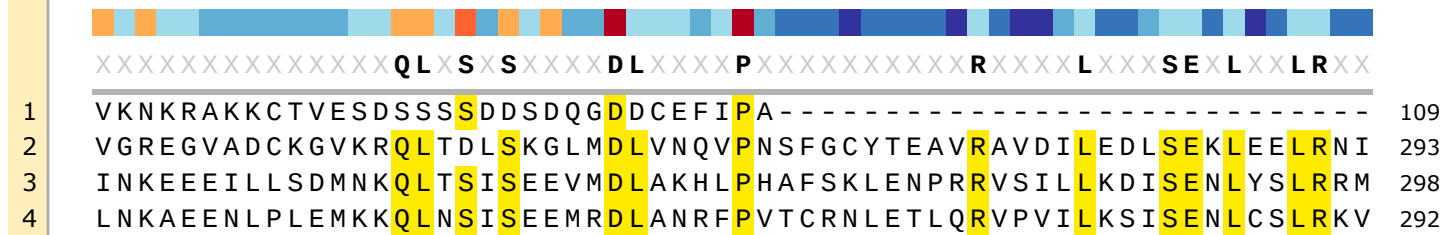
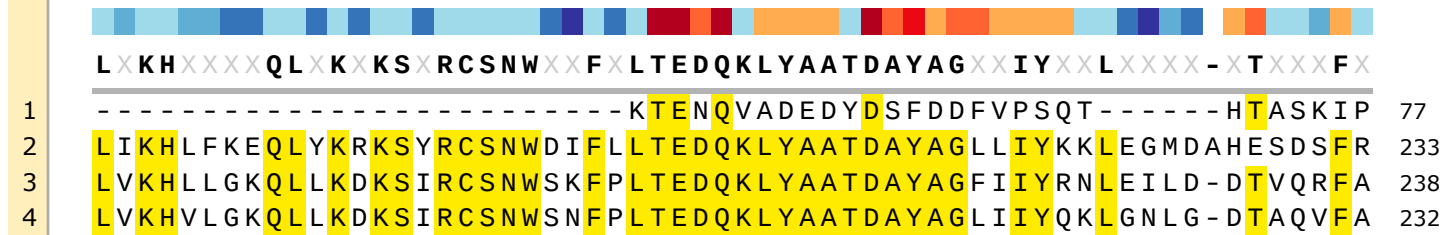
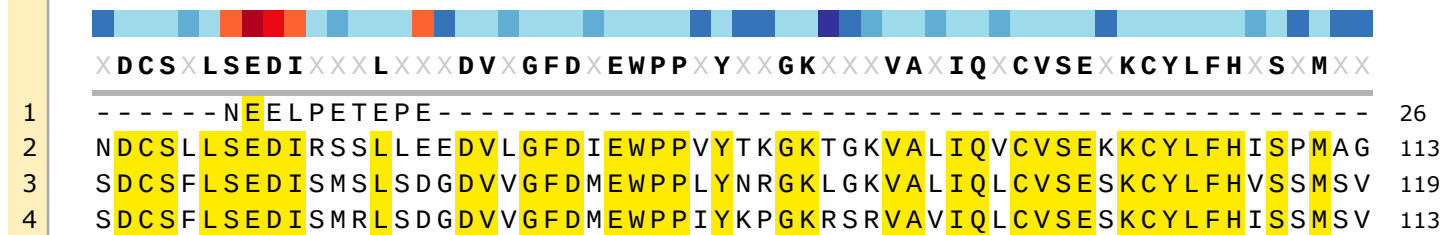
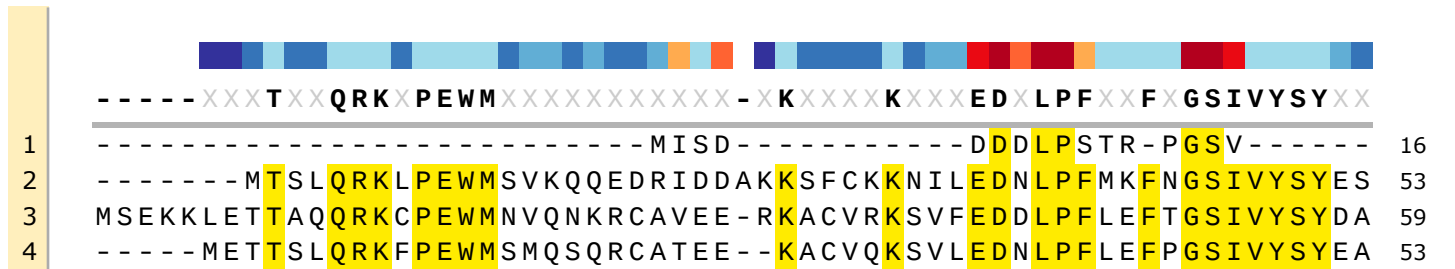


**Consensus**

1. sp|Q19546|WRN\_CAEL
2. sp|O93530|WRN\_XENLA
3. sp|Q14191|WRN\_HUMAN
4. sp|O09053|WRN\_MOUSE







LXXXXGITLIAIDEAHCISEWGHDFRXXSXXLXGSL--KXXLPXVPXXALTATASXSIREDD

1	TSCRKHISLLAIDEAHCVSQWGHDFRNSYRHLAEIRNRSDLCNIPMIALTATATVRVRDD	395
2	LDNRYGITLIAIDEAHCISEWGHDFRSAYRSLGSL--KRMLPNVPIVALTATASPSIRED	654
3	LEADIGITLIAVDEAHCISEWGHDFRDSFRKLGSL--KTALPMVPIVALTATASSSIREDD	713
4	LDSSI GITLIAVDEAHCISEWGHDFRSSFRMLGSL--KTALPLVPVIALSATASSSIREDD	677



IXXXXLNLXXPQITCTXFDRPNLYLVXRKTXXNIXXDLXXFLXXX-XXSXXWFEFEGPTIIYC

1	VIANLRLRKPLITTTSFDRKNLYISV-HSSKDMAEDLGLFMKTD-EVKGRHFGGPTIIYC	453
2	ITKSLNLHNPQVTCTSFDRPNLYLDVARKTTNISIDLQRFLIKKQQGSGWFEFEGATIVYC	714
3	IVRCLNLRNPQITCTGFDRPNLYLEVRKKTGNILQDLQPFLVK--TSSHWEFEGPTIIYC	771
4	IISCLNLKDPQITCTGFDRPNLYLEVGRKTGNILQDLKPFLVRK-ASSAWEFEGPTIIYC	736



PXXRKMXXQVTXELXKLXXXCXTYHAGMXXXXRXXXHHRFXRDEIXCVVATVAFGMGINKX

1	QTKQM VDDVNCVLRRIQVRSAYHYHAGLTKNQR EKAHTDFMRDKITTI VATVAFGMGIDKP	513
2	PTRKTSEQVTAELIKLGIACGTYHAGMGIKQREVVHHRFMRDEIHCVVATVAFGMGINKP	774
3	PSRKMTQQVTGELRKLNLSCGTYHAGMSFSTRKDIHHRFVRDEIQCVIATIAFGMGINKA	831
4	PSRKMTEQVTAELGKLNLCRTYHAGMKISERKDVHHRFLRDEIQCVVATVAFGMGINKA	796



DIRXVIHYGAPKXMESYYQEIGRAGRDGLXSXCHXLWAPADXXRXXLXEIXXXXFRXY

1	DVRNVIHYGCPNNIESYYQEIGRAGRDGSPSICRVFWAPKDLNTIKFKLRNSQQKEEVVE	573
2	DIRKVIHYGAPKEMESYYQEIGRAGRDGLPSCCHALWAQADMNFNRHMLGEIPNKGFREY	834
3	DIRQVIHYGAPKDMESYYQEIGRAGRDGLQSSCHVLWAPADINLNRHLLTEIRNEKFRLY	891
4	DIRKVIHYGAPKEMESYYQEIGRAGRDGLQSSCHLLWAPADFNTRSNLLIEIHDEKFRLY	856



KLKMMXK-MEKYLXSSXCRRXIILSHFEDKXXXKASXXIMGTEKCCDNCXXRLXXXXXX

1	NLTMMLRQLELVLTTVGCRRYQLLKHFDPSYAKPPTM---QADCCDRCTEMLNGN---Q	626
2	KLKMLTK-MEKYLNSSTCRRKIILSHFEDKQLRKASSGIMGTEKCCDNCCTRLICNISIN	893
3	KLKMMAK-MEKYLHSSRCRRQIILSHFEDKQVQKASLGIMGTEKCCDNCRSRLDHCYSMD	950
4	KLKMMVK-MEKYLHSSQCRRRIILSHFEDKCLQKASLDIMGTEKCCDNCRPRLNHCLTAN	915



DSEDXXXDFGPQAXLXSAV-DXLXXKFGIGXPILFLRGSXSQ--RXXDXXRXXLFGXG

1	DSSSSIVDVTTESKWLFQVINEMYNGKTGIGKPIEFLRGS SKEDWRIKTTTSQ-QK LFGIG	685
2	DTEDNLQDFGPQAYKFISAV-DV LGQKFGTGPVLPVFLRGS TSQ--RVPDRFRNHSLFSSG	950
3	DSEDTSWDFGPQAFKLLSAV-DILGEKFGIGLPILFLRGS NSQ--RLADQYRRHSLFGTG	1007
4	NSEDASQDFGPQAFQLLSAV-DILQEKFGIGIPILFLRGS NSQ--RLPKYRGHRLFGAG	972

K X Q X E X W W K X L X X X L I X E G X L X E V X - X X X K F X X X C X L T X K G X X W L - - X K A X X X X X S L L L

1 KHIPDKWVKALAAASLRIAGYLGEVRLMQMKFGSCITLSELGERWLLTGKEMKIDATPIILL 745  
2 KDQTEAFWKVLRQLITEGYLQESS-GQTKFSTICGLT SKGSNWL--IKANNEQCP SLLL 1007  
3 KDQTESWVKAFSRQLITEGFLVEVS-RYNKFMKICALT KKG RNWL--HKANTES-QSLIL 1063  
4 KEQAESWVKTL SHHLIAEGFLVEVP-KENKYIKTCSLT KKG RKWL--GEASSQSPP SLLL 1029

Q X N X E X X X X X X X X X - - - - - X X X X X X X X X X P X X X X X X X X X X P X X X X T - K X X X L X X X X S Y X X X X X

1 QGKKEK-----AAPSTVPGASRSQSTKSSTEIPT-KILGANKIREYEPANE 790  
2 PSNNE LCLQRTRVSNFSSAQAHSSMVPHASSNTRSSMPKAGP--EKMELKDKFSYQEAER 1065  
3 QANEELCPKLLLP-----SSKTVSSGTKEHCYNQVPVELSTEKKS NLEKLYSYKPCDK 1117  
4 QANEEMFPRKVLLP-----SSNPVSPETTQHSSNQNPAGLTT-KQSNLERTHSYKVPEK 1082

X S X X X N X X K X S X X X X X P X K X X X X X X P X X S X X E X X X X X X X L Y X R L V X A R Q K X A N X X D V X P A X

1 NEQLMNLKKQEVT-GLPEKIDQ-----LRSRLDDIRVGIANMHEVAPFQ 833  
2 LSKAAGVSKSSFKLQTPCKLSRPPEPEVSPRERELQTTLYGRLVVARQKIASERDILPAV 1125  
3 ISSGSNISKKSIMVQSPEKAYSSSQPVISAQE QETQIVLYGKLV EARQKHANKMDVPPAI 1177  
4 VSSGTNIPKKS AVMPSPGTSSSPLEPAISAQELDARTGLYARLVEARQKHANKMDVPPAI 1142

L A T N K V L X D M A K X R P T T X E N X K X I D G V S E X K X A X L A P - L L E V X K X F C X X X S X X T D X X S X X

1 IVSNTVLD CFANLRPTSASNLEMIDGMSAQQKSRYGKRFVDCVVQFSKETGIATN VNAND 893  
2 LATNKVLVDMAKLRPTTSENMKKLDGVSEAKSAMLAP-LLEVVKEFCIANS LKVDVFSGS 1184  
3 LATNKILVDMAKMRPTTVENVKRIDGVSEGKAAMLAP-LLEVIKHFCQTN SVQTDLFSST 1236  
4 LATNKVLLDMAKMRPTTVENMKQIDGVSEGKAALLAP-LLEVIKHFCQVTSVQTDLLSSA 1201

X X X X E X X X X X X X X X X X X X X L X X S X X X X Y X L F Q E X X X X L K X I A X X R X L X X X X X G M H L X Q A V K

1 MIPPE-----LISKMQVLSDAVRRVYTEHLISRSTAKEVATARGISEGTVYSYLA MAVE 948  
2 VSQSESTFFTPREQERISLPESQRMSYS L F Q E Q N L S L K K I A D V R C L S M A V V G M H L W Q A L K 1244  
3 KPQEEQKTSLVAKNKICTLSQSMAITYSLFQEKKMP LK S I A E S R I L P L M T I G M H L S Q A V K 1296  
4 KPHKEQEKSQEMEKKDCSLPQSVAVTYTLFQEKKMP L H S I A E N R L L P L T A A G M H L A Q A V K 1261

A G X P L D X X R A G L T P E X X K X I X X X I R X P P X N S D X X X X X - - X I R M X V P X N X D X Y X I X M A I X I

1 KGLPLHLDKLNVS RKNIAMALNAVR-VHLGSNVAVLTWPVEAMGVVPDFNQLKLIRAILI 1007  
2 AGYSFDVQRAGLTPEMKKLI TYA I K K P P I N S D L S S F K - - A I R E Y V P A N I D G Y P I R M V I S L 1302  
3 AGCPLDLERAGLTPEVQKIIADVIRNPPVNSDMSKIS--LIRMLVPENIDTYLIHMAIEI 1354  
4 AGYPLDMERAGLTPE TWK I I M D V I R N P P I N S D M Y K V K - - L I R M L V P E N I D T Y L I H M A I E I 1319



LXXGXD-SXXQXXXD-----XXXXXXXXXPXXE

1	YEYGLDTSENQEKPD-----	1022
2	LEKEGS-SGAQGQPEFPTQKTLIQTEENPKNVSVQNTKHKVTMGKSMWIEKKPTQPATAE	1361
3	LKHGPD-SGLQPSCD-----VNRRCFPGSEE	1380
4	LQSGSD-SRTQPPCD-----SSRKRFPSSAE	1345



X-----XXSXXXXXEXXXXXTXSXXXXXRRLPWF--XKXXXXXX

1	-----IQSMPSTSNPSTIKTVPSTPSSSLRAPPL-----	1051
2	LEVTKGKALAPIMLASWNEASLDADTEELFSESQSSSTRPRRRLPEWFGSTKGNAAATRCI	1421
3	I-----CSSSKRSKEEVDGINTETSSAERKRRLPVWF--AKGSDTSKKL	1421
4	S-----CESCKESKEAVT-ETKASSSESKRKLPEWF--AKGNVPSADT	1385



XXXXXXXXXXKKXXLFX

1	-----KKFKL--	1056
2	QESKNLGE-EKGSFFD	1436
3	-----MDKTKRGG LFS	1432
4	GSSSSMAKTKKKGLFS	1401

**Consensus Threshold:** >50%

**Compare to:** the consensus

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

**Created:** 30 Jan 2020

**Last Modified:** 30 Jan 2020