Align

How to use this tool

Align two or more protein sequences with the Clustal Omega program (see also this FAQ) to view their characteristics alongside each other.

1. Enter either protein sequences in FASTA format or UniProt identifiers into the form field, for example:
   TPA_HUMAN
   TPA_PIG

2. Click the *Run Align* button.

Help Align help video Other tutorials and videos Downloads

Alignment

How to print an alignment in color

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Q8IZJ1 UNC5B_HUMAN          1   MGARSGARGALLLALLLCWDPRLSQAGTDSGSEVLPDSFPSAPAEPLPYFLQEPQDAYIV       60
K7DDY1 K7DDY1_PANTR         1   MWARSGARGALLLALLLCWDPRLSQAGTDSGSEVLPDSFPSAPAEPLPYFLQEPQDAYIV       60
K7B3D8 K7B3D8_PANTR         1   MWARSGARGALLLALLLCWDPRLSQAGTDSGSEVLPDSFPSAPAEPLPYFLQEPQDAYIV       60
K7BVI5 K7BVI5_PANTR         1   MWARSGARGALLLALLLCWDPRLSQAGTDSGSEVLPDSFPSAPAEPLPYFLQEPQDAYIV       60
H2NAM6 H2NAM6_PONAB         1   ------------------------------------------------------------       0
G7N281 G7N281_MACMU         1   MWTRSGARDALLLALLLCWDPRLSQAGTDSGSEALPDSFPSAPAEPLPYFLQEPQDAYIV       60
F6UDU4 F6UDU4_MACMU         1   MWTRSGARDALLLALLLCWDPRLSQAGTDSGSEALPDSFPSAPAEPLPYFLQEPQDAYIV       60
F6UDV7 F6UDV7_MACMU         1   MWTRSGARDALLLALLLCWDPRLSQAGTDSGSEALPDSFPSAPAEPLPYFLQEPQDAYIV       60
F7A1Z5 F7A1Z5_CALJA         1   -------------------------GTDSGSEVLPDSFPSAPAEPLPYFLQEPQDAYIV       34
U3F339 U3F339_CALJA         1   MWARSGARGVLLLALLLCWDARLSQAGTDSGSEVLPDSFPSAPAEPLPYFLQEPQDAYIV       60

Q8IZJ1 UNC5B_HUMAN         61   KNKPVELRCRAFPATQIYFKCNGEWVSQNDHVTQEGLDEATGLRVRE--VQIEVSRQQVE       118
K7DDY1 K7DDY1_PANTR        61   KNKPVELRCRAFPATQIYFKCNGEWVSQNDHVTQEGLDEATGLRVRE--VQIEVSRQQVE       118
K7B3D8 K7B3D8_PANTR        61   KNKPVELRCRAFPATQIYFKCNGEWVSQNDHVTQEGLDEATGLRVRE--VQIEVSRQQVE       118
K7BVI5 K7BVI5_PANTR        61   KNKPVELRCRAFPATQIYFKCNGEWVSQNDHVTQEGLDEATGLRVRE--VQIEVSRQQVE       118
H2NAM6 H2NAM6_PONAB         1   ------------------------------------------------------------       0
G7N281 G7N281_MACMU        61   KNKPVELRCRAFPATQIYFKCNGEWVSQNDHVTQEGLDEATGLRVRE--VQIEVSRQQVE       118
F6UDU4 F6UDU4_MACMU        61   KNKPVELRCRAFPATQIYFKCNGEWVSQNDHVTQEGLDEATGLRVRE--VQIEVSRQQVE       118
F6UDV7 F6UDV7_MACMU        61   KNKPVELRCRAFPATQIYFKCNGEWVSQNDHVTQEGLDEATGLRVRE--VQIEVSRQQVE       118
F7A1Z5 F7A1Z5_CALJA        35   KNKPVELRCRAFPATQIYFKCNGDWVSQNDHVTHERISEPVGLKPYSKREFLRETKQHIE        94
U3F339 U3F339_CALJA        61   KNKPVELRCRAFPATQIYFKCNGDWVSQNDHVTQEGLDEATGLRVRE--VQIEVSRQQVE       118

Q8IZJ1 UNC5B_HUMAN        119   ELFGLEDYWCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPE       178
K7DDY1 K7DDY1_PANTR       119   ELFGLEDYWCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPE       178
K7B3D8 K7B3D8_PANTR       119   ELFGLEDYWCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPE       178
K7BVI5 K7BVI5_PANTR       119   ELFGLEDYWCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPE       178
H2NAM6 H2NAM6_PONAB         1   ------------------------------------------------------------       0
G7N281 G7N281_MACMU       119   ELFGLEDYWCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPE       178
F6UDU4 F6UDU4_MACMU       119   ELFGLEDYWCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPE       178
F6UDV7 F6UDV7_MACMU       119   ELFGLEDYWCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPE       178
F7A1Z5 F7A1Z5_CALJA        95   ELFGLEDYWCQCVAWSSAGTTRRGKFPEQRPDLRKNFDQEPLGKEVPLDHEVLLQCRPPE       154
U3F339 U3F339_CALJA       119   ELFGLEDYWCQCVAWSSAGTTKSRRAYVRIAYLRKNFDQEPLGKEVPLDHEVLLQCRPPE       178

Q8IZJ1 UNC5B_HUMAN        179   GVPVAEVEWLKNEDVIDPTQDTNFLLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTT       238
K7DDY1 K7DDY1_PANTR       179   GVPVAEVEWLKNEDVIDPTQDTNFLLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTT       238
K7B3D8 K7B3D8_PANTR       179   GVPVAEVEWLKNEDVIDPTQDTNFLLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTT       238
K7BVI5 K7BVI5_PANTR       179   GVPVAEVEWLKNEDVIDPTQDTNFLLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTT       238
H2NAM6 H2NAM6_PONAB         1   ------------------------------------------------------------       0
G7N281 G7N281_MACMU       179   GVPVAEVEWLKNEDVIDPTQDTNFLLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTT       238
F6UDU4 F6UDU4_MACMU       179   GVPVAEVEWLKNEDVIDPTQDTNFLLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTT       238
F6UDV7 F6UDV7_MACMU       179   GVPVAEVEWLKNEDVIDPTQDTNFLLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTT       238
F7A1Z5 F7A1Z5_CALJA       155   GMPVAEVEWLKNEDVIDPTQDTNFLLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTT       214
U3F339 U3F339_CALJA       179   GMPVAEVEWLKNEDVIDPTQDTNFLLTIDHNLIIRQARLSDTANYTCVAKNIVAKRRSTT       238

Q8IZJ1 UNC5B_HUMAN        239   ATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQAFQKTACTTI       298
K7DDY1 K7DDY1_PANTR       239   ATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQAFQKTACTTI       298
K7B3D8 K7B3D8_PANTR       239   ATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQAFQKTACTTI       298
K7BVI5 K7BVI5_PANTR       239   ATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPAPLNGGAFCEGQAFQKTACTTI       298
H2NAM6 H2NAM6_PONAB         1   ----------------------------------------MSLCA-----HAPVYHA        12
G7N281 G7N281_MACMU       239   ATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPTPLNGGAFCEGQAFQKTACTTI       298
F6UDU4 F6UDU4_MACMU       239   ATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPTPLNGGAFCEGQAFQKTACTTI       298
F6UDV7 F6UDV7_MACMU       239   ATVIVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPTPLNGGAFCEGQAFQKTACTTI       298
F7A1Z5 F7A1Z5_CALJA       215   ATVTVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPTPLNGGAFCEGQAFQKTACTTV       274
U3F339 U3F339_CALJA       239   ATVTVYVNGGWSSWAEWSPCSNRCGRGWQKRTRTCTNPTPLNGGAFCEGQAFQKTACTTV       298
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Q8IZJ1 UNC5B_HUMAN        299   CPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKK       358
K7DDY1 K7DDY1_PANTR       299   CPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKK       358
K7B3D8 K7B3D8_PANTR       299   CPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKK       358
K7BVI5 K7BVI5_PANTR       299   CPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKK       358
H2NAM6 H2NAM6_PONAB        13   LTVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKK        72
G7N281 G7N281_MACMU       299   CPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKK       358
F6UDU4 F6UDU4_MACMU       299   CPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQ---       355
F6UDV7 F6UDV7_MACMU       299   CPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKK       358
F7A1Z5 F7A1Z5_CALJA       275   CPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKK       334
U3F339 U3F339_CALJA       299   CPVDGAWTEWSKWSACSTECAHWRSRECMAPPPQNGGRDCSGTLLDSKNCTDGLCMQNKK       358
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Q8IZJ1 UNC5B_HUMAN          359   TLSDPNSHLLEASGDAALYAGLVVAIFVVVAILMAVGVVVYRRNCRDFDTDITDSSAALT       418
K7DDY1 K7DDY1_PANTR         359   TLSDPNSHLLEASGDAALYAGLVVAVFVVVAILMAVGVVVYRRNCRDFDTDITDSSAALT       418
K7B3D8 K7B3D8_PANTR         359   TLSDPNSHLLEASGDAALYAGLVVAVFVVVAILMAVGVVVYRRNCRDFDTDITDSSAALT       418
K7BVI5 K7BVI5_PANTR         359   TLSDPNSHLLEASGDAALYAGLVVAVFVVVAILMAVGVVVYRHNCRDFDTDITDSSAALT       418
H2NAM6 H2NAM6_PONAB          73   TLSDPNSHLLEASGDAALYAGLVVAIFVVVAILMAVGVVVYRRNCRDFDTDITDSSAALT       132
G7N281 G7N281_MACMU         359   TLSDPNSHLLEASGDAALYAGLVVAVFVVVAILMAVGVVVYRRNCRDFDTDITDSSAALT       418
F6UDU4 F6UDU4_MACMU         356   --------MLEASGDAALYAGLVVAVFVVVAILMAVGVVVYRRNCRDFDTDITDSSAALT       407
F6UDV7 F6UDV7_MACMU         359   TLSDPNSHLLEASGDAALYAGLVVAVFVVVAILMAVGVVVYRRNCRDFDTDITDSSAALT       418
F7A1Z5 F7A1Z5_CALJA         335   TLSDPNSHLLEASGDAALYAGLVVAVFVVVAVLMAVGVVVYRRNCHDFDTDITDSSAALT       394
U3F339 U3F339_CALJA         359   TLSDPNSHLLEASGDAALYAGLVVAVFVVVAVLMAVGVVVYRRNCHDFDTDITDSSAALT       418
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Q8IZJ1 UNC5B_HUMAN          419   GGFHPVNFKTARPSNPQLLHPSVPPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLP       478
K7DDY1 K7DDY1_PANTR         419   GGFHPVNFKTARPSNPQLLHPSVPPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLP       478
K7B3D8 K7B3D8_PANTR         419   GGFHPVNFKTARPSNPQLLHPSVPPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLP       478
K7BVI5 K7BVI5_PANTR         419   GGFHPVNFKTARPSNPQLLHPSVPPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLP       478
H2NAM6 H2NAM6_PONAB         133   GGFHPVNFKTARPSNPQLLHPSVPPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLP       192
G7N281 G7N281_MACMU         419   GGFHPVNFKTARPNNPQLLHPSVPPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLP       478
F6UDU4 F6UDU4_MACMU         408   GGFHPVNFKTARPNNPQLLHPSVPPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLP       467
F6UDV7 F6UDV7_MACMU         419   GGFHPVNFKTARPNNPQLLHPSVPPDLTASAGIYRGPVYALQDSTDKIPMTNSPLLDPLP       478
F7A1Z5 F7A1Z5_CALJA         395   GGFHPVNFKTARPSNPQLLHPSVPPDLTASAGIYRGPMCALQDSTDKILMTNSPLLDPLP       454
U3F339 U3F339_CALJA         419   GGFHPVNFKTARPSNPQLLHPSVPPDLTASAGIYRGPMCALQDSTDKILMTNSPLLDPLP       478
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Q8IZJ1 UNC5B_HUMAN          479   SLKVKVYSSSTTGSGPGLADGADLLGVLPPGTYPSDFARDTHFLHLRSASLGSQQLLGLP       538
K7DDY1 K7DDY1_PANTR         479   SLKVKVYSSSTTGSGPGLADGADLLGVLPPGTYPSDFARDTHFLHLRSASLGSQQLLGLP       538
K7B3D8 K7B3D8_PANTR         479   SLKVKVYSSSTTGSGPGLADGADLLGVLPPGTYPSDFARDTHFLHLRSASLGSQQLLGLP       538
K7BVI5 K7BVI5_PANTR         479   SLKVKVYSSSTTGSGPGLADGADLLGVLPPGTYPSDFARDTHFLHLRSASLGSQQLLGLP       538
H2NAM6 H2NAM6_PONAB         193   SLKVKVYSSSTTGSGPGLADGADLLGVLPPGTYPSDFAQDTHFLHLRSASLGSQQLLGLP       252
G7N281 G7N281_MACMU         479   SLKVKVYSSSTTGSGPGLADGADLLGVLPPGTYPSDFARDTHLLHLRSASLGSQQLLGLP       538
F6UDU4 F6UDU4_MACMU         468   SLKVKVYSSSTTGSGPGLADGADLLGVLPPGTYPSDFTRDTHLLHLRSASLGSQQLLGLP       527
F6UDV7 F6UDV7_MACMU         479   SLKVKVYSSSTTGSGPGLADGADLLGVLPPGTYPSDFTRDTHLLHLRSASLGSQQLLGLP       538
F7A1Z5 F7A1Z5_CALJA         455   SLKVKVYSSSTTGSGQGLTDGADLLGVLPPGTYPSDFTRDSHFLHLRSASLGSQQLLGLP       514
U3F339 U3F339_CALJA         479   SLKVKVYSSSTTGSGQGLTDGADLLGVLPPGTYPSDFTRDSYFLHLRSASLGSQQLLGLP       538
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Q8IZJ1 UNC5B_HUMAN          539   RDPGSSVSGTFGCLGGRLSIPGTGVSLLVPNGAIPQGKFYEMYLLINKAESTLPLSEGTQ       598
K7DDY1 K7DDY1_PANTR         539   RDPGSSVSGTFGCLGGRLSIPGTGVSLLVPNGAIPQGKFYEMYLLINKAESTLPLSEGTQ       598
K7B3D8 K7B3D8_PANTR         539   RDPGSSVSGTFGCLGGRLSIPGTGVSLLVPNGAIPQGKFYEMYLLINKAESTLPLSEGTQ       598
K7BVI5 K7BVI5_PANTR         539   RDPGSSVSGTFGCLGGRLSIPGTGVSLLVPNGAIPQGKFYEMYLLINKAESTLPLSEGTQ       598
H2NAM6 H2NAM6_PONAB         253   RDPGSSVSGTFGCLGGRLSIPGTGVSLLVPNGAIPQGKFYEMYLLINKAESTLPLSEGTQ       312
G7N281 G7N281_MACMU         539   RDPGSSVSGTFGCLGGRLSIPGTGVSLLVPNGAIPQGKFYEMYLLINKAESTLPLSEGTQ       598
F6UDU4 F6UDU4_MACMU         528   RDPGSSVSGTFGCLGGRLSIPGTGVSLLVPNGAIPQGKFYEMYLLINKAESTLPLSEGTQ       587
F6UDV7 F6UDV7_MACMU         539   RDPGSSVSGTFGCLGGRLSIPGTGVSLLVPNGAIPQGKFYEMYLLINKAESTLPLSEGTQ       598
F7A1Z5 F7A1Z5_CALJA         515   RDPGSSVSGTFGCLGGRLSIPGTGVSLLVPSGAIPQGKFYEMYLLINKAESTLPLSEGTQ       574
U3F339 U3F339_CALJA         539   RDPGSSVSGTFGCLGGRLSIPGTGVSLLVPSGAIPQGKFYEMYLLINKAESTLPLSEGTQ       598
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Q8IZJ1 UNC5B_HUMAN          599   TVLSPSVTCGPTGLLLCRPVILTMPHCAEVSARDWIFQLKTQAHQGHWEEVVTLDEETLN       658
K7DDY1 K7DDY1_PANTR         599   TVLSPSVTCGPTGLLLCRPVILTMPHCAEVSARDWIFQLKTQAHQGHWEEVVTLDEETLN       658
K7B3D8 K7B3D8_PANTR         599   TVLSPSVTCGPTGLLLCHPVILTMPHCAEVSARDWIFQLKTQAHQGHWEEVVTLDEETLN       658
K7BVI5 K7BVI5_PANTR         599   TVLSPSVTCGPTGLLLCHPVILTMPHCAEVSARDWIFQLKTQAHQGHWEEVVTLDEETLN       658
H2NAM6 H2NAM6_PONAB         313   TVLSPSVTCGPTGLLLCRPVILTLPHCAEVSARDWIFQLKTQAHQGHWEEVVTLDEETLN       372
G7N281 G7N281_MACMU         599   TVLSPSVTCGPTGLLLCRPVILTVPHCAKVSVGDWIFQLKTQAHQGHWEEVVTLDEETLN       658
F6UDU4 F6UDU4_MACMU         588   TVLSPSVTCGPTGLLLCRPVILTVPHCAKVSVGDWIFQLKTQAHQGHWEEVVTLDEETLN       647
F6UDV7 F6UDV7_MACMU         599   TVLSPSVTCGPTGLLLCRPVILTVPHCAKVSVGDWIFQLKTQAHQGHWEEVVTLDEETLN       658
F7A1Z5 F7A1Z5_CALJA         575   TVLSPSVTCGPAGLLLCRPVILTVPHCAEVSAGDWIFQLKTQAHQGHWEEVVTLDEETLN       634
U3F339 U3F339_CALJA         599   TVLSPSVTCGPAGLLLCRPVILTVPHCAEVSAGDWIFQLKTQAHQGHWEEVVTLDEETLN       658
                                  ***********:*****:*****:****:**. **************************

Q8IZJ1 UNC5B_HUMAN          659   TPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVKRLQLAVFAPALCTSLEYSLRVYCLE       718
K7DDY1 K7DDY1_PANTR         659   TPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVKRLQLAVFAPALCTSLEYSLRVYCLE       718
K7B3D8 K7B3D8_PANTR         659   TPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVKRLQLAVFAPALCTSLEYSLRVYCLE       718
K7BVI5 K7BVI5_PANTR         659   TPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVKRLQLAVFAPALCTSLEYSLRVYCLE       718
H2NAM6 H2NAM6_PONAB         373   TPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVKRLQLAVFAPALCTSLEYSLRVYCLE       432
G7N281 G7N281_MACMU         659   TPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVKRLQLAVFAPALCTSLEYSLRVYCLE       718
F6UDU4 F6UDU4_MACMU         648   TPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVKRLQLAVFAPALCTSLEYSLRVYCLE       707
F6UDV7 F6UDV7_MACMU         659   TPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVKRLQLAVFAPALCTSLEYSLRVYCLE       718
F7A1Z5 F7A1Z5_CALJA         635   TPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVKRLQLAVFAPSLCTSLEYSLRVYCLE       694
U3F339 U3F339_CALJA         659   TPCYCQLEPRACHILLDQLGTYVFTGESYSRSAVKRLQLAVFAPSLCTSLEYSLRVYCLE       718
                                  *******************************************:****************

Q8IZJ1 UNC5B_HUMAN          719   DTPVALKEVLELERTLGGYLVEEPKPLMFKDSYHNLRLSLHDLPHAHWRSKLLAKYQEIP       778
K7DDY1 K7DDY1_PANTR         719   DTPVALKEVLELERTLGGYLVEEPKPLMFKDSYHNLRLSLHDLPHAHWRSKLLAKYQEIP       778
K7B3D8 K7B3D8_PANTR         719   DTPVALKEVLELERTLGGYLVEEPKPLMFKDSYHNLRLSLHDLPHAHWRSKLLAKYQEIP       778
K7BVI5 K7BVI5_PANTR         719   DTPVALKEVLELERTLGGYLVEEPKPLMFKDSYHNLRLSLHDLPHAHWRSKLLAKYQEIP       778
H2NAM6 H2NAM6_PONAB         433   DTPVALKEVLELERTLGGYLVEEPKPLMFKDSYHNLRLSLHDLPHAHWR-KLLAKYQEIP       491
G7N281 G7N281_MACMU         719   DTPVALKEVLDLERTLGGYLVEEPKPLMFKDSYHNLRLSLHDLPHAHWRSKLLAKYQEIP       778
F6UDU4 F6UDU4_MACMU         708   DTPVALKEVLDLERTLGGYLVEEPKPLMFKDSYHNLRLSLHDLPHAHWRSKLLAKYQEIP       767
F6UDV7 F6UDV7_MACMU         719   DTPVALKEVLDLERTLGGYLVEEPKPLMFKDSYHNLRLSLHDLPHAHWRSKLLAKYQEIP       778
F7A1Z5 F7A1Z5_CALJA         695   DTPVALKEVLELERTLGGYLVEEPKPLVFKDSYHNLRLSLHDLPHAHWRSKLLAKYQEIP       754
U3F339 U3F339_CALJA         719   DTPVALKEVLELERTLGGYLVEEPKPLVFKDSYHNLRLSLHDLPHAHWRSKLLAKYQEIP       778
                                  **********:****************:********************** **********

Q8IZJ1 UNC5B_HUMAN          779   FYHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEGQIFQLHT-----TLAETPA       833
K7DDY1 K7DDY1_PANTR         779   FCHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEGQIFQLHT-----TLAETPA       833
K7B3D8 K7B3D8_PANTR         779   FCHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEGQIFQLHT-----TLAETPA       833
K7BVI5 K7BVI5_PANTR         779   FCHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEGQIFQLHT-----TLAETPA       833
H2NAM6 H2NAM6_PONAB         492   FYHIWSGSQKALHCTFTLERHSLASTELICKICVRQVEGEGQIFQLHT-----TLAETPA       546
G7N281 G7N281_MACMU         779   FYHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEGQIFQLHT-----TLAETPA       833
F6UDU4 F6UDU4_MACMU         768   FYHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEGQIFQLHTTTLLHTTLAETPA       827
F6UDV7 F6UDV7_MACMU         779   FYHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEGQIFQLHT-----TL--TPA       831
F7A1Z5 F7A1Z5_CALJA         755   FYHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEGQIFQLHT-----TLAETPA       809
U3F339 U3F339_CALJA         779   FYHIWSGSQKALHCTFTLERHSLASTELTCKICVRQVEGEGQIFQLHT-----TLAETPA       833
                                  * ************************* ******************     **  ***

Q8IZJ1 UNC5B_HUMAN          834   GSLDTLCSAPGSTVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRMLAQKLSMDRYL       893
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K7BD08 K7BD08_PANTR        834   GSLDTLCSAPGSTVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRMLAQKLSMDRYL       893
K7BVI5 K7BVI5_PANTR        834   GSLDTLCSAPGSTVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRMLAQKLSMDRYL       893
H2NAM6 H2NAM6_PONAB        547   GSLDTLCSAPGSTITTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRMLAQKLSMDRYL       606
G7N281 G7N281_MACMU        834   GSLDTLCSAPGSAVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRMLAQKLSMDRYL       893
F6UDU4 F6UDU4_MACMU        828   GSLDTLCSAPGSAVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRMLAQKLSMDRYL       887
F6UDV7 F6UDV7_MACMU        832   GSLDTLCSAPGSAVTTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRMLAQKLSMDRYL       891
F7A1Z5 F7A1Z5_CALJA        810   GSLDTLCSAPGGAITTQLGPYAFKIPLSIRQKICNSLDAPNSRGNDWRMLAQKLSMDRYL       869
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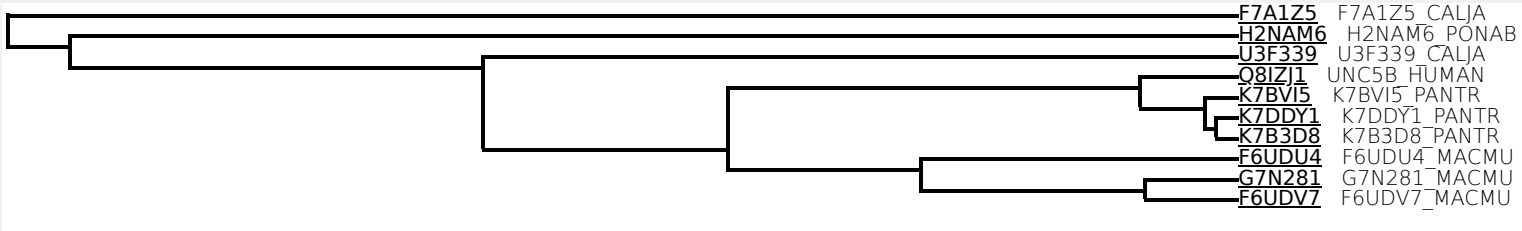
You may add additional sequences to this alignment (in FASTA format)

Tree



Highlight Taxonomy

Result information

Query sequences

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Date of job execution	Mar 16, 2018
Job identifier	A2018031683C3DD8CE55183C76102DC5D3A26728B0D5B59R (jobs are stored for 7 days)
Running time	23 seconds
Identical positions	601
Identity	63.13%
Similar positions	29
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Default parameters	Default parameters: The default transition matrix is Gonnet, gap opening penalty is 6 bits, gap extension is 1 bit. Clustal-Omega uses the HHalign algorithm and its default settings as its core alignment engine. The algorithm is described in Söding, J. (2005) 'Protein homology detection by HMM–HMM comparison'. Bioinformatics 21, 951-960.

	Entry	Entry name	Protein names	Organism	Gene name
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K7DDY1	K7DDY1_PANTR	**Unc-5 homolog B**	Pan troglodytes (Chimpanzee)	**UNC5B**	
K7B3D8	K7B3D8_PANTR	**Unc-5 homolog B**	Pan troglodytes (Chimpanzee)	**UNC5B**	
K7BVI5	K7BVI5_PANTR	**Unc-5 homolog B**	Pan troglodytes (Chimpanzee)	**UNC5B**	
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G7N281	G7N281_MACMU	**Uncharacterized protein**	Macaca mulatta (Rhesus macaque)	EGK_19753	
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F6UDV7	F6UDV7_MACMU	**Unc-5 netrin receptor B**	Macaca mulatta (Rhesus macaque)	**UNC5B**	
F7A1Z5	F7A1Z5_CALJA	**Unc-5 netrin receptor B**	Callithrix jacchus (White-tufted-ear marmoset)	**UNC5B**	
U3F339	U3F339_CALJA	**Netrin receptor UNC5B isoform 1**	Callithrix jacchus (White-tufted-ear marmoset)	**UNC5B**	