

CLUSTAL O(1.2.4) multiple sequence alignment

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NC_014479      MAYEEKTDWLPDDPINEDDVNRWEKGIKDAHTDLAAHKNDMNNPHNTTKAQVGLGNVDNV      60
NC_000964      MAYEEKTDWLPDDPINEDDVNRWEKGIKDAHTDLAAHKNDMNNPHNTTKAQIGLGNVDNV      60
NC_022898      MAYEEKTDWLPDDPINEDDVNRWEKGIKDAHTDLAAHKNDMNNPHNTTKAQIGLGNVDNV      60
NC_018520      MAYEEKTDWLPDDPINEDDVNRWEKGIKDAHTDLAAHKNDMNNPHNTTKAQIGLGNVDNV      60
NZ_CP017314    MAYEEKTDWLPDDPINEDDVNRWEKGIKDAHTDLAAHKNDMNNPHNTTKAQIGLGNVDNV      60
NC_014976      MAYEEKTDWLPDDPINEDDVNRWEKGIKDAHTDLAAHKNDMNNPHNTTKAQIGLGNVDNV      60
NC_017195      MAYEEKTDWLPDDPINEDDVNRWEKGIKDAHTDLAVHKNDMNNPHNTTKAQIGLGNVDNV      60
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NC_014479      KQAAKDFDQHDQDQVRHIAEEEREKWNNGQLSKITKDDGSVFITID-NGQDFNEVAAQQ      119
NC_000964      QQASKTEFNEHNHDSTRHITSVERDEWNAKETPAGAQYKADQ-----      102
NC_022898      QQASKTEFNEHNHDSTRHITSVERDEWNAKETPAGAQYKADQ-----      102
NC_018520      QQASKTEFNEHNHDSTRHITSVERDEWNAKETPAGAQYKADQ-----      102
NZ_CP017314    QQAAKDFDKHEQDQVRHITSTERENWNAKETPGEAQNKADQ-----      102
NC_014976      QQAAKDFEKHVNDGTIHIITAERSKWNNAQLSKISGDDGRVFKSVTEITDYNDL----      116
NC_017195      QQAAKDFDKHISDETIHISSERTKWNNAQLTKLTDEKGKYLASIQN-GLDFHKIVEEL      119
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NC_014479      KKSFTFYTVKTGLNTPPQPTKGIYLYSENDGEAIAMTNDGG----IWR-KTLTSGEWS      173
NC_000964      -----A-----EANAAYTD-----NFAAR-----      117
NC_022898      -----A-----EANAAYTD-----NFAAR-----      117
NC_018520      -----A-----EANAAYTD-----NFAAR-----      117
NZ_CP017314    -----A-----EANAAYTD-----SFAAR-----      117
NC_014976      TDTGMYLIYNDGLNGPGLNQCFLLVMSYKN--TLVQIAYDGIKGEQSFFRIRKNDSTTWT      174
NC_017195      GQTFFFYTDKTGINPPFATRGL-YIGKYSYGEALAMDYEGG----TWR-KSLNDSGWT      172
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NC_014479      EWASFETEAGSKSKAAQ-----      190
NC_000964      -----RD-----      119
NC_022898      -----RD-----      119
NC_018520      -----RD-----      119
NZ_CP017314    -----RD-----      119
NC_014976      AWIESETTEGSQKKIDAHANKTDIHVTKSDKDKWNDSQLFKITQDNGLAKYCEDA--DFN      232
NC_017195      DWVQLETSEGAQFKVRSHEEKTEIHVNSDKDKWNSGQLFKVTADNGTQKINLSSGSFYD      232

NC_014479      -----      190
NC_000964      -----NPNQVT-KA----Q-----VGLGNV-----      134
NC_022898      -----NPNQVT-KA----Q-----VGLGNV-----      134
NC_018520      -----NPNQVT-KA----Q-----VGLGNV-----      134
NZ_CP017314    -----NPNQVT-KA----Q-----VGLGNV-----      134
NC_014976      TVIETGFYYMSGATTTLNAPVNN--NGYLMVYNFSTYAYQEYTSYSSSDTISTGRRKFMR      290
NC_017195      SLKDVGTVTFYGTNAVTDNPSNTSLRGMQLVGQLG-----IGMGYAVDVGGNAWWF      283

NC_014479      -----AEKNAKNYIDNHTDNSSIHIITNDERVKWNGAQLTKLTKDNGRRT      234
NC_000964      -----ENVKQASLADFDAHLSNSKVVHVSEGERNKWNAQLIKLTGDDGKRI      180
NC_022898      -----ENVKQASLADFDAHLSNSKVVHVSEGERNKWNAQLIKLTGDDGKRI      180
NC_018520      -----ENVKQASLADFDAHLSNSKVVHVSEGERNKWNAQLIKLTGDDGKRI      180
NZ_CP017314    -----ENVKQASQADFDAHLSNTKVVHVSEGERNKWNAQLIKLTGDDGKRI      180
NC_014976      NKVANSDVWTSWREIESVEGSQIKVDAHANKTDIHVTTSDKDKWNNALYRLTDTQGCR      350
NC_017195      -FYNANDSAINWYQIESITGAQSKIDAHANKTDIHVTTSDKDKWNNALYRLTDTQGCR      342

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[illegible]

NC_014479	WVPDGTDLISLSTGFYYGVGKYVVNNPVDDDNAWYNYDVIE - GESGRKTIVAYQSFEVTM	293
NC_000964	QLQDGTDLITLSSGFYCAVGQSVVNNPVEGDAAWYNYDIVE - GSGRKTIVAYQSWGSM	239
NC_022898	QLQDGTDLITLSSGFYCAVGQSVVNNPVEGDAAWYNYDIVE - GSGRKTIVAYQSWGSM	239
NC_018520	QLQDGTDLITLSSGFYCAVGQSVVNNPVEGDAAWYNYDIVE - GSGRKTIVAYQSWGSM	239
NZ_CP017314	QLQDGTDLITLSSGFYCAVGQSVVNNPVEGDATWYNYDIVE - GSGRKTIVAYQSWGSM	239
NC_014976	KIPDGTDLLTLP SGFYALGNVITNPNVSGDGSWYNYDIETEGGRKTIASRSYDGT	410
NC_017195	KIPDGTDLLTLP SGFYAVGNVIINNPVLGDGSWYNYDIETGGGRKTIASRSFDGT	402
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[illegible]

NC_014479	WIGMVHTDGKFRGWKRLVTSEELNSENINKITDESLEYQDAAYSGNNYPIGITTVAILQGS	353
NC_000964	WIGMVHTDGEFRGWKQIATTDIDRVQTELDLH-----ENDKTNPHSVTK-----	284
NC_022898	WIGMVHTDGEFRGWKQIATTDIDRVQTELDLH-----ENDKTNPHSVTK-----	284
NC_018520	WIGMVHTDGEFRGWKQIATTDIDRVQTELDLH-----ENDKTNPHSVTK-----	284
NZ_CP017314	WIGMVHTDGKFRGWKQIATTDIDRVQSELDIH-----KNDKTNPHSVTK-----	284
NC_014976	WTATIHTDGVFKGWNKIETE-----	430
NC_017195	WMATIHTDGVFKGWNKIETE-----	422
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NC_014479	TGYPYELGEVLNIKSSKYRFAQFFFYAGNTGQKKVFIIRHWYDTVGWTDFTITIPSSSEEL	413
NC_000964	--QQVGLGNVENVKQETPDGAQ-----KKADTALNQSKDYTNSTAFITRPLNS----	330
NC_022898	--QQVGLGNVENVKQETPDGAQ-----KKADTALNQSKDYTNSTAFITRPLNS----	330
NC_018520	--QQVGLGNVENVKQETPDGAQ-----KKADTALNQSKDYTNSTAFITRPLNS----	330
NZ_CP017314	--QQVGLGNVENVKQETPDGAQ-----KKADTALNQSKDYTNSTAFITRPLNS----	330
NC_014976	-----	430
NC_017195	-----	422

NC_014479	VLNTAKLYTDSHANNTEIHVTQNDKTKWNSQIFKL TQDDGLGKFYNEDLNNITKTGFY	473
NC_000964	ITDANDL-----NLP--PGT---YRLDTNYMNAN---	354
NC_022898	ITDANDL-----NLP--PGT---YRLDTNYMNAN---	354
NC_018520	ITDANDL-----NLP--PGT---YRLDTNYMNAN---	354
NZ_CP017314	ITDANDL-----NLP--PGT---YRLDTNYMNAN---	354
NC_014976	-----	430
NC_017195	-----	422

NC_014479	YIYSSITTELNAPINRNGYLLVYNVETYPYQEFTSYSGYTD SIPDNRRKFIRNKKQDSEEW	533
NC_000964	--PVLQNQFPLNDNRTGLLLIYPSANK-----WATRQDWF S ISTKTLYTRVAVNGTDY	405
NC_022898	--PVLQNQFPLNDNRTGLLLIYPSANK-----WATRQDWF S ISTKTLYTRVAVNGTDY	405
NC_018520	--PVLQNQFPLNDNRTGLLLIYPSANK-----WATRQDWF S ISTKTLYTRVAVNGTDY	405
NZ_CP017314	--PELQNQFPLNDNRTGLLLIYPSANK-----WATRQDWF S ISTKTLYTRVAVNGTEY	405
NC_014976	-----	430
NC_017195	-----	422

NC_014479	TPWMEI EYSQGAQAKADKALADAKNYVDNTYTNQKLT KL TGSNAIQDARTGGDEYPPQGLT	593
NC_000964	SGWYI LENSEGSQNKADKALADAKNYVETNYTNQKLT VLTGTSNAIQDARISGNDYKYGIT	465
NC_022898	SGWYI LENSEGSQNKADKALADAKNYVETNYTNQKLT VLTGTSNAIQDARISGNDYKYGIT	465
NC_018520	SGWYI LENSEGSQNKADKALADAKNYVETNYTNQKLT VLTGTSNAIQDARISGNDYKYGIT	465
NZ_CP017314	TDWYI LETSEGSQSKADKALADAKNYVDSNYTNKKLT VLTGTSNAIQDARTSGNEYPPAGLT	465
NC_014976	-----VSAQTKADKALADAKNYVDSNYTNKKLT VLTGTSNAIQDARTGGNEYPPGLT	481
NC_017195	-----ASAQTKADKALSDAKNYVETNYTNQKLT VLTGTSNAIQDARISGNDYKYGIT	473

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NC_014479	LIDIGQGNNTGYPLRYGFVKNEKYSDFRFAQYFYGTGNESGSYIDSTGTWIRHWWSGSGW	653
NC_000964	FMDIGANNTTGYPLTYGFVKNEKHSNYRFTQYFYGNADTTSGSYDHVGTWIRHWWADSGW	525
NC_022898	FMDIGANNTTGYPLTYGFVKNEKHSNYRFTQYFYGNADTTSGSYDHVGTWIRHWWADSGW	525
NC_018520	FMDIGANNTTGYPLTYGFVKNEKHSNYRFTQYFYGNADTTSGSYDHVGTWIRHWWADSGW	525
NZ_CP017314	FMDIGANNTTGYPLTYGIVKNEKYSNYRFAQYFYGTGNESNSYFTSTGSWIRHWWSDSGW	525
NC_014976	LMDIGQGNNTGYPLGYGIVKNEKYSDFRFTQYFYGTGNESNSYIDSTGTWVRHWWSGSGW	541
NC_017195	FMDIGANNTTGYPLTYGFVKNEKHSNYRFTQYFYGNADTTSGSYDHVGTWIRHWWADSGW	533

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NC_014479	TAWHKISGFAHAYIRTTGIQYLDKAAHTKIQFNRIKIDSHNAFDTKNSRFVAPNDGMFLV	713
NC_000964	TAWQKISGFAHANIGTTGRQALIKGENNIIKYNRIIKDSHKLFDTKNNRFVASHAGMHLV	585
NC_022898	TAWQKISGFAHANIGTTGRQALIKGENNIIKYNRIIKDSHKLFDTKNNRFVASHAGMHLV	585
NC_018520	TAWQKISGFAHANIGTTGRQALIKGENNIIKYNRIIKDSHKLFDTKNNRFVASHAGMHLV	585
NZ_CP017314	TAWHKISGFAHANIGTTGKQQLIKGELQKVKNRIKIDSHNTFDTKNNRFIVPNDGMFLV	585
NC_014976	TAWQKISGFAHANIGTTGRQALIKGENNIIKYNRIIKDSHKLFDTKNNRFVASHAGMHLV	601
NC_017195	TAWQKISGFAHANIGTTGRQALIKGENNIIKYNRIIKDSHKLFDKNNRFVASHAGMHLV	593

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NC_014479	GVGLYMINTPAYINFHLKLYLNGSLYKPIDHKRGDFV--DKENEMNLDLNGNVTPMKNKG	771
NC_000964	SASLYIENTERYSNFELYVVVNGTKYKLMNQFRMPTPSNNSDNEFNATVTGSVTVPLDAG	645
NC_022898	SASLYIENTERYSNFELYVVVNGTKYKLMNQFRMPTPSNNSDNEFNATVTGSVTVPLDAG	645
NC_018520	SASLYIENTERYSNFELYVVVNGTKYKLMNQFRMPTPSNNSDNEFNATVTGSVTVPLDAG	645
NZ_CP017314	NAGLYIENYQRYVNYELDIYLNQVRYKNIAHYRANPGDQSDTTEINVGLYGAATVPANQG	645
NC_014976	SASLYIENTERYSNFELYVVVNGTKYKLMNQFRMPTPSNNSDNEFNATVTGSVTVPLDAG	661
NC_017195	SASLYIENTERYSNFELYVVVNGTKYKLMNQFRMPTPSNNSDNEFNATVTGSVTVPLDAG	653

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NC_014479	DYIEIYCYCNYHGTDRRGVSDYNEVYNYIDIQELGGLNYPTV	813
NC_000964	DYVEIYVVVGYSGDVTRYVTDSENGALNYFDVLELGGRNYPRV	687
NC_022898	DYVEIYVVVGYSGDVTRYVTDSENGALNYFDVLELGGRNYPRV	687
NC_018520	DYVEIYVVVGYSGDVTRYVTDSENGALNYFDVLELGGRNYPRV	687
NZ_CP017314	DYIEIYLYVGYNGGTTRYTTESSGWYNYFDITEIGGRNYPRV	687
NC_014976	DYVEIYVVVGYSGDVTRYVTDSENGALNYFDVLELGGRNYPRV	703
NC_017195	DYVEIYVVVGYSGDITRYVTDSENGVLYNYFDVLELGGRNYPRV	695

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