

Muscle

Multiple Sequence Alignment (MSA)

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muscle-I20250718-063307-0344-23525757-p1m

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CLUSTAL multiple sequence alignment by MUSCLE (3.8)

1VHB_1 Chains	-MLDQQTINIILKATVPVLKEHGVTTTFYKNLFAKHPEVRPLF----DM-----GRQ
1GCW_2 Chains	VHWTQEERDEISKTFQGT--DMKTVVTQALDRMFVYPWTNRYFQKRTDFRS-----
1GCW_1 Chains	-AFTACEKQTIGKIAQVLAKSPEAYGAECLARLFVTHPGSKSYFEYK-DYSA----AGA
1HBR_2 Chains	VHWTAEEKQLITGLWGKV--NVAECGAEALARLLIVYPWTQRFFASFGNLSSPTAILGNP
2D5X_2 Chain	VQLSGEEKAAVLAWDKV--NEEEVGGEALGRLLVVYPWTQRFFDSFGDLSNPGAVMNP
1HDA_2 Chains	-MLTAAEKAAVTAFWGKV--KVDEVGGEALGRLLVVYPWTQRFFESFGDLSTADAVMNP
1A3N_2 Chains	VHLTPEEKSAVTALWGKV--NVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAMGNP
1HBR_1 Chains	-MLTAEDKKLIQQAWEKAASHQEEFGAEALTRMFTTYPQTKTYFPHF-DLSP----GSD
1HDA_1 Chains	-VLSAADKGKVNKAAGKVGHHAAEYGAEALERMFLSFPTTKTYFPHF-DLSH----GSA
1A3N_1 Chains	-VLSPADKTNVKAAGKVGGAHAGEYGAEALERMFLSFPTTKTYFPHF-DLSH----GSA
2D5X_1 Chain	-VLSAADKTNVKAASKVGHHAGEYGAEALERMFGLGFPTTKTYFPHF-DLSH----GSA
	: .: . * . * : .
1VHB_1 Chains	ESLEQPALKAMTVLAAAQNIEENLPAILPAVKKIHAVKHCQA-GVAAAHYPIVGQELLGAIK
1GCW_2 Chains	--SIHAGIVVGALQDAVKHMDDVKTLFKDLSKK---HADDLHVDPGSFHLLTDCIIVELA
1GCW_1 Chains	KVQVHGGKVIRAVVKAEEHVDDLHSHLETALT---HGKKLLVDPQNFPMLSECIIVTLA
1HBR_2 Chains	MVRAHGKKVLTSFGDAVKNLDNIKNTFSQLSEL---HCDKLHVDPENFRLLGDILIIIVLA
2D5X_2 Chain	KVKAHGKKVLHSFGEVHHLDNLKGTFAAALSEL---HCDKLHVDPENFRLLGNVLVVVLA
1HDA_2 Chains	KVKAHGKKVLDSFSNGMKHLDLKGTFAAALSEL---HCDKLHVDPENFKLLGNVLVVVLA
1A3N_2 Chains	KVKAHGKKVLGAFSDGLAHDNLKGTFATLSEL---HCDKLHVDPENFRLLGNVLVCVLA
1HBR_1 Chains	QVRGHGKKVLGALGNAVKNDNLSQLAMAELSRL---HAYNLRVDPVNFKLLSQCIQVVL
1HDA_1 Chains	QVKGHGAKVAAALTКАVEHLDLPGALSESDL---HAHKLRVDPVNFKLLSHSLLVTLA
1A3N_1 Chains	QVKGHGKKVADALTNAVAVDDMPNALSALSDL---HAHKLRVDPVNFKLLSHCLLVTLA
2D5X_1 Chain	QVKAHGKKVGDALTLAVGHLDLPGALSNSLSDL---HAHKLRVDPVNFKLLSHCLLSTLA
	: : : . . ::::: : : * * . : :: : : :
1VHB_1 Chains	EVLGDAATDDILDIAWGKAYGVIADVFIQVEADLYAQAVE
1GCW_2 Chains	YLRKDCFTPPIQGIWDKFFEVIDAI---SKQY----
1GCW_1 Chains	THL-TEFSPDTHCAVDKLLSAICQEL---SSRYR----
1HBR_2 Chains	AHFSKDFTPECQAAWQKLVRVVAHAL---ARKYH----
2D5X_2 Chain	RHFGKDFTPELQASYQKVVAGVANAL---AHKYH----
1HDA_2 Chains	RNFGKEFTPVLQADFQKVVAGVANAL---AHRYH----
1A3N_2 Chains	HHFGKEFTPQAAVQKVVAGVANAL---AHKYH----
1HBR_1 Chains	VHMGKDYTPEVHAFDKFLSAVSAVL---AEKYR----
1HDA_1 Chains	SHLPSDFTPAVHASLDKFLANVSTVL---TSKYR----
1A3N_1 Chains	AHLPAEFTPQAVHASLDKFLASVSTVL---TSKYR----
2D5X_1 Chain	VHLPNDFTPAVHASLDKFLSSVSTVL---TSKYR----
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Alignment with colours

Hide

CLUSTAL multiple sequence alignment by MUSCLE (3.8)

1VHB_1 Chains	-MLDQQTINI IKAT VPVL KEHGVT ITTTFY KNLFAK HPEVRPLF-----DM-----GRQ
1GCW_2 Chains	VHWTQEERDEIS KTFQGT --DMKT VV TQALDRMF KVYP WTNRYF QKRTDFRS -----
1GCW_1 Chains	-AFTACE KQTIGKIA QVLA KSPEAYGA ECLARLFVTHPGSKSYFEYK-DYSA-----AGA
1HBR_2 Chains	VHWT AEKQLITGLWGKV --NVAECGA EALARLLIVY PWTQRFFASFGNLSSPTAILGNP
2D5X_2 Chain	VQLSGEEKAAV LALWDKV --NEEEVGGEALG RLLVVY PWTQRFFDSFGDLSNP GAVMGNP
1HDA_2 Chains	-MLTAEEKA AVTAFWGKV --KVDEV GGEALG RLLVVY PWTQRFFESFGDL STADAVMNNP
1A3N_2 Chains	VHLT PEEKSAVTALWGKV --NVDEV GGEALG RLLVVY PWTQRFFESFGDL STPD AVMGNP
1HBR_1 Chains	-MLTAEDKKLI QQAWEKAASHQEEFGAEALTRMFTTY PQT KTYFPHF -DLSP-----GSD
1HDA_1 Chains	-VLSAAD KGNVKA AWG KVGGHAAEYGAEALERMF LSFP TTKTYFPHF -DLSH-----GSA
1A3N_1 Chains	-VLSPAD KTNVKA AWG KVGAHAGEYGAEALERMF LSFP TTKTYFPHF -DLSH-----GSA
2D5X_1 Chain	-VLSAAD KTNVKA AW SKVGGHAGEYGAEALERMF LGFP TTKTYFPHF -DLSH-----GSA
	: .:: .* . * :
1VHB_1 Chains	ESLEQP KALAMTVLAAAQNIE NLPAILPAVK KIAVKHCQA -GVAAAHYP IVGQELLGAIK
1GCW_2 Chains	--SIHAGIVVGAL QDAVKHMDDV KTLFK DLSKK ---HADDL HVDPGSFHLLTDCIIVELA
1GCW_1 Chains	KVQV HGGKVIRAVV KAAEH VHDDLHS LET LA L---HGKKL LVDPQNFPM LSECIIV VTLA
1HBR_2 Chains	MVRAHG KKVLTSFGDAVNLDNI KNT SQLSEL ---HCDKL HVDPENFRLLGDIL IIV VLA
2D5X_2 Chain	KVKAHG KKVLHSFGEVHH DLNK GTFAALSEL ---HCDKL HVDPENFRLLGNV L VVVLA
1HDA_2 Chains	KVKAHG KKVLDSFSNGMKHLDL K GTFAALSEL ---HCDKL HVDPENFKLLGNV L VVVLA
1A3N_2 Chains	KVKAHG KKVLGA F SDSLGAHLDLN L KGTFAALSEL ---HCDKL HVDPENFRLLGNV L LCVLA
1HBR_1 Chains	QVRGHG KKVLGALGN A KVNVDNL S QAMAELSNL ---HAYN LRVDPVNFKLLSQCIQV VLA
1HDA_1 Chains	QVK GHGAKVAAALTKA VE HLDLPGALSELSDL ---HAHKLR RVDPVNFKLLSH SLV LT LA
1A3N_1 Chains	QVK GHGKKVADALTN A VAVHDDMPNALSALSDL ---HAHKLR RVDPVNFKLLSH CL LVT LA
2D5X_1 Chain	QVK AHGKKVGDALT LAV GHLDDLPGALSNLSDL ---HAHKLR RVDPVNFKLLSH CL LST LA
	: : .: . ::::: : : * * . : :: : : :
1VHB_1 Chains	EVLGDAAT DDILD AWG KAYGVIADVF IQ VEADLYAQAVE
1GCW_2 Chains	YL RKDCFTPHIQG I WDKFFEVVIDAI ---SK QY -----
1GCW_1 Chains	THL-TEF SPDTCAVDKL LSAIC CQEL ---SS RYR -----
1HBR_2 Chains	AHFSK DFTPECQAAWQ K LVRVVAHAL ---ARKYH-----
2D5X_2 Chain	RHFGK DFTPELQASYQ K VVAGVANAL ---AHKYH-----
1HDA_2 Chains	RNFGK EFTPVLQADFQ K VVAGVANAL ---AHRYH-----
1A3N_2 Chains	HHFGK EFTPPVQAA YQ VVAGVANAL ---AHKYH-----
1HBR_1 Chains	VHMGK DYTPEVHAAFDKFL SAV S AVL---AEKYR-----
1HDA_1 Chains	SHLPSDFTPAV HASLDKF LAN VSTVL ---TSKYR-----
1A3N_1 Chains	AHLPAEFTPAV HASLDKF LASV VSTVL ---TSKYR-----
2D5X_1 Chain	VHLPNDFTPAV HASLDKF LSSV VSTVL ---TSKYR-----