

Clustal Omega

Multiple Sequence Alignment (MSA)

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clustalo-I20250718-063254-0826-7058527-p1m

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Phylogenetic Tree

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CLUSTAL O(1.2.4) multiple sequence alignment

1VHB_1 Chains	-MLDQQTINI IKATVPVLKEHGVTITTFYKNLFAKHPEVRPLFDMG-----RQ 48
1GCW_2 Chains	VHWTQEERDEISKTFQGTD--MKT VVTQALDRMFKVYPWTNRYFQKRTDF----- 48
1GCW_1 Chains	-AFTACEKQTIGKIAQVLA KSPEAYGAECLARLFVTHPGSKSYFEYKDY-----SAAGA 53
1HBR_2 Chains	VHWTAEKQLITGLWGKV N--VAECGAELARLLIVYPWTQRFFASFGNLSSPTAILGNP 58
2D5X_2 Chain	VQLSGEEKA AVLALWDKV N--EEEVGGEALGR LLVVYPWTQRFFDSFGDLSNPGAVMNP 58
1A3N_2 Chains	VHLTPEEKSAVTALWGKV N--VDEVGGEALGR LLVVYPWTQRFFESFGDLSTPDAMGNP 58
1HDA_2 Chains	-MLTAEEKA AVTAFWGKV K--VDEVGGEALGR LLVVYPWTQRFFESFGDLSTADAVMNP 57

1HBR_1 Chains	-MLTAEDKKLIQQAWEKAASHQEEFGAEALTRMFTTYPQTCKTYFPHFDL-----SPGSD 53
1A3N_1 Chains	-VLSPADKTNVKAAGWKVGAHAGEYGAEALERMFLSFPTTKTYFPHFDL-----SHGSA 53
1HDA_1 Chains	-VLSAADKGNVKAAGWKVGGHAAEYGAEALERMFLSFPTTKTYFPHFDL-----SHGSA 53
2D5X_1 Chain	-VLSAADKTNVKAAWSKVGGHAGEYGAEALERMFGLGFPTTKTYFPHFDL-----SHGSA 53
	: .:: .* . *
1VHB_1 Chains	ESLEQP KALAMTVLAAAQNIE NLPAILPAVKKIAVKHCQ-AGVAAA HYP IVGQELL GAIK 107
1GCW_2 Chains	RSSIHAGIVVGALQDAVKHMDDVKTLFKD--LSKKHADDLHVDPGSFHLLTDCIIVELA 105
1GCW_1 Chains	KVQVHGGKVKIRAVVKA AEHVDDLHSHLET-LAL THGKKLLVDPQNPMLSECII VTLA 110
1HBR_2 Chains	MVRAHGKKVLTSFGDAVKNLDNIKNTFSQ--LSELHCDKLHVDPENFRLLGDILIIIVLA 115
2D5X_2 Chain	KVKAHGKKVLHSFGEGVHLDNLKGTFAA--LSELHCDKLHVDPENFRLLGNVLVVLA 115
1A3N_2 Chains	KVKAHGKKVLGAFSDGLAHL DNLKGTFAT--LSELHCDKLHVDPENFRLLGNVLVCVLA 115
1HDA_2 Chains	KVKAHGKKVLDSFSNGMKHDDLKGTFAA--LSELHCDKLHVDPENFKLLGNVLVVLA 114
1HBR_1 Chains	QVRGHGKKVLGALGNAVKVNVDNLSQAMAE--LSNLHAYNLRVDPVNFKLLSQCIQVVLA 110
1A3N_1 Chains	QVKGHGKKVADALTNAVAHVDDMPN ALSA--LSDLHAHKLRVDPVNFKLLSHSLLVT LA 110
1HDA_1 Chains	QVKGHGAKVAAALT KAVEHLDLPGALSE--LSDLHAHKLRVDPVNFKLLSHSLLVT LA 110
2D5X_1 Chain	QVKAHGKKVGDALTAVGHLDLPGALSN--LSDLHAHKLRVDPVNFKLLSHC LLSTLA 110
	: : . . ::::: : :: * * : :: . : :
1VHB_1 Chains	EVLGDAATDDILDIAWGKAYGVIADVFIQVEADLYAQAVE 146
1GCW_2 Chains	YLRKDCFTP HIQGIWDKF FEV VIDAISKQY----- 135
1GCW_1 Chains	THL-TEFSPDTHCAVDKL LSAICQELSSRYR----- 140
1HBR_2 Chains	AHFSKDFTPECQAAWQKL VRVVAHALARKYH----- 146
2D5X_2 Chain	RHFGKDFTEPELQASYQKV VAGVANALAHKYH----- 146
1A3N_2 Chains	HHFGKEFTP VQAA YQKV VAGVANALAHKYH----- 146
1HDA_2 Chains	RNFGKEFTP VLQADFQ KV VAGVANALAHRYH----- 145
1HBR_1 Chains	VHMGKDYTPEVHA AFDKFLSAVSAV LAE KYR----- 141
1A3N_1 Chains	AHLPAEFTP AVHASLDKFLASVSTV LSKYR----- 141
1HDA_1 Chains	SHLPSDFTP AVHASLDKFLANVSTV LSKYR----- 141
2D5X_1 Chain	VHL PNDFTP AVHASLDKFLSSVSTV LSKYR----- 141
	: * : :

Alignment with colours

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CLUSTAL O(1.2.4) multiple sequence alignment

1VHB_1 Chains	-MLDQQTINI I KATVPVLKEHGVTITTFYK NLFAKHPEVRPL FDMG-----RQ 48
1GCW_2 Chains	VHW TQEERDEISKT FQGT D--MKT VVT QALDRMF KV VPWTNRYFQKRTDF----- 48
1GCW_1 Chains	-AFTACEK QTIGKIAQVLA KSPEA YGAE CLARLFV THPGS KSYF EYKDY-----SAAGA 53
1HBR_2 Chains	VHW TAEEKQLITGLWGKV N--VAECGA E ALARLLIVY PWTQRFF ASFGN LSSPTA ILGNP 58
2D5X_2 Chain	VQLSGEEKA AAVLALWDKV N--EEEV GGEAL GRLL VVY PWTQRFF DSFGDL S NP GAVMGNP 58
1A3N_2 Chains	VHL TPEEKSA VTALWGKV N--VDEV GG EAL GRLL VVY PWTQRFF ESFG DL STPD AVMGNP 58
1HDA_2 Chains	-MLTAA EKA AAVT AFWG KV K--VDEV GG EAL GRLL VVY PWTQRFF ESFG DL STAD AVMNNP 57
1HBR_1 Chains	-MLTAEDKKLIQQAWEKAASHQEEFGAEALTRMFTTYPQTCKTYFPHFDL-----SPGSD 53
1A3N_1 Chains	-VLSPADKTNVKAAGWKVGAHAGEYGAEALERMFLSFPTTKTYFPHFDL-----SHGSA 53
1HDA_1 Chains	-VLSAADKGNVKAAGWKVGGHAAEYGAEALERMFLSFPTTKTYFPHFDL-----SHGSA 53
2D5X_1 Chain	-VLSAADKTNVKAAWSKVGGHAGEYGAEALERMFGLGFPTTKTYFPHFDL-----SHGSA 53
	: .:: .* . *
1VHB_1 Chains	ESLEQP KALAMTVLAAAQNIE NLPAILPAVKKIAVKHCQ-AGVAAA HYP IVGQELL GAIK 107

1GCW_2 Chains	RSSIHAGIVVGALQDAVKHMDDVKTLFKD--	LSKKHADDLHVDPGSFHLLTDCIIVELA	105
1GCW_1 Chains	KVQVHGGKVIRAVVKAAEHVDDLHSHLET--	LALTHGKKLLVDQPQNFPMLECIIVTLA	110
1HBR_2 Chains	MVRAHGKKVLTSFGDAVKNLDNIKNTFSQ--	LSELHCDKLHVDPENFRLLGDILIIVLA	115
2D5X_2 Chain	KVKAHGKKVLHSFGEGVHHLDNLKGTFAA--	LSELHCDKLHVDPENFRLLGNVLVVVLA	115
1A3N_2 Chains	KVKAHGKKVLGAFSDGLAHLDNLKGTFAT--	LSELHCDKLHVDPENFRLLGNVLVCVLA	115
1HDA_2 Chains	KVKAHGKKVLDSFSNGMKHLDDLKGTFAA--	LSELHCDKLHVDPENFKLLGNVLVVVLA	114
1HBR_1 Chains	QVRGHGKKVLGALGNAVKNVDNLSQAMAE--	LSNLHAYNLRVDPVNFKLLSQCIQVVLA	110
1A3N_1 Chains	QVKGHGKKVADALTNAAVAHVDDMPNALSA--	LSDLHAHKLRVDPVNFKLLSHCLLVTLA	110
1HDA_1 Chains	QVKGHGAKVAAALTKAVEHLDLPGALSE--	LSDLHAHKLRVDPVNFKLLSHSLLVTLA	110
2D5X_1 Chain	QVKAHGKKVGDALTAVGHLDDLPGALSN--	LSDLHAHKLRVDPVNFKLLSHCLLSTLA	110
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1VHB_1 Chains	EVLGDAATTDDILDAWGKAYGVIAVFIQVEADLYAQAVE		146
1GCW_2 Chains	YLRKDCFTPHIQGIWDKFFEVVIDAIISKQY-----		135
1GCW_1 Chains	THL-TEFSPDTHCAVDKLLSAICQELSSRYR-----		140
1HBR_2 Chains	AHFSKDFTPECQAQWQKLVRVVAHALARKYH-----		146
2D5X_2 Chain	RHFGKDFTPELQASYQKVVAGVANALAHKYH-----		146
1A3N_2 Chains	HHFGKEFTPVQAAQKVVAGVANALAHKYH-----		146
1HDA_2 Chains	RNFGKEFTPVLQADFQKVVAGVANALAHRYH-----		145
1HBR_1 Chains	VHMGKDYTPEVHAAFDKFLSAVSAVLAEKYR-----		141
1A3N_1 Chains	AHLPAEFTPAPVHASLDKFLASVSTVLTSKYR-----		141
1HDA_1 Chains	SHLPSDFTPAVHASLDKFLANVSTVLTSKYR-----		141
2D5X_1 Chain	VHLPNDFTPAPVHASLDKFLSSVSTVLTSKYR-----		141

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