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Muscle

Multiple Sequence Alignment (MSA)

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Results for Job ID

muscle-I20250718-063307-0344-23525757-p1m

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Tool Output

Alignments

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Result Fi

Tool output

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CLUSTAL multiple sequence alignment by MUSCLE (3.8)

```

1VHB_1|Chains      -MLDQQTINIIKATVPVLKEHGVTTITTTFYKNLFAKHPEVRPLF----DM-----GRQ
1GCW_2|Chains      VHWTQEERDEISKTFQGT--DMKTVVTQALDRMFKVYPWNTNRYFQKRTDFRS-----
1GCW_1|Chains      -AFTACEKQTIGKIAQVLAKSPEAYGAECLEARLFVTHPGSKSYFEYK-DYSA-----AGA
1HBR_2|Chains      VHWTAEKQLITGLWGKV--NVAECGAELARLLIVYPWTQRFFASFGNLSPTAILGNP
2D5X_2|Chain       VQLSGEEKAAVLALWDKV--NEEEVGGEALGRLLVVYPWTQRFFDSFGDLSPGAVMGNP
1HDA_2|Chains      -MLTAEKAAVTAFWGKV--KVDEVGGEALGRLLVVYPWTQRFFESFGDLSTADAVMNNP
1A3N_2|Chains      VHLTPEEKSAVTALWGKV--NVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDVAVMGNP
1HBR_1|Chains      -MLTAEDKKLIQQAWEKAASHQEEFGAEALTRMFTTYPQTKTYFPHF-DLSP-----GSD
1HDA_1|Chains      -VLSAADKGNVKAAGWKVGGHAAEYGAELERMFLSFPTTKTYFPHF-DLSH-----GSA
1A3N_1|Chains      -VLSPADKTNVKAAGWKVGAHAGEYGAELERMFLSFPTTKTYFPHF-DLSH-----GSA
2D5X_1|Chain       -VLSAADKTNVKAAWSKVGGHAGEYGAELERMFLGFPTTKTYFPHF-DLSH-----GSA
                  :                .::  .*  .  *      :

```

```

1VHB_1|Chains      ESLEQPKALAMTVLAAAQNIENLPAILPAVKKIAVKHCQA-GVAAAHYPIVGQELLGAIK
1GCW_2|Chains      --SIHAGIVVGALQDAVKHMDVKTFLFKDLSKK--HADDLHVDPGSFHLLTDCIIVELA
1GCW_1|Chains      KVQVHGGKVIRAVVKAEEHVDLHSHLETALT---HGKKLLVDPQNFPMSECIIIVTLA
1HBR_2|Chains      MVRAGHKKVLTSGDAVKNLDNKNTFSQLSEL---HCDKLHVDPENFRLLGDILIIIVLA
2D5X_2|Chain       KVKAHGKKVLHSGEGVHLDNLKGTFAALSEL---HCDKLHVDPENFRLLGNVLVVVLA
1HDA_2|Chains      KVKAHGKKVLDGSFNGMKHLDDLKGTFAALSEL---HCDKLHVDPENFKLLGNVLVVVLA
1A3N_2|Chains      KVKAHGKKVLGAFSDGLAHLNLDNLKGTFAATLSEL---HCDKLHVDPENFRLLGNVLVCVLA
1HBR_1|Chains      QVRGHGKKVLGALGNAVKNVDNLSQAMAELSNL---HAYNLRVDPVNFKLLSQCIQVVLA
1HDA_1|Chains      QVKGHGAKVAAALTKAVEHLDDLPGALSELSDL---HAHKL RVDPVNFKLLSHSLLVTLA
1A3N_1|Chains      QVKGHGKKVADALTNAVAHVDDMPNALSALSDDL---HAHKL RVDPVNFKLLSHCLLVTLA
2D5X_1|Chain       QVKAHGKKVGDAALTAVGHLDLPGALSNDLSDL---HAHKL RVDPVNFKLLSHCLLSTLA
                  :   :   :.  .  :::::  :   :   *   *  .  :  ::  :   :

```

```

1VHB_1|Chains      EVLGDAATDDILDWAGKAYGVIADVFIQVEADLYAQAVE
1GCW_2|Chains      YLRKDCFTPHIQGIWDKFFEVVIDAI----SKQY-----
1GCW_1|Chains      THL-TEFSPDTHCAVDKLLSAICQEL----SSRYR----
1HBR_2|Chains      AHFSKDFTPECQAAWQKLVVRVAHAL----ARKYH----
2D5X_2|Chain       RHFGKDFTPELQASYQKV VAGVANAL----AHKYH----
1HDA_2|Chains      RNFGKEFTPVLQADFQKV VAGVANAL----AHRYH----
1A3N_2|Chains      HHFGKEFTPPVQAAYQKV VAGVANAL----AHKYH----
1HBR_1|Chains      VHM GKDYTPEVHAAFDKFLSAVSAVL----AEKYR----
1HDA_1|Chains      SHLP SFTPAVHASLDKFLANVSTVL----TSKYR----
1A3N_1|Chains      AHLPAEFTPAVHASLDKFLASVSTVL----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      -MLDQQTINIIKATVPVLKEHGVTTTTFYKNLFAKHPEVRPLF-----DM-----GRQ
1GCW_2|Chains      VHWTEERDEISKTFQGT--DMKTVVTQALDRMFKVYPWTNRYFQKRTDFRS-----
1GCW_1|Chains      -AFTACEKQTIQKIAQVLAKSPEAYGAECARLFVTHPGSKSYFEYK-DYSA-----AGA
1HBR_2|Chains      VHWTAEEKQLITGLWGKV--NVAECGAELARLLIVYPWTQRFASFNGLSSPTAILGNP
2D5X_2|Chain       VQLSGEEKA AVLALWDKV--NEEEVGGEGALRLLVVYPWTQRFDSFGDLSPGAVMGNP
1HDA_2|Chains      -MLTAEEKAAVTAFWGKV--KVDEVGGEGALRLLVVYPWTQRFESFGDLSTADAVMNNP
1A3N_2|Chains      VHLTPEEKSAVTALWGKV--NVDEVGGEGALRLLVVYPWTQRFESFGDLSTPDVAVMGNP
1HBR_1|Chains      -MLTAEDKKLIQQAWEKAAHQEEFGAEALTRMFTTYPQTCTYFPHF-DLSP-----GSD
1HDA_1|Chains      -VLSAADKGNVKAAGKVGGAHAEYGAELERMFLSFPTTKTYFPHF-DLSH-----GSA
1A3N_1|Chains      -VLSPADKTNVKAAGKVGGAHAEYGAELERMFLSFPTTKTYFPHF-DLSH-----GSA
2D5X_1|Chain       -VLSAADKTNVKAAGSKVGGHAEYGAELERMFLGFPTTKTYFPHF-DLSH-----GSA
                  :                               .:: .* . *      :

1VHB_1|Chains      ESLEQPKALAMTVLAAQNIENLPAILPAVKKIIVKHCQA-GVAAAHYPIVGQELLGAIK
1GCW_2|Chains      --SIHAGIVVGALQDAVKHMDVKTLFKDLSKK--HADDLHVDPGSFHLLTDCIIVELA
1GCW_1|Chains      KVQVHGGKVIKAVVKAEEHVDLHSHLETALT--HGKLLVDPQNFPMLECIIVTLA
1HBR_2|Chains      MVRAGHKKVLTSGDAVKNLNLIKNTFSQSEL---HCDKLHVDPENFRLLGDILIIVLA
2D5X_2|Chain       KVKAHGKKVLHSFGEGVHHLNLIKGTFAALSEL---HCDKLHVDPENFRLLGNVLVVLA
1HDA_2|Chains      KVKAHGKKVLDSFSGMKHLDDLKGTFAALSEL---HCDKLHVDPENFKLLGNVLVVLA
1A3N_2|Chains      KVKAHGKKVLGAFSDGLAHLNLIKGTFAALSEL---HCDKLHVDPENFRLLGNVLVCLLA
1HBR_1|Chains      QVRGHGKKVLGALGNAVKNVDNLSQAMAELSNL---HAYNLRVDPVNFKLLSQCIQVLA
1HDA_1|Chains      QVKGHGAKVAAALTKAVEHLDDLPGALSELSDL---HAHKLVRDPVNFKLLSHSLLVTLA
1A3N_1|Chains      QVKGHGKKVADALTNAVAHVDDMPNALSALSDL---HAHKLVRDPVNFKLLSHCLLVTLA
2D5X_1|Chain       QVKAHGKKVGDAALTAVGHLDDLPGALSNLSDL---HAHKLVRDPVNFKLLSHCLLVTLA
                  :   :   : . . : : : :   :   :   *   * . : : :   :   :

1VHB_1|Chains      EVLGDAATDDILDWAGKAYGVIADVFIQVEADLYAQAVE
1GCW_2|Chains      YLRKDCFTPHIQGIWDKFFEVVIDAI----SKQY-----
1GCW_1|Chains      THL-TEFSPDTHCAVDKLLSAICQEL----SSRYR-----
1HBR_2|Chains      AHFSKDFTPECQAQWQKLVVVVAHAL----ARKYH-----
2D5X_2|Chain       RHFGKDFTPELQASYQKVVAGVANAL----AHKYH-----
1HDA_2|Chains      RNFGKEFTPVLQADFQKVVAGVANAL----AHRYH-----
1A3N_2|Chains      HHFGKEFTPPVQAAYQKVVAGVANAL----AHKYH-----
1HBR_1|Chains      VHMKGDTPEVHAADFDFLSAVSAVL----AEKYR-----
1HDA_1|Chains      SHLPDFTPAVHASLDKFLANVSTVL----TSKYR-----
1A3N_1|Chains      AHLPAEFTPAVHASLDKFLASVSTVL----TSKYR-----
2D5X_1|Chain       VHLPNDFTPAVHASLDKFLSSVSTVL----TSKYR-----

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