

Multiple sequence alignment of rh10, AAV1, AAV2, AAV3, AAV7, and AAV8 using Clustal Omega:

CLUSTAL O(1.2.4) multiple sequence alignment

```

AAV7      MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRGLVLPGYKYLGPFGNGLD 60
rh10      MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFGNGLD 60
AAV8      MAADGYLPDWLEDNLSEGIREWWALKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFGNGLD 60
AAV1      MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFGNGLD 60
AAV2      MAADGYLPDWLEDNLSEGIRQWWKLKPGPPPKPAERHKDDSRGLVLPGYKYLGPFGNGLD 60
AAV3      MAADGYLPDWLEDNLSEGIREWWALKPGVPQPKANQQHQDNRRGLVLPGYKYLGPFGNGLD 60
          *****.*****: ** ***** * ** :::*: ***** *****

AAV7      KGEFVNAAAADAALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQ 120
rh10      KGEFVNAAAADAALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQ 120
AAV8      KGEFVNAAAADAALEHDKAYDQQLQAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQ 120
AAV1      KGEFVNAAAADAALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQ 120
AAV2      KGEFVNAAAADAALEHDKAYDRQLDSDGNPYLKYNHADADEFQERLKEDTSFGGNLGRAVFQ 120
AAV3      KGEFVNAAAADAALEHDKAYDQQLKAGDNPYLKYNHADADEFQERLQEDTSFGGNLGRAVFQ 120
          ***** *****:*.:.:*****:*****:*****:*****

AAV7      AKKRVLEPLGLVEEGAKTAPAKKRPVEPSPQRSPTSSTGIGKKGQQPARKRLNFGQTGDS 180
rh10      AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPTSSTGIGKKGQQPARKRLNFGQTGDS 180
AAV8      AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPTSSTGIGKKGQQPARKRLNFGQTGDS 180
AAV1      AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTGQQPARKRLNFGQTGDS 179
AAV2      AKKRVLEPLGLVEEPVKAPGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDA 179
AAV3      AKKRILEPLGLVEEAAKTAPGKKGAVDQSPQ-EPDSSSGVGKSGKQPARKRLNFGQTGDS 179
          ****:*****.*****. ** *: ** .*****: * ** *:***:*****:

AAV7      ESVPDPQPLGEPPAAPSSVSGTVAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDVR 240
rh10      ESVPDPQPIGEPPAGPSGLSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDVR 240
AAV8      ESVPDPQPLGEPPAAPSGVGPNMTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDVR 240
AAV1      ESVPDPQPLGEPPATPAAVGPTTMAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDVR 239
AAV2      DSVDPDPQPLGQPPAAPSGLGTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDRV 239
AAV3      ESVPDPQPLGEPPAAPTSLGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSTWLGDVR 239
          :*****:*.*** *::.: **:*.*****:*****:*****:*****

AAV7      ITTSTRTWALPTYNNHLYKQISSET-AGSTNDNTYFGYSTPWGYFDNRFHCHFSRWDQ 299
rh10      ITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDNRFHCHFSRWDQ 300
AAV8      ITTSTRTWALPTYNNHLYKQISNGTSGGATNDNTYFGYSTPWGYFDNRFHCHFSRWDQ 300
AAV1      ITTSTRTWALPTYNNHLYKQISSAS-TGASNDNHYFGYSTPWGYFDNRFHCHFSRWDQ 298
AAV2      ITTSTRTWALPTYNNHLYKQISSQ--SGASNDNHYFGYSTPWGYFDNRFHCHFSRWDQ 297
AAV3      ITTSTRTWALPTYNNHLYKQISSQ--SGASNDNHYFGYSTPWGYFDNRFHCHFSRWDQ 297
          *****.*****. *::*** *****

AAV7      RLINNNWGFPRPKKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDEYQLPYVLGSA 359
rh10      RLINNNWGFPRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSA 360
AAV8      RLINNNWGFPRPKRLSFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSA 360
AAV1      RLINNNWGFPRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDEYQLPYVLGSA 358
AAV2      RLINNNWGFPRPKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSA 357
AAV3      RLINNNWGFPRPKKLSFKLFNIQVRGVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSA 357
          *****: * *****: ** *:*.*****:***:*****

AAV7      HQGCLPPFPADVFMIPQYGYLTLNNGSQSVGRSSFYCLEYFPSQMLRTGNNFEFSYSYFED 419
rh10      HQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFEFSYQFED 420
AAV8      HQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFEFSYQFED 420

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AAV1	HQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNTFSYTFEE	418
AAV2	HQGCLPPFPADVFMVFPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNTFSYTFED	417
AAV3	HQGCLPPFPADVFMVFPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNTQFSYTFED	417
	*****:*****:***** *: *	
AAV7	VPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQSNPGGTAGNRELQFYQGGPSTMAEQAKN	479
rh10	VPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQS-TGGTAGTQQLLFSQAGPNNMSAQAKN	479
AAV8	VPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQT-TGGTANTQTLGFSQGGPNTMANQAKN	479
AAV1	VPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQN-QSGSAQNKDLLFSRGSPAGMSVQPKN	477
AAV2	VPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTN-TPSGTTTQSRLOFSQAGASDIRDQSRN	476
AAV3	VPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQGTTSGTTNQSRLLFSQAGPQMSLQARN	477
	***** *: .*: * * :. : *	
AAV7	WLPGPCFRQQRVSKTLDQNNNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDEDRFFPS	539
rh10	WLPGPCYRQQRVSTTSLQNNNSNFAWTGATKYHLNGRDSLNVNPGVAMATHKDDEERFFPS	539
AAV8	WLPGPCYRQQRVSTTTGQNNNSNFAWTAGTKYHLNGRNSLANPGIAMATHKDDEERFFPS	539
AAV1	WLPGPCYRQQRVSKTKTDNNNSNFTWTGASKYNLNGRESIINPGTAMASHKDDEDKFFPM	537
AAV2	WLPGPCYRQQRVSKTSADNNNSSEYSWTGATKYHLNGRDSLNVNPGPAMASHKDDEEKFFPQ	536
AAV3	WLPGPCYRQQRSLKTANDNNNSNFPWTAASKYHLNGRDSLNVNPGPAMASHKDDEEKFFPM	537
	*****:*****:*. * :*****: * .: **:*****: * : *** ***:*****:***	
AAV7	SGVLIFGKTGATNK-TTLENVMTNEEEIRPTNPVATEEYGVSSNLQAANTAAQTQVVN	598
rh10	SGVLMFGKQGAGKDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQQQNAAPIVGAVN	599
AAV8	NGILIFGKQNAARDNADYSDVMLTSEEEIKTTNPVATEEYGVVADNLQQQNTAPQIGTVN	599
AAV1	SGVMIFGKESAGASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVH	597
AAV2	SGVLIFGKQGSEKTNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVN	596
AAV3	HGNLIFGKEGTTASNAELDNVMITDEEEIRTTNPVATEQYGTVANLQSSNTAPTGTGVN	597
	* :*** .: . .*:*.*****: *****:*. * : *:* . *	
AAV7	NQALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQILIKNTPVPAN	658
rh10	SQALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQILIKNTPVPAD	659
AAV8	SQALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQILIKNTPVPAD	659
AAV1	AMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPQILIKNTPVPAN	657
AAV2	TQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPAN	656
AAV3	HQALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQIMIKNTPVPAN	657
	*.*****:*****:*****:*****:*****:*****:	
AAV7	PPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNFEKQTGVDFAVDS	718
rh10	PPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTNVDFAVNT	719
AAV8	PPTTFNQSKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTSVDFAVNT	719
AAV1	PPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNYAKSANVDFTVDN	717
AAV2	PSTTFSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDT	716
AAV3	PPTTFSPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDT	717
	* * .*: *****:*****: *****: *...***:*.:	
AAV7	QGVYSEPRPIGTRYLTRNL 737	
rh10	DGTYSEPRPIGTRYLTRNL 738	
AAV8	EGVYSEPRPIGTRYLTRNL 738	
AAV1	NGLYTEPRPIGTRYLTRPL 736	
AAV2	NGVYSEPRPIGTRYLTRNL 735	
AAV3	NGVYSEPRPIGTRYLTRNL 736	
	: * *:***** *	

Pairwise sequence alignment of rh10 and AAV1 using EMBOS Needle:

rh10	201	SGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTSTRTWAL	250
AAV1	200	PTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWAL	249
rh10	251	PTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQ	300
AAV1	250	PTYNNHLYKQISSASTGAS-NDNHYFGYSTPWGYFDFNRFHCHFSPRDWQ	298
rh10	301	RLINNNWGFPRKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSE	350
AAV1	299	RLINNNWGFPRKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFS DSE	348
rh10	351	YQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEY	400
AAV1	349	YQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEY	398
rh10	401	FPSQMLRTGNNFEFSYQFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSR	450
AAV1	399	FPSQMLRTGNNFTFSYTFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLSR	448
rh10	451	TQSTGGTAGTQQLLFSQAGPNMSAQAKNWLPGPCYRQQRVSTTLSQNNN	500
AAV1	449	TQNQSGSAQNKDLLFSRGSPPAGMSVQPKNWLPGPCYRQQRVSKTKTDNNN	498
rh10	501	SNFAWTGATKYHLNGRDSLVPNGVAMATHKDDEERFFPSSGVLMFGKQGA	550
AAV1	499	SNFTWTGASKYNLNGRESIINPGTAMASHKDDKFFPMSGVMIFGKESA	548
rh10	551	GKDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQQQNAAPIVGAVNS	600
AAV1	549	GASNTALDNVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPATGDVHA	598
rh10	601	QGALPGMVWQNRDVYLQGPWAKIPHTDGNFHPSPMLMGGFGLKHPPPQIL	650
AAV1	599	MGALPGMVWQDRDVYLQGPWAKIPHTDGHFHPSPMLMGGFGLKNPPPQIL	648
rh10	651	IKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENS KRWNPE	700
AAV1	649	IKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENS KRWNPE	698
rh10	701	IQYTSNYYKSTNVDFAVNTDGTYSEPRPIGTRYLTRNL	738
AAV1	699	VQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRPL	736

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Pairwise sequence alignment of rh10 and AAV2 using EMBOSS Needle:

```
#####
# Program: needle
# Rundate: Fri 15 Nov 2024 23:25:10
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20241115-232506-0064-13031896-plm.asequence
#   -bsequence emboss_needle-I20241115-232506-0064-13031896-plm.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#=====
#
# Aligned_sequences: 2
# 1: rh10
# 2: AAV2
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 738
# Identity:      620/738 (84.0%)
# Similarity:    667/738 (90.4%)
# Gaps:          3/738 ( 0.4%)
# Score: 3405.5
#
#
#=====

rh10          1 MAADGYLPDWLEDNLSEGIREWWDLPKPGAPKPKANQQKQDDGRGLVLPGY      50
               |||||||||||||.|||||:|.|||||.|||...:|.|||||||
AAV2          1 MAADGYLPDWLEDTLSEGIQWWKLKPGPPPPKPAERHKDDSRGLVLPGY      50

rh10          51 KYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEF    100
               |||||||||||||.|||||:|.|.|||||:|||||||
AAV2          51 KYLGPFNGLDKGEPVNEADAAALEHDKAYDRQLDSDGNPYLKYNHADAEF    100

rh10          101 QERLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEPSP    150
               |||:|||||||||||||||||||||||.|||||||.||
AAV2          101 QERLKEDTSFGGNLGRAVFQAKKRVLEPLGLVEEPVKTPAGKKRPVEHSP    150

rh10          151 QRSPDSSTGIGKKGQQPAKKRLNFGQTDGSESVDPDPQPIGEPPAGPSGLG    200
               .|.||||:|.|||.|||||:|||||||:|:|||||:|.|||||
AAV2          151 V-EPDSSSGTGKAGQQPARKRLNFGQTDGADSVDPDPQPLGQPPAAPSGLG    199
```

rh10	201	SGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDREVITTSTRTWAL	250
AAV2	200	TNTMATGSGAPMADNNEGADGVGNSSSGNWHCDSTWMGDRVITTSTRTWAL	249
rh10	251	PTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQ	300
AAV2	250	PTYNNHLYKQIS--SQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQ	297
rh10	301	RLINNNWGFPRKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSE	350
AAV2	298	RLINNNWGFPRKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSE	347
rh10	351	YQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEY	400
AAV2	348	YQLPYVLGSAHQGCLPPFPADVFMVPPQYGYLTLNNGSQAVGRSSFYCLEY	397
rh10	401	FPSQMLRTGNNFEFSYQFEDVPPFHSSYAHSQSLDRLMNPLIDQYLYLSR	450
AAV2	398	FPSQMLRTGNNFTFSYTFEDVPPFHSSYAHSQSLDRLMNPLIDQYLYLSR	447
rh10	451	TQSTGGTAGTQQLLFSQAGPNNMSAQAKNWLPGPCYRQQRVSTTLSQNNN	500
AAV2	448	TNTPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGPCYRQQRVSKTSADNNN	497
rh10	501	SNFAWTGATKYHLNGRDSLVPNGVAMATHKDDEERFFPSSGVLMMFGKQGA	550
AAV2	498	SEYSWTGATKYHLNGRDSLVPNGPAMASHKDDEEKFFPQSGVLIFGKQGS	547
rh10	551	GKDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQQQNAAPIVGAVNS	600
AAV2	548	EKTNDVIEKVMITDEEEIRTNPVATEQYGSVSTNLQRGNRQAATADVNT	597
rh10	601	QGALPGMVWQNRDVYLQGPWAKIPHTDGNFHPSPLMGGFGLKHPPPQIL	650
AAV2	598	QGVLPGMVWQDRDVYLQGPWAKIPHTDGHFHPSPLMGGFGLKHPPPQIL	647
rh10	651	IKNTPVPADPPTTFSSQAKLASFITQYSTGQVSVEIEWELQKENSQRWNPE	700
AAV2	648	IKNTPVPANPSTTFSSAAKFASFITQYSTGQVSVEIEWELQKENSQRWNPE	697
rh10	701	IQYTSNYYKSTNVDFAVNTDGTYSERPIGTRYLTRNL	738
AAV2	698	IQYTSNYSKSVNVDFTVDTNGVYSERPIGTRYLTRNL	735

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Pairwise sequence alignment of rh10 and AAV3 using EMBOSS Needle:

```
#####
# Program: needle
# Rundate: Fri 15 Nov 2024 23:31:39
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20241115-233134-0706-54638021-plm.asequence
#   -bsequence emboss_needle-I20241115-233134-0706-54638021-plm.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#=====
#
# Aligned_sequences: 2
# 1: rh10
# 2: AAV3
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 739
# Identity:      629/739 (85.1%)
# Similarity:    675/739 (91.3%)
# Gaps:          4/739 ( 0.5%)
# Score: 3458.5
#
#
#=====

rh10          1 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGY      50
               |||||||||||||||||||||.|||||.:|||||.||:|||||||
AAV3          1 MAADGYLPDWLEDNLSEGIREWWALKPGVPQPKANQQHQDNRRGLVLPGY      50

rh10          51 KYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEF    100
               |||||.|||||||.|||||||||||||||||||||:|||||||
AAV3          51 KYLGPGNGLDKGEPVNEADAAALEHDKAYDQQLKAGDNPYLKYNHADAEF    100

rh10          101 QERLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEPSP    150
               |||||||||||||||||||:|||||||.|||||||.||:..||
AAV3          101 QERLQEDTSFGGNLGRAVFQAKKRILEPLGLVEEAAKTAPGKKGAVDQSP    150

rh10          151 QRSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVDPDPQPIGEPPAGPSGLG    200
               |.|||||:|:|.||:|:|||||||||||||||||:|||||.||:..||
AAV3          151 Q-EPDSSSGVGKSGKQPARKRLNFGQTGDSESVDPDPQPLGEPPAAPTSLG    199
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rh10	201	SGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGD RVITTSTRTWAL	250
AAV3	200	SNTMASGGGAPMADNNEGADGVGNSSSGNWHCD SQWLGD RVITTSTRTWAL	249
rh10	251	PTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQ	300
AAV3	250	PTYNNHLYKQIS--SQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQ	297
rh10	301	RLINNNWGFPRKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSE	350
AAV3	298	RLINNNWGFPRKKLSFKLFNIQVRGVTQNDGTTTIANNLTSTVQVFTDSE	347
rh10	351	YQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEY	400
AAV3	348	YQLPYVLGSAHQGCLPPFPADVFMVMPQYGYLTLNNGSQAVGRSSFYCLEY	397
rh10	401	FPSQMLRTGNNFEFSYQFEDVVPFHSSYAHSQSLDRLMNPLIDQYLYLSR	450
AAV3	398	FPSQMLRTGNNFQFSYTFEDVVPFHSSYAHSQSLDRLMNPLIDQYLYLNR	447
rh10	451	TQ-STGGTAGTQQLLFSQAGPNNMSAQAKNWLPGPCYRQQRVSTTLSQNN	499
AAV3	448	TQGTTSGETTNQSRLLFSQAGPQSMQLQARNWLPGPCYRQQRLSKTANDNN	497
rh10	500	NSNFAWTGATKYHLNGRDSLVPNGVAMATHKDDEERFFPSSGVL MFGKQG	549
AAV3	498	NSNFPWTAASKYHLNGRDSLVPNGPAMASHKDDEEKFFPMHG NLI FGKEG	547
rh10	550	AGKDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQQQNAAPIVGAVN	599
AAV3	548	TTASNAELDNVMITDEEEIRTTNPVATEQYGTVANNLQSSNTAPT TGTVN	597
rh10	600	SQGALPGMVWQNRDVYLQGPWAKIPHTDGNFHPSPLMGGFGLKHPPPQI	649
AAV3	598	HQGALPGMVWQDRDVYLQGPWAKIPHTDGHFHPSPLMGGFGLKHPPPQI	647
rh10	650	LIKNTVPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENS KRWNP	699
AAV3	648	MIKNTVPVPANPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENS KRWNP	697
rh10	700	EIQYTSNYYKSTNVDFAVNTDGTSEPRPIGTRYLTRNL	738
AAV3	698	EIQYTSNYSKSVNVDFVTDTNGVYSEPRPIGTRYLTRNL	736

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Pairwise sequence alignment of rh10 and AAV7 using EMBOSS Needle:

```
#####
# Program: needle
# Rundate: Fri 15 Nov 2024 23:33:42
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20241115-233337-0776-26048654-plm.asequence
#   -bsequence emboss_needle-I20241115-233337-0776-26048654-plm.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#=====
#
# Aligned_sequences: 2
# 1: rh10
# 2: AAV7
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 739
# Identity:      655/739 (88.6%)
# Similarity:    692/739 (93.6%)
# Gaps:          3/739 ( 0.4%)
# Score: 3578.0
#
#
#=====

rh10          1 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGY      50
               |||
AAV7          1 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRGLVLPGY      50

rh10          51 KYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEF    100
               |||
AAV7          51 KYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEF    100

rh10          101 QERLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEPSP    150
               |||
AAV7          101 QERLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPAKKRPVEPSP    150

rh10          151 QRSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVDPDPQPIGEPPAGPSGLG    200
               |||
AAV7          151 QRSPDSSTGIGKKGQQPARKRLNFGQTGDSESVDPDPQPLGEPPAAPSSVG    200
```

rh10	201	SGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTSTRTWAL	250
		: :	
AAV7	201	SGTVAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTSTRTWAL	250
rh10	251	PTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQ	300
		:..:	
AAV7	251	PTYNNHLYKQISSETA-GSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQ	299
rh10	301	RLINNNWGFPRKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSE	350
		: . .:. :	
AAV7	300	RLINNNWGFPRPKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDE	349
rh10	351	YQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEY	400
		:	
AAV7	350	YQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQSVGRSSFYCLEY	399
rh10	401	FPSQMLRTGNNFEFSYQFEDVPFHSSYAHSQSLDRLMNPLIDQYLYLSR	450
		. :	
AAV7	400	FPSQMLRTGNNFEFSYSFEDVPFHSSYAHSQSLDRLMNPLIDQYLYLAR	449
rh10	451	TQST-GGTAGTQQLLFSQAGPNNMSAQAKNWLPGPCYRQQRVSTTLSQNN	499
		. .:.	
AAV7	450	TQSNPGGTAGNRELQFYQGGPSTMAEQAKNWLPGPCFRQQRVSKTLDQNN	499
rh10	500	NSNFAWTGATKYHLNGRDSLVPNGVAMATHKDDEERFFPSSGVLFGKQG	549
		: : : .	
AAV7	500	NSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDEDRFFPSSGVLIFGKTG	549
rh10	550	AGKDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQQQNAAPIVGAVN	599
		..::: : : : : : : : : : : : : : : : :	
AAV7	550	A-TNKTTLENVLMTNEEEIRPTNPVATEEYGIVSSNLQAANTAAQTQVVN	598
rh10	600	SQGALPGMVWQNRDVYLQGPWAKIPHTDGNFHPSPLMGGFGLKHPPPQI	649
		:	
AAV7	599	NQGALPGMVWQNRDVYLQGPWAKIPHTDGNFHPSPLMGGFGLKHPPPQI	648
rh10	650	LIKNTVPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSQRWNP	699
		: .. : . .	
AAV7	649	LIKNTVPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSQRWNP	698
rh10	700	EIQYTSNYYKSTNVDFAVNTDGTSEPRPIGTRYLTRNL	738
		: . . . : . .	
AAV7	699	EIQYTSNFEKQGTGVDFAVDSQGVYSEPRPIGTRYLTRNL	737

#-----
#-----

Pairwise sequence alignment of rh10 and AAV8 using EMBOSS Needle:

```
#####
# Program: needle
# Rundate: Mon 18 Nov 2024 04:56:18
# Commandline: needle
#   -auto
#   -stdout
#   -asequence emboss_needle-I20241118-045614-0421-63917963-plm.asequence
#   -bsequence emboss_needle-I20241118-045614-0421-63917963-plm.bsequence
#   -datafile EBLOSUM62
#   -gapopen 10.0
#   -gapextend 0.5
#   -endopen 10.0
#   -endextend 0.5
#   -aformat3 pair
#   -sprotein1
#   -sprotein2
# Align_format: pair
# Report_file: stdout
#####

#=====
#
# Aligned_sequences: 2
# 1: rh10
# 2: AAV8
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 738
# Identity:      690/738 (93.5%)
# Similarity:    713/738 (96.6%)
# Gaps:          0/738 ( 0.0%)
# Score: 3795.0
#
#
#=====

rh10          1 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGY      50
               |||
AAV8          1 MAADGYLPDWLEDNLSEGIREWWALKPGAPKPKANQQKQDDGRGLVLPGY      50
               |||

rh10          51 KYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEF    100
               |||
AAV8          51 KYLGPFNGLDKGEPVNAADAAALEHDKAYDQQLQAGDNPYLRYNHADAEF    100
               |||

rh10          101 QERLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEPSP    150
               |||
AAV8          101 QERLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKTAPGKKRPVEPSP    150
               |||

rh10          151 QRSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVDPDPQPIGEPPAGPSGLG    200
               |||
AAV8          151 QRSPDSSTGIGKKGQQPARKRLNFGQTGDSESVDPDPQPLGEPPAAPSGVG    200
               |||
```

rh10	201	SGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTSTRTWAL	250
AAV8	201	PNTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTSTRTWAL	250
rh10	251	PTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQ	300
AAV8	251	PTYNNHLYKQISNGTSGGATNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQ	300
rh10	301	RLINNNWGFPRKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSE	350
AAV8	301	RLINNNWGFPRKRLSFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSE	350
rh10	351	YQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEY	400
AAV8	351	YQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEY	400
rh10	401	FPSQMLRTGNNFEFSYQFEDVVPFHSSYAHSQSLDRLMNPLIDQYLYLSR	450
AAV8	401	FPSQMLRTGNNFQFTYTFEDVVPFHSSYAHSQSLDRLMNPLIDQYLYLSR	450
rh10	451	TQSTGGTAGTQQLLFSQAGPNNMSAQAKNWLPGPCYRQQRVSTTLSQNNN	500
AAV8	451	TQTTGGTANTQTLGFSQGGPNTMANQAKNWLPGPCYRQQRVSTTTGQNNN	500
rh10	501	SNFAWTGATKYHLNGRDSLVPNGVAMATHKDDEERFFPSSGVLMMFGKQGA	550
AAV8	501	SNFAWTAGTKYHLNGRNSLANPGIAMATHKDDEERFFPSNGILIFGKQNA	550
rh10	551	GKDNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQQQNAAPIVGAVNS	600
AAV8	551	ARDNADYSDVMLTSEEEIKTTNPVATEEYGIVADNLQQQNTAPQIGTVNS	600
rh10	601	QGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQIL	650
AAV8	601	QGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQIL	650
rh10	651	IKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSkrwnPE	700
AAV8	651	IKNTPVPADPPTTFNQSKLNSFITQYSTGQVSVEIEWELQKENSkrwnPE	700
rh10	701	IQYTSNYYKSTNVDFAVNTDGTysePRPIGTRYLTRNL	738
AAV8	701	IQYTSNYYKSTSVDFAVNTEGVysePRPIGTRYLTRNL	738

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