Supplementary Information

Plasmodium vivax ligand-receptor interaction: *Pv*AMA-1 domain I contains the minimal regions for specific interaction with CD71^{+} reticulocytes

Gabriela Arévalo-Pinzón [1, 2, +], Maritza Bermúdez [1, 3, +], Diana Hernández [1], Hernando Curtidor [1, 4], Manuel Alfonso Patarroyo [1, 4 *]

[1] Fundación Instituto de Inmunología de Colombia (FIDIC), Carrera 50 # 26-20, Bogotá, Colombia.

[2] PhD Program in Biomedical and Biological Sciences, Universidad del Rosario, Carrera 24 # 63C-69, Bogotá, Colombia.

[3] MSc Program in Biological Sciences, Pontificia Universidad Javeriana, Carrera 7 # 40-62, Bogotá, Colombia.

[4] School of Medicine and Health Sciences, Universidad del Rosario, Carrera 24 # 63C-69, Bogotá, Colombia.

+Equal contributors

Supplementary Table S1. A list of the primers used for amplifying *Pv*AMA-1 fragments. The restriction sites for each one are highlighted in bold.

Recombinant fragments	Primers	Used	Sequence
*Pv*AMA1	Ectodo 1	Heterologous Expression (*E. coli*)	5'-CG**G GAT CC**C CTA CCG TTG AGA GAA GCA-3'
	Ectodo 2		5'-ACG C**GT CGA C**TA GTA GCA TCT GCT TGT TCG-3'
*Pv*DI-II	Ectodo 1		5'-CG**G GAT CC**C CTA CCG TTG AGA GAA GCA-3'
	DI-DIIR		5'-ACG C**GT CGAC** TTA CTC CAG GTC TAC TTC TTG-3'
*Pv*DII-DIII	DII-DIIIF		5'-CG**G GAT CC**C GTA AAA ATT TAG GAA ACG CC-3'
	Ectodo 2		5'-ACG C**GT CGA C**TA GTA GCA TCT GCT TGT TCG-3'
*Pv*AMA1	AMA-1Cos-7F	Expression on COS7 cells	5'-GAA **TTT AAA** CCTA CCG TTG AGA GAA GC-3'
	AMA-1Cos-7R		5'-GAT **GGG CCC** TAG TAG CAT CTG CTT GTT CG-3'
*Pv*DI-II	AMA-1Cos-7F		5'-GAA **TTT AAA** CCTA CCG TTG AGA GAA GC-3'
	AMA-1Cos-7EctoI-IIR		5'-GCA **GGG CCC** CTC CAG GTC TAC TTC TTG-3'
*Pv*DII-DIII	AMA-1Cos-7EctoII-IIIF		5'-AGC **CAG CTG** GTG CGT AAT GAT TGG GAT AAA-3'
	AMA-1cos-7R		5'-GAT **GGG CCC** TAG TAG CAT CTG CTT GTT CG-3'

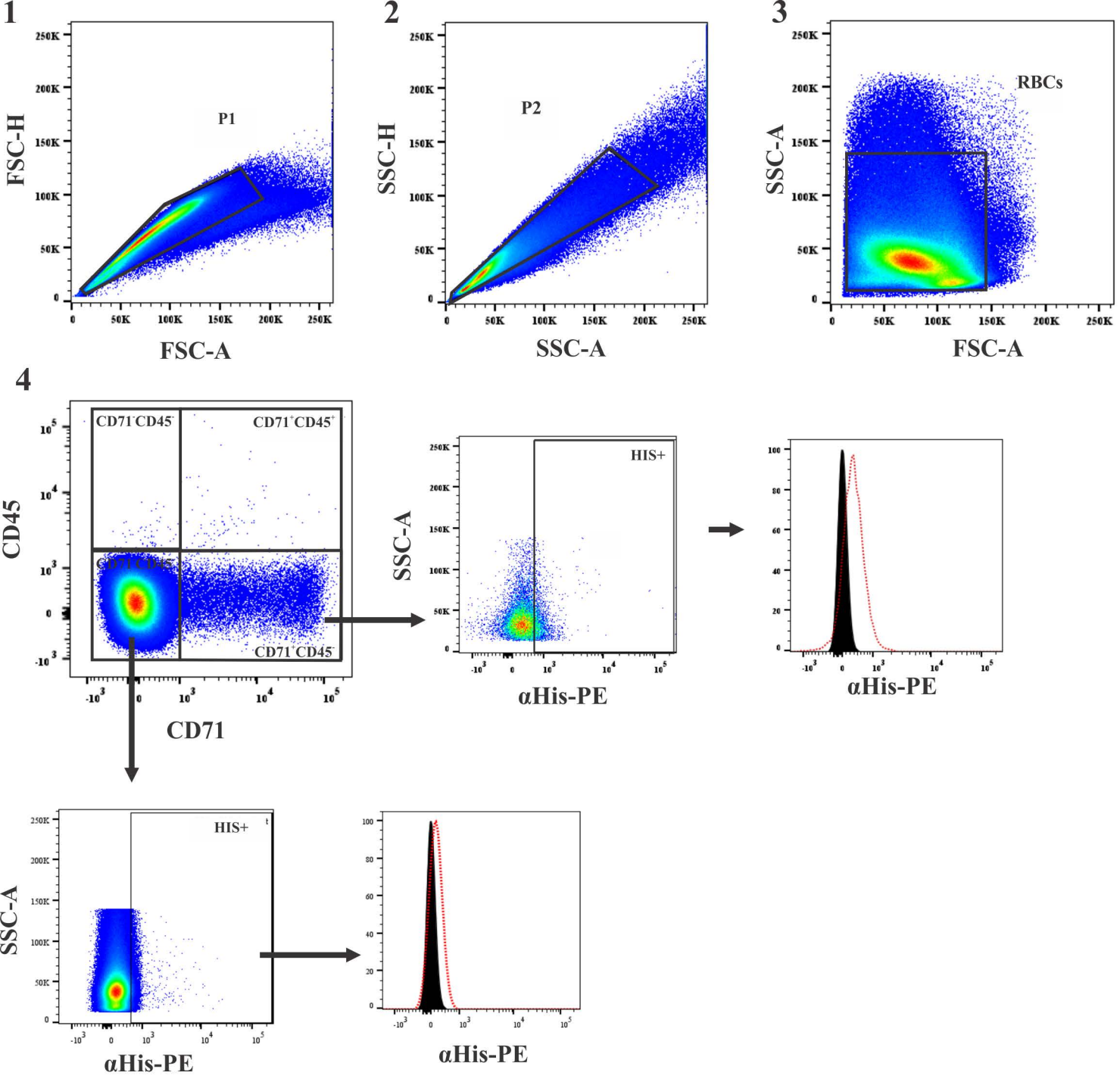


Figure S1. Flow chart used for selecting the study population by flow cytometry. Gating the general population regarding acquired events (P1, P2) for selecting RBC. Data was analyzed regarding CD45 labeling compared to CD71. Recombinant binding was compared to that of PE conjugated anti-histidine antibody binding to $CD71^{+}CD45^{-}$ (reticulocytes) or $CD71^{-}CD45^{-}$ cells (normocytes and older reticulocytes).

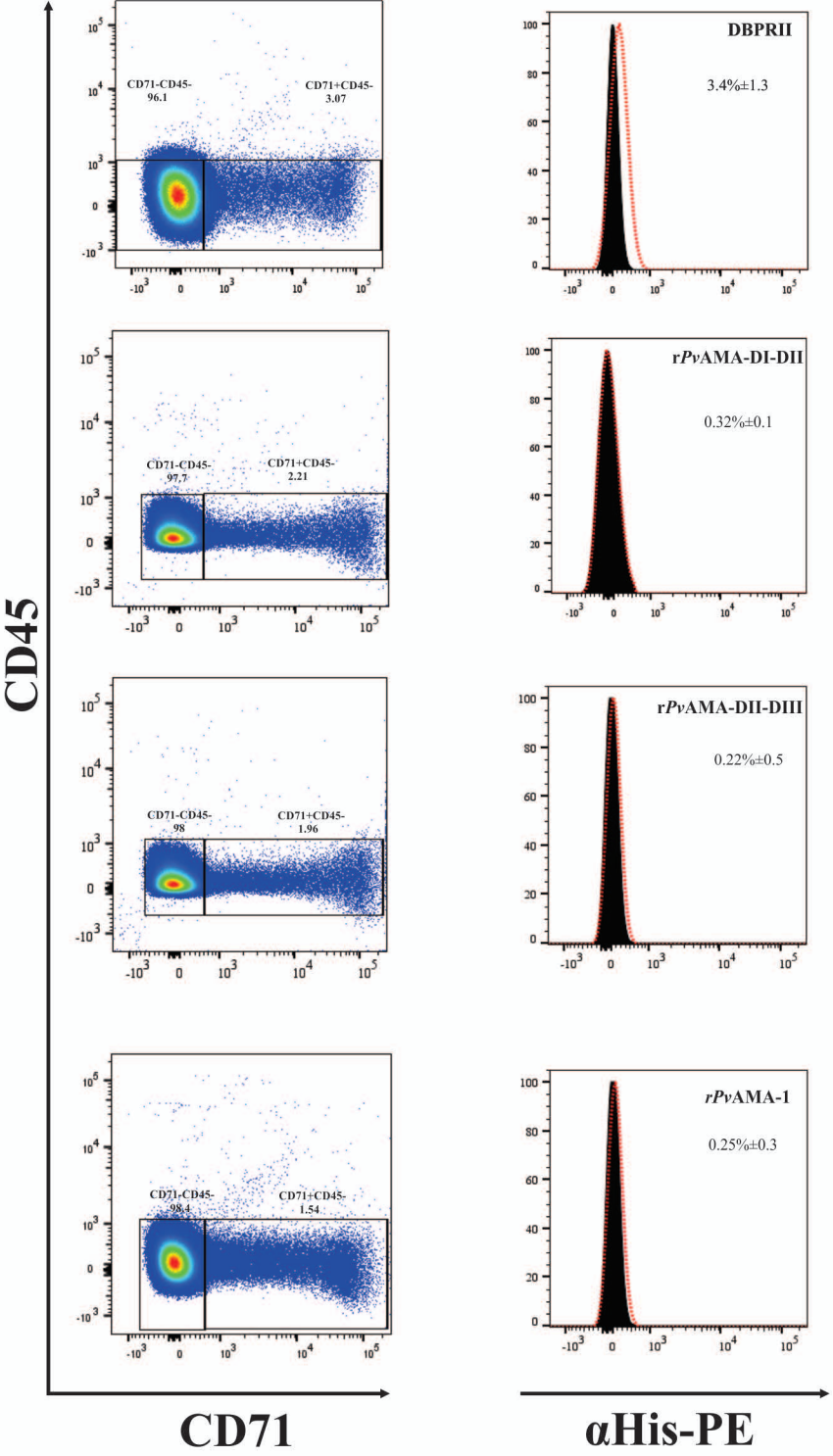
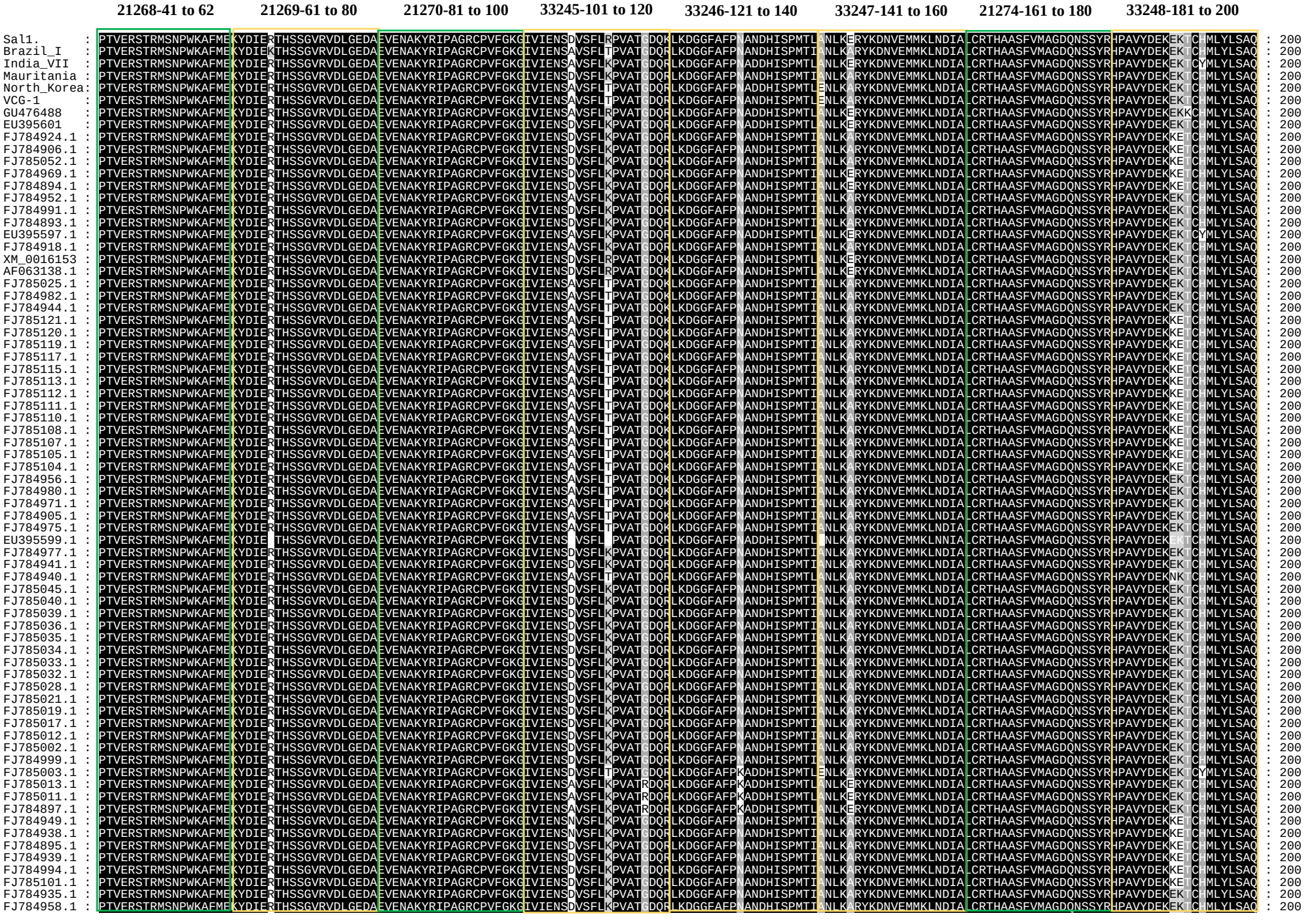


Figure S2. Flow cytometry CD71$^-$CD45$^-$ cell binding experiments. Binding to normocytes was determined by gating the CD71-CD45- population. CD71+CD45- cell binding percentages for each protein are shown on the X axis.


21268-41 to 62
21269-61 to 80
21270-81 to 100
33245-101 to 120
33246-121 to 140
33247-141 to 160
21274-161 to 180
33248-181 to 200
Sal1. : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLRPVATGDQRLKDGGFAFPNANDHISPMTLANLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
Brazil_I : PTVERSTRMSNPWKAFMEKYDIEKTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTINLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
India_VII : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLKPVATGDQRLKDGGFAFPNADDHISPMTLANLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICYMLYLSAQ : 200
Mauritania : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTLANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
North_Korea: PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNADDHISPMTLENLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
VCG-1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTLENLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
GU476488 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLRPVATGDQRLKDGGFAFPNADDHISPMTLANLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKKCHMLYLSAQ : 200
EU395601 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNADDHISPMTLANLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784924.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784906.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785052.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784969.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784894.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784952.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784991.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784893.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
EU395597.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLKPVATGDQRLKDGGFAFPNADDHISPMTLANLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICYMLYLSAQ : 200
FJ784918.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
XM_0016153 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLRPVATGDQRLKDGGFAFPNANDHISPMTLANLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
AF063138.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLRPVATGDQRLKDGGFAFPNANDHISPMTLANLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785025.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784982.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784944.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785121.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785120.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785119.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785117.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785115.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785113.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785112.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
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FJ785110.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785108.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785107.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785105.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
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FJ784956.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784980.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784971.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784905.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784975.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
EU395599.1 : PTVERSTRMSNPWKAFMEKYDIE THSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENS VSFL PVATGDQRLKDGGFAFPNADDHISPMTLNLKARYKDNVEMMKLNNIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKTCHMLYLSAQ : 200
FJ784977.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
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FJ784940.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLTPVATGDQRLKDGGFAFPNANDHISPMTLANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKNKICHMLYLSAQ : 200
FJ785045.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785040.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785039.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785036.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785035.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785034.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785033.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785032.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785028.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785021.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785019.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785017.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785012.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785002.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784999.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785003.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLTPVATGDQRLKDGGFAFPKADDHISPMTIENLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICYMLYLSAQ : 200
FJ785013.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLKPVATRDQRLKDGGFAFPKADDHISPMTLANLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ785011.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLKPVATRDQRLKDGGFAFPKADDHISPMTLANLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784897.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSAVSFLKPVATRDQRLKDGGFAFPKADDHISPMTLANLKERYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784949.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSNVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784938.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSNVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784895.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784939.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
FJ784994.1 : PTVERSTRMSNPWKAFMEKYDIERTHSSGVRVDLGEDAEVENAKYRIPAGRCPVFGKGIVIENSDVSFLKPVATGDQRLKDGGFAFPNANDHISPMTIANLKARYKDNVEMMKLNDIALCRTHAASFVMAGDQNSSYRHPAVYDEKEKICHMLYLSAQ : 200
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FJ784947.1 : PTVERSTRMSNPWKAFME KYDIERTHSSGVRVDLGEDA EVENAKYRIPAGRCPVFGKG IVIENS AVSFL KPVAT GDQR LKDGGFAFP KADDHISPMTL ANLK ERYKDNVEMMKLNDIA LCRTHAASFVMAGDQNSSYR HPAVYDEK EKI CHMLYLSAQ : 200
FJ784948.1 : PTVERSTRMSNPWKAFME KYDIERTHSSGVRVDLGEDA EVENAKYRIPAGRCPVFGKG IVIENS AVSFL TPVAT GDQR LKDGGFAFP KADDHISPMTI ANLK ARYKDNVEMMKLNDIA LCRTHAASFVMAGDQNSSYR HPAVYDEK EKI CHMLYLSAQ : 200
FJ785023.1 : PTVERSTRMSNPWKAFME KYDIERTHSSGVRVDLGEDA EVENAKYRIPAGRCPVFGKG IVIENS AVSFL TPVAT GDQR LKDGGFAFP KADDHISPMTL ANLK ERYKDNVEMMKLNDIA LCRTHAASFVMAGDQNSSYR HPAVYDEK EKI CHMLYLSAQ : 200
FJ785010.1 : PTVERSTRMSNPWKAFME KYDIERTHSSGVRVDLGEDA EVENAKYRIPAGRCPVFGKG IVIENS AVSFL TPVAT GDQR LKDGGFAFP KADDHISPMTL ANLK ERYKDNVEMMKLNDIA LCRTHAASFVMAGDQNSSYR HPAVYDEK EKI CHMLYLSAQ : 200
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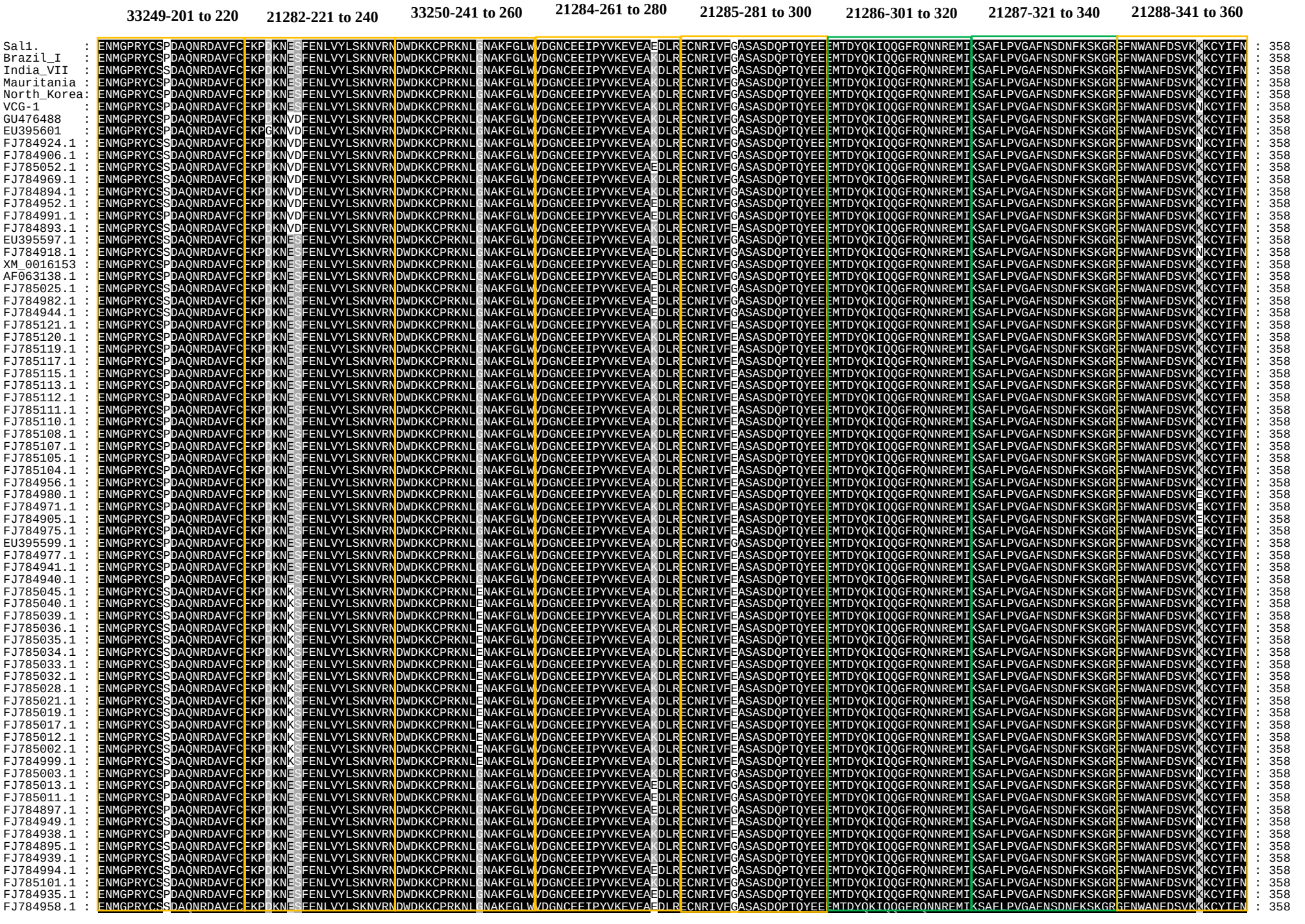
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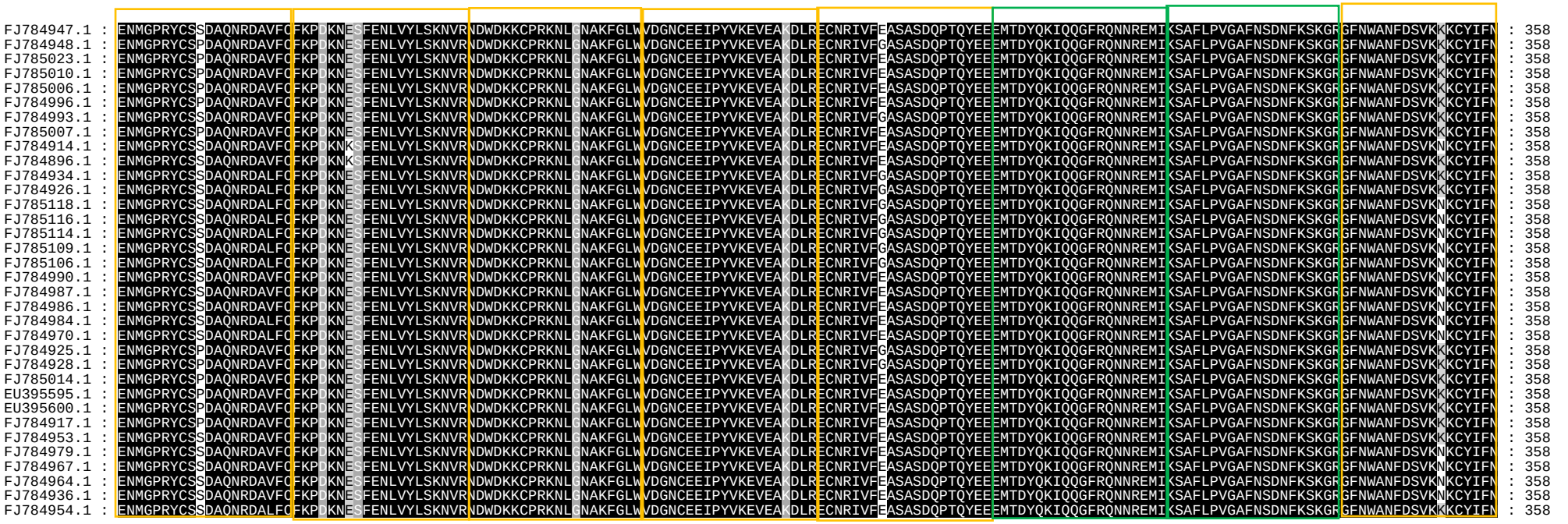
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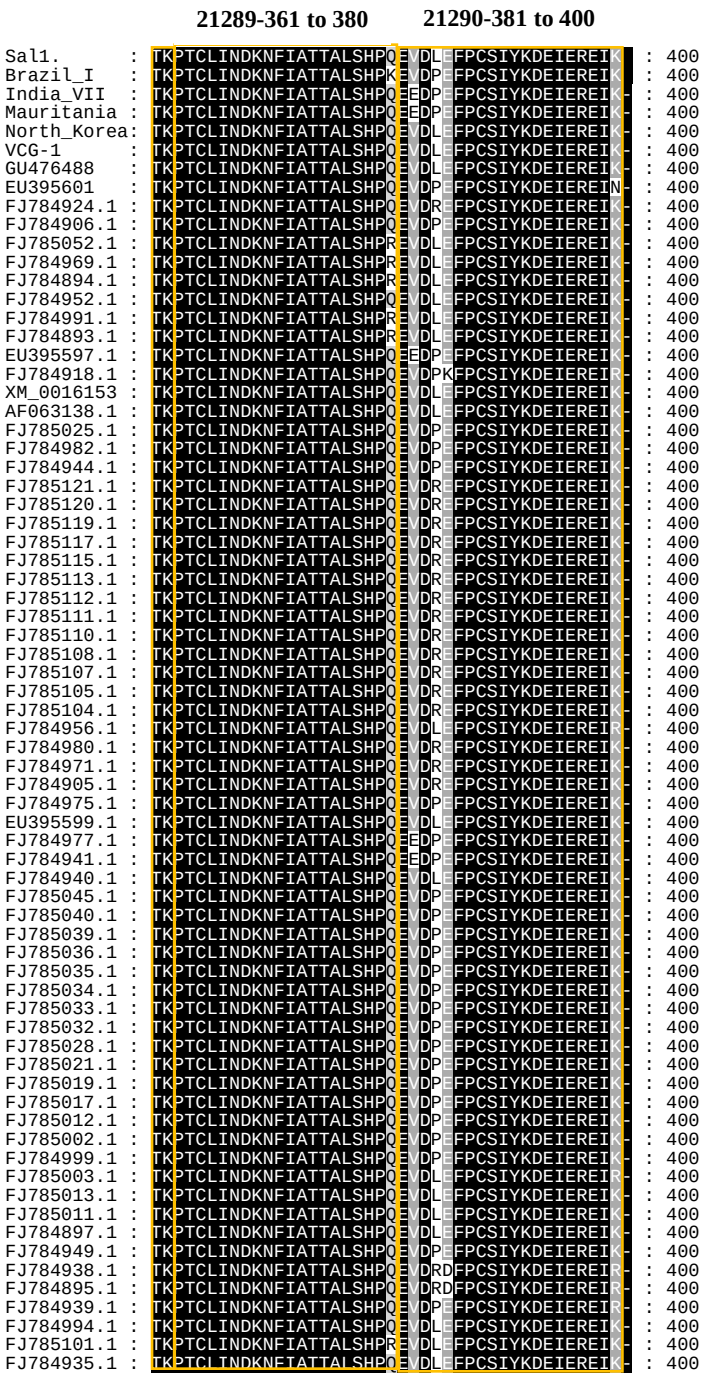
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FJ784935.1 : TKPTCLINDKNFIATTALSHPQEVDLEFPCSIYKDEIEREIK- : 400

Figure S3. Aligning *Pv*AMA-1 domain I and domain II amino acids. The Sal-1 strain (PVX_092275) was taken as reference. Black highlights residues which were conserved in all the strains' and clinical isolates' sequences. The position and sequence of each synthetic peptide evaluated in inhibition and specific binding assays are shown. The yellow boxes show the variable peptides and the green ones the conserved peptides.

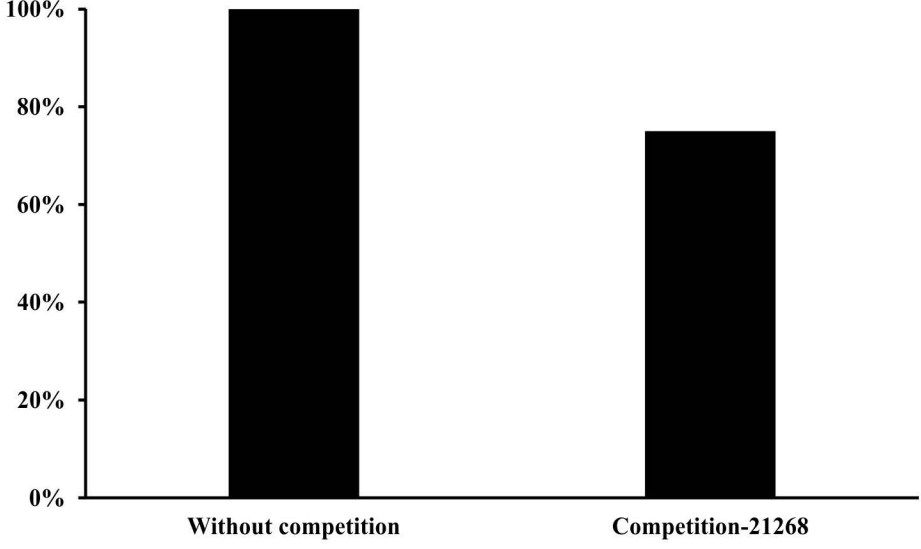

Figure S4. Rosette formation inhibition assay with peptide 21268. The values shown are the average relative percentages for *Pv*AMA-DI-II binding to UCB RBC in the absence (100%) or presence of peptide 21268. Standard deviations were below 5%.