

Clustal Omega

Multiple Sequence Alignment (MSA)

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clustalo-I20250718-063254-0826-7058527-p1m

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Alignments

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Phylogenetic Tree

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Result

Tool output

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CLUSTAL O(1.2.4) multiple sequence alignment

1VHB_1 Chains	-MLDQQTINIIKATVPVLKEHGVTTTTFYKNLFAKHPEVRPLFDMG-----RQ	48
1GCW_2 Chains	VHWTQEERDEISKTFQGTD--MKTVVTQALDRMFKVYPWTNRYFQKRTDF-----	48
1GCW_1 Chains	-AFTACEKQTIGKIAQVLAKSPEAYGAECARLFVTHPGSKSYFEYKDY-----SAAGA	53
1HBR_2 Chains	VHWTAEKQLITGLWGKVN--VAECGAEALARLLIVYPWTQRFFASFGNLSSPTAILGNP	58
2D5X_2 Chain	VQLSGEEKA AVLALWDKVN--EEEVGGEALGRLLVVYPWTQRFFDSFGDLSNPGAVMGNP	58
1A3N_2 Chains	VHLTPEEKSAVTALWGKVN--VDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNP	58
1HDA_2 Chains	-MLTAEKAAVTAFWGKVK--VDEVGGEALGRLLVVYPWTQRFFESFGDLSTADAVMNNP	57

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1HBR_1|Chains      -MLTAEDKKLIQQAWEKAASHQEEFGAEALTRMFTTYPQTKTYFPHFDL-----SPGSD 53
1A3N_1|Chains      -VLSPADKTNVKAAWGKVGGAHAGEYGAEALERMFLSFPTTKTYFPHFDL-----SHGSA 53
1HDA_1|Chains      -VLSAADKGNVKAAWGKVGGAHAGEYGAEALERMFLSFPTTKTYFPHFDL-----SHGSA 53
2D5X_1|Chain       -VLSAADKTNVKAWSKVGGHAGEYGAEALERMFLGFPTTKTYFPHFDL-----SHGSA 53
                   :                               .::  .*  .  *

1VHB_1|Chains      ESLEQPKALAMTVLAAAQNIENLPAILPAVKKIAVKHCQ-AGVAAAHYPVIGQELLGAIK 107
1GCW_2|Chains      RSSIHAGIVVGALQDAVKHMDVKTFLKFD--LSKKHADDLHVDPGSFHLLTDCIIVELA 105
1GCW_1|Chains      KVQVHGGKVIRAVVKAEEHVDDLHSHLET---LALTHGKKLLVDPQNFPMSECIIIVTLA 110
1HBR_2|Chains      MVRAGHKKVLTSFGDAVKNLDNINKTFSQ---LSELHCDKLHVDPENFRLLGDILIIIVLA 115
2D5X_2|Chain       KVKAHGKKVLHSHFGEGVHHLNLTGTFAT---LSELHCDKLHVDPENFRLLGNVLVVVLA 115
1A3N_2|Chains      KVKAHGKKVLGAFSDGLAHLNLTGTFAT---LSELHCDKLHVDPENFRLLGNVLVCVLA 115
1HDA_2|Chains      KVKAHGKKVLDSFSGMGMKHLDDLKGTFAA---LSELHCDKLHVDPENFKLLGNVLVVVLA 114
1HBR_1|Chains      QVRGHGKKVLGALGNVKNVDNLSQAMAE---LSNLHAYNLRVDPVNFKLLSQCIQVVLA 110
1A3N_1|Chains      QVKGHGKKVADALTNVAHVDDMPNLSA---LSDLHAHKLRVDPVNFKLLSHCLLVTLA 110
1HDA_1|Chains      QVKGHGAKVAAALTKAVEHDDLPGALSE---LSDLHAHKLRVDPVNFKLLSHSLLVTLA 110
2D5X_1|Chain       QVKAHGKKVGDAALTAVGHLDDLPGALSN---LSDLHAHKLRVDPVNFKLLSHCLLSTLA 110
                   :   :  :.  .  ::::  :   ::  *   *   :  :.  :   :

1VHB_1|Chains      EVLGDAATDDILDWAGKAYGVIADVFIQVEADLYAQAVE      146
1GCW_2|Chains      YLRKDCFTPHIQGIWDKFFEVIDAISKQY-----      135
1GCW_1|Chains      THL-TEFSPDTHCAVDKLLSAICQELSSRYR-----      140
1HBR_2|Chains      AHFSKDFTPECQAAWQKLVRVVAHALARKYH-----      146
2D5X_2|Chain       RHFGKDFTPELQASYQKVVGAVANALAHKYH-----      146
1A3N_2|Chains      HHFGKEFTPPVQAAYQKVVGAVANALAHKYH-----      146
1HDA_2|Chains      RNFGKEFTPVLQADFQKVVGAVANALAHRYH-----      145
1HBR_1|Chains      VHMKGDYTPEVHAADFDFLSAVSAVLAEKYR-----      141
1A3N_1|Chains      AHLPAEFTPAVHASLDKFLASVSTVLTISKYR-----      141
1HDA_1|Chains      SHLPSDFTPAVHASLDKFLANVSTVLTISKYR-----      141
2D5X_1|Chain       VHLPNDFTPAVHASLDKFLSSVSTVLTISKYR-----      141
                   :           *   :   :

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Alignment with colours

Hide

CLUSTAL O(1.2.4) multiple sequence alignment

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1VHB_1|Chains      -MLDQQTINIIKATVPVLKEHGVTTTTFYKNLFAKHPEVRPLFDMG-----RQ 48
1GCW_2|Chains      VHWTEERDEISKTFQGTD--MKTVVTTQALDRMFKVYPWTRRYFQKRTDF----- 48
1GCW_1|Chains      -AFTACEKQTIQKIAQVLAKSPEAYGAELARLFVTHPGSKSYFEYKDY-----SAAGA 53
1HBR_2|Chains      VHWTAEEKQLITGLWGKVN--VAECGAELARLLIVYPWTQRFFASFGNLSPTAILGNP 58
2D5X_2|Chain       VQLSGEEKAAVLALWDKVN---EEVGGGALGRLLVVYPWTQRFFDSFGDLSPGAVMGNP 58
1A3N_2|Chains      VHLTPEEKSAVTALWGKVN--VDEVGGGALGRLLVVYPWTQRFFESFGDLSTPDAVMGNP 58
1HDA_2|Chains      -MLTAEKAAVTAFWGKVK--VDEVGGGALGRLLVVYPWTQRFFESFGDLSTADAVMNNP 57
1HBR_1|Chains      -MLTAEDKKLIQQAWEKAASHQEEFGAEALTRMFTTYPQTKTYFPHFDL-----SPGSD 53
1A3N_1|Chains      -VLSPADKTNVKAAWGKVGGAHAGEYGAEALERMFLSFPTTKTYFPHFDL-----SHGSA 53
1HDA_1|Chains      -VLSAADKGNVKAAWGKVGGAHAGEYGAEALERMFLSFPTTKTYFPHFDL-----SHGSA 53
2D5X_1|Chain       -VLSAADKTNVKAWSKVGGHAGEYGAEALERMFLGFPTTKTYFPHFDL-----SHGSA 53
                   :                               .::  .*  .  *

1VHB_1|Chains      ESLEQPKALAMTVLAAAQNIENLPAILPAVKKIAVKHCQ-AGVAAAHYPVIGQELLGAIK 107

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1GCW_2 Chains	RSSIHAGIVVGALQDAVKHMDVKTLFKD---LSKKHADDLHVDPGSFHLLTDCIIVELA	105
1GCW_1 Chains	KVQVHGGKVIKRAVVKAAEHVDDLHSHLET---LALTHGKKLLVDPQNFPMLECIIVTLA	110
1HBR_2 Chains	MVRAHGKKVLTSGDAVKNLDNIKNTFSQ---LSELHCDKLHVDPENFRLLGDIILIVLA	115
2D5X_2 Chain	KVKAHGKKVLHSGEGVHHLDNLKGTFAA---LSELHCDKLHVDPENFRLLGNVLVVVLA	115
1A3N_2 Chains	KVKAHGKKVLGAFSDLAHLNLDNLKGTFAA---LSELHCDKLHVDPENFRLLGNVLVVCVLA	115
1HDA_2 Chains	KVKAHGKKVLDSFSNGMKHLDLNLKGTFAA---LSELHCDKLHVDPENFKLLGNVLVVVLA	114
1HBR_1 Chains	QVRGHGKKVLGALGNVKNVDNLSQAMAE---LSNLHAYNLRVDPVNFKLLSQCIQVVLA	110
1A3N_1 Chains	QVKGHGKKVADALTNVAHVDDMPNLSA---LSDLHAHKLVRDPVNFKLLSHCLLVTLA	110
1HDA_1 Chains	QVKGHGAKVAAALTKAVEHLDDLPGALSE---LSDLHAHKLVRDPVNFKLLSHSLLVTLA	110
2D5X_1 Chain	QVKAHGKKVGDAALTAVGHLDDLPGALSN---LSDLHAHKLVRDPVNFKLLSHCLLVTLA	110
	: : . . : : : : : : * * : : . : :	
1VHB_1 Chains	EVLGDAATDDILDWAGKAYGVIAADVFIQVEADLYAQAVE	146
1GCW_2 Chains	YLRKDCFTPHIQGIWDKFFEVVIDAISKQY-----	135
1GCW_1 Chains	THL-TEFSPDTHCAVDKLLSAICQELSSRYR-----	140
1HBR_2 Chains	AHFSKDFTPECQAAWQKLVVRVVAHALARKYH-----	146
2D5X_2 Chain	RHFGKDFTPELQASYQKVVAGVANALAHKYH-----	146
1A3N_2 Chains	HHFGKEFTPPVQAAYQKVVAGVANALAHKYH-----	146
1HDA_2 Chains	RNFGKEFTPVLQADFQKVVAGVANALAHRYH-----	145
1HBR_1 Chains	VHMGKDYTPEVHAADFDFLSAVSAVLAEKYR-----	141
1A3N_1 Chains	AHLPAEFTPAVHASLDKFLASVSTVLTSKYR-----	141
1HDA_1 Chains	SHLPDFTPAVHASLDKFLANVSTVLTSKYR-----	141
2D5X_1 Chain	VHLPNDFTPAVHASLDKFLSSVSTVLTSKYR-----	141
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