


Aligned using an external algorithm


Consensus

- 1. SP|Q19546|WRN_CAEEL
- 2. SP|Q14191|WRN_HUMAN
- 3. SP|O09053|WRN_MOUSE
- 4. SP|O93530|WRN_XENLA




--- -XXXTXXQRKXPEWMXXXXXXXXXXXXX-KXXXXKXXXEDXLPFXXFXGSIVYSYXX

| | | |
|---|--|----|
| 1 | ----- | |
| 2 | MSEKKLETTAQQRKCPPEWMLNVQNKRCAVEE-RKACVRKSVFEDDLPFLEFTGSIVYSYDA | 59 |
| 3 | -----METTSLQRKFPPEWMSMQSQRCATEE--KACVQKSVLEDNLPFLEFPGSIVYSYEA | 53 |
| 4 | -----MTSLQRKLPPEWMSVKQQEDRIDDAKKSFCCKNILLEDNLPFMKFNIGSIVYSYES | 53 |




XDCSXLSEDIXXXLXXXDVXGFDXEWPPYXXGKXXXVAXIQXCVSEXKCYLFHXSXMXX

| | | |
|---|--|-----|
| 1 | ----- | |
| 2 | SDCSFLSEDISMSLSDGDVVGFDMEWPPLYNRGKLGKVALIQLCVSESKCYLFHVSSMSV | 119 |
| 3 | SDCSFLSEDISMRLSDGDVVGFDMEWPPIYKPGKRSRVAVIQLCVSESKCYLFHISSMSV | 113 |
| 4 | NDCSLLESDIRSSLLEEDVLGFDIEWPPVYTKGKTGKVALIQLCVSEKCYLFHISPMA | 113 |




FPXGLKXLLEXXXXXXKXGVGIEGDQWKLXXDXXXKLXXFXELXXXANXKLXCXEXWXXNX

| | | |
|---|---|-----|
| 1 | ----- | |
| 2 | FPQGLKMLLENKAVKKAGVGVGIEGDQWKL LRD FDIKKNFVELTDVANKKLCCTETWSLNS | 179 |
| 3 | FPQGLKMLLENKSIKAGVGVGIEGDQWKL LRD FDKLESFVELTDVANEKLCKAETWSLNG | 173 |
| 4 | FPKGLKRLLLEDVSRKVG VGVGIEGDQWKLMSDYELKLGFIELSEMANQKLRCKEKWTFNG | 173 |




LXKHXXXXQLXKXKSXRCSNWXFXLTEDQKLYAATDAYAGXXIYXXLXXXXXX-XXXFX

| | | |
|---|---|-----|
| 1 | ----- | |
| 2 | LVKHL L GKQLLKD KSI RCSNWSKFP LTEDQKLYAATDAYAG FIIYRNLEILDDT-VQRF | 238 |
| 3 | LVKHVLGKQLLKD KSI RCSNWSNFP LTEDQKLYAATDAYAG LIYQKLGNLGDT-AQV | 232 |
| 4 | LIKHL FKEQLYKR KSYRCSNWDIF L LTEDQKLYAATDAYAG LLIYKLEGMDAHESSFR | 233 |



XXXXXXXXXXXXXXXXXXQLXXXSXXXXDLXXXXPXXXXXXXXXXXXRXXXXLXXXSEXLXLRXX

| | | |
|---|---|-----|
| 1 | ----- | |
| 2 | INKEEEI L LSDMNKQLTSISEEVMDLAKHLP HAFSKLENPRRVSILLKDISENLYSLRRM | 298 |
| 3 | LNKAEENLPLEMKKQLNSISEEMRDLANRFPVTCRNLETLRVPIVILKDISENLCSLRKV | 292 |
| 4 | VGREGVADCKGVKRQLTDLSKGLMDLVNQV P NSFGCYTEAVRAVDILEDLSEKLEELRNI | 293 |



XXXXXXXXXXEXXXXPGXXXXLXXEDXXXXXXXXXXXXKXIXXXXXXXXXXXXXXXXXXPXXXXLXXXX

| | | |
|---|---|-----|
| 1 | MISDDDDLPSTRPGSVNEEL-----PETE----PEDNDELPEPEPESDSD | 41 |
| 2 | IIGSTNIE TELRP SNLNL L SFEDSTTGGVQQKQIREHEVLIHVEDETWDP TLDHLAKHD | 358 |
| 3 | ICGPTNTE TRLKP GSSFN L SSED SAAAGEKE KQI GKHS TFAKIKEEPWPPELDSLVKQE | 352 |
| 4 | MKEASKAE-----GNGLHFQNS EDCS---KKDKSILHVACK-----ESLAEH- | 332 |



XXXVXXNKXXXXXXXX-XXXXXXXXXDXXXXEXXXXXXXXXXXXXIEXELXXXEXXXXXXXXXXD

| | | |
|---|--|-----|
| 1 | KPTVTSNK TEN----- | 57 |
| 2 | GEDVLGNKVERKED-GFEDGVEDNKLKENMERACLMSLDITEHELQILEQQSQEEYLSDI | 417 |
| 3 | EVDVFRNQVKQKEG-ESENEIEDNLLREDMERTCVIP-SISENELQDLEQQAKEEKYNDV | 410 |
| 4 | -----KMDCKNADSQNNKDIIDSCQENRDEDFDFMTLGISEEELYMMEREDDKKQTN-- | 383 |



XX--XXXXDXEXDXXSYXIESDEDXEXE

| | | |
|---|--|-----|
| 1 | DYDSFDDFVPSQHTASKIPVKNKRAKKCTVESDSSSSDSDSQQGDDCEFIPACDETQEV | 117 |
| 2 | AYKSTEHLSPNDNENDTSYVIESDEDLEMEMLKH---LSPNDNENDTSYVIESDEDLEME | 474 |
| 3 | SHQ-----LSEH---LSPNDNENDSSYVIESDEDLEME | 440 |
| 4 | -----PDYKLNKD---SCDTNEEKDMSYVIESDEDLDFSE | 414 |



XX-----KSLXLNXXXVEPXXXXXXXXXXXXXXXXXX

| | | |
|---|--|-----|
| 1 | KIKRGYTLRTRASVKNKCDDSWDDGIDEEDVSKRSEDTLNDSFVDPFEMDSVL-DNQLTI | 176 |
| 2 | ML-----KSLLENLNSGTVEPTHSKCLKMERNLGL | 503 |
| 3 | ML-----KSLLENLNSDVVEPTHSTWLEMGTNRL | 469 |
| 4 | II-----KSLLEDLNDSTEEALGTGVP---QAGLI | 440 |



PXKX-XXXXXXXXXXXXXXXX-XXEXXXXXDXXXPXXXXXCLKXYFGHSSFKPVQWKVX

| | | |
|---|---|-----|
| 1 | KGKKQFLDDGEFFDRNVPQIDEATKMKWASMTSPQEALNALNEFFGHKGFREKQWDVV | 236 |
| 2 | PTKE-EEEDDENEAN-----EGEEDDDKDFLWPAPNEEQVTCCLKMYFGHSSFKPVQWKVI | 557 |
| 3 | PPEE-EDGHGN--EA-----IKEEQEEEDHLLPEPNAKQINCLKTYFGHSSFKPVQWKVI | 521 |
| 4 | PAKS-VDTVADEEEDEGI-EEEDDDDDWDPSMPEPSAQHISCLKTYFGHSSFKPVQWKVV | 498 |



HSVLXERRDNXVVMATGYGKSLCXQXPPVYXXXIGXVISPLISLMEDQVLQLXSNIXAC

| | | |
|---|---|-----|
| 1 | RNVLGG-KDQFVLMSTGYGKSVCYQLPSLLLNSMTVVVSP LISLMNDQVTTLVSKGIDAV | 295 |
| 2 | HSVLEERRDNVAVMATGYGKSLCFYPPVYVGKIGLVISPLISLMEDQVLQLKMSNIPAC | 617 |
| 3 | HSVLEERRDNVVVMATGYGKSLCFYPPVYTGKIGIVISPLISLMEDQVLQLELSNVPAC | 581 |
| 4 | HSVLRERRDNLVVMATGYGKSLCYQFAPVYTSGIGIVICPLISLMEDQVLQLEM SNISSC | 558 |



XLGSAQSXNLX--DXKXGKXRXYIXTPEXCSXXXXLLQLXXXXGITLIAXDEAHCISE

| | | |
|---|--|-----|
| 1 | KLDGHSTQIEWDQVANMHRIRFIYMSP E MVTSQKGLELLTSCRKHTISLLAIDEAHCVSQ | 355 |
| 2 | FLGSAQSENVLT--DIKLGK YRIVYVTPEYCSGNMGLLQQL EADIGITLIAVDEAHCISE | 675 |
| 3 | LLGSAQSKNILG--DVKLGK YRVYITPEFCSGNLDLLQQLDSSIGITLIAVDEAHCISE | 639 |
| 4 | FLGSAQSKNVLQ--DVKD GKM RVIYMTPEFCRGISLLQLDNRYGITLIAIDEAHCISE | 616 |



WGHDFRXXRXLGLSLKX--XLPXVPXXALTATASXSIREDIXXXLNLXXPQITCTXFDRP

| | | |
|---|---|-----|
| 1 | WGHDFRNSYRH LAEIRNRSDL CNIPMIALTATATVRRDDVIANLRLRKPLITTTSFDRK | 415 |
| 2 | WGHDFRDSFRKLGSLKT--ALPMVPIVALTATASSSIREDIVRCLNLRNPQITCTGFDRP | 733 |
| 3 | WGHDFRSSFRMLGSLKT--ALPLVPVIALSATASSSIREDIISCLNLRNPQITCTGFDRP | 697 |
| 4 | WGHDFRSAYRSLGSLKR--MLPNVPIVALTATASPSIREDI TKSLNLHNPQVTCTSFDRP | 674 |

NLYLXVXRKTXNIXXDLXXFLXKXXXXSXWFEFEGPTIIYCPXRKMXXQVTXELXKLXXXC

1 NLYISVHSS-KDMAEDLGLFM-KTDEVKGRHFGGPTIIYCQTKQMVDVNCVLRRIQVRS 473
2 NLYLEVRRKTGNI LQDLQPFVLK--TSSHWEFEGPTIIYCP SRKMTQQVTGELRKLNLSC 791
3 NLYLEVGRKTGNI LQDLKPFVLVRK-ASSAWEFEGPTIIYCP SRKMTQVTAELGKLNLC 756
4 NLYLDVARKTTNISIDLRFLLIKKQQGSWFEFEGATIVYCPTRKTSEQVTAELIKLGIAC 734

XYTHAGMXXXXRXXHHRFXRDEIXCVVATVAFGMGINKXDIRXVIHYGAPKXMESYYQE

1 AHYHAGLTKNQREKAHTDFMRDKITTTIVATVAFGMGIDKPDVNRNVIHYGCPNNIESYYQE 533
2 GTYHAGMSFSTRKDIHHRFVRDEIQCVIATIAFGMGINKADIRQVIHYGAPKDMESYYQE 851
3 RTYHAGMKISERKDVHHRFLRDEIQCVVATVAFGMGINKADIRKVIHYGAPKEMESYYQE 816
4 GTYHAGMGIKQRREVHHRFMRDEIHCVVATVAFGMGINKPDIRKVIHYGAPKEMESYYQE 794

IGRAGRDLXSXCHXLWAPADNXRXLXEIXXXXFRXYKL-KMXXKMEKYLXSSXCR

1 IGRAGRDGSPSICRVFWAPKDLNLIKFKLRNSQQKEEVVENLTMMLRQLELVLTTVGCRR 593
2 IGRAGRDLQSSSCHVLWAPADINLNRHLLTEIRNEKFRLYKL-KMMAKMEKYLHSSRCRR 910
3 IGRAGRDLQSSSCHLLWAPADFNTRSRLIEIHDEKFRLYKL-KMMVKMEKYLHSSQCRR 875
4 IGRAGRDLPSCHALWAQADMNFNRHMLGEIPNKGFRYKYL-KMLTKMEKYLNSSTCRR 853

XIILSHFEDKXXXKASXXIMGTEKCCDNCXXRLXXXXXXXXXXSEDXXXDFGPQAXXXXSAV

1 YQLLKHFDPYAKPPT----MQADCCDRCTEMLNGNQDSSSSIVDVT--TESKWLQVIN 647
2 QIILSHFEDKQVQKASLIMGTEKCCDNCRSRLDHCYSMDSDSDTSWDFGPQAFKLLSAV 970
3 RIILSHFEDKCLQKASLDIMGTEKCCDNCRPNLNHCLTANNSEDASQDFGPQAFQLLSAV 935
4 KIILSHFEDKQLRKASSGIMGTEKCCDNCRTLICNISINDTEDNLQDFGPQAYKFISAV 913

DXLXXKFGIGXPILFLRGSXSQRXXD-XXRXHLFGXGKXQXEWKXLXXXLIEGXLX

1 EMYNGKTFGIGKPIEFLRGS SKEDWRIKTTSSQQKLFYIGKHIPDKWVKALAAASLRIAGYLG 707
2 DILGEKFGIGLPIFLRGSNSQR LAD-QYRRHSLFGTGKDQTESWVKAFSRQLITEGFLV 1029
3 DILQEKFGIGIPIFLRGSNSQR LAD-KYRGHSLFGAGKEQAESWVKTLSSHLLIAEGFLV 994
4 DVLGQKFGTGVPVFLRGS TSQRVDP-RFRNHSLFSSGKDQTEAFWVKLARQLITEGYLQ 972

EVXXX-XKFXXXCLTXKGXWLVXXAXXXX--XXSLLLQXNEXXXXXXXXXXXXXSXSS--

1 EVRLMQMKFGSCITLSELGERWLLTGKEMKIDATPI LLQGGKEKAAPSTVPGASRSQS-- 765
2 EVSRY-NKFMKICALTKKGRNWLHKANTES--QSLILQANEELCPKLLLPSSKTVS-- 1083
3 EVPKE-NKYIKTCSLTKKGRKWLGEASSQS--PPSLLLQANEEMFPRKVLPLPSSNPVS-- 1049
4 ESSGQ-TKFSTICGLTSKGSNWLIKANNEQ--CPSLLLPSNNEELCLQRTRVSNFSSAQAH 1029

XXXXXXXXHXXXXXXXXXPXXXXXXXXXXLXXXXSYXXXXXXXXSXNXXKXSXXXXXXXXPXXXXXXXX

1 -----TKSSTEIP TKIL-----GANKIREYEPANENEQLMNLKKQEV-TG----- 804
2 SGTKEHCYNQ--VPVELSTEKSNLEKLYSYKPCDKISSGSNISKKSIMVQSP EKAYSSS 1141
3 PETTQHSSNQ--NPAGLTT-KQSNLERTHSYKVPEKVS SGTNIPKKS AVMPSPGTSSSPL 1106
4 SSMVPHASSNTRSSMPKAGPEKME LKDKFSYQEAERLSKAAGVSKSSFKLQTPCKLSRPP 1089

XPXXSXXEXEXXXXLYXRLVXARQKXANXXDVXPAXLATNKVLXDMAKXRPTT XenXKXI

1 ---LPEKIDQLRSRLDDIRVGIANMHEVAPFQIVSNTVLD CFANLRPTSASNLEM I 857
2 QPVISAEQETQIVLYGKLV EARQKHANKMDVPPA I LATNKILV DMAKMRPTT VENVKRI 1201
3 EPAISAEELDARTGLYARLVEARQKHANKMDVPPA I LATNKVLL DMAKMRPTT VENMKQI 1166
4 EPEVSPRERELQTTLYGRLVV ARQKIASERDILPAV LATNKVLV DMAKLRPTT SENMKKL 1149

DGVSEXXAXLA-PLLEVXKXFCXXXSXXTDXXSXXXXXXXXXXXXXXXXXXXXXXXXLXXSXX

1 DGMSAQQKSRYGKRFVDCVVQFSKETGIATNVNANDMIPPEL----ISKMQKVLSDAVR 912
2 DGVSEGKAAMLA-PLLEVIKHFCQTNSVQTDLFSSTKPQEEQKTSLVAKNKICTLSQSMA 1260
3 DGVSEGKAALLA-PLLEVIKHFCQVTSVQTDLLSSAKPHKEQEKSQEMEKKDCSLPQSVA 1225
4 DGVSEAKSAMPLA-PLLEVVKFCIANSLKVDVFSGSVVSQSESTFFTPREQERISLPESQR 1208

XXYXLFQEXXXXLKXIAXXRXLXXXXGMHLXQAVKAGXPLDXXRAGLTPEXXKXIXXXI

1 RVYTEHLISRSTAKEVATARGISEGTVYSYLAMAVEKGLPLHLDKLNVS RKNIAMALNAV 972
2 ITYSLFQEKKMP LKSIAESRILPLMTIGMHL SQAVKAGCPLD LERAGLTPEVQKIIADV I 1320
3 VTYTLFQEKKMP LHSIAENRLLPLTAAGMHLAQAVKAGYPLD MERAGLTPETWKIIMDVI 1285
4 MSYSLFQEQNLSLKKIADVRCLSMAVVGMHLWQALKAGYSFDVQRAGLTPEMKKLITYAI 1268

R-----XPPXNSDXXXXKLIRXXVPXNDXYXIXMXIXILXXGXDSE-XXQ

1 RVHLGSNVAVLTPWVEAMGVVPDFNQLKLIRAIL-----IYEYGLDTSENQ 1018
2 R-----NPPVNSDMSKISLIRMLV PENIDTYLIHMAIEILKHGPDS-GLQ 1364
3 R-----NPPINSDDMYKVKLIRMLV PENLDTYLIHMAIEILQSGSDS-RTQ 1329
4 K-----KPPINSDLSSFKAIREYVPANIDGYPIRMVISLLEKEGSS-GAQ 1312

XXXDXXXXXXXXXPXXXE-XXXXX-----XXXXXXXXXXXXXXXXXX-XXXXXX

1 EKPDI---QSMPLSTSN-PSTIK-----TVPSTPSSSL---RAPPLKK 1053
2 PSCDVNKRRCFP GSEE-----IC----- 1382
3 PPCDSSRKRFPSSAE-----SC----- 1347
4 GQPEFPTQKTLIQTEENPKNVSVQNTKHKVMTGKSMWIEKKPTQPATAELEVTKGKALAP 1372

XXX-----SXXXXXXXXXXXXXXXXSXXXXRXLXWFXXXXXXXXXXXXXXXXXXXXXXXX-XX

1 FKL----- 1056
2 -----SSKRSEEVGIN TETS SAERKRRLPVWF AKGSDTS-----KKLMDKTK-RG 1428
3 -----ESCKESKEAVT-ETKASSSESKRKLPEWFAKGNVPSADTGSSSSMAKTK-KK 1397
4 IMLASWNEASLDADTEELFSESQSS TTRPRRLPEWFGSTKGNAATRCCIQUESKNLGEEKG 1432

XXFX

1 --- 1056
2 GLFS 1432
3 GLFS 1401
4 SFFD 1436

Consensus Threshold: >50%

Compare to: the consensus

Amino acids that match the reference are marked with yellow highlighting.

Created: 29 Jan 2020

Last Modified: 29 Jan 2020