Residue # 1 11 21 31 41 51 61 71 81 91

Consensus m e v l y s l s - - - k t l k d a r d k i v e g t l y s n v s d l i q q f n q m i v t m n g n d f q t g g i g n l p i r n w t f d f g l l g t t l l n l d a n y v e n a r t t i e y fi d f i d a v c m

Conservation

RV Group A [subgroup I]	MDVLYSLS - - - KTLKDARDKIVEGTLYSNVSDLIQQFNQMIITMNGNEFQTGGIGNLPIRNWNFDFGLLGTTLLNLDANYVETARNTIDYFVDFVDNVCM
RV Group A [subgroup II]	MEVLYSLS - - - KTLKDARDKIVEGTLYSNVSDLIQQFNQMIVTMNGNDFQTGGIGNLPVRNWTFDFGLLGTTLLNLDANYVENARTTIEYFIDFIDNVCM
RV Group A [non-subgroup I & II]	MEVLYSLS - - - KTLKDARDKIVEGTLYSNVSDLIQQFNQMIVTMNGNDFQTGGIGNLPIRNWTFDFGLLGTTLLNLDANYVETARTTIEYFIDFIDNVCM
RV Group B	MDLIETVNACVKLQKRVLGLAPNTNLNTAGQSVLNDYNALASRVNGKTYALLNQI - AVYTPYTINAPIISLAVR - ISTDDYDDMRSGIESILDVLAAAIR
RV Group C	MEVLYSLS - - - KTLKDARDKIVEGTLYSNVSDLIQQFNQMIVTMNGNDFQTGGIGNLPIRNWTFDFGLLGTTLLNLDANYVENARTTIEYFIDFIDNVCM
RV Group D	MEALSSIA - - - LTVREAREKIINGTIYSNVSDVIQQFNQMVRVLNGSTFTTGGLATMPLREWTFDLPQLGTTLLNIDANYVESMTPTLDMLTEFVIAVCE
RV Group F	MEAIYSIA - - - RTIADAEEKIVVGTLFSNVQQIVMQMNEVIKVMNGSQFLTGGVGNMGVTQWTFNHGQLGVAPLYVDENYREELMQTINYYKRFVHAVCE
RV Group G	MDLIETVNAVVDLQKRIYELSSNTNLSSKGQQVVNDYNALASRVNGKTYALHDQT - AVLTPYIINMNLISISTR - ISTDDYEAMKEGMNGLLDVIAAAIR

Residue # 101 111 121 131 141 151 161 171 181 191

Consensus d e m a r e s q r n g i a - p q s e a l r k l s g i k f k r i n f d n s s e y i e n w n l q n r r q r t g - - - - - - - - - - - - - - f v f h k p n i f p y s a s i t l n r s q p a h d n l m g t r w l

Conservation

RV Group A [subgroup I]	DEMVRESQRNGIA - PQSDSLRKLSGIKFKRINFDNSSEYIENWNLQNRRQRTG - - - - - - - - - - - - - FTFHKPNIFPYSASFTLNRSQPAHDNLMGTMWL
RV Group A [subgroup II]	DEMARESQRNGVA - PQSEALRKLAGIKFKRINFDNSSEYIENWNLQNRRQRTG - - - - - - - - - - - - - FVFHKPNIFPYSASFTLNRSQPMHDNLMGTMWL
RV Group A [non-subgroup I & II]	DEMARESQRNGVA - PQSEALRKLAGIKFKRINFNNSSEYIENWNLQNRRQRTG - - - - - - - - - - - - - FVFHKPNIFPYSASFTLNRSQPMHDNLMGTMWL
RV Group B	TEGSRPTRVIERRVLEPNVKQLIDDLRLKSLVSDLSIANLAAVDT - - AMIQPEVIETENPLYADIIEQIVHRPNIGMTGGNIRAT - - - - - - - - - LGRWS
RV Group C	DEIARESQRNGIA - PQSEALRKLSGIKFKRINFDNSSDYIENWNLQNRRQRTG - - - - - - - - - - - - - FVFHKPNILPYSASFTLNRSQPAHDNLMGTMWI
RV Group D	TELLVDNNRNGAY - PQSEALRLLSNNKYVFLNMDLGSKYISEWHYRLSARDPM - - - - - - - - - - - - - FSNHVPYIFPYDMAIAYDRVTAAYDNVSGTRFA
RV Group F	TEMCLESQRGGAT - MQSAAMQALQTVKFKNLSYDYSENYIKQWALQKVRVRTA - - - - - - - - - - - - - YSSRNPYVVPELNTITYRRSQAAMDNVAGTRVM
RV Group G	TECSRRVRAIEQRVLEPVVKMLIEDIRLRAQVSKIAIANMSAYDT - - AKLEPQIVNIENPLRPGIVDDVLQRPNFTQRGGGIRYT - - - - - - - - - TGRWS

Residue # 201 211 221 231 241 251 261 271 281 291

Consensus n - a g s e i q v a g f d y s c a - n a p a n i q q f e h i v q l r r a l t t a t i t l l p d a e r f s f p r v i n s a d g a t t w f f n p v i l r p n - - n v e v e f l l n g q i i n t y q a r f g t

Conservation

RV Group A [subgroup I]	N - AGSEIQVAGFDYSCAINAPANTQQFEHIVQLRRVLTTATITLLPDAERFSFPRVINSADGATTWYFNPVILRPN - - NVEVEFLLNGQIINTYQARFGT
RV Group A [subgroup II]	N - AGSEIQVAGFDYSCAINAPANIQQFEHIVQLRRALTTATITLLPDAERFSFPRVINSADGATTWFFNPVILRPN - - NVEVEFLLNGQIINTYQARFGT
RV Group A [non-subgroup I & II]	N - AGSEIQVAGFDYSCALNAPANIQQFEHIVQLRRALTTATITLLPDAERFSFPRVINSADGATTWFFNPIILRPN - - NVEVEFLLNGQIINTYQARFGT
RV Group B	GNKGVVTCMSGMD - - - - - - - - - - - SEHRFTVELKTRTCGIINIVYIPTSGTILIPMPAGR - - NREGDLIDVSAEMMADDFAIDFMDDDNIIQTE - TGVGV
RV Group C	N - AGSEIQVAGFDYSCAFNAPANIQQFEHVVPLRRALTTATITLLPDAERFSFPRVINSADGTTTWYFNPVILRPS - - NVEVEFLLNGQIINTYQARFGT
RV Group D	S - LNNAIHFAAFDQDFVRGQPANARQFEYLYNLRTPVSNATIVIHPISDILSVPSMIRNQAATHYWPYNPYNIPTFRDDIRVEFQLAGQVIYVA - ANLGM
RV Group F	A - IGDTIKFAVFDQDFARTEPGQMWESNFEYNMPVPISDATIQVGTDASGLLNDQVLITNTYNTTWLYVPFQVPLT - - RFTIEFYNTGNLVYQIVA - PGM
RV Group G	GNKGIVTCVSGTD - - - - - - - - - - - GVHTIEIQLRTTLTGILNLLYVPAPGKIVQSRGRAQGVPVTLRCSDVSPDMARGDIVIEFLRNGAVVDAE - GGSGT

Residue # 301 311 321 331 341 351 361 371 381 391

Consensus i i a r n f d t i r l s f q l m r p p n - - - - - m t p a v a n l f p q a q p f - h h a t v g - l t l r i e s a v c e s v l a d - - - - a n e t l y a n v t a v r q e y a i p v g p v f p p g m n w t e

Conservation

RV Group A [subgroup I]	IIARNFDTIRLSFQLMRPPN - - - - - MTPTVAALFPNAQPFEHHATVG - LTLRIESAVCESVLAD - - - - ASETMLANVTSVRQEYAIPVGPVFPPDMNWTD
RV Group A [subgroup II]	IIARNFDTIRFIFQLMRPPN - - - - - MTPAVNALLPQAQPFQHHATVG - LTLRIESAVCESVLAD - - - - ANETLLANVTAVRQEYAIPVGPIFPPDMNWTE
RV Group A [non-subgroup I & II]	IVARNFDTIRLSFQLMRPPN - - - - - MTPAVNALFPQAQPFQHHATVG - LTLRIESAVCESVLAD - - - - ANETLLANVTAVRQEYAIPVGPVFPPGMNWTE
RV Group B	YSFPMCNRIRFRINPWNNQKDDDNLGTVHMVNWAQGTAP - - - KQPAISFMFETRRTFTEGDYQHLSRCAPKAQYMMDTQ - - - - - FNDVSFTNRPAVDWNI
RV Group C	IIARNFDTIRLSFQLVRPPN - - - - - MTPAVNLFPQAPPFIFHATVG - LTLRIESAVCESVLAD - - - - ASETLLANVTAVRQEYAIPVGPVFPPGMNWTE
RV Group D	HTIPQFDAVNIILTMRRLPL - - - - - - LADLQNIFPAGNPSATHQAVISTKIEVLNATTETTVPS - - - - INEHLYALIVGTRGRYQMQAGPVFPPGMRWDD
RV Group F	HCVPTFNSIIFRLRIVRPAV - - - - - LSQQLQQYFPAQNPGNVHATVV - ISLQIKSCVTDVVLAD - - - - PDSTHYARITNVRTLYGIPVGPVFPPNMAWDT
RV Group G	FQFTQCDTIRIRVEPWSIVKNLN - - PTPDFANWNQNQAN - - - SQPTVLIMFEIRQAYTQLENDEMSADAPKVQYYLDTI - - - - - FTQDSFVRHPNVLWRT

Figure S1. Alignment of group A and non-group A rotavirus VP6 sequences showing conservation of the negatively-charged surface electrostatic potential in the VP6 trimer. Alignment of representative sequences from group A and non-group A rotavirus VP6 sequences (specific strains are shown in table below) was performed using ClustalW2, the multiple sequence alignement computer program. Numbers at the top indicate the residue number. Small letters represent 1-letter residue abbreviations of the consensus VP6 sequence based on the aligned representative VP6 sequences. The gray bar graphs represent identity histograms showing conservation levels of individual residues at each position. The dashes within the sequences indicate absence of residues from the specific strain sequences accessed from Genbank. Residues below the solid black line indicate those that are shown to contribute to the negatively-charged electrostatic patch within the VP6 trimers.