

**CRY2** 1 MAATVATAAAVAPAPAPGCTDSASSVHWFR---KGLRL----HNPALLAAV-RGARCRC-----  
**SPATA31A1** 166 PQAKHPQDLASTPSEPEMTTSVSSLSASQPPPEPSLPLEHPSPEPPALFPHPFHTPDPACSPPPPKGFTA

**CRY2** 53 ----VYIDWFAASSVGNRWRFLQSLLEDLDTSLRKNSRLFVIRGQPADVFPRLFKEWGVTRL-T  
**SPATA31A1** 237 PPLRDSTLITPSHCDSVALPAGTVFQSLSPHEDLVASIPALIS----GLGGNSH--VSASSRWQETARTS

**CRY2** 117 FEYDS-----EPEGKERDAAIK-M--AKEACVEVVTENSHTLYDLDRILELNGQKPLTYKR  
**SPATA31A1** 307 CAENSSVQDHLRHPPEYQMEAGSLFLSSDCQNAVGIQVTEAKVNIWEKEN-----

**CRY2** 172 FQAIISRMELEKPKVGLVTSQQMESCRAEIQENHDETYGVFS-----LEELGFTEGLGPAVWGGGETE  
**SPATA31A1** 377 VGSFTDRMT-PEKHINSI-----RNLAKSI DAEQDTTNPKEFWNMGENSKQIPGQKLSDEPRLWQESFWK

**CRY2** 236 ALARL-----DKHLERKAWVANYERPRMNANSLLASPIGTSFYLRFGCISCRLFYRLWDLYKKIKR  
**SPATA31A1** 447 NYSQIFWGLPSLHSESLVANAWVTDRSYTLQSPPELFNEMSNVCEIQRETTISPLIFQAQPPSH---LGP

**EBV-BPLF1** 451 VPPHRPPSAARLPPVPIPIHQSPPASPTPHAPVSTIAPSVTPSERLPLQIETPLPQAAPSNPKIPLTTPSEPTAAAPPTTTLSPP  
**SPATA31A1** 166 -----PQAKHPQDLASTPSEPEMTTSVSSLSASQPPPEPSLPLEHPSPEPPALFPHPF----PHLEDELACSEFPKGFMAP

**EBV-BPLF1** 541 TQQQPQQAAPAPSPLEPQQQPTPSAAPAPSPLLPQQQPPPSAARAPSPLEPQQQPLPSATPAPPPAQQLPSPAITLEPEKNPPAADRA  
**SPATA31A1** 256 LRDSTLIIPSHCDVALPLG-----TVFQSLSPHEDLVASVVP-----AISGLGGNSHVSASSRW

**EBV-BPLF1** 631 GTEISPPPEGQPSFGDDASGGGLVRMLSLLEEFILSMDSSEETESDASDIPTTEDEDMPEDEVFNSLSLESGSSAPTSPITLDTARS  
**SPATA31A1** 356 QETARTSCAFN--SSVQDHLRHPPEYQMEAGSLFLSSD---CQNAVGIQVTEAKVNIWEKENVGSFT-----