

# Mcl-1

## Homo sapiens:

>Q07820 MCL1 HUMAN Induced myeloid leukemia cell differentiation protein Mcl-1 OS=Homo sapiens OX=9606 GN=MCL1 PE=1 SV=3  
MFLGKRNAVIGLNLVYCGGAGLGAGGGGATRPGGRLLA TEKEASARREIGGEGAGAVIGGS  
AGASPPSTLTTPDSRRVA**SPPTGAE**VPDVTATPARLLFFAPTRRAAPLEEMEA PAADAIM  
SPEEELDGYEPEPLGKRPAVLPLELVLGSEGNNTSTDGSLPSTPPPAAEEDELYRQSL  
EIIISRYLREQATGAKDTPKPMGRSGATSRKALETLRVVG DG VQRNHETAFQGMRLKLDIKNE  
DDVKLSLRVMIHVFS DGV TNWGRIVTLISFGAFVAKHLKTINQESCIEPLAESITDVLVR  
TKRDWLVKQRGWDGFVEFFHVEDLEGGIRNVLLAFAGVAGVGAGLAYLIR

## Pongo abelii:

>XP\_002810320.1 induced myeloid leukemia cell differentiation protein Mcl-1 isoform X1 [Pongo abelii]  
MFLGKRNAVIGLNLVYCGGAGLGAGSGATPPGGRLLA TEKEASARREIGGEGAGAVIGSAGASPPSTLT  
PDSRRVA**SPPTGAE**VPDVTATPARLFFAPTRRAAPLEEMEA PAADAIMSPEEELDGYEPEPLGKRPAV  
LPLELVLGSEGNNTSTDGSLPSTPPPAAEEDELYRQSL EIIISRYLREQATGAKDTPKLRSGATCRKAL  
ETLRVRVG DG VQRNHETAFQGMRLKLDIKNE DDVKLSLRVMHVFS DGV TNWGRIVTLISFGAFVAKHLKT  
INQESCIEPLAESITDVLVTRTKRDWLVKQRGWDGFVEFFHVEDLEGGIRNVLLAFAGVAGVGAGLAYLIR

## Mus musculus:

>NP\_032588.1 induced myeloid leukemia cell differentiation protein Mcl-1 homolog [Mus musculus]  
MFLGKRNAVIGLNLVYCGGASLGAGGSGPAGARLVAEEAKARREGGGEAALLPGARVVA**SPFVQAE**DPDV  
TASAERLRHKSPGLLAVPPEEMAASAAAAIVSPEEELDGCEPEAIGKRPAVLPLLERVSEAAKSSGADGS  
LPSTPPPPEEEEDDLVRQSL EIIISRYLREQATGSKDSKPLGEAGAAGRRALETLRVRVG DG VQRNHETAFQ  
GMRLKLDIKNEG DVKFSRVMHVFKDGV TNWGRIVTLISFGAFVAKHLKSVNQESFIEPLAETITDVLV  
RTRRDWLVKQRGWDGFVEFFHVQDLEGGIRNVLLAFAGVAGVGAGLAYLIR

## Gallus gallus:

>NP\_001244212.2 induced myeloid leukemia cell differentiation protein Mcl-1 isoform 1 [Gallus gallus]  
MFAVKRNAVIGFNLVYCGGGSPGLVPASPAGEQTTPPPAAAAAPAAAAATVAEVPRLIGSAGLWAAAGRAEA  
**FPAPFSGSQA**PHAPIGSAARAPFDSTSRFVALWSPEEELDGCEPESERGPGGDSLPGTTPPELFDLIPD  
ELRQESLELILNLVREAGAEAFVQVKLEPGLLQCGPFCRASSAVMEKALETLRARVGDGVNQKHELAFQ  
GMLRKLILIKKEDDLQAVCEVAHVNDGV TNWGRIVTLISFGAFVAKHLKSIINQEK CITSLAGIITDALV  
SSKREWLMSQGGWEGVDFVRVEDLESSIRNVLMFAFAGVAGLGA SLAYMIRKWRSS

## Xenopus laevis:

>NP\_001131055.1 MCL1, BCL2 family apoptosis regulator L homeolog [Xenopus laevis]  
MMHQSVIAKQRPSTSFILIPQCFYCSGGSSSEKTL SARGASPWDPDMDTHRPO LNLGFGNNNGSLPCSQED  
ELDEIDMNGSQGSTSPDPSPVC PKDGLYMDTQQ LILAFYRVYSGEESGELEASCLLQHG VHHKALETL LRL  
VGGEIIEKH HMAFTGMLQRLSIHSREDLQKLS E V PALVFNDGV TNWGRIVTVISFGAFVAKHLKSLNLED  
CIGVLA EFTQFLMMSKKDWIIQEKGWDGFVDFFHIEDYESGLKT VLMAFSSVAVLGAGLAYMIR

## Salmo salar:

>NP\_001117034.1 myeloid leukemia differentiation protein homologue [Salmo salar]  
MSLSNSITRATTMTLHFQNGGSSYLADDARPLY YFQGAGACAGASPKSKVDLGNGTGDTPPRPPTTLGVN  
VVKSNGLDNHLSDRSNDDSLPCTPQMASEC GP ELSNCPSGDEVLEH DTRQLIENFLG DYTGLSQFRWQT  
SKPLTTMKRVVEDVIAKHRYAYNGMVAKLDLDDRCDDMGVINSVAKTFMSD GITNWGRIASLVAFGA VVS  
QHLKERGRGHGVELVQG EIAKYL LDDQS DWLKNNAWNGFVEFFHVQDPESSVRNTLLAFAGVAGIGATL  
AMFIR

## Petromyzon marinus:

>XP\_032829936.1 anti-apoptotic protein NR13-like [Petromyzon marinus]  
MVA DGT HAGI FAADRLQQQAGSGPPNSPSPRDNDTATAPAIGEACGAPPTTPATSADSVSHSAADIQAT  
RSGGSRPYND DALTVETANFITGYMAHLTPTEQPPHQQLSSASELLKSMGDSLLEQHRAAISGMVSRVE  
AQTDFPELRGSALGVAREMFS DGHMNGRVVALVVF CALLVKRLKASGR L SDAEARAVADEVA AFLVSSR  
KAMFVQQGGWNGFVREFERETPDSALKNTLMAVAGFGAMTALAALGV RKLISGFC

## Branchiostoma belcheri:

>XP\_019634801.1 PREDICTED: bcl-2-related ovarian killer protein homolog B-like [Branchiostoma belcheri]  
MDLTRRESAVEQPLPSLDEEHEHDS DGEPESVDSRREETGGVPARVWTF LREFSVRDWLRNAKDAALD  
LRQYVLDPETIKGLWSQAAPTEKSVI DESRQLRDYINGRLKKS NLRGRLPDAKRRPT EVSSQLQKM  
GGELERMYPHLYRDVSRQINITLSSESIETSFETVANELFSTGITWARI VAMFAVAGAFVDCVHQGHP  
MFTRRLVDVVDFTRKLSAWLVQEGGWYGLVKHFRGDGRTHMFWAISGIAAIGLAATFFVIDP

## Drosophila melanogaster:

No homolog found.

## Hydra vulgaris:

>XP\_001626412.1 apoptosis regulator Bcl-2 [Nematostella vectensis]  
MPTREGYDNANAVARKMKTP EEKIAHELA KDFIGYKLGKGR LNTKSALILRKLSNQIENKH EFLRNM  
CDRLDIQHNAPETFKQVADEIFGDGINWGRIVVLYTFAGK VAKYQENQLDNAENVATWVGNYVASKSD  
WVKKAGGWEAFNEQFKVDQVEHEKFWWNSLLC TTLGLGSLA AVL YMKSS

## Nematostella vectensis:

>XP\_047134887.1 apoptosis regulator BAX [Hydra vulgaris]  
MGPFPAQPKPTIENNQPLNEEAPSLD TVDGRPQRFNNGGTRLRNQPRNVVNVNNSN QVIESTPELFTQF  
LVNRNENDNI EVPEELRNRSRNGTVNKEVAHCLKRIGDDL VNNHQLNHLISSIQVTRETAYKTFFDVASH  
VFADGTINWGRVTVLFYFAYKLAIQV VNLPLVEIVIGMWQKFVTDRLAQWIAERG GWNAVQEYFGSTTV  
QFVGVFAGFLFAYILTKVFRR

## Amphimedon queenslandica:

>XP\_003386733.1 PREDICTED: bcl-2-like protein 1 [Amphimedon queenslandica]

MALVVPAPVQHQQYHHKNSPKRRGSPVQDDKFYEETRNLITACIESASGKEPLSVKLSEEALRIVGMVQQ  
TLKADEIFFRKLCEELELTATNLFSKLMDVWGMFSDGQVNI GRLLALLAFQCQCVTVYCRSVGLPSIESS  
VPHWASIFISTTHLKDWITNRGGWDAISKELMLRTSATNSSTSSRTASNGGWLQWGVSGIALAISVFDAL  
HNSS

## Alignment

XP_019634801.1[B.belcheri]	-----	0
XP_00386733.1[A.queenslandica]	-----	0
XP_047134887.1[H.vulgaris]	-----	0
XP_001626412.1[N.vectensis]	-----	0
XP_032829936.1[P.marinus]	-----	0
NP_001117034.1[S.salar]	MSL-----SNSITRATTMTLHFQNGSGS-----	23
NP_001131055.1[X.laevis]	MMHQSVIAKQRPSTSLIPICQFYCSGGGSEKT-----	33
NP_001244212.2[G.gallus]	-----MFAVKRNAVIGFNLYCGGSGPGLVPAS--PAGEQTTPPAAAAFAAAATVAE	50
NP_032588.1[M.musculus]	-----MFGLRRNAVIGLNLYCGGASLGAGGGS--PAGARLVAAEA--KARR-EGGGE	47
Q07820[H.sapiens]	-----MFGLKRNAVIGLNLYCGGAGLGAGSGGATPGRRLATEKEASARREIGGGE	52
XP_002810320.1[P.abelii]	-----MFGLKRNAVIGLNLYCGGAGLGAGSGGATPPGGRLLATEKEASARREIGGGE	52
XP_019634801.1[B.belcheri]	-----MD	2
XP_00386733.1[A.queenslandica]	-----	0
XP_047134887.1[H.vulgaris]	-----	0
XP_001626412.1[N.vectensis]	-----	0
XP_032829936.1[P.marinus]	-----MV	2
NP_001117034.1[S.salar]	-----YLADDARPLYFQGAGAT-----	41
NP_001131055.1[X.laevis]	-----L	34
NP_001244212.2[G.gallus]	VPRPLIGSAGLW-----AAAGRAEAPKAPTGSGAA-----PHAPI-GSAAARRAPPPDS--	97
NP_032588.1[M.musculus]	-----AALLPGARVVAKPPFVVALDPDVTASAERRLHKSPLGLLAVPPEEMA	93
Q07820[H.sapiens]	AGAVIGGSAGASPPSTLTPDSRRVAKPPFVVALVDPVTATPARLLFFAFPTRAAPLEEME	112
XP_002810320.1[P.abelii]	AGAVIGGSAGASPPSTLTPDSRRVAKPPFVVALVDPVTATPARLLFFAFPTRAAPLEEME	112
XP_019634801.1[B.belcheri]	LT-----RRESAVEQPLPLDEEHEHSDGEGPES	32
XP_00386733.1[A.queenslandica]	-----	0
XP_047134887.1[H.vulgaris]	-----MGPPPAQPKPTIENNQPLNEEAPSLDVTVDGRPQRF-----	34
XP_001626412.1[N.vectensis]	-----	0
XP_032829936.1[P.marinus]	ADGTHAGIFAADRLQQQGA--GSPFNSPSPR-DNDTA--TAPAIGE-----	43
NP_001117034.1[S.salar]	-----CAGASPKSKVDLNGTGDTPRPTTLGVN-----VVKSNGLDNHLSDRS	85
NP_001131055.1[X.laevis]	SARG-ASPWDPMDTH-----RPQLNGLGFNNGG--SLPCSQ-EDELEDMD-----	76
NP_001244212.2[G.gallus]	TSRP-VALWSPPEELD-----GCEPESERG-----	121
NP_032588.1[M.musculus]	ASAA-AAIVSPPEELD-----GCEPEAI GK R-PA--VLPLLERVSEAAKSS-----	135
Q07820[H.sapiens]	APAA-DAIMSPPEELD-----GYEPEPLGKR-PA--VLPLLELVGESGNN-----	154
XP_002810320.1[P.abelii]	APAA-DAIMSPPEELD-----GYEPEPLGKR-PA--VLPLLELVGESGNN-----	154
XP_019634801.1[B.belcheri]	VDSRREETGGVPARVWTFLREFSVRDWLRNAKDAALDLRQYVLDVPETI-----K-G	84
XP_00386733.1[A.queenslandica]	-----MA-----LVVNPAPVQHQY-----HHKNS	19
XP_047134887.1[H.vulgaris]	-----NNGGTR-----LRNQPRWVNVN-----	54
XP_001626412.1[N.vectensis]	-----	6
XP_032829936.1[P.marinus]	-----ACG-AP-----PPTTATSADSVSHSAADIQAT	70
NP_001117034.1[S.salar]	-----NND-DS-----LPCTPQMASEC-----G	102
NP_001131055.1[X.laevis]	-----DNG-SQ-----GSTSPDPSVVC-----P	93
NP_001244212.2[G.gallus]	-----PGG-DS-----LPGTPELPDL-----I	138
NP_032588.1[M.musculus]	-----GAD-GS-----LPSTPPP-PEE-----E	151
Q07820[H.sapiens]	-----STD-GS-----LPSTPPP-AEE-----E	170
XP_002810320.1[P.abelii]	-----STD-GS-----LPSTPPP-AEE-----E	170
XP_019634801.1[B.belcheri]	SLWSQAAPTEKSVIDESRQLIRDYINGRLKKSNLTRGR-----LPDAKRRPTE	132
XP_00386733.1[A.queenslandica]	PKRRGSPVQDDKFEYETRNLTACIESASGKEPLSV-----KLSE	59
XP_047134887.1[H.vulgaris]	-----SSNQVIESTPELFTQLFLVNRMDNDNIIEVP EE-----LRNRSRNGTVNKE	98
XP_001626412.1[N.vectensis]	-----YDNANAVAARKMKTPEEKIAHELAKDFIGY-----KLGGKTRLNTK	47
XP_032829936.1[P.marinus]	RSGGSRPYNDALTIVETANFITGYMAHLTPTEQPPH-----QQQLSS	112
NP_001117034.1[S.salar]	PELSNCPSPGDEVLEHDTLRLIENFLGDYTGLSQP-----RWTQSK	142
NP_001131055.1[X.laevis]	K-----DGLYMDTQQLLILAFPRVYSGEESGEL-----BASCLLQHGWHHK	133
NP_001244212.2[G.gallus]	P-----DELROSELELLLYLREAGGEAFQVKLFPGLLQGPGRPCFCASSAVMEK	189
NP_032588.1[M.musculus]	E-----DDLYRQSL E I I SRYLREQATGSKD-----SKPLGEAGAAGR	189
Q07820[H.sapiens]	E-----DELYRQSL E I I SRYLREQATGAKD-----TKPLGRSGATSRK	208
XP_002810320.1[P.abelii]	E-----DELYRQSL E I I SRYLREQATGAKD-----TKPLGRSGATCRK	208
XP_019634801.1[B.belcheri]	VSSQLQKMGGELERMPHLYRDVSRQINITLSSESILETSFETVANELFSTGI-TWARIV	191
XP_00386733.1[A.queenslandica]	EALRIVGMVQOTLKADEIFFRKLCELELAT--N-LFSKLMVDVGMFSDGQVNI GRLL	116
XP_047134887.1[H.vulgaris]	VAHCLKRI GDDLNNHQLN--HLISSIQVTR--T-AYKTFDFVASHVFDAGTINWGRVV	153
XP_001626412.1[N.vectensis]	SALILRKLSNQIENKHELFLRNMCDRLDIRQH--N--APETFFQVADEIFGDGI--NWGRIV	103
XP_032829936.1[P.marinus]	ASELLKSMGDSLLEQHRAAISGMVSRVEAQTDPEE-LRGSALGVAREMFSDGHMNGRIV	171
NP_001117034.1[S.salar]	PLTTMKRVVEDVIAKHRYAYNGMVAKLDDLRCD--MG-VINSVAKTMFSDGITNWGRIA	200
NP_001131055.1[X.laevis]	ALETLLRVGG E I I EKHMAFTGMLQRLSIHSR-ED-LQ-KLSEVPALVFNDGVTNWGRIV	190
NP_001244212.2[G.gallus]	ALETLLRRVGDGVQKHELAFQGMRLKLEIKKE-DD-LQ-AVCEVAHVFDNGVTNWGRVV	246
NP_032588.1[M.musculus]	ALETLLRRVGDGVQRNHETAFQGMRLKLDIKNE-GD-VK-SFSRVMVHVFDGVTNWGRIV	246
Q07820[H.sapiens]	ALETLLRRVGDGVQRNHETAFQGMRLKLDIKNE-DD-VK-SLSRVMVHVFDGVTNWGRIV	265
XP_002810320.1[P.abelii]	ALETLLRRVGDGVQRNHETAFQGMRLKLDIKNE-DD-VK-SLSRVMVHVFDGVTNWGRIV	265
XP_019634801.1[B.belcheri]	AMFAVAGAFVDCVHQGHMPF--TRRLVD/VVDFTD-RKLSAWLVQEGGWGLVKHFRGD	248
XP_00386733.1[A.queenslandica]	ALLAFQCQCVTYCRSVGLPSI--ESSVPHMAISFISTTHLKDWITNRRGWD AISKELMLR	174
XP_047134887.1[H.vulgaris]	TLFYFAYKLAIQV--VNQLPL--VEIVIGWQKFVT--DRLAQWIAERGGWNAVQEYFGST	208
XP_001626412.1[N.vectensis]	VLYTFAGVKAKYQENQLDNA--ENVATW-VGNVY-ASKSDWVKAGGWAFAFQFKDV	158
XP_032829936.1[P.marinus]	ALVVFCALLVKRLKASGRLSDAEARAVADEVA AFLV--SSRKAWFVQGGWNGFVREFERE	230
NP_001117034.1[S.salar]	SLVAFGAVVSQHLKERGRGHC--VELVGEIAKYLL--SDQSDWL IKNNAWNGFVEFFHVQ	230
NP_001131055.1[X.laevis]	TVISFGAFVAKHLKSLNLEDC--IGVLAEHFTQFLM--MSKKDW I I QEKWMDGFVDFHIE	247
NP_001244212.2[G.gallus]	TLISFGAFVAKHLKSLNQEK--ITSLAGIITDVLV--SSKREWLMSQGGWEGFVDFFRVE	257
NP_032588.1[M.musculus]	TLISFGAFVAKHLKSLVQESF--IEPLAETITDVLV--RTKRDWLVKQRGWDGFVEFFHVQ	303
Q07820[H.sapiens]	TLISFGAFVAKHLKLTINQESC--IEPLAESITDVLV--RTKRDWLVKQRGWDGFVEFFHVE	322
XP_002810320.1[P.abelii]	TLISFGAFVAKHLKLTINQESC--IEPLAESITDVLV--RTKRDWLVKQRGWDGFVEFFHVE	322
XP_019634801.1[B.belcheri]	GRTHM-----FWAISGIGAAIGLAATFFVIDP-----	275
XP_00386733.1[A.queenslandica]	TSATNSSTSSRTASNGMWLQWGV S-GIALAISVFDALHNSS	214
XP_047134887.1[H.vulgaris]	T-----VQFVGVFAA-GFLFAYILTKVFR--	232
XP_001626412.1[N.vectensis]	QEEHEKFW--WNSLLCTTLGLGSL-AAVLYM--KS-----	188
XP_032829936.1[P.marinus]	TPDSA--L--KNTL-MAVAGFGAM-TALAALGVRKILSGFC	265
NP_001117034.1[S.salar]	DPES--V--RNTL-LAFAGVAGI-GATLAMP I R--	285
NP_001131055.1[X.laevis]	DYESG--L--KTVL-MAFSSVAVL-GAGLAYMIR-----	275
NP_001244212.2[G.gallus]	DLESS--I--RNVL-MAFAGVAGL-GASLAYMIRKWR S--	335
NP_032588.1[M.musculus]	DLEGG--I--RNVL-LAFAGVAGV-GAGLAYLIR-----	331
Q07820[H.sapiens]	DLEGG--I--RNVL-LAFAGVAGV-GAGLAYLIR-----	350
XP_002810320.1[P.abelii]	DLEGG--I--RNVL-LAFAGVAGV-GAGLAYLIR-----	350