

Figure 1

CLUSTAL O(1.2.4) multiple sequence alignment

ctg9-2-a	MKISVETISREMIKPSTPTPNHLRHYHFSYLDQTAPLYMSLLYFYHLDDHKLVSNNHHL	60
ctg9-1-c	MKIDVETISREMIKPSTPTPNHLRHYQFSLHDQIGPPFYISLLYFYHLDDDKLVSNNRHL	60
ctg9-1-a	MKIDVETISREMIKPSTPTPNHLRHYQFSLHDQIGPPFYISLLYFYHLDDDKLVSNNRHL ***.*****.***.***.***.***.*****.*****.***	60
ctg9-2-a	FINSLKSSLSNVLTKEYPLAGRVKNYVDCNDEGVVFSGAKVSCLLSEIINE--LPSEFN	118
ctg9-1-c	FSDSLKSSLSNVLTKEYPLAGRIKNYVDCNDEGVVFSEAKVSCQLSEIINEPEFPSEFK	120
ctg9-1-a	FSDSLKSSLSNVLTKEYPLAGRIKNYVDCNDEGVVFSEAKVSCQLSEIINEPEFPSEFK * :*****.*****.*** ***** ***** :****:	120
ctg9-2-a	KLHPFDQEKDVVSINGLPIAIQVNMFCNCGSVAIAVMI FK HKIADAASLITFTKNWAAAARG	178
ctg9-1-c	KLLPFDQEKDVVSFDSLAI AI QVNMFCNCGNAVAVMI SH KIADGSSLSTFTKNWAAAARG	180
ctg9-1-a	KLLPFDQEKDVVSFDSLAI AI QVNMFCNCGNAVAVMI SH KIADGSSLSTFTKNWAAAARG ** *****.:. * *****.***.*** *****.:. * *****	180
ctg9-2-a	GSGNVFPFVAARLFPQDAGGSGSVSDPRPKKIVLKKFLFEGPKITALRDKYGLDNGI	238
ctg9-1-c	ESENVFPFVAARLFPEDAGGSGTSFDPKPKVVLKKFLFEGSKITALRDKYGFNDRI	240
ctg9-1-a	ESENVFPFVAARLFPEDAGGSGTSFDPKPKVVLKKFLFEGSKITALRDKYGFNDRI * *****.***.***.***.*****.***** *****.*** *	240
ctg9-2-a	YPTRVEALS AF IWSRLAASTRIKISPERPYMLVHLVNLKRKRMEPPLPDDSGFNGI I GA AVT	298
ctg9-1-c	YPTRVEALS AF LWSRLAASNRIKVSSE RP CM LI HAVNLRKR VE PQLPADSFGNLF AF AVT	300
ctg9-1-a	YPTRVEALS AF LWSRLAASNRIKVSSE RP CM LI HAVNLRKR VE PQLPADSFGNLF AF AVT *****.*****.***.*** *****.*** *****.*** *****.:. ***	300
ctg9-2-a	VLEND DD DRMVNKF RA ICKVDKDYLKVMKLEHSEL TD LVI T NGEIVDRGELGYCFFSS	358
ctg9-1-c	VLDEND--DGMVNK FR DAISKIDKDYLKAKKVEHSEL IDL GIN GE KFGGELGYCIISS	359
ctg9-1-a	VLDEND--DGMVNK FR DAISKIDKDYLKAKKVEHSEL IDL GIN GE KFGGELGYCIISS ***.*** *****.***.*****.*** ***** ***** . *****.***	359
ctg9-2-a	LCKFPVYEAD F GLGKPMWVWAGRLPYKNI I HLIDTKSGDGE IA W I HLEEEVMAK F GN DQ E	418
ctg9-1-c	LCKFPVYEAD F GLGKPTWVWAGCFPYKNV I HFIDAKSGDGEV V W H LEKEVMAK F END Q E	419
ctg9-1-a	LCKFPVYEAD F WLGKPTWVWAGCFPYKNV I HFIDAKSGDGEV V W H LEKEVMAK F END Q E ***** ***** ***** :****.***.***.*****.***.*** ***** *****	419
ctg9-2-a	LLAYVSP 425	
ctg9-1-c	LLAYVST 426	
ctg9-1-a	LLAYVST 426 *****	

Figure 2

>AAT9-1-c

ATGAAAATCGATGTTGAAACAATCTCTAGAGAAATGATCAAACCATCAACTCCTACCCCAAACACCTTCGCCA
TTACCAATTTTCCCATCTTGATCAAATTGGTCCACCATTTTATATTTCTTTACTATACTTCTATCATCTTGATGATG
ACAAACTTGTTAGCAACAACCGCCACCTATTTAGCGACTCTCTTAAATCATCATTGTCCAATGTGCTAACCAAGT
ACTATCCTTTAGCCGGACGCATCAAGAACAACCTACGTAGATTGCAATGATGAGGGAGTCTTTTTCTCGGAGGCT
AAAGTCAGTTGCCAACTTTCCGAAATCATCAATGAACCTGAATTTCCAAGCGAGTTCAAAAACTTCTCCCATTT
GATCAGGAAAAAGATGTTGTTAGTTTCGATAGTTTAGCCATTGCTATTCAGGTTAACATGTTCAACTGTGGCAA
TG TAGCTGTTGCTGTGATGATTTCTCACAAGATAGCAGATGGTTCGTCTTTGAGCACGTTTACCAAAAACTGGG
CTGCTGCTGCTCGTGGCGAGAGTGAAAATGTTTTCCGGAGTTTGTGGCCGCCAGGCTCTTTCCCCCGAGGAT
GCAGGAGGCGGCTCCGGAACGAGTTTCGATCCTAGGCCAAAGAAAGTTGTGTTGAAGAAATTTCTATTTGAG
GGGTCTAAGATAACTGCTCTTAGAGACAAATATGGGTTTCGACAACAGGATATATCCAACCCGTGTTGAGGCAT
TGTCAGCTTTTTTATGGAGTCGTCTTGCTGCTTCAACCGTATCAAGGTTAGTTCTGAAAGACCTTGTATGCTGA
TCCATGCAGTGAATTTGCGTAAGAGGGTGGAACACAGCTGCCAGCCGATTCTTTGGGAATCTCTTGCATTT
GCTGTGACAGTTTTAGATGAAAATGATGATGATGGAATGGTAAACAAGTTCAGAGACGCTATAAGCAAATA
GACAAGGACTATCTGAAAGCAAAGAAGGTCGAACACTCAGAACTCATAGACTTGGGCATAACGAATGGTGAA
AAATTTGGCGGAGGAGAATTGGGTTATTGCATCATCTCAAGTTTATGTAAGTTTCCTGTTTATGAAGCAGACTT
TGGGTTGGGGAAGCCTACTTGGGTTGCTTGGGTTGTTTTCTTATAAGAACGTAATTCATTTATTGACGCCA
AATCTGGAGATGGAATTGAGGTATGGGTTCACTTGGAGAAAGAAGTTATGGCCAAATTCGAAAATGACCAGG
AACTACTTGCTTATGTTTCACTTAG

>AAT9-1-c

MKIDVETISREMIKPSTPTPNHLRHYQFSHLDQIGPPFYISLLYFYHLDDDKLVSNNRHLFSDSLKSSLSNVLTKEYPLA
GRIKNNYVDCNDEGVFFSEAKVSCQLSEIINEPEFPSEFKLLPFDQEKDVVSFDSLAIQVNMFNCGNVAVAVMIS
HKIADGSSLSTFTKNWAAAARGESENVFPEFVAARLFPPEDAGGSGTSFDPKPKVVLKKFLFEGSKITALRDKYGF
DNRIYPTREALS AFLWSRLAASNRIKVSSERPCMLIHAVNLRKRVEPQLPADSFGNLF AFAVTVLDENDDGMVN
KFRDAISKIDKDYLKAKKVEHSELIDLGITNGEKFGGGELGYCISSLCKFPVYEADFGLGKPTWVAWGCFYPYKNVIHFI
DAKSGDGIEVWVHLEKEVMAKFENDQELLAYVST

Figure 3

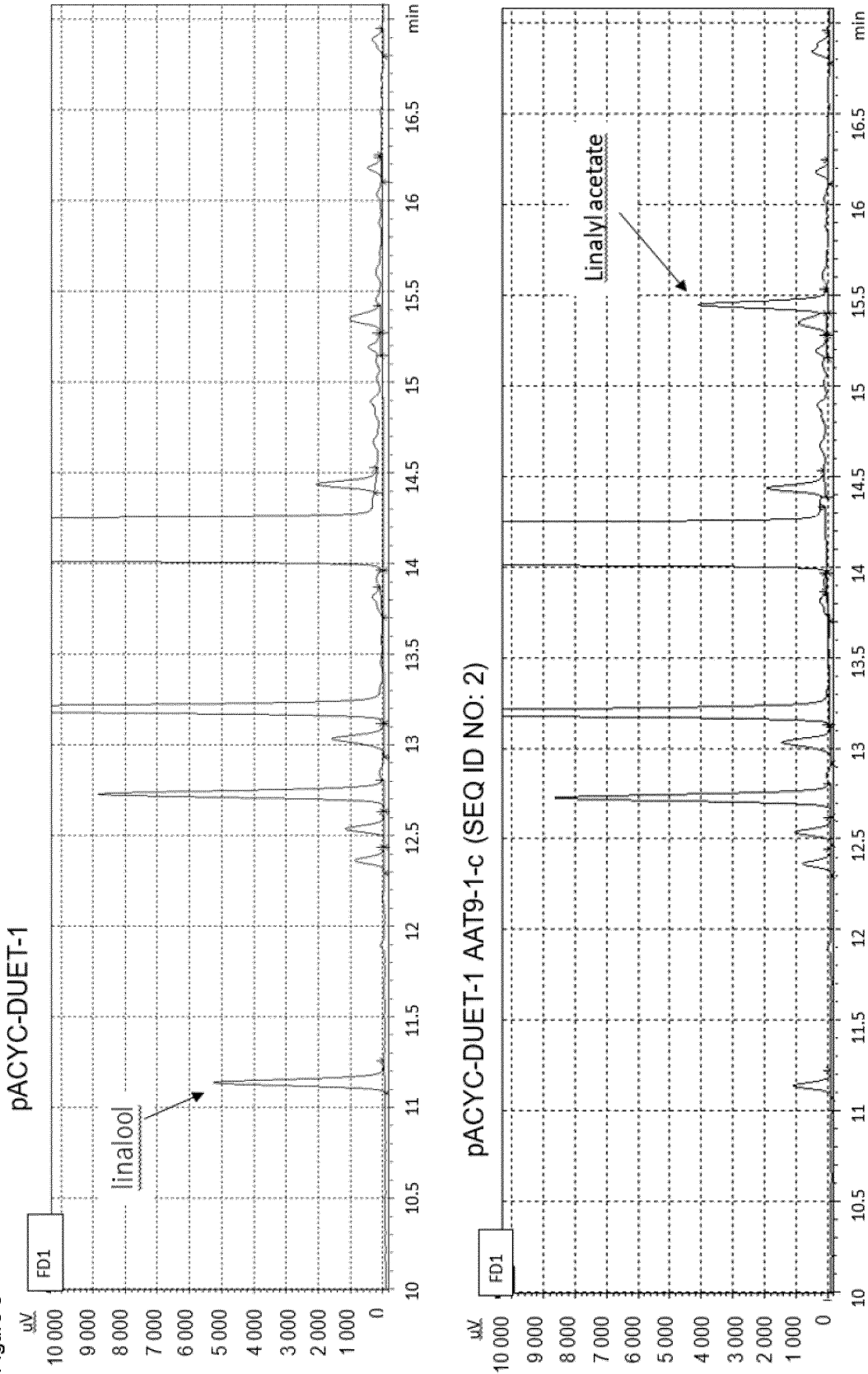


Figure 4 (cont.)

Figure 5

CLUSTAL O(1.2.4) multiple sequence alignment

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AAT9-1-c      10      20      30      40      50      60      70
10056      MKIDVETISREMIKPSPTPNHLRHYQFSLDDQICPPFYISLLYFYHLDLDDKLVSNRHLFSDSLKSSLS
1461      MEIETRIVISTEIIKPSSPTPKFLQNHRLSELDQIAPPFMPVVFYVESN.TKFPNSQQ...SNHLKNSLS
Consensus  M IE E IS E IKPSSPTP LR LSFLDQI PPFIPL YFY D K VN SD LK SLS

AAT9-1-c      80      90      100     110     120     130     140
10056      NVLTKEFYPLAGRLVGNLYVDCDDGCVFVEAEANFDLSQIITNP.NPRNMSKFLPYNES....HDFCM
1461      DALAKFYPLAGRMKGQISVDCNDQGVLCTEAIANANVLDIVSSE.DPLVLDKLIPIYVTN.GFYSSAQEQL
Consensus  VLTKFYPLAGR KGN YVDCND GV F EA AN LS II P P KLLPY VS

AAT9-1-c      150     160     170     180     190     200     210
10056      AIQVNMFCNNVAVAVMISHKIADCSSELTETKNFAAAH.GESEN.VFPEFVAARLEPPED...AGGG
1461      AVQATYFRCCGVAVGLLVSHKIADALSFFLFANFSAVARSGEGGGGQPPKFDVATYFPPRD...ISG.
Consensus  AIQ T FNCGGVAVG SHKIADASSLS F K WAA AR GE V P F ATLFPPRD G

AAT9-1-c      220     230     240     250     260     270     280
10056      SGTSPDPRPKKVLKKFLFEGSKITALRDKYGFDN.....RIYPTRVEALSAFILSRLAASNRIKVS
1461      YEPSTGIMKEEITTRIFTSDKKHVLREKYAATGSGGDGLPQRRPTRVEALSAFILTRFINSTGVKSD
Consensus  TSPSVRLAPNLVIKRFLESSQSNAMKLEVSRSR.....ILNPTRVEVVLTALINRCVVAKGIERS
PS P V K FLFS KI ALR KY PTRVEALSAFIW R S GIK S

AAT9-1-c      290     300     310     320     330     340     350
10056      SERPCMLIHAVNLRKRVEPGLPADSFGNLFAFAVTVLDENDD...DG...MVNKFRLAIS..KIDKDYLK
1461      PNKIYTMHAVNLRITHTDPLTEYHFGNISRLAIANPDVGESGVTGGVELMQRVREAIK..AVDGAYVA
Consensus  NRS..VAYHTLNLRG.KIPALSERSEGNLFQMIKVESEAETT....WILLVEKLRSAFEGFDVKKQLLG
HAVNLR R P L E SFGNLF A D DG LV K R AI VDK YL

AAT9-1-c      360     370     380     390     400     410     420
10056      AKKVHSELIDLGITNGEKFGGGELGYCIISSLCFFPVYADFCGLKFTLVAVWGCFFPYKNVIHFIDAK.S
1461      DLK.GGEKHLSLMREKMAQANKGELVSEFTSLCRFPVLYADFCGCKPVVVGSAFAVKNLVTFMDTR.D
Consensus  EKGFENAKENFMETISQLLRAG..NVEVERFSSYCRNAVYADFCGCKPVVVSNSCYRNKNCVFLFDSVGS
KK E K L I AG GEL F FSSLCRFPVYADFGWGKPVVW CF YKN V F D S

AAT9-1-c      430     440     450
10056      GDGIEVIVHLEKEVMKKFENDQBELAYVST.....
1461      GDGIEAVIHSRREDMEKFEVDLELQDFLSHDKSSLISLV
Consensus  RGGIEAVIVMSERDMERLEODLEFKRFASF.....
GDGIEAVIH EDMKFE DLEL F S

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☐ non-conserved
☒ ≥ 50% conserved
☒ all match

Figure 6

