Figure 25

Human PVRIG WT Full length

Human PVRIG sequence starting from position 21 - alternative methionine

MGHRTLVLPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIR QWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGSLPPSSDPGLSAPPTPAPILRADLAGILGV SGVLLFGCVYLLHLLRRHKHRPAPRLQPSRTSPQAPRARAWAPSQASQAALHVPYATINTSCRPATLDTAHPHGGPSW WASLPTHAAHRPQGPAAWASTPIPARGSFVSVENGLYAQAGERPPHTGPGLTLFPDPRGPRAMEGPLGVR (SEQ ID NO:8)

Human PVRIG sequence starting from position 1 methionine

MRTEAQVPALQPPEPGLEGAMGHRTLVLPWVLLTLCVTAGTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWG GPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGSLPPSSDPG LSAPPTPAPILRADLAGILGVSGVLLFGCVYLLHLLRRHKHRPAPRLQPSRTSPQAPRARAWAPSQASQAALHVPYATIN TSCRPATLDTAHPHGGPSWWASLPTHAAHRPQGPAAWASTPIPARGSFVSVENGLYAQAGERPPHTGPGLTLFPDPR GPRAMEGPLGVR (SEQ ID NO:9)

Alternative signal P with three C to S Mutations at the Fc domain
CGEN-PVRIGHH-2 Alternative SP (MGWSCIILFLVATATGVHS ((SEQ ID NO:10) + CGEN-PVRIG (41-171 of PVRIG_HUMAN) + Human IgG1 Fc mutated at C220S, C226S, C229S of hinge

MGWSCIILFLVATATGVHSTPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQW APARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGSLPPSSDPGLSAPPTPAPILRADEPKSSDKTHT SPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO:11)

Figure 63C

Name	Hcdr1	SEQ ID NO:	Hcdr2	SEQ ID NO:	Hcdr3	SEQ ID NO:	Lcdr1	SEQ ID NO:	Lcdr2	SEQ ID NO:	Lcdr3	SEQ ID NO:
CPA.7.031	GGTFSSSA	1240	IIPIYGIT	1241	ARDDTARRVRGVPYYYYYAMDV	1242	QSLLDSDDGNIH	1243	TLS	1244	MQRKEFPLT	1245
CPA.7.032	GFTFSSYG	1246	ISYDGSNK	1247	AKEDRLRFLEWLFYGMDV	1248	HDIYTY	1249	DAS	1250	QQYDNHPPEVT	1251
CPA.7.033	GGTFSSSA	1252	IIPIYGIT	1253	ARDDTARRVRGVPYYYYYAMDV	1254	QDIDDD	1255	EAS	1256	LQHDNLPLT	1257
CPA.7.034	GYTLTELS	1258	FDPEDGET	1259	ATEDPGPVAGPYYYYGMDV	1260	QSLLYINGYHY	1261	LGS	1262	MQALQTPPT	1263
CPA.7.035	GYMFTNYP	1264	INAGTGNT	1265	AREGMFYYGLESYYKGGWFDP	1266	QSLLHRNGYNY	1267	LAS	1268	MQALQTPLT	1269
CPA.7.036	GGTFSSSA	1270	IIPIYGIT	1271	ARDDTARRVRGVPYYYYYAMDV	1272	QSLLDSDDGNTY	1273	TLS	1274	MQRLQFPLT	1275
CPA.7.037	TYTFTTYY	1276	IYPSGGNT	1277	VRDQNYYYSAMDV	1278	QDIRNY	1279	DAS	1280	QQFENLPIT	1281
CPA.7.038	GGTFSSSA	1282	IIPIYGIT	1283	ARDDTARRVRGVPYYYYYAMDV	1284	RDISDS	1285	DAS	1286	HQYDNLPLT	1287
CPA.7.039	GFNFRGYA	1288	ISGSGGTT	1289	AQSYAQIGYGGHIDH	1290	SGIDVATYM	1291	YKSDSDK	1292	LIWHGSHYV	1293
CPA.7.040	GYTLTELS	1294	FDPEDGET	1295	ATGVPAAIGVYYYYYYMDV	1296	QSLLYRNGYNY	1297	WGS	1298	MQAVQNPPT	1299
CPA.7.041	GGTFSSSA	1300	IIPIYGIT	1301	ARDDTARRVRGVPYYYYYAMDV	1302	QNIDSS	1303	YAS	1304	HQSSSLPLT	1305
CPA.7.042	GGTFSSSA	1306	IIPIYGIT	1307	ARDDTARRVRGVPYYYYYAMDV	1308	QSVYNNY	1309	DAS	1310	QQYNSWPPYT	1311
CPA.7.043	GGTFSSYA	1312	IIPIFGTA	1313	ARDAYYYDSSGYYNPDAFDI	1314	QSLLYSNGYNY	1315	LGS	1316	MQARQTPYT	1317
CPA.7.044	GGTFSSSA	1318	IIPIYGIT	1319	ARDDTARRVRGVPYYYYYAMDV	1320	ESVTTF	1321	DAS	1322	HQHTNWPLT	1323
CPA.7.045	GYTLTELS	1324	FDPEDGET	1325	ATEVGYCSGGSCYISYYYGMDV	1326	QSLLYRNGHNF	1327	LGS	1328	MQALQTPPT	1329
CPA.7.046	GGTFSSSA	1330	IIPIYGIT	1331	ARDDTARRVRGVPYYYYYAMDV	1332	QTMNNY	1333	DAS	1334	QQYGDWLPIT	1335

Figure 103AW

>PVRIG_Mouse_WT_ECD_(without_SP) SEQ ID NO: 1515

SPEVWVQVQMEATNLSSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMGQSKARSSLANTTFCCEFVTFPHGSRV
ACRDLHRSDPGLSAPTPALNLQAD

Figure 103AX

>PVRIG_Mouse_WT_ECD_(with_SP) SEQ ID NO: 1516

MGQMQTLVLFSTLLTLCVSEASPEVWVQVQMEATNLSSFSVHCGVLGYSLISLVTVSCEGFVDAGRTKLAVLHPEFGTQQWAPARQAHWETPNSVSVTLTMGQSKA
RSSLANTTFCCEFVTFPHGSRVACRDLHRSDPGLSAPTPALNLQAD

Figure 103AY

>PVRIG_HH-1_(Human_ECD_+_human_IgG1_Fc_mutated_C220S_at_hinge)_-_without_SP SEQ ID NO: 1517

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPCANTTFCCKFASFPEGSWEACGS
LPPSSDPGLSAPPTPAPILRADEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

Figure 103AZ

>PVRIG_HH-1-1_(Human_ECD_with_C127F_and_C147S_mutations_+_human_IgG1_Fc_mutated_C220S_at_hinge)_-_without_SP SEQ ID NO: 1518

TPEVWVQVRMEATELSSFTIRCGFLGSGSISLVTVSWGGPNGAGGTTLAVLHPERGIRQWAPARQARWETQSSISLILEGSGASSPFANTTFCCKFASFPEGSWEASGSL
PPSSDPGLSAPPTPAPILRADEPKSSDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV
LTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSLSLSPGK