

ORF-GIF Family Alignment

GIF_ORFVgORF117	MA[C]..LRVFLAVFAL[CGS]...VHSAQWIGERDF[CM]AHAQDVFARLQVWMRIDR	48
GIF_SB87_gp117	MAADGLRLLLALAAVLGGGPARARAHKGFHGGGE.DF[C]RAHERDIYPSLQIWVRVDR	55
GIF_PCPV_gp121	MA[C]..LRVFLAVLAL[CGS]...VHSTPWIGERDF[CA]AHAQDVFSRLOQVWIRIDR	48
GIF_ORFVgORF117	[NVT]AAD[NNS]A[CG]ALAIETPPSNFDADVYVAAAGI[NVS]VSAIN[CG]FFSNMRQVETTYDT	104
GIF_SB87_gp117	DPGVARNAST[CT]LNVEAHPSGFDAAHAYVAAAGV[NVSLATKHFGKFSMLRRTTFSP	111
GIF_PCPV_gp121	[NVT]TAD[NNS]A[CG]ALAIETPPSNFDADVYVAAAGI[NVS]VSAIN[CG]FFSNMRQVEATYDT	104
GIF_ORFVgORF117	ARRQMYYVMDTWDPWVLDDPQPLFS..QEYE[NET]LP.YLLEVLLELARLYIRVG[CTV	157
GIF_SB87_gp117	EKDKIYVYLDWSWPWTR..SVDPLFR[NCS]GADN[CT]DPNLLLEVLLETARLSVEVG[CSA	166
GIF_PCPV_gp121	ARRQMYYVYTDTWDPWVLDPNPQPIFS..QEYE[NDT]LP.YLLEVLLEFSRMYIRVG[CTV	157
GIF_ORFVgORF117	PGEQPFVEVITGIDYPHTSMFELQHVLRPNRRFAPAKLHMDLEVDYR[CV]SAVYVKAF	213
GIF_SB87_gp117	PGFRPDLADP..LETHADPDLLTLTDTHDRKRDPGAVEVDLRVDER[CV]RSAYVKVV	220
GIF_PCPV_gp121	PGEQPFVEVIGIDYPHHSMEFLQLQHVQRPNRRFSPAKLHIDLEVDYR[CV]SAHVKAFA	213
GIF_ORFVgORF117	LQDA[C]S..ARKAR..TPLYFAGHGSNHPDRRPKNPVP RPQHVSSPMSRK[CL]MQTAR	265
GIF_SB87_gp117	LRDA[C]FQQAMHHRQRPRRRLPRQSRRLQQLKLPQPPQHQS[CR]NERRKIQ...	272
GIF_PCPV_gp121	LQDA[C]S..ARKAR..TPLYFAGHGSNHPDRRPKNPVP RPQQVWSSSSRK[CL]RMQTVR	265

Figure S13. Sequence alignment of the ORF-GIF family members. Cysteine residues are boxed in yellow. Predicted N-linked glycosylation sites are boxed in blue.

Orphan Alignment

COTV030	MNSLKLIIIFILYVSTIYSFNYSNV[NITI]EINDVNSDYNIK[NY]TLNLIY	50
CPXV_GER91_007_	MGRSIIIFLALIG[CA]ISNYVTPKQPTDNQFNNVEITFFMTPNIEGKYTTY	50
SCPlike_COTV007	MIIMKHIIILFINFVSFVYSEKFNKVDINLYIFSL[NNT]DYDIYTLSDNQYK	50
SCPlike_COTV179	MIIMKHIIILFINFVSFVYSEKFNKVDINLYIFSL[NNT]DYDIYTLSDNQYK	50
A41-like_COTV011	MNTHLLLLLVGVISS[CY]YAG..NKNWVKPELVSI FSDTENPLTKVFKV[CD]TE	49
A41-like_COTV175	MNTHLLLLLVGVISS[CY]YAG..NKNWVKPELVSI FSDTENPLTKVFKV[CD]TE	49
SB87_gp113	MKTLLLAAVIISLANSLP LLLSNKDAF[CS]STKEEIHQIMIAMRI[NRT]VV	50
DPXV_-016	MIKYTLTTSFIFFIT[CY]YHVSXVSNEEIQNKFTMFVDLTVYDKNLINDVS[CG]	50
BPSVgORF117	MWLPRALLALSVI[CG]TASSYRGMHDGGEF[CR]AHSREIFTSFQMWMRIQRN	50
COTV030	KIITQDFTIELTKRSKQRFIYTDYVNIINNTGIATFYTDIGNRFSYRGSYS	100
CPXV_GER91_007_	SHRRFHAVNSDKWIVGITA INLDLPNK[NITI]LTQLVPS[NATI]IVKFTFGSND	100
SCPlike_COTV007	V[NITI]EVSIIYITAYDIPLEFKNVYIEQIQDLSVINLSTDTGIFQTG[NKSI]I	100
SCPlike_COTV179	V[NITI]EVSIIYITAYDIPLEFKNVYIEQIQDLSVINLSTDTGIFQTG[NKSI]I	100
A41-like_COTV011	NVFMGMYLNI FAKVNKYTPR[CT]SLDIKKDNAYVVGGVV I[NNT]LQD[CP]FP	99
A41-like_COTV175	NVFMGMYLNI FAKVNKYTPR[CT]SLDIKKDNAYVVGGVV I[NNT]LQD[CP]FP	99
SB87_gp113	SEP KTY[CE]LDMQDDLLLEGT FMDSTAYFEANGV[NATI]VSIMGEGIDMTLSSL	100
DPXV_-016	KRYDHDNFYSMYI IDNF[NVS]ITLSD[CG]DAGFTEGYVTNVRNNTMELGYFT	100
BPSVgORF117	VQTAR[NATI]Q[CA]LDVEAPPDMSITDVLVAYANTAGI AVTVATANVGRVDVRTLQ	100
COTV030	I E L T [C] E S I F N I Y G D Y L Y [C] D N T N T [N Y T] N N K I K N F F T I Y G S [C] V K K A K I K F V	150
CPXV_GER91_007_	I F Q T K K V K F I I G I T [C] K E T T A K T L R S L N L R M S S L D K H F T E Y I N T N H V S Y Y G	150
SCPlike_COTV007	Y L D I D [C] N N K N I S D N K K M L K G I W N I N I F K R Y M D F V Y I H G S [C] I D R V N A R I R Y	150
SCPlike_COTV179	Y L D I D [C] N N K N I S D N K K M L K G I W N I N I F K R Y M D F V Y I H G S [C] I D R V N A R I R Y	150
A41-like_COTV011	V S T V A E E V Y D D S I L N V I F S T V N P I T D K D K T N F I T K D E S K N I P K K [C] K V F V S	149
A41-like_COTV175	V S T V A E E V Y D D S I L N V I F S T V N P I T D K D K T N F I T K D E S K N I P K K [C] K V F V S	149
SB87_gp113	R V E Y T P T T D A E I M Y A F I S S W A P W V K N N K D L A L N N R E E L A [NFT] N K L N I A L K	150
DPXV_-016	P I I M K Y K G L N F D S R [C] I V R I I I T [C] D G D N N L V M T P Q R F K P K K Q K H A D H I E K	150
BPSVgORF117	V L Y S T [NKS] S M F V Y L D T W S P W T K Y T R P L Y S [NAS] A D A H [NET] I D [C] L L E V L D L N	150
COTV030	Y L N T L T K K I L L I I Y I L E T A L L F N Q K V K K I K Y H K F V Y K M D A D Y I F	195
CPXV_GER91_007_	N [C] F N Y L S V D I N Y K N T E T I G V Y D F Y Y S T N S A Q Y V D K G S I V K I	191
SCPlike_COTV007	S N T K S R L F E S S Y F T N N F	167
SCPlike_COTV179	S N T K S R L F E S S Y F T N N F	167
A41-like_COTV011	M K [C] K Q D E H F S E E S F D E H E Y D D D Y E E A V P I N V D N E I L A T F N R N K A P I K V N D	199
A41-like_COTV175	M K [C] K Q D E H F S E E S F D E H E Y D D D Y E E A V P I N V D N E I L A T F N R N K A P I K V N D	199
SB87_gp113	V D [C] D H Q K F P V P T T E A P T P T T E S P T T T I S V T E T R [NET] T P S V D E E D D E	200
DPXV_-016	L I L Y G K [C] I D G I K A D V T Y D Y G S V R D T S S I I Y G T I S D I S G L L P N T [C] P K	196
BPSVgORF117	K V H V D V G [C] A V E D I P V D V V D P I D Y P R V Y D P D L L R Y V I P K N R K Q N P G Y V F V D	200
COTV030	195
CPXV_GER91_007_	191
SCPlike_COTV007	167
SCPlike_COTV179	167
A41-like_COTV011	I L T L D I D K S [C] V Q E V V S R L R I N D L [C] E S V K R Y P E S S Y V Q E V S Y P E S S K F E D F	249
A41-like_COTV175	I L T L D I D K S [C] V Q E V V S R L R I N D L [C] E S V K R Y P E S S Y V Q E V S Y P E S S K F E D F	249
SB87_gp113	E P P V D V H T N R K H E P M D I S F S T M I N Q Q [C] I Q D L A V R V V I R D A [C] E Y R K T E T P L	250
DPXV_-016	196
BPSVgORF117	L S V D S Y [C] V H S V N V K T V L R D A [C] I H H K N E T P L N F Y G R E N F P L H K S P N S V I P T	250
COTV030	195
CPXV_GER91_007_	191
SCPlike_COTV007	167
SCPlike_COTV179	167
A41-like_COTV011	E K N T P G Y P T L [C]	260
A41-like_COTV175	E K N T P G Y P T L [C]	260
SB87_gp113	G M L G T H G N D F R Q E L K K M K T K R T [C] S M H L K N E E T V D E E V S E L S E	292
DPXV_-016	196
BPSVgORF117	H K R G F S T [C] E M I T G Q	264

Figure S14. Sequences of orphan PIE domains. Cysteine residues are boxed in yellow. Predicted N-linked glycosylation sites are boxed in blue.