

CLUSTAL W (1.83) multiple sequence alignment

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1912748405 -----
2127213838 MTLVSFTITIVCIVSITRLPKFATEIPNKNTLQTYIVHVEGPDDQQ-HES
2127213839 ML-----SFITCPAFSANTQKQTS�PTYIVHVEASHAQLSSES
2127214961 ML-----SFITCPAVSANTQEQTSLPTYIVHVEASHAQLSSES
2236153894 MASFS-KITQILLISLIFHSTITQAIDEIDDLITYIVHVDPSDTSL----

1912748405 -----
2127213838 QDLQSWYRSFLPAATTSSSGEDEARLVYSYRHVFKGFAAKLSTDEVNEME
2127213839 SQLENWYRSFLPATTTASADEGEARMVYSYRSVFKGFAARLSADEVKEMA
2127214961 SQLESWYRSFLPATTTASADEGEARMVYSYRSVFKGFAARLSADEVKEMA
2236153894 EELESWYRSFLGNS-----NPSRIVHTYKHVIKGFAARLTPDEVAIIQ

1912748405 -----MYQLSTTRSPSFLGLHQGTGLWNQSNNGGKGVIIIGVIDT
2127213838 KKEGFISARPQKQLSLHTTHSPNFLGLNLRNVGFWKDSNYGKDVIIGVMDT
2127213839 KKEGFISARPEKILSLHTTHSPNFLGLNQNMGLWKDSNYGKGVIIIGVLDT
2127214961 KKEGFISARPEKILSLHTTHSPNFLGLNQNMGLWKDSNYGKGVIIIGVLDT
2236153894 KYDGFLHARPQRQLPLHTHTPNFLGLHRETGLWEASNYGEGVIGVLDT
                * *:.*.*****:  *:.* ** *:.******:**

1912748405 GVFPSHPSFSGANMLPPPAKWKGKCEFPNKTDCCNKLIGARLFNRAVSSA
2127213838 GVLPEHPSFSAGGMPPPPAKWKGRCFNH-TTCNNKIIGARYFNA-----
2127213839 GILPEHPSFSDEGMPPPPAKWKGRCEFSN-TTCNNKIIGARFFGS-----
2127214961 GILPEHPSFSDEGMPPPPAKWKGRCEFMN-TTCNNKIIGARFFGS-----
2236153894 GISPDHPSFSDEGMPPPPAKWKKGKCELNT-TACNNKLIGARYFTF-----
                *: *.***** .* *****:.*:  * *****:***** *

1912748405 ASILDEETVVDREHGHTHISGTAAGVFVENACFLGSACGTAVGMAPRAHL
2127213838 ----DDQSPLDDDGHTHTASTAAGTFVGGANLLGSANGTAVGIAPLAHL
2127213839 ----DATSPFDEDGHTHTAGTAAGSFVKGANVFGNAYGTAAGIAPMAHL
2127214961 ----DATSPFDEDGHTHTAGTAAGSFVKGANVFGNAYGTAAGIAPMAHL
2236153894 ----GQGTSLDENGHTHVAGTAAGSFVAGANSFRRANGTAAGIAPRAHI
                . : .* :***** :.**** ** .* :  * ***.*:** **

1912748405 AIYKVCTK--SGCSSINMLAGLDAAIEDGVDVISLSLSHQSIPIFYDDHTA
2127213838 AIYKVC-----CGEVDVLAGEAEDGVDVISISLGLGDGDFFENSIA
2127213839 AIYRVCTP--S-CSDSRVLAGIDAAIDDGVDVLSISLGMLENSFAQDYTA
2127214961 AIYRVCTP--S-CSDSRVLAGIDAAIEDGVDVLSISLGLTNSFAQDYIA
2236153894 AVYKVCTDTGH-CESDVLAAAMDFAIEDGVDVISLSVGLGQDPFAFNAIS
                *:.*:**  *. . :**.* * :.******:.*:  * : :

1912748405 IGTFAAVKKGIFVSCSGGNHGPFKKSIRSEAPWVLTVGASTIDRSLRATA
2127213838 IGAFSAMEKGILVSCSAGNDGPFSSVENGAPWILTVGASTIDRKL TAKA
2127213839 IGAFSAMEKGILVSCSAGNFGPFNFVENEAPWILTVGASTLDRKLAATA
2127214961 IGAFSAMEKGILVSCSAGNFGPFNFSENEAPWILTVGASTLDRKLAATA
2236153894 LGAYGAVKKGIVFVSCSAGNNGPSHGTLSENEAPWVLTVGASTVDRKLLAVA
                :*::.*:**:****.* ** :. . ***:*****:*** * *

1912748405 KLGDGQEFDGESVYQQKDFPDGTMPLVYRA-----SCA-GNTSL
2127213838 VLGNNKQFDGESAFQPKHFPQ-TLLPLVYAGMLNASDDYAPYCFYDTFNH
2127213839 VLGNNQTFDGETVFQPKDFPS-KLLPLVYAGDINTSDPYVKFCYDESLNN

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[illegible]

2127213838	HSVRSPIAVLS-----
2127213839	HSVRSPIAVILQ-----
2127214961	HSVRSPIAVILQ-----
2236153894	YEVRSPIVAMMIDWEF-
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