

Supplemental Figure 1

zAe3	M-----	-----GRSYNEKDFEYHRHTFHHTHHPSTHLP--QFRKRVLSMDRRRKRKRKKKKTSMPPS	58
hbAe3	MANGVIPPGGASPLPQVRVPLEEPPLSPDVEEEDDLGKTLAVSRFGDLISKPPAWDPEKPSRSYSERDFEFHRHTSHHTHHPSTHLP--QFRKRVLSMDRRRKRKRKKKKTSMPPS	120	
rbAe3	MANGVIPPGGASPLPQVRVPLEEPPLSPDVEEEDDLGKTLAVSRFGDLISKTPAWDPEKPSRSYSERDFEFHRHTSHHTHHPSTHLP--QFRKRVLSMDRRRKRKRKKKKTSMPPS	120	
zAe3	DVTPTIHE-----VDEEFAESEIFGQCQAATPTTP----SEELPQLSLGSEEDLAADLPLSSFHMESERPASSEETLPSASMEEKEETQQPPDGGEHKDIS---NSFSPSPEAASMTTR	166	
hbAe3	EGTPPIQEEGGAGVDEEEEEEEEEEGESHAEPVPPPPSGTPQKAKFSIGSDED---DSP-----GLPGRAAV-----TKPLPSVGPHTDKSPQHSSSSSSPRARASRLA	216	
rbAe3	EGTPPIQEEGGAGVDEEEEEEEEEEGESHAEPVPPPPSGTPQKAKFSIGSDED---DSP-----GLS IKAP-----AKALPSVGLPSDQSPQRSGSSSPRARASRLA	216	
zAe3	GWFRKPVHRLAGAQRTSYDLRERICIGSMTAMETAVYQKVPTDEAEAQMLASADLDDMKSHRFEDNPGVRRHLVKKSSRCQLPRSSN--GSPPLSSLKRRKRMDKKTHEVFVELNELIV	284	
hbAe3	GEKSRP-----WSPSASYDLRERLCPGSALGNPGGPEQVPTDEAEAQMLGASADLDDMKSHRLEDNPGVRRHLVKKPSRTQGGRGSPSGLAPILRRRKRKKKLDKRRPHEVFVELNELML	330	
rbAe3	TEKSRP-----WSPSASYDLRERLCPGSALGNPG-PEQRVPTDEAEAQMLGASADLDDMKSHRLEDNPGVRRHLVKKPSRIQGGRGSPSGLAPILRRRKRKKKLDKRRPHEVFVELNELML	329	
zAe3	DKNQEMRWKERARWIKFEDVEEETDRWGKPHVASLSFRSLELRRTITHGAIMLDDQSTLPGIAHLMVETMISDQIRAEDRANVLRALLKHSHPNDEKE-GLFHRNHSVTSLSGFR	403	
hbAe3	DRSQEPHWRETARWIKFEDVEEETDRWGKPHVASLSFRSLELRRTIAHGAALLDLEQTTLPGIAHLMVETMIVSDQIRPEDRASVLRLLLLKHSHPNDDKDSGFFPRNPSSSSMNSVL	450	
rbAe3	DRSQEPHWRETARWIKFEDVEEETDRWGKPHVASLSFRSLELRRTIAQGAALLDLEQTTLPGIAHLMVETMIVSDQIRPEDRASVLRLLLLKHSHPNDDKDSGFFPRNPSSSSVNSVL	449	
zAe3	HNHN----HVHDTSLPLVSQDHEEMHDSKAAEHD-KEKSLHPIPAEGHAASRSKLLAKIPKDAEATVVLVGVVEFLEKPAAMAFVRLNESILLESILEVVPPIRFIVVLLGPTQTNDVYH	518	
hbAe3	GNHHPTPSHGPDGAVPTMADDLGEPAPLWPHDPDAKEKPLHMPGGDGRGK-SLKLEKIPEDAETVVLVGVVPFLEQPAAAFVRLNEAVLLESVLEVPVVRFLFVMLGPSHTSTDYH	569	
rbAe3	GNHHPTPSHGPDGAVPTMADDLGEPAPLWPHDPDAKEKPLHMPGGDGRGK-SLKLEKIPEDAETVVLVGVVPFLEQPAAAFVRLSEAVLLESVLEVPVVRFLFVMLGPSHTSTDYH	568	
zAe3	EIGRSFSTLMSDKNFHEVAYFADDRQDLLNGINEFLDCSIVIPPSDVEGKDLLKTVASFQKQMLRKRKERELKCASTVTGALET-KDVNIEEQEEDQFDVDPDKRSVIPFGGLIHD	637	
hbAe3	ELGRSIATLMSDKLFHEAAYQADDRQDLLSAISEFLDGSIVIPSEVEGRDLLRSVAAFQRELLRKRREREQTKVEMTRGGYTAPGKELSLELGGSEATPEDDPLLRGTSVFGGLVRDV	689	
rbAe3	ELGRSIATLMSDKLFHEAAYQADDRQDLLGAISEFLDGSIVIPSEVEGRDLLRSVAAFQRELLRKRREREQTKVEMTRGGYVAPGKELSLEMGGSEATSEDDPLQRTGTSVFGGLVRDV	688	
zAe3	RRRYPRYISDLKDALDTCIAAVFIYFAALSPTITFGGLGKTEQGMGVSELIISTATVGVLFSLLAGOPLLIIGFSGPLLVEEAFYKFCQAQGFYLTGRVWIGFWLIFIVLVIVA	757	
hbAe3	RRRYPHYPSDLRDALHSQVAAVLFYFAALSPTITFGGLGKTEGLMGVSELIVSTAVLGVLFSLLAGOPLLVVGFSGPLLVEEAFYKFCRAQDLEYLTGRVWVGLVWVFLALVA	809	
rbAe3	KRRYPHYPSDLRDALHSQVAAVLFYFAALSPTITFGGLGKTEGLMGVSELIVSTAVLGVLFSLLAGOPLLVVGFSGPLLVEEAFYKFCRAQDLEYLTGRVWVGLVWVFLALVA	808	
zAe3	AEGSFLVRYISPFTQEIFAFLISLIFIYETFSKLIKVFQEHPLMMSYT-SAAFKHSQDQSSVIGEPI-----LNQPNTALLSMVLMGTFFTAFFLRKLNRNRFLLGGKVRVIGD	867	
hbAe3	AEGSFLVRYISPFTQEIFAFLISLIFIYETFYKLYKVFTEHPLLPFYPPPEGALEGLDAGLEPNGSALPPTTEGPPSPRNQPNTALLSLILMLGTFFFIAFFLRKFRNSRFLGGKARRIIGD	929	
rbAe3	AEGSFLVRYISPFTQEIFAFLISLIFIYETFFKLYKVFTEHPLLPFYPPPEEAE-----PGLLELNSALPPTTEGPPGPRNQPNTALLSLILMLGTFLLIAFFLRKFRNSRFLGGKARRVIGD	924	
zAe3	FGIPISILISVLVDILIPDTYTQKLNVPSSGFSVTSPPDKRGWFI SPPGDKQFPVWMMGASVIPALLVFLIFMETQITTLIVSKKERRLMKSGGFHLDLLIVTLGAIPLFGLPWLTA	987	
hbAe3	FGIPISILVMVLVDYSITDITYTQKLTVPGLSVTSPDKRSWFI PPLGSRPFPVWMMVAAVALLVLLIFMETQITLIVSQKARRLLKSGGFHLDLLIGSLGGLGLFGLPWLTA	1049	
rbAe3	FGIPISILVMVLVDYSITDITYTQKLTVPGLSVTSPHKRTWFI PPLGSRPFPVWMMVAAVALLVLLIFMETQITLIVSQKARRLLKSGGFHLDLLIGSLGGLGLFGLPWLTA	1044	
zAe3	TVRSVTHVNALTVMSKATAPGEKPMIQEVKEQRVTGMQVAILVGLSIVMTDVLRHIPLAVLFGIFLYMGITSLTGIQLYERITLMTVPKAKHHPDHVYTKVKTWRMMFTVIQLLCIVLL	1107	
hbAe3	TVRSVTHVNALTVMRTAIAPGDKPQIQEVREQRVTGVLIASLVGLSIVMGAVLRRIPLAVLFGIFLYMGVTSLSGIQLSQRLLLILMPAKHHPDQPYVTKVKTWRMHLFTCIQLGCIALL	1169	
rbAe3	TVRSVTHVNALTVMRTAIAPGDKPQIQEVREQRVTGVLIASLVGLSIVMGAVLRRIPLAVLFGIFLYMGVTSLSGIQLSQRLLLIFMPAKHHPDQPYVTKVKTWRMHLFTFIQLGCIALL	1164	
zAe3	WVKSTVASLAFPPFILIMTVPLRRLILTRIFEERELAALDADESPNFDEDGRDEYNEIHMLV	1170	
hbAe3	WVKSTAASLAFPPFLLLTVPLRRCLLPRLFQDRELQALDSEDAEPNFDEDGQDEYNEIHMPV	1232	
rbAe3	WVKSTVASLAFPPFLLLTVPLRRCLLPRLFQDRELQALDSEDAEPNFDEDGQDEYNEIHMPV	1227	