKGKSRLI-ASSLNDSVAMRQTFGNLYKTFHLNPGVVTGSAVGCDPDLFWSKIPVM---HLIAFDYSGYDASLSPVWFACLK--- 250_A
3DDK_A.s_300_389      75.6  301_A ---INNIIRTLMLKVYKGIDLDQFRMIAYGDDVIASYPWPIDASLLAEAGKGYGLIMTPADKGECFNEVTWTNVTFLKRYFRADEQYPFLVH--- 390_A
3DDK_A.s_277_366      74.4  278_A ---DKHYFVRGGMPSGCSGTSIFNSMINNIIIRTLMLKVYKGIDLDQFRMIAYGDDVIASYPWPIDASLLAEAGKGYGLIMTPADKGECFNEV--- 367_A
3DDK_A.s_254_343      73.3  263_A ---TNYIDYLCNSHHLYRDKHYFVRGGMPSGCSGTSIFNSMINNIIIRTLMLKVYKGIDLDQFRMIAYGDDVIASYPWPIDASL--- 343_A
3DDK_A.s_231_320      73.3  232_A ---FDYSGYDASLSPVWFACLKMILEKLGY---TNYIDYLCNSHHLYRDKHYFVRGGMPSGCSGTSIFNSMINNIIIRTLMLKVYKGIDLD--- 320_A
3DDK_A.s_93_182       72.2   94_A ---PMKLEDAVYGTEGLEALDLTTSAGYPYVALGIKKRDILSKKTKDLTKLKECMDKYGLNLPMVTYVKDELRSIEKVAKGKSRLI--- 176_A
3DDK_A.s_70_159       72.2   70_A ---VDEYMLEAVDHYAGQLATLDISTEPMKLEDAVYGTEGLEALDLTTSAGYPYVALGIKKRDILSKKTKDLTKLKECMDKYGLNLPMVTYVK--- 159_A
3DDK_A.s_1_90         72.2    2_A -EIEFIESSKDAGFPVINTPSKTKLEPSVFHQVFEGNKEPAVLRSGDPRLKANFEEAIFSKYIGNVN-HVDEYMLEAVDHYAGQLATLD--- 89_A
3DDK_A.s_139_228      71.1  140_A ---KLKECMDKYGLNLPMVTYVKDELRSIEKVAKGKSRLI-ASSLNDSVAMRQTFGNLYKTFHLNPGVVTGSAVGCDPDLFWSKIPVM--- 224_A
3DDK_A.s_116_205      71.1  117_A ---GYPYVALGIKKRDILSKKTKDLTKLKECMDKYGLNLPMVTYVKDELRSIEKVAKGKSRLI-ASSLNDSVAMRQTFGNLYKTFHLNPGV--- 204_A
3DDK_A.s_208_297      70.0  209_A ---AVGCDPDLFWSKIPVM---HLIAFDYSGYDASLSPVWFACLKMILEKLGY---TNYIDYLCNSHHLYRDKHYFVRGGMPSGCSGTSIF--- 297_A
3DDK_A.s_185_274      70.0  186_A ---AMRQTFGNLYKTFHLNPGVVTGSAVGCDPDLFWSKIPVM---HLIAFDYSGYDASLSPVWFACLKMILEKLGY---TNYIDYLCNSHH--- 274_A
1XR7_A.s_300_389      63.3  299_A ---INNIIRTLVLDAYKHIDLDKLKIIAYGDDVIFSYKYKLDMEAIAKEGQKYGLTITPADKSSEFKELDYGNVTFLKRGFRQDDKYKFLIH--- 388_A
1XR7_A.s_277_366      63.3  276_A ---STYYEVEGGVPSGCSGTSIFNSMINNIIIRTLVLDAYKHIDLDKLKIIAYGDDVIFSYKYKLDMEAIAKEGQKYGLTITPADKSSEFKEL--- 365_A
1XR6_A.s_300_389      63.3  299_A ---INNIIRTLVLDAYKHIDLDKLKIIAYGDDVIFSYKYTLDMEAIANEGKKYGLTITPADKSTEFKKLDYNNVTFLKRGFKQDEKHTFLIH--- 388_A
1XR6_A.s_277_366      63.3  276_A ---STYYEVAGGVPSGCSGTSIFNTMINNIIIRTLVLDAYKHIDLDKLKIIAYGDDVIFSYKYTLDMEAIANEGKKYGLTITPADKSTEFKKL--- 365_A
1XR6_A.s_231_320      62.5  233_A ---FDYTNYDGSIHPVWFQALKKVLENLSF---NLIDRLCYSKHLFKSTYYEVAGGVPSGCSGTSIFNTMINNIIIRTLVLDAYKHIDLD--- 318_A
1XR7_A.s_369_458      61.1  368_A ---GNVTFLKRGFRQDDKYKFLIHPTFPVEEIYESIRWTKKPSQMQEHVLSLCHLMWHNGPEIYKDFETKIRSVSAGRALYIPPYELLRHEWY--- 457_A
1XR7_A.s_346_435      61.1  345_A ---EGQKYGLTITPADKSSEFKELDYGNVTFLKRGFRQDDKYKFLIHPTFPVEEIYESIRWTKKPSQMQEHVLSLCHLMWHNGPEIYKDFETK--- 434_A
1XR7_A.s_231_320      60.2  233_A ---FDYTNYDGSIHPIWFKALGMVLDNLS------LINRLCNSKHIFKSTYYEVEGGVPSGCSGTSIFNSMINNIIIRTLVLDAYKHIDLD--- 318_A
1XR7_A.s_372_461      60.0  371_A ---TFLKRGFRQDDKYKFLIHPTFPVEEIYESIRWTKKPSQMQEHVLSLCHLMWHNGPEIYKDFETKIRSVSAGRALYIPPYELLRHEWYEKF 460_A
1XR6_A.s_346_435      60.0  345_A ---EGKKYGLTITPADKSTEFKKLDYNNVTFLKRGFKQDEKHTFLIHPTFPVEEIYESIRWTKKPSQMQEHVLSLCHLMWHNGRKVYEDFSSK--- 434_A
1XR6_A.s_162_251      60.0  163_A ---RKKEKISAGKTRVIEASSINDTILFRTTFGNLFSKFHLNPGVVTGSAVGCDPETFWSKIPVM----IMAFDYTNYDGSIHPVWFQALK--- 251_A
1XR6_A.s_254_343      59.1  261_A ---SNLIDRLCYSKHLFKSTYYEVAGGVPSGCSGTSIFNTMINNIIIRTLVLDAYKHIDLDKLKIIAYGDDVIFSYKYTLDMEA--- 341_A
1XR6_A.s_208_297      59.1  209_A ---AVGCDPETFWSKIPVM----IMAFDYTNYDGSIHPVWFQALKKVLENLSF---NLIDRLCYSKHLFKSTYYEVAGGVPSGCSGTSIF--- 295_A
1XR7_A.s_323_412      58.9  322_A ---IIAYGDDVIFSYKYKLDMEAIAKEGQKYGLTITPADKSSEFKELDYGNVTFLKRGFRQDDKYKFLIHPTFPVEEIYESIRWTKKPSQMQE--- 411_A
1XR6_A.s_369_458      58.9  368_A ---NNVTFLKRGFKQDEKHTFLIHPTFPVEEIYESIRWTKKPSQMQEHVLSLCHLMWHNGRKVYEDFSSKIRSVSAGRALYIPPYDLLKHEWY--- 457_A
1XR6_A.s_323_412      58.9  322_A ---IIAYGDDVIFSYKYTLDMEAIANEGKKYGLTITPADKSTEFKKLDYNNVTFLKRGFKQDEKHTFLIHPTFPVEEIYESIRWTKKPSQMQE--- 411_A
1XR6_A.s_372_461      57.8  371_A ---TFLKRGFKQDEKHTFLIHPTFPVEEIYESIRWTKKPSQMQEHVLSLCHLMWHNGRKVYEDFSSKIRSVSAGRALYIPPYDLLKHEWYEKF 460_A
1XR7_A.s_254_343      56.8  263_A ---LINRLCNSKHIFKSTYYEVEGGVPSGCSGTSIFNSMINNIIIRTLVLDAYKHIDLDKLKIIAYGDDVIFSYKYKLDMEA--- 341_A
1XR6_A.s_185_274      56.8  186_A ---LFRTTFGNLFSKFHLNPGVVTGSAVGCDPETFWSKIPVM----IMAFDYTNYDGSIHPVWFQALKKVLENLSF---NLIDRLCYSKH--- 272_A
1XR7_A.s_162_251      56.7  163_A ---RKKDKIAAGKTRVIEASSINDTILFRTVYGNLFSKFHLNPGVVTGCAVGCDPETFWSKIPLM----IMAFDYTNYDGSIHPIWFKALG--- 251_A
1XR6_A.s_93_182       55.6   93_A ---KPIALEDSVFGIEGLEALDLNTSAGFPYVTMGIKKRDLINNKTKDISRLKEALDKYGVDLPMITFLKDELRKKEKISAGKTRVIEASSIN--- 182_A
1XR6_A.s_24_113       55.6   25_A ---LQPSVFYDVFPGSKEPAVLTDNDPRLKVNFKEALFSKYKGNTE-SLNQHMEIAIAHYSAQLITLDIDSKPIALEDSVFGIEGLEALDL--- 112_A
1XR6_A.s_139_228      55.6  140_A ---RLKEALDKYGVDLPMITFLKDELRKKEKISAGKTRVIEASSINDTILFRTTFGNLFSKFHLNPGVVTGSAVGCDPETFWSKIPVM--- 224_A
1XR7_A.s_93_182       54.4   93_A ---QPIAMEDSVFGMDGLEALDLNTSAGYPYVTLGIKKKDLINNKTKDISKLKLALDKYGVDLPMITFLKDELRKKDKIAAGKTRVIEASSIN--- 182_A
1XR7_A.s_47_136       54.4   48_A ---PRLKVDFDSALFSKYKGNTE-SLNEHIQVAVAHYSAQLATLDIDPQPIAMEDSVFGMDGLEALDLNTSAGYPYVTLGIKKKDLINNKT--- 135_A
1XR7_A.s_24_113       54.4   25_A ---LQPSVFYDIFPGSKEPAVLTEKDPRLKVDFDSALFSKYKGNTE-SLNEHIQVAVAHYSAQLATLDIDPQPIAMEDSVFGMDGLEALDL--- 112_A
1XR7_A.s_1_90         54.4    2_A -QIQISKHVKDVGLPSIHTPTKTKLQPSVFYDIFPGSKEPAVLTEKDPRLKVDFDSALFSKYKGNTE-SLNEHIQVAVAHYSAQLATLD--- 89_A
1XR6_A.s_47_136       54.4   48_A ---PRLKVNFKEALFSKYKGNTE-SLNQHMEIAIAHYSAQLITLDIDSKPIALEDSVFGIEGLEALDLNTSAGFPYVTMGIKKRDLINNKT--- 135_A
1XR6_A.s_1_90         54.4    2_A -QIKISKHANECGLPTIHTPSKTKLQPSVFYDVFPGSKEPAVLTDNDPRLKVNFKEALFSKYKGNTE-SLNQHMEIAIAHYSAQLITLD--- 89_A
1XR6_A.s_116_205      54.4  116_A ---AGFPYVTMGIKKRDLINNKTKDISRLKEALDKYGVDLPMITFLKDELRKKEKISAGKTRVIEASSINDTILFRTTFGNLFSKFHLNPGVV--- 205_A
1XR7_A.s_208_297      53.4  209_A ---AVGCDPETFWSKIPLM----IMAFDYTNYDGSIHPIWFKALGMVLDNLS------LINRLCNSKHIFKSTYYEVEGGVPSGCSGTSIF--- 295_A
1XR7_A.s_139_228      52.2  140_A ---KLKLALDKYGVDLPMITFLKDELRKKDKIAAGKTRVIEASSINDTILFRTVYGNLFSKFHLNPGVVTGCAVGCDPETFWSKIPLM--- 224_A
1XR7_A.s_116_205      52.2  116_A ---AGYPYVTLGIKKKDLINNKTKDISKLKLALDKYGVDLPMITFLKDELRKKDKIAAGKTRVIEASSINDTILFRTVYGNLFSKFHLNPGVV--- 205_A
1XR7_A.s_185_274      50.0  186_A ---LFRTVYGNLFSKFHLNPGVVTGCAVGCDPETFWSKIPLM----IMAFDYTNYDGSIHPIWFKALGMVLDNLS------LINRLCNSKH--- 272_A
1XR7_A.s_70_159       48.9   70_A ---LNEHIQVAVAHYSAQLATLDIDPQPIAMEDSVFGMDGLEALDLNTSAGYPYVTLGIKKKDLINNKTKDISKLKLALDKYGVDLPMITFLK--- 159_A
1XR6_A.s_70_159       48.9   70_A ---LNQHMEIAIAHYSAQLITLDIDSKPIALEDSVFGIEGLEALDLNTSAGFPYVTMGIKKRDLINNKTKDISRLKEALDKYGVDLPMITFLK--- 159_A
1U09_A.s_277_366      43.3  288_A ---KRITVEGGMPSGCSATSIINTILNNIYVLYALRRHYEGV----TMISYGDDIVVASDYDLDFEALKPHFKSLGQTITP--- 366_A
1U09_A.s_254_343      38.2  271_A ---AEWILKTLVNTEHAYENKRITVEGGMPSGCSATSIINTILNNIYVLYALRRHYEGV----TMISYGDDIVVASDYDLDFEA--- 352_A
1U09_A.s_300_389      37.1  311_A ---NNIYVLYALRRHYEGV----TMISYGDDIVVASDYDLDFEALKPHFKSLGQTITP---------SITDVTFLKRHFHMDYGT--- 396_A
1U09_A.s_231_320      35.6  239_A ---VDYSAFDANHCSDAMNIMF-----------WILKTLVNTEHAYENKRITVEGGMPSGCSATSIINTILNNIYVLYALRRHYEGV--- 326_A
1U09_A.s_208_297      35.2  214_A ---AVGCNPDVDWQRFGTH------VDYSAFDANHCSDAMNIMF-----------WILKTLVNTEHAYENKRITVEGGMPSGCSATSII--- 306_A
1KHW_B.s_93_182       34.8  110_B ---NLNFKAAFN-----TLDLSTSCG-------KKIDH--------------------YACGLKDELRPLDKVKEGKKRLLWGCDV--- 195_B
1U09_A.s_323_412      34.1  334_A ---ISYGDDIVVASDYDLDFEALKPHFKSLGQTITP---------SITDVTFLKRHFHMDYGT---YKPVMASKTLEAILSFARR--- 417_A
1U09_A.s_1_90         33.3    2_A -LIVDTRD-------RVHVM-KTKLAPTVAHGV--PEFGPAALSNKDPRL----DEVIFSKHKGDTK----ALFRRCAADYASRLHS--- 87_A
1U09_A.s_346_435      33.0  357_A ---FKSLGQTITP--------HSITDVTFLKRHFHMDYGT---YKPVMASKTLEAILSFARR---IQEKLISVAGLAVHSGPDEYRRLFE--- 444_A
1U09_A.s_24_113       33.0   21_A ---LAPTVAHGV--PEFGPAALSNKDPRL--VLDEVIFSKHKGDTK-------RRCAADYASRLHS--TANAPLSIYEAIKGVDGLDAMEP--- 113_A
1U09_A.s_372_461      31.3  385_A ---FLKRHFHMDYGTG---KPVMASKTLEAILSFARR---IQEKLISVAGLAVHSGPDEYRRLFEPFQ------LFEIPSYRSLYLRWVNA- 465_A
1U09_A.s_369_458      31.3  382_A ---DVTFLKRHFHMDYGT---YKPVMASKTLEAILSFARR---IQEKLISVAGLAVHSGPDEYRRLFEPFQ------LFEIPSYRSLYLRW---- 462_A
1KHV_A.s_70_159       30.9   85_A ---DEFIERAAADVLGYLRFL--RQANLNFKAAFN-----TLDLSTSCG-------KKIDH--------------------YACGL--- 172_A
1U09_A.s_47_136       29.9   53_A ---DEVIFSKHKGDT-----LFRRCAADYASRLHS--TANAPLSIYEAIKGVDGLDAMEPDTAPGLPWALQGKRRGALI--- 132_A
1KHV_A.s_93_182       29.7  110_A ---NLNFKAAFN---------STSCG---------------------IYACGLKDELRPL-----KKRLLWGCDV--- 195_A
1SH0_B.s_277_366      29.2  290_B ---FTISINEGLPSG-PCTSQWNSIAHWLLTLCALSEVTN------LFSFYGDDEIVSTDIKLDPEKLTAKLKEYGLKPTRPDKTE--- 376_B
1U09_A.s_139_228      28.7  142_A ---EVEAA---FACQTFLKDEIRPMEKVRAGKTRIVDVLPVEHILYTRMMIGRFCAQMHSNNGPQIGSAVGCNPDVDWQRFGTH--- 229_A
1SH0_B.s_93_182       28.2  103_B ---KWSFAQACA------SLDKTTSSGHPH------KNDCW-------------------TPVYTGALKDELVKTDK-----KRLLWGSDL--- 189_B
1U09_A.s_162_251      27.8  168_A ---RPMEKVRAGKTRIVDVLPVEHILYTRMMIGRFCAQMHSNNGPQIGSAVGCNPDVDWQRFGTH------VDYSAFDANHCSDAMNIM--- 256_A
1U09_A.s_185_274      27.3  191_A ---YTRMMIGRFCAQMHSNNGPQIGSAVGCNPDVDWQRFGTH------VDYSAFDANHCSDAMNIMF-----------WILKTLVNTEH--- 283_A
1KHW_B.s_70_159       27.3   85_B ---DEFIERAAADVLGYLRFL----ANLNFKAAFN---------STSCG--------KKIDH--------------------YACGL--- 172_B
1KHW_B.s_24_113       26.8   45_B ---KTGYRPANL---------------------KLDKVDEFIERAAADVLGYLRFL----ANLNFKAAFN--- 118_B
1KHW_B.s_116_205      26.7  133_B ---KKIDH--------------------YACGLKDELRPLDKVKEGKKRLLWGCDVGVAVCAAAVFHNICYKLKMVA--- 216_B
1KHV_A.s_47_136       26.1   80_A ---KLDKVDEFIERAAADVLGYLRFL---QANLNFKAAFN-----TLDLSTSCG--- 127_A
2CKW_A.s_208_297      25.9  216_A ---AVGINMD--MQVMNDS-------LDYSKWDSTQNPAVTAASLAILERF-------------AEGYVNDIKFVTRGGLPSGMPFTSVV--- 308_A
1KHV_A.s_277_366      25.8  298_A ---MIVQTKRGLPSGMPFTSVINSICHWLLWSAAVYKSC-------APFFYTYGDDGVY------LPAIIENLRDYGLSPTAADKT--- 388_A
1SH0_B.s_323_412      25.6  339_B ---SFYGDDEIVSTDIKLDPEKLTAKLKEYGLKPTRPD-----LNGLTFLRRTVTRD-----WFGKLEQSSILRQMYWT--- 418_B
1KHW_B.s_277_366      25.6  298_B ---MIVQTKRGLPSGMPFTSVINSICHWLLWSAAVYKSC-------APFFYTYGDDGVY------LPAIIENLRDYGLSPTA-DKTEFIDV--- 393_B
2YI8_A.s_93_182       25.4  242_A ---TIKSSAGLPY----KTKGDT-------------------GLLFPKGERY--------TRNIWSAPY--- 326_A
1KHV_A.s_116_205      25.4  133_A ---KKIDH--------------------YACGLKDELRPL--------KKRLLWGCDVGVAVCAAAVFHNICYKLKMVA--- 216_A
1SH0_B.s_300_389      25.3  313_B ---HWLLTLCALSEVTN------LFSFYGDDEIVSTDIKLDPEKLTAKLKEYGLKPTRPDKTE-----LNGLTFLRRTVTRD--- 398_B
1KHW_B.s_323_412      25.3  350_B ---YTYGDDGVY----------IIENLRDYGLSPTA-DKTEFIDVCPLNKISFLKRTFEL------WVSKLDKSSILRQLEWSK--- 430_B
1U09_A.s_93_182       25.0   95_A ---PLSIYEAIKGVDGLDAMEPDTAPGLPWALQGKRRGALI-FENGT-------------FACQTFLKDEIRPMEKVRAGKTRIVDVLPV--- 186_A
2YI8_A.s_208_297      24.7  355_A ---LYGFSP-----------------IDLEKGEANCTPQHMQAMMYYLLT---------PSMVVDS-CLLMNLQLKT--- 466_A
1U09_A.s_116_205      24.7  118_A ---GLPWALQGKRRGALI-FENGT-------------FACQTFLKDEIRPMEKVRAGKTRIVDVLPVEHILYTRMMIGRFCAQMHSNNGP--- 209_A
1SH0_B.s_254_343      24.7  273_B ---QVVAEDLL--VVDVGDFTISINEGLPSG-PCTSQWNSIAHWLLTLCALSEVTN------LFSFYGDDEIVSTDIKLDPEK--- 357_B
1SH0_B.s_116_205      24.7  127_B ---KNDCW-------------------TPVYTGALKDELVKTDK-----KRLLWGSDLATMIRCARAFGGLMDELKTHC--- 210_B
1KHW_B.s_139_228      24.7  167_B ---IYACGLKDELRPLDKVKEGKKRLLWGCDVGVAVCAAAVFHNICYKLKMVA------AVGVDMT--VDVIINN--- 238_B
1KHW_B.s_47_136       24.6   64_B ---LMNIAVK-----KLDKVDEFIERAAADVLGYLRFL---QANLNFKAAFN--------DLSTSCG--- 127_B
1KHW_B.s_1_90         24.6   21_B ---VGAEP-----GTRYAKV-----YKTGYRPANLGRSDPD-------KLDKVDEFIERAAADVLGYLRFL--- 102_B
1KHW_B.s_346_435      24.4  375_B ---LRDYGLSPTA-DKTEFIDVCPLNKISFLKRTFEL------GWVSKLDKSSILRQLEWSK---RGVQLEELQVAAAAHGQEFFNFVCR--- 473_B
1KHW_B.s_208_297      24.4  222_B ---AVGVDMT--VDVIINN-------LDYSKWDSTMSPCVVRLAIDIL----------------PMTILDAMIVQTKRGLPSGMPFTSVI--- 316_B
1KHV_A.s_346_435      24.4  375_A ---LRDYGLSPTAADKT-FIDVCPLNKISFLKRTFEL------GWVSKLDKSSILRQLEWSK---RGVQLEELQVAAAAHGQEFFNFVCR--- 473_A
1KHV_A.s_208_297      24.4  222_A ---AVGVDMT--VDVIINN----FLCLDYSKWDSTMSPCVVRLAIDILA----------------PMTILDAMIVQTKRGLPSGMPFTSVI--- 316_A
1MUK_A.s_277_366      24.3  682_A ---SGSTATSTEHTANNSTMMETFL-------------YVCQGDDGL-------LELISKYGEEFGWKY--- 771_A
2PGG_A.s_93_182       24.2  252_A ---INLKSSSG-------RTKGET-------------------SCGLLFPKAERYDKST-----TRNIWSAPS--- 342_A
2CKW_A.s_277_366      24.1  290_A ---IKFVTRGGLPSGMPFTSVVNSINHMIYVAAAILQAY-------TIHTYGDDCMY---------TVLANLTSYGLK--- 374_A
1KHW_B.s_162_251      24.1  177_B ---RPLDKVKEGKKRLLWGCDVGVAVCAAAVFHNICYKLKMVA------AVGVDMT--VDVIINN-------LDYSKWDSTMSPCVVRLA--- 266_B
2CKW_A.s_93_182       23.7  102_A ---VLTYHQACE-------LERTTSCG--------GLKGDYWDEE-------------AYKLALKDELRPIEKNKAG-RRLLWGCDA--- 189_A
2YI8_A.s_116_205      23.6  254_A ---KTKGDT----------LVLAD------CGLLFPKGERYTQVD-----TRNIWSAPYPTHLLLSMVSTPVMNE--- 342_A
2CKW_A.s_323_412      23.6  343_A ---HTYGDDCMY---------VLANLTSYGLK-----------------VFLKRTFTQT------IRALLDITSITRQFYWLK--- 421_A
1KHV_A.s_323_412      23.5  350_A ---YTYGDDGVY------LPAIIENLRDYGLSPTAADKT-FIDVCPLNKISFLKRTFEL------WVSKLDKSSILRQLEWSK--- 430_A
1N35_A.s_277_366      23.3  673_A ---FTHMT---FPSGSTATSTEHTANNSTMMETFL-------------YVCQGDDGL-------LELISKYGEEFGWKY--- 771_A
1KHV_A.s_24_113       23.2   70_A ---KNLQV----KLDKVDEFIERAAADVLGYLRFL---QANLNFKAAFN--- 118_A
2CKW_A.s_231_320      22.6  241_A ---LDYSKWDSTQNPAVTAASLAILERF-------------AEGYVNDIKFVTRGGLPSGMPFTSVVNSINHMIYVAAAILQAY--- 325_A
1KHV_A.s_300_389      22.4  321_A ---HWLLWSAAVYKSC------DAPFFYTYGDDGVY------LPAIIENLRDYGLSPTAADKT-FIDVCPLNKISFLKRTFEL--- 408_A
1KHW_B.s_300_389      22.1  321_B ---HWLLWSAAVYKSC-------APFFYTYGDDGVY------LPAIIENLRDYGLSPTA-DKTEFIDVCPLNKISFLKRTFEL--- 408_B
1KHW_B.s_231_320      22.1  249_B ---LDYSKWDSTMSPCVVRLAIDILAD-------------HPMTILDAMIVQTKRGLPSGMPFTSVINSICHWLLWSAAVYKSC--- 333_B
1KHV_A.s_231_320      22.1  249_A ---LDYSKWDSTMSPCVVRLAIDILAD--------------PMTILDAMIVQTKRGLPSGMPFTSVINSICHWLLWSAAVYKSC--- 333_A
1N35_A.s_300_389      21.9  695_A ---NSTMMETFL-------------YVCQGDDGL-------ELISKYGEEFGWKYD------------EYLKLY--- 785_A
1KHV_A.s_162_251      21.7  187_A ---KRLLWGCDVGVAVCAAAVFHNICYKLKMVA------AVGVDMT--VDVIINN----FLCLDYSKWDSTMSPCVVRLA--- 266_A
1MUK_A.s_300_389      21.5  695_A ---NSTMMETFL-------------YVCQGDDGL-------LELISKYGEEFGWKY----------AEYLKLY--- 785_A
2CKW_A.s_162_251      21.4  171_A ---RPIEKNKAG-RRLLWGCDAATTLIATAAFKAVATRLQVVT------AVGINMD--MQVMNDS-------LDYSKWDSTQNPAVTAASL--- 259_A
1SH0_B.s_231_320      21.4  241_B ---ADYSRWDSTQQRAVLAAALEIMVKFS---QVVAEDLL--VVDVGDFTISINEGLPSG-PCTSQWNSIAHWLLTLCALSEVTN--- 326_B
1SH0_B.s_208_297      21.4  216_B ---RVGMNMNEDGPIIFER------ADYSRWDSTQQRAVLAAALEIMVKFS---QVVAEDLL--VVDVGDFTISINEGLPSG-PCTSQW--- 308_B
1SH0_B.s_162_251      21.4  170_B ---VKTDK-----KRLLWGSDLATMIRCARAFGGLMDELKTHC------RVGMNMNEDGPIIFER------ADYSRWDSTQQRAVLAAAL--- 259_B
1KHV_A.s_1_90         21.4   22_A ---GAEPRPPV-GTRYAK-------------------VKNLQV----KLDKVDEFIERAAADVLGYLRFL--- 102_A
2CKW_A.s_300_389      21.3  313_A ---HMIYVAAAILQAY-------TIHTYGDDCMY------FHTVLANLTSYGLK--------------VFLKRTFTQT--- 400_A
2R7X_A.s_254_343      21.1  562_A ---KQTQINLMDSYVQIPIKKIQY------GEKQTKAANSIANLALIKTVLSRIS--------IRVDGDDN--- 633_A
1KHV_A.s_139_228      21.1  167_A ---IYACGLKDELRPL--------RLLWGCDVGVAVCAAAVFHNICYKLKMVA------AVGVDMT--VDVIINN--- 238_A
2R7X_A.s_231_320      21.0  519_A ---TDVSQWDS---QPFFRKGIIMGLDIL-----QTQINLMDSYVQIPIKKIQY------GEKQTKAANSIANLALIKTVLSRI--- 615_A
2PGG_A.s_116_205      20.8  265_A ---RTKGET-------IAISN----SCGLLFPKAERYDKST-----TRNIWSAPSPTHLMISMITWPVMSN--- 358_A
1SH0_B.s_139_228      20.7  158_B ---TPVYTGALKDELVKTDK-----KRLLWGSDLATMIRCARAFGGLMDELKTHC------RVGMNMNEDGPIIFER--- 231_B
2J7U_A.s_323_412      20.5  659_A ---AISGDDCVV------FANAL---LNDMG------------------VPFCSHHFHELI-----------PQDELIGRARISQ--- 742_A
1U09_A.s_70_159       20.5   72_A ---ALFRRCAADYASRLHS--TANAPLSIYEAIKGVDGLDAMEPDTAPGLPWALQGKRRGALI-FENGT-------------FACQTFL--- 163_A
1N35_A.s_254_343      20.3  673_A ---FTHMT---FPSGSTATSTEHTANNSTMMETF--------------YVCQGDDGL--- 737_A
1MUK_A.s_254_343      20.3  659_A ---FSYRV--FTHMT---FPSGSTATSTEHTANNSTMMETF--------------YVCQGDDGL--- 737_A
1KHW_B.s_254_343      20.2  291_B ---PMTILDAMIVQTKRGLPSGMPFTSVINSICHWLLWSAAVYKSC-------APFFYTYGDDGVY--- 358_B
2YI8_A.s_231_320      20.0  402_A ---DLEKGEANCTPQHMQAMMYYLLT--------APSMVVDS-CLLMNLQLKT-----SGNAFTFLNN-----TIVVAEW--- 491_A
2CKW_A.s_346_435      20.0  368_A ---LTSYGLK-------------------VFLKRTFTQT------IRALLDITSITRQFYWL-----RSAQLENALAYASQHGPVMFDTVRQ--- 463_A
2CKW_A.s_116_205      20.0  125_A ---LKGDYWD--------------YKLALKDELRPIEKNKAG-RRLLWGCDAATTLIATAAFKAVATRLQVVT--- 210_A
1SH0_B.s_372_461      20.0  390_B ---FLRRTVTR-------FGKLEQSSILRQMYWT---SQRPIQLMSLLGEAAL-GPAFYSKISKLVI------FYVPRQEPMFRWM--- 485_B
1KHV_A.s_254_343      20.0  291_A ---PMTILDAMIVQTKRGLPSGMPFTSVINSICHWLLWSAAVYKSC-------DAPFFYTYGDDGVY--- 358_A
1NB4_A.s_116_205      19.7  104_A ---GAKDV-----------RAVNH-------DTTIMAKSEVF---------ARLIVFPDLGVRVCEKMALYDVVST--- 181_A
2CKW_A.s_185_274      19.5  194_A ---IATAAFKAVATRLQVVT------AVGINMD--MQVMNDS-------LDYSKWDSTQNPAVTAASLAILER-----SCAIEALS--- 280_A
2CKW_A.s_139_228      19.5  161_A ---AYKLALKDELRPIEKNKAG-RRLLWGCDAATTLIATAAFKAVATRLQVVT------AVGINMD--MQVMNDS--- 232_A
1NB7_A.s_116_205      19.4  104_A ---GAKDV----------------------TTIMAKSEVF---------RLIVFPDLGVRVCEKMALYDVVS--- 180_A
2CKW_A.s_254_343      19.3  283_A ---AEGYVNDIKFVTRGGLPSGMPFTSVVNSINHMIYVAAAILQAY-------TIHTYGDDCMY--- 351_A
1S48_A.s_277_366      19.3  395_A ---EVYIRNGQRGSGQPDTSAGNSXLNVLTXXYAFCESTG-------RIHVCGDDG-----------ANKGXQILHEAGKPQ--- 477_A
2R7X_A.s_277_366      19.2  582_A ---KIQY------GEKQTKAANSIANLALIKTVLSRIS--------IRVDGDDN--------SNDVRETYARMNAKV--- 666_A
2J7U_A.s_277_366      19.2  590_A ---DIISRKDQRGSGQVGTYGLNTFTNMEAQLVRQME----------MAISGDDCVV--------ALNDMG--- 685_A
1SH0_B.s_346_435      19.2  368_B ---KPTRP---GPLVI--NGLTFLRRTVTRD-----WFGKLEQSSILRQMYWT---SQRPIQLMSLLGEAAL-GPAFYSKI--- 458_B
1KHW_B.s_185_274      19.1  200_B ---CAAAVFHNICYKLKMVA------AVGVDMT--VDVIINN-------LDYSKWDSTMSPCVVRLAIDIL--- 270_B
1SH0_B.s_47_136       18.8   65_B ---DQLKP----------SVLEAAKKTIINVLE---------WSFAQACA-----SLDKTTSSGHPH------KNDCW--- 131_B
1SH0_B.s_1_90         18.8   18_B ---SAPKLSTKTKFWR----------TYEPAYL-----------MRDQLKP----------SVLEAAKKTIINVLEQ--- 96_B
1S48_A.s_254_343      18.8  378_A ---DTITDHXTEVPVI--GEVYIRNGQRGSGQPDTSAGNSXLNVLTXXYAFCESTGV------RIHVCGDDG--- 450_A
1RTD_A.s_277_366      18.8  142_A ---IRYQYN---PQGWKGSPAIFQSSMTKILE--------------------------IEELRQHLLRWGLTT--- 216_A
1KHV_A.s_185_274      18.8  200_A ---CAAAVFHNICYKLKMVA------AVGVDMT--VDVIINN----FLCLDYSKWDSTMSPCVVRLAIDILAD--- 272_A
2PGG_A.s_254_343      18.6  462_A ---PALVVDS-CLIMNLQIKTY---GSGNAATFINNHLLSTLVLDQWNL--- 506_A
1KHV_A.s_369_458      18.5  398_A ---KISFLKRTFELT-----GWVSKLDKSSILRQLEWSK---RGVQLEELQVAAAAHGQEFFNFVCREL----------VYSYDAARK--- 494_A
2PGG_A.s_208_297      18.4  416_A ---DLEKGEANCTRQHMQAAMYYILT---------APALVVDS-CLIMNLQIK---QGSGNAAT--- 489_A
1SH0_B.s_70_159       18.3   81_B ---SVLEAAKKTIINVLEQT---DKWSFAQACA-----SLDKTTSSGHPH------KNDCW-----------------TPVYTGAL--- 165_B
1SH0_B.s_369_458      18.3  387_B ---GLTFLRRTVTR--------FGKLEQSSILRQMYWT---SQRPIQLMSLLGEAAL-GPAFYSKISKLVI------FYVPRQEPMFR--- 483_B
2HCS_A.s_162_251      18.2  481_A ---LGARFLEFEALGFLNED------------EGLGLQKLGYILREV-------DDTAGWDTRITRADLENEA--- 553_A
2HMI_A.s_277_366      17.9  142_A ---IRYQYN---PQGWKGSPAIFQSSMTKIL-------------------------IEELRQHLLRWGLTTP--- 217_A
2HCS_A.s_346_435      17.6  686_A ---LNAMS-------------WQQVPFCSNHFTELI----LVTPC-GQDELVGRARI----RDTACLAKSY--- 763_A
2HCS_A.s_254_343      17.5  610_A ---YALNTFTNLAVQLVRMM------------MAVSGDDCVV--- 672_A
2CKW_A.s_369_458      17.5  390_A ---PVFLKRTFTQT------IRALLDITSITRQFYWL-----RSAQLENALAYASQHGPVMFDTVRQIAI------------NYDQA--- 484_A
1S48_A.s_231_320      17.2  344_A ---FDTKAWDTQVTSKDLQLIGEIQKYYY-------TDHXTEVPVI--GEVYIRNGQRGSGQPDTSAGNSXLNVLTXXYAFCESTGV--- 432_A
1N35_A.s_323_412      17.2  730_A ---VCQGDDGL---------ELISKYGEEFGWKY--------------AEYLKLY----------------PNLSRH--- 798_A
1MUK_A.s_323_412      17.2  730_A ---VCQGDDGL---------ELISKYGEEFGWKY--------------AEYLKLY----------------PNLSRH--- 798_A
2J7U_A.s_300_389      17.1  613_A ---NMEAQLVRQMEG-----------MAISGDDCVV---------LALNDMG-----------------WQQVPFCSHHFHELI--- 717_A
1SH0_B.s_185_274      17.1  194_B ---RCARAFGGLMDELKTHC------RVGMNMNEDGPIIFER------ADYSRWDSTQQRAVLAAALEIMVKFS---QVVAEDLL--- 280_B
1KHW_B.s_372_461      16.9  401_B ---FLKRTFEL------GWVSKLDKSSILRQLEW----ERGVQLEELQVAAAAHGQEFFNFVCRELER-------VYSYDAARKILA--- 497_B
2J7U_A.s_369_458      16.7  705_A ---QVPFCSHHFHELI-----------PQDELIGRARIS--- 741_A
2J7U_A.s_346_435      16.7  681_A ---LNDMG--------------------VPFCSHHFHELI----LVVPC-PQDELIGRARIS-----LGKAYAQM--- 761_A
2CKW_A.s_70_159       16.7   78_A ---QLLSRAVTHVRSYIE----RSPVLTYHQACE------LLERTTSCG---------KGDYWD--------------------YKLAL--- 166_A
2CKW_A.s_372_461      16.7  392_A ---FLKRTFTQT------IRALLDITSITRQFYWL-----RSAQLENALAYASQHGPVMFDTVRQIAI------------NYDQAL--- 485_A
1NB7_A.s_277_366      16.2  280_A ---RASGVLTTSCGNTLTCYLKATAACRAA--------CTMLVNGDDLVVIC-------AFTEAMTRYSAP--- 349_A
2R7X_A.s_208_297      16.0  532_A ---QPFFRKGIIMGLD---------QTQINLMDSYVQIPIKKIQY------GEKQTKAA--- 599_A
1NB4_A.s_277_366      16.0  280_A ---RASGVLTTSCGNTLTCYLKATAACRAA--------CTMLVNGDDLVVICES---LRAFTEAMTRYSAP--- 349_A
2CKW_A.s_47_136       15.9   63_A ---NGLKP-----------LLSRAVTHVRSYIE----SPVLTYHQACE------LLERTTSCG-----------KGDYWD--- 131_A
2CKW_A.s_1_90         15.9   15_A ---LDVGGMP-GTRYHRS---------THAPAP-----------EMLVNGLKP-----------LLSRAVTHVRSYIETI--- 94_A
1S48_A.s_139_228      15.9  257_A ---YETAIPKNEK----------PRVIQ-PEAKTRLAITKVXYNW---------------EGKTPLFNIFDKVRK--- 331_A
2J7U_A.s_254_343      15.7  572_A ---YQNKVVKV-MDIISRKDQRGSGQVGTYGLNTFTNMEAQLVRQ-------------MAISGDDCVV--- 667_A
1KHW_B.s_369_458      15.7  398_B ---KISFLKRTFEL------GWVSKLDKSSILRQLE-----EERGVQLEELQVAAAAHGQEFFNFVCRELER---------VYSYDAARKIL--- 496_B
1KHV_A.s_372_461      15.7  401_A ---FLKRTFEL------GWVSKLDKSSILRQLE----EERGVQLEELQVAAAAHGQEFFNFVCRELER---------VYSYDAARK---- 494_A
2HCS_A.s_185_274      15.6  486_A ---LEFEALGFLNED----------GVEGLGLQKLGYILR---------DDTAGWDTRITRADLENEA----------RAIIEL--- 573_A
1MUK_A.s_231_320      15.6  585_A ---DISACDASITW--LSVIMAAIHEG--------------FSYRV--FTHMT---FPSGSTATSTEHTANNSTMME--- 700_A
2YI8_A.s_139_228      15.4  299_A ---CGLLFPKGERYTQVD----TRNIWSAPYPTHLLLSMVSTPVMNES-----------YGFSP---MDRIMTI--- 371_A
2HCS_A.s_323_412      15.4  664_A ---AVSGDDCVV-----------SLHFLNAMS-----------------------VPFCSNHFTELI-----------GQDELVGRARI--- 745_A
1N35_A.s_231_320      15.4  584_A ---IDISACDASITW--LSVIMAAIHEG-------------------FTHMT---FPSGSTATSTEHTANNSTMM--- 699_A
2HCS_A.s_372_461      15.2  713_A ---FCSNHFTEL-----------GQDELVGRARI---------------LLLYF--- 772_A
1S48_A.s_208_297      15.1  317_A ---EGKTPLFNIFDKVRK-----AVSFDTKAWDTQVTSKDLQLIGEIQKYYY-------TDHXTEVPVI--GEVYIRNGQRGSGQPDTSAG--- 413_A
2PGG_A.s_231_320      14.9  416_A ---DLEKGEANCTRQHMQAAMYYIL---------APALVVDS-CLIMNLQIKTYGQ-------------------LSTLVLDQWN--- 505_A
2HCS_A.s_231_320      14.9  535_A ---DDTAGWDTRITRADLENEA-----------------------------TYALNTFTNLAVQLVRMMEG--- 628_A
2HCS_A.s_208_297      14.9  509_A ---VEGLGLQKLGYILRE-------DDTAGWDTRITRADLENEA------------RAIIEL--- 573_A
1RT1_A.s_254_343      14.9  142_A ---IRYQY---LPQGWKGSPAIFQSSMTKILE-------------DIVIYQYMDD--- 186_A
1NB4_A.s_162_251      14.9  157_A ---ARLIVFPDLGVRVCEKMALYDVVST---------------SPKQRVEFL-----------YDTRCFDSTVTESDIRVEE--- 237_A
1RTD_A.s_254_343      14.8  142_A ---IRYQY---LPQGWKGSPAIFQSSMTKILE--- 169_A
2HCS_A.s_300_389      14.7  617_A ---NLAVQLVRMME---------MAVSGDDCVV----------HFLNAMS----------------WQQVPFCSNHFTELI--- 722_A
1NB4_A.s_139_228      14.7  136_A ---TTIMAKSEVFC---------ARLIVFPDLGVRVCEKMALYDVVST--------------SPKQRVEFLV--- 205_A
2PGG_A.s_139_228      14.5  315_A ---CGLLFPKAERYDKST----TRNIWSAPSPTHLMISMITWPVMS----------YKFNP---LNRIVEW--- 388_A
1NB7_A.s_162_251      14.5  157_A ---ARLIVFPDLGVRVCEKMALYDVVS---------------SPKQRVEFLVN-----GFSYDTRCFDSTVTESDIRVEE--- 237_A
1NB7_A.s_139_228      14.5  136_A ---TTIMAKSEVFC---------ARLIVFPDLGVRVCEKMALYDVVST--------------SPKQRVEFLV--- 205_A
1N35_A.s_208_297      14.5  585_A ---DISACDASITW--LSVIMAAI-------------------------FTHMT---FPSGSTATSTE--- 690_A
1MUK_A.s_208_297      14.5  585_A ---DISACDASITW--LSVIMAAIHEG--------------FSYRV--FTHMT---FPSGSTATSTE--- 690_A
2PGG_A.s_369_458      14.3  571_A ---LGWSATYSK--------VLDKERLFCSAA------KVVRYEALRLV----------LLNKA--- 640_A
2HCS_A.s_369_458      14.1  710_A ---QVPFCSNHFTELI-----------GQDELVGRARI--------------------LMANA--- 783_A
1HHS_A.s_231_320      13.9  323_A ---TDVSDHDTFWPGWLRDLI----------------------LPVYV-----------LSSGQGATDLMGTLLMSITYLVMQLD--- 416_A
2J7U_A.s_372_461      13.8  708_A ---FCSHHFHELI-----------PQDELIGRARIS-----------------LASNAI--- 779_A
2YI8_A.s_254_343      13.3  448_A ---APSMVVDS-CLLMNLQLKTY---GSGNAFTFLNNHLMSTIVVAEWV--- 492_A
1NB7_A.s_254_343      13.3  281_A ---ASGVLTTSCGNTLTCYLKATAACRAA--------CTMLVNGDDLVVIC--- 324_A
1NB4_A.s_254_343      13.3  264_A ---GPLTN----------ASGVLTTSCGNTLTCYLKATAACRAA--------CTMLVNGDDLVVICE--- 325_A
2J7U_A.s_162_251      13.2  478_A ---LGARYLEFEALGFLNED--------------GLHKLGYILRD---------DDTAGWDTRITEDDLHNEE--- 550_A
2CKW_A.s_24_113       13.2   40_A ---THAPAP-----------NGLKP----------LLSRAVTHVRSYIE----SPVLTYHQACE--- 110_A
1HI0_P.s_300_389      13.1  406_P ---MSITYLVMQLDH----------QISKSDDAMLGW----------------KISYE-------------AFLGD--- 499_P
1HI0_P.s_231_320      13.1  323_P ---TDVSDHDTFWPGWLRDLICDELL--------VKLFETSLKLPVYV----------GLSSGQGATDLMGTLLMSITYLVMQLD--- 416_P
2PGG_A.s_162_251      13.0  325_A ---YDKSTWL---TRNIWSAPSPTHLMISMITWPVMSN------------LNRIVEW--- 388_A
2J7U_A.s_231_320      12.9  532_A ---DDTAGWDTRITEDDLHNEE---------------YQNKVVKV-MDIISRKDQRGSGQVGTYGLNTFTNMEAQLVRQMEG--- 624_A
2J7U_A.s_208_297      12.9  510_A ---GLHKLGYILR---------DDTAGWDTRITEDDLHNEE---------------YQNKVVKV-MDIISRKDQRGSGQVGTYGL--- 608_A
2YI8_A.s_162_251      12.7  309_A ---YTQVDWD---TRNIWSAPYPTHLLLSMVSTPVMNES--------------MDRIMTI-------IDLEKGEAN--- 409_A
1S48_A.s_300_389      12.5  418_A ---NVLTXXYAFCESTG--------RIHVCGDDG----------ANKGXQILHEAGKPQ-------------EDIEFCSHTPVPVR--- 505_A
1NB4_A.s_323_412      12.5  314_A ---LVNGDDLVVICE------AFTEAMTRYSAPP-------------ELITSCSSNVSVA-----------DPTTPLARAA--- 396_A
1HI0_P.s_277_366      12.5  391_P ---LSSGQGATDLMGTLLMSITYLVMQLDH----------QISKSDDAMLGW----------------KISYE--- 491_P
1HHS_A.s_277_366      12.5  391_A ---LSSGQGATDLMGTLLMSITYLVMQLDH----------QISKSDDAMLGW----------------KISYE--- 491_A
3DU6_A.s_254_343      12.3  292_A ---FVAFRRKIYKW---LLQGDPLSGCLCELYMAFMDRLY--- 328_A
1HI0_P.s_208_297      12.2  323_P ---TDVSDHDTFWPGWLRDLICD----------VKLFETSLKLPVYV---------GLSSGQGATDLM--- 401_P
1HHS_A.s_208_297      12.2  323_A ---TDVSDHDTFWPGWLRDLIC----------VKLFETSLKLPVYV---------GLSSGQGATDLM--- 401_A
2PGG_A.s_372_461      12.1  571_A ---LGWSATYSKDL-----VLDKERLFCSAA------KVVRYEALRLV---------PLLNKA--- 640_A
2PGG_A.s_323_412      12.1  398_A ---LVYADNIYI------------KSIED--INFKI-----------------LGWSATYSKDLG--- 582_A
1S48_A.s_162_251      12.0  284_A ---PRVIQ-PEAKTRLAITKVXYN-----------------EGKTPLFNIFDKVRK----AVSFDTKAWDTQVTSKDLQLIG--- 362_A
2PGG_A.s_346_435      11.9  524_A ---LGINFK-------------------LGWSATYSKDLG-----VLDKERLFCSAAY------KVVRYEALRLV--- 629_A
2HCS_A.s_277_366      11.9  608_A ---VTYALNTFTNLAVQLVRMME---------MAVSGDDCVV---------HFLNAMS--- 690_A
1S48_A.s_323_412      11.8  444_A ---HVCGDDG--------ANKGXQILHEAGKPQ-------------EDIEFCSHTPVPVR----SHXAG-DTAVILSKXA--- 527_A
1NB4_A.s_300_389      11.8  295_A ---CYLKATAACRAA--------CTMLVNGDDLVVICES---LRAFTEAMTRYSAPP-------------LELITSCSSNVSV--- 372_A
1HHS_A.s_254_343      11.8  354_A ---VKLFET-LKLPVYV----------LSSGQGATDLMGTLLMSITYLVMQLDH---------QISKSDDAMLGW--- 459_A
1HI0_P.s_254_343      11.7  354_P ---VKLFET-LKLPVYV----------LSSGQGATDLMGTLLMSITYLVMQLDH---------QISKSDDAMLGW--- 459_P
3DU6_A.s_208_297      11.6  249_A ---KVDIRDAYGN-----IPVLCKLIQSI---------DHISN-FVAFRRKIYKWN-GLLQGDPLSGCL--- 316_A
2R7X_A.s_185_274      11.6  468_A ---EYFIAQHAVVEKMLI----------------TDVSQWDS---QPFFRKGIIMGLDIL----YKQTQINLMDSYV--- 573_A
1HHS_A.s_300_389      11.5  406_A ---MSITYLVMQLDH----------QISKSDDAMLGW----------------MKISYE-------------AFLGD--- 499_A
2YI8_A.s_372_461      10.9  560_A ---LLGWSAIYSRQM---------------------------YQIVRYEAIRLV--- 619_A
1NB7_A.s_323_412      10.8  314_A ---LVNGDDLVVIC------AFTEAMTRYSAPP-------------ITSCSSNVSVA-----------DPTTPLARAA--- 396_A
1NB7_A.s_300_389      10.8  295_A ---CYLKATAACRAA--------CTMLVNGDDLVVIC-----LRAFTEAMTRYSAPP-------------LELITSCSSNVSV--- 372_A
1NB7_A.s_208_297      10.8  196_A ---SPKQRVEFLVN----GFSYDTRCFDSTVTESDIRVEESIYQCC--------------GPLTN----GYRRC---SGVLTTSCG--- 290_A
1NB4_A.s_208_297      10.8  196_A ---SPKQRVEFLVN--------YDTRCFDSTVTESDIRVEESIYQCC--------------GPLTN-----------SGVLTTSCG--- 290_A
3DU6_A.s_231_320      10.4  251_A ---DIRDAYGNVKIPVLCKLIQ-----------------FVAFRRKIYKW---LLQGDPLSGCLCELYMAFMDRLYF--- 329_A
1SH0_B.s_24_113       10.3   64_B ---RDQLKP----------SVLEAAKKTIINVLEQ-------WSFAQACA--- 111_B
1S48_A.s_185_274      10.3  297_A ---AITKVXYNW--------------EGKTPLFNIFDKVRK-----AVSFDTKAWDTQVTSKDLQLIGEIQKYYY-------TDHXTEVPV--- 389_A
1NB7_A.s_231_320      10.3  219_A ---YDTRCFDSTVTESDIRVEESIYQCCD--------------GYRRC---SGVLTTSCGNTLTCYLKATAA--- 302_A
1NB4_A.s_231_320      10.0  219_A ---YDTRCFDSTVTESDIRVEESIYQCC--------------GPLTN---GYRRC---SGVLTTSCGNTLTCYLKATAACRAA--- 306_A
2J7U_A.s_185_274       9.9  483_A ---LEFEALGFLNED--------GLHKLGYILR---------DDTAGWDTRITEDDLHNEE--------------YQNKVV--- 577_A
1NB4_A.s_369_458       9.7  362_A ---LITSCSSNVSVA-----------DPTTPLARAA-----------WLGNIIMYAP---------LMTHFFS--- 431_A
1S48_A.s_346_435       9.6  470_A ---LHEAGKPQ-------------EDIEFCSHTPVPV-----SHXAG-DTAVILSKX--------KAVAFSFLLXYSW--- 555_A
1NB4_A.s_185_274       9.3  170_A ---CEKMALYDVVS-----------------SPKQRVEFLVN--------YDTRCFDSTVTESDIRVEESIYQCC--- 243_A
1NB7_A.s_185_274       9.2  170_A ---CEKMALYDVVS-----------------SPKQRVEFLV-------FSYDTRCFDSTVTESDIRVEESIYQCC--- 243_A
2YI8_A.s_369_458       8.4  560_A ---LLGWSAIYSRQME-----VLENERLIASAA------YQIVRYEAIRLV---------NPLLETA--- 630_A
1S48_A.s_369_458       7.9  493_A ---DIEFCSHTPVPV-----------DTAVILSKXA---------EKAVAFSFLLXYS--- 554_A
2YI8_A.s_346_435       7.2  560_A ---LLGWSAIYSRQME-----------------------YQIVRYEAIRLV--- 619_A
1NB7_A.s_369_458       7.2  362_A ---LITSCSSNVS-------------DPTTPLARAA-----------WLGNIIMYAPT----------THFFS--- 431_A
1HI0_P.s_185_274       6.9  282_P ---PIMAVAQPVRNKIY----------------RLNKEEK------------TDVSDHDTFWPGWLRDLI-------------VKLFETSLKLPV--- 365_P
1HI0_P.s_162_251       6.8  274_P ---GGPFALNAPIMAVAQPVRNKIY--------------RLNKEEK----------TDVSDHDTFWPGWLR--- 337_P
1HHS_A.s_185_274       6.8  282_A ---PIMAVAQPVRNKIYS-------------------NKEEK-------------TDVSDHDTFWPGWLRDLIC-----------VKLFETSLKLPV--- 365_A
1NB4_A.s_346_435       6.2  345_A ---RYSAP-------------LELITSCSSNVSVA-----------DPTTPLARA------------WLGNIIMYAP--- 417_A
1HHS_A.s_116_205       6.1  199_A ---YYVVYRA---------------------GGPFALNAPIMAVAQPVRNKIY--- 295_A
1HHS_A.s_162_251       5.8  274_A ---GGPFALNAPIMAVAQPVRNK-------------------LNKEEK--------TDVSDHDTFWPGWLR--- 337_A
1HI0_P.s_116_205       4.7  199_P ---YYVVYRA---------------------GGPFALNAPIMAVAQPVRNKIY--- 295_P
1HHS_A.s_139_228       4.3  199_A ---YYVVYRA---------------------GGPFALNAPIMAVAQPVRNKIY--------------RLNKEEK--- 313_A
1HI0_P.s_139_228       3.0  199_P ---YYVVYR-----------------------GGPFALNAPIMAVAQPVRNKIY------------------RLNKEEK--- 313_P
END_of_job
```