

CLUSTAL X (1.83) multiple sequence alignment

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hsIL-12Rb2      -CIQKGEQG----TVACTWERGR-DTHLYTEYTLQLSG-----PKNLTWQKQC
mmIl-12rb2     -CVQEGENG----TVACSWNSGK-VTYLKTNYTLQLSG-----PNNLTCQKQC
hsLIFR_CHD1    -CVTNNLQ-----VWNCWSWKAPS-GTGRGTDYEVCIE-----RSRSCYQLEK--TS
mmLifr_CHD1    -CTTNNMR-----VWDCTWPAPL-GVSPGTVKDICIKD-----RFHSCHPLET--TN
hsOSMR_CHD0.5  -----
mmOsmr_CHD0.5  -----
hsIL-12b1      -CYRISSD-----RYECSWQYEG-PTAGVSHFLRCCLS-----SG--RCCYFAAG--SA
mmIl-12b1      -CYRVSKT-----DYECWQYDG-PEDNVSHVLWCCFVPPNHTHTGQERCRYFSSG--PD
hsOBR_CHD1     -CWLKGDG-----KLFICYVESL-FKNLFRNYNYKVHLLYVLPVELEDSPLVPKGSFQM
mmObr_CHD1     -CWMKGDG-----TLFICHMEPL-PKNPFKNYDSKVHLLYDLPEVIDDSPLPPLKDSFQT
hsOBR_CHD2     -CETDGYL-----TKMTCRWSTS-TIQSLAESTLQLRYHRSLSLYCSDIPSIHPI---EP
mmObr          -CETDGYL-----TKMTCRWSPS-TIQSLVGSTVQLRYHRRSLYCPDPSIHPPTS--EP
hsGCSFR        -CLMNLTT-----SLICQWEPGP-ETHLPTSFTLKSFK-----SRGNCQTQGDS
mmGcsfr        -CLMHLTT-----SLVCQWEPGP-ETHLPTSFILKSFR-----SRADCQYQGDT
hsIL-23R       -CVIYEYSG----NMTCTWNAGK-LTYIDTKYVVHVKSLETEEEQQ-----
mmIl-23r       -CVIYEYSG----NMTCTWNTGK-PTYIDTKYIVHVKSLETEEEQQ-----
hsOSMR_CHD2    -CETEDFK-----TLHCTWDPGT-DTALGWSKQPSQSYYTLFESFSG-----
mmOsmr_CHD2    -CETRDFK-----TLDCSWEPGV-DTTLTWRKQRFQNYTLCEFSK-----
hsLIFR_CHD2    -CETHDLK-----EIICSWNPGR-VTALVGPR--TSYTLVESFSGK-----YV
mmLifr_CHD2    -CETHDLK-----EIICSWNPGR-ITGLVGPRN--TEYTLFESISGK-----SA
drlifr.b_CHD2  -CITRDL-----SVECQWKLGR-KTQLYG-TRA-TNYTLNGRKC-----
drlifr.a_CHD2  -CETRDLA-----SAKCSWKKGR-DTRLKKNRNSR-TNYTLNGRVCG-----
hsGP130        -CIVNEGK-----KMRCWDGGR-ETHLETNFTLKS-EWATHK-----
mmGp130        -CIVNEGK-----NMLCQWDPGR-ETYLETNYTLKS-EWATEK-----
hsIL-27R       -CYGVGPLG-----DLNCSWEPLG-DLGAPSELHLSQKYSRNSK-----
mmIl-27r       -CYSVGPLG-----ILNCSWEPLG-DLETTPVLYHQSKYHPNR-----
hsGLMR         -CVYYYRK-----NLCTWSPGK-ETSYTQYTVKRTYAFGEKHDNC-----
mmGlmr         -CVFYFDR-----NLCTWRPEK-ETNDTSYIVTLTYSYGK-----
drlifr.a_CHD0.5 -----
drlifr.b_CHD0.5 -----
drosmr_CHD0.5  -----
drgp130        -CIALQRKKDISPDLNCYWEPGLRDPPLATNYTLYAQVGQDLYN-----
dril-12rb2.a   -CIRKTEFG----NVSCTWTTGR-DTKIVTTCQLRVQGDPHHG-----
drgcsfr        -CALTLVKMP---SLRCDWNPVQEIKNLPINYLHVFRAKSQK-----
drobr_CHD2     -CESEYSYVD---TMICKWNQSNWAQARLLYRQYRSKCTEEAEEDTS-----
drosmr_CHD2    -CETADMHN-----IHCSWEILR-APNLNGSYRRTYTLISDS-----
dril-23r       -CVTHQHS-----KFVNCYLTATTETYLFTNFRVTFRNRTSLLG-----
dril-12rb2.b   -CVIEDLVK---EDIYCSWTISD-EPMITTVYTLHWQDYEGNVN-----
drobr_CHD1     -CWLEGERE---NLICNAKTRRAAAAAASTLVSVSPHQLVVQMDVHS-----DETN

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hsIL-12Rb2	KD---IYCDYLDGFINLTPESPESNFTAKVTAVNSLGSSS-----SLPSTFTFLDIVRPL
mmIl-12rb2	FSDNRQNCNRLDLGINLSPDLAESRFIVRVTAINDLGNSS-----SLPHTFTFLDIVIPL
hsLIFR_CHD1	IKIPALSHGDYEITINSLHDFGSSTSKFTLNEQNVSLIPD-----TPEILNLSADFSTST
mmLifr_CHD1	VKIPALSPGDHEVTINYLNLFQS---KFTLNEKDVSLIPE-----TPEILDLSADFFSTSS
hsOSMR_CHD0.5	-----
mmOsmr_CHD0.5	-----
hsIL-12b1	TRLQFSDQAGVSVLYTVTLWVESWARNQTEKSPEVTLQLYNSVKYEPPLGDIKVSKLAGQ
mmIl-12b1	RTVQFWEQDGIPLVLSKVNFWVESRLGNRTMKSQKISQYLYNWTKTTPPLGHIKVSQSHGQ
hsOBR_CHD1	VHCNCSVHECCECLVPVPTAKLNDTLLMCLKITSGGVIFQ-----SPLMSVQPINMVKPD
mmObr_CHD1	VQCNCSLRG-CECHVPVPRAKLNYALLMYLEITSAGVSFQ-----SPLMSLQPMLVVKPD
hsOBR_CHD2	KDCYLQSDGFYECIFQP--IFLLSGYTMWIRINHSLGSLD-----SPPTCVLPDSVVKPL
mmObr	KNCVLQRDGFYECVFQP--IFLLSGYTMWIRINHSLGSLD-----SPPTCVLPDSVVKPL
hsGCSFR	ILDVCPKDGQSHCCIPRKHLLLYQNMGIWVQAENALGTSM-----SPQLCLDPMDVVKLE
mmGcsfr	IPDCVAKKRQNNCSIPRKNLLLYQYMAIWVQAENMLGSSE-----SPKLCLDPMDVVKLE
hsIL-23R	-----YLTSSYINISTDSLQGGKKYLWVWQAANALGMEESK-----QLQIHLDDIVIP
mmIl-23r	-----YLASSYVKISTDSLQGSRKYLWVWQAANSLGMENSQ-----QLHVHLDDIVIP
hsOSMR_CHD2	---EKKLCTHKNWCNWQITQDSQETYNFTLIAENYLRKRSVN-----ILFNLTHRVYLM
mmOsmr_CHD2	---RCEVSNYRNSYTWQITEGSQEMYNFTLTAENQLRKRVSVN-----INFNLTHRVHPK
hsLIFR_CHD2	RLKRAEAPTNEYSYQLLFQMLPNQEIYNFTLNHNPLGRSQST-----ILVNI TEKVYPH
mmLifr_CHD2	VFHRIEGLTNETYRLGVQMHPGQEIHNFTLTGRNPLGQAQSA-----VVINVTERVAPH
drliffr.b_CHD2	-----EFNRCDPLELKKQITN-----WTLIARNALGEKIVT-----DTGDPTHRVLK
drliffr.a_CHD2	-----EANEGKSWECSEVWEK---NWTLVARNPIGTIQLT-----DSAQITDRVHLL
hsGp130	FADCKAKRDTPTSTCTVDYSTVYFVNIEVWVEAENALGKVTSDH-----INFDPVYKVKPN
mmGp130	FPDCQSKHG--TSCMVSYPMTYYVNIWVVEAENALGKVSSSES-----INFDPVDKVKPT
hsIL-27R	TQTVAVAAGRSWVAIPREQLTMSDKLLVWGTKA---GQPLWPP-----VFNLETQMKPN
mmIl-27r	VWEVKVPSKQSWVTIPREQFTMADKLLIWGTQK---GRPLWSS-----VSVNLETQMKPD
hsGLMR	TTNSSTSENRASCSFFLPRITIPDNYTIEVEAENGDVVKSVM-----TYWRLENIKAKTE
mmGlmr	-SNYSDNATEASYSPRSCAMPPDICSVEVQAQNGDGKVKSDI-----TYWHLISIAKTE
drliffr.a_CHD0.5	-----
drliffr.b_CHD0.5	-----
drosmr_CHD0.5	-----
drgp130	--STCKQSLARSCTVNLSSTYPVHMTLKVWVEVKNSLGSERSDE-----HEYDSLVLVKPN
dril-12rb2.a	--YESVMNSSGFCWATFPKSRMSQLTVSLNVSNSLGSNT-----SVQPS
dragsfr	--VYAVPPGQHFYVVPDAYGYFSELEISVTAANVLGNNTSDP-----LKLTPLNVTVKFD
drobr_CHD2	LVKECPKAGDHRQCTLSQISMIFCYKFWLEVEGGRGQSFP-----VYVTPIDYVKPS
drosmr_CHD2	---RTVSCNFNPPSCSFKVVPHQITYNVTLLVRNSLGRESESD-----IFNITDRVFPK
dril-23r	----PYEINKGHISLQSLFNFESMTYNVHVIGHNALGQSLST-----FNFSIWDIVIPS
dril-12rb2.b	----SAESDCEMAIINRDKYTKGTQMTVWVTARNVLGYARSEE-----SVFNTGHIRRPD
drobr_CHD1	STAQCVGEETAICSVSLHGGDATVSLVIIISENGTTAQSQK-----MQVSTYELQAGD

hsIL-12Rb2 PPWDIRIKF-----QKASVSRCTLYW-RDEGLVLLNRLRYRPSNSRLWNMVNVTAKGRH
mmIl-12rb2 PPWDIRINF-----LNASGSRGTLQW-EDEGQVVLNQLRYQPLNSTSWNMVNATNAKGY
hsLIFR_CHD1 LYLKWNDRG-----SVFPHRSNVIWE-IKVLKRESMELVKLVTHNTTLNGKDTLHHWSWA
mmLifr_CHD1 LLLKWNDRG-----SALPHPSNATWE-IKVLQNPRTPEPVALVLLNTMLSGKDTVQHWNWT
hsOSMR_CHD0.5 ----WTVHN-----LPYHQELKMFVQ-IQISRIETSNIWVGNYSTTVK-WNQVLHWSWE
mmOsmr_CHD0.5 ----WTVPA-----LT-HEELNMIFQ-IEISRLNISNTIWVENYSTTVK-REEAVRWNWT
hsIL-12b1 LRMEWETPD-----NQVGAEVQFRHR-TPSSPWKLGDCGPDQDD-----TES
mmIl-12b1 LRMDWNVS-----EEAGAEVQFRRR-MPTTNWTLGDCGPQVNSGSGVL-GDICGSMSES
hsOBR_CHD1 PPLGLHMEI-----TD-DGNLKISWS-SPPLVPFPLQYQVKYSENSTTVIREADKIVSAT
mmObr_CHD1 PPLGLHMEV-----TD-DGNLKISWD-SQTMAPPFLQYQVKYLENS-TIVREAAEIVSAT
hsOBR_CHD2 PPSVKAIEI-----TINIGLLKISWE-KPVFPENNLQFQIRYGLSGKEVQWKMYEVYDAK
mmObr PPSNVKAEI-----TVNTGLLKVSWE-KPVFPENNLQFQIRYGLSGKEIQWKTHEVFDK
hsGCSFR PPMLRTMDPSPEAAPPQAGCLQLCWEPWQPGLHINQKCELRHKPQRGEASWALVGPLPLE
mmGcsfr PPMLQALDIGPDVSHQPGCLWLSWKPWKPSEYMEQECELRYQPQLKANWTLVFLPSS
hsIL-23R SAAVISRAETINATVPKTIYWDSQTTIEK---VSCEMRYK--ATTNQTWNVKEFDNTFT
mmIl-23r SASIISRAETTNDTVPKTIVYWKSKTMIEK---VFCMRYK--TTTNQTWSVKEFDANFT
hsOSMR_CHD2 NPFVNFENVN-ATNAIMTWKVSIRNNFT---YLCQIELHGEGKMMQY-NVSIK--VNG
mmOsmr_CHD2 APQDVTLKIIIG-ATKANMTWKVHSHGNNT---LLCQVKLQYGEVIHEH-NVSVH--MSA
hsLIFR_CHD2 TPPTSFKVKDIN-STAVKLSWHLPGNFAKIN---FLCEIEIKKSNSVQEQNRNVTIKGVENS
mmLifr_CHD2 DPTSLKVKDIN-STVVTFSWYLPGNFTKIN---LLCQIEICKANSKKEVRNATIRGAEDS
drlifr.b_CHD2 APHNI SHAAHARNATVHWSWSVT-EYASLL---MICQK-----TFSGK----G
drlifr.a_CHD2 APVNV MADPKAWNATLRWNWTVE-AYKKLE---MICQMKLI-SRQLSSTRNYSGT----G
hsGp130 PPHNLSVIN-SEELSSILKLTWTPNSIKSV-IILKYNIQYRTKDASTWSQIPPEDTAST-
mmGp130 PPYNLSVTN-SEELSSILKLSWVSSGLGGL-LDLKSDIQYRTKDASTWIVPLEDTMSP-
hsIL-27R APRLGPDVDFSEDDPLEATVHWAPPTWPSH-KVLICQFHYRRCQEAAWTLLEPELKTIP-
mmIl-27r TPQIFSQVDISEEATLEATVQWAPPVWPPQ-KALTCQFRYKQCQAEAWTRLEPQLKTGD-
hsGLMR PPKIF-RVKPVLGIKRMIIQIEWIKPELAPVSSDLKYTLRFRTVNSTSWMEVNFANRDKK
mmGlmr PPIIL-SVNPIC--NRMFQIQW-KPREKTRGFPLVCMRLRFRTVNSSRWTEVNFENCK---
drlifr.a_CHD0.5 ----WQSDS-----SLFD-IEIFHTEFMNVVLNETVAVNTDPVTGQHSWTWH
drlifr.b_CHD0.5 ----WTDEN-----NEFEKVSVD-IEIHTEQMRTVHFENIHVKPD-KSSHVHWKWT
drosmr_CHD0.5 ----WNINQ-----NKQRIEVYEQVGRTKNMDIISVNVN-----RGLHAVIWS
drgp130 PPNVEVKVEEDFPTS FVVKWEYDIEDTTMR---FSSAIRYCQVGSDDWKKVP-ENYTNVH
dril-12rb2.a LPKIKHVDC-----SSRWCHLHTDNHSMNLVEVQYKSPKG-----IWKKVQING
drgcsfr PPSITRIEAKHYGCLKYSWLSLSETQKWLQLTFIVQLRLKTVSNQPNKD---LVYTSRQLQ
drobr_CHD2 PPFDELAIT-----LPSKTL SVRWKRPSPVYGMQYELQFKALAGMANTQWKVIGPLL
drosmr_CHD2 PQRLEATAG-----VFDLSVILHLNFSFGLQLICQIELEPGGTVQES--VQDGSDSVQ
dril-23r TPDIMQILLE-----NGSRFPTIYWNGSDNHFKPSLRYRRAHG-NHAWVLGNIAVVRI
dril-12rb2.b PPYNMTHMF-----TPLEIFWDMDCDIMGTLDECHVQYHMQNHLMLDWTEVDDC
drobr_CHD1 PSRELKPSP-----LSMKSPVFKHFGFPVSYVDNVRVVDKKTQFCKLCYVLKVEGR

hsIL-12Rb2	DLLDLK----PFTEYEFQISSK-LHLYKGSWSDWS
mmIl-12rb2	DLRDLR----PFTEYEFQISSK-LHLSGGSWSNWS
hsLIFR_CHD1	SDMPLE-CAIHFVEIRCYIDNL-HFSGLEEWSDWS
mmLifr_CHD1	SDLPLQ-CATHSVSIRWHIDSP-HFSGYKEWSDWS
hsOSMR_CHD0.5	SELPLE-CATHFVRIKSLVDDA-KFPEPNFWSNWS
mmOsmr_CHD0.5	SDIPLQ-CVKHFIRIRALVDDT-KSLPQSSWGNWS
hsIL-12b1	CLCPLEMNVAQEFQLRRRQ----LGSQGSSWSKWS
mmIl-12b1	CLCPSE-NMAQEIQIRRRRRLS-SGAPGGPWSWDS
hsOBR_CHD1	SLLVDSILP--GSSYEVQVRGK-RLDGPGIWSWDS
mmObr_CHD1	SLLVDSVLP--GSSYEVQVRGK-RLDGSGVWSWDS
hsOBR_CHD2	SKSVSLPVPDLCAVYAVQVRCK-RLDGLGYWSNWS
mmObr	SKSASLLVSDLCVYVQVRCR-RLDGLGYWSNWS
hsGCSFR	ALQYELCGLLPATAYTLQIRCI-RWPLPGHWSWDS
mmGcsfr	KDQFELCGLHQAPVYTLQMRCI-RSSLPGFWSWDS
hsIL-23R	YVQQSEFYLEPNIKYVFQVRCQ-ETGKRY-WQPWS
mmIl-23r	YVQQSEFYLEPDSKYVFQVRCQ-ETGKRN-WQPWS
hsOSMR_CHD2	EYFLS--ELEPATEYMARVRCA-DASHFWKWEWS
mmOsmr_CHD2	NYLFS--DLDPDTKYKAFVRCA-SANHFWKWSDWT
hsLIFR_CHD2	SYLVALDKLNPTYTLYTFRIRCS--TETFWKWSKWS
mmLifr_CHD2	TYHVAVDKLNPTYTAYTFRVRCR--SKTFWKWSRWS
drliffr.b_CHD2	LASVLEHLQPFTKYTAKVSCG-SHEHFFQWGDWS
drliffr.a_CHD2	LSSVLEDLWPDVDYTVTVRCA-SKQSFWKWGDES
hsGp130	RSSFTVQDLKPFTEYVFRIRCM-KEDGKGYWSDWS
mmGp130	RTSFTVQDLKPFTEYVFRIRSI-KDSGKGYWSDWS
hsIL-27R	LTPVEIQDLELATGYKVYGRCA-MEKEEDLWGEWS
mmIl-27r	LTPVEMQNLEPGTCYQVSGRCQ-VEENG-YPWGEWS
hsGLMR	NQTYNLTGLQPFTEYVIALRCA-VKES-KFWSWDS
mmGlmr	-QVCNLTGLQAFTEYVIALRFR-FNDS-RYWSKWS
drliffr.a_CHD0.5	SPLPLQ-----CTSHSVQIRAR-NQSQSISPWS---
drliffr.b_CHD0.5	SPIPLQ-----CTSHSVRLRRR-DQLRISEWT---
drosmr_CHD0.5	SQLPLN-----CVNHAVRIRLITAASTFSSWSPWK
drgp130	ITSYRLQSLEPYTEYVQMRSI--GEHYTIWSEWS
dril-12rb2.a	KKSLNISLLEPYTKYMFQIRRK-INQTMGLWSYWS
drgcsfr	LNP IEVCSLLHWTDYRSTVRVK--YYATSEWSEWS
drobr_CHD2	EPQAEIQLEESCQVFKVEVRCK-DVNDTGYWSDWS
drosmr_CHD2	LYLFRLQNLKPKSTQYASRGRCA---VQKHWSHWT
dril-23r	GCVFLQEPLEPLISYQFELRVCVSSANCSMWS---
dril-12rb2.b	QSMFRIEDPQPFQYSFRVRCR-CGHEEKVMSNWS
drobr_CHD1	SWVALN-ELSSDIRYTVQVRCQ---NHLGYWSEWS