

## CHAPTER 12

# Appendix

### 12.1 Tables of Peptides, Synthesized on Membranes

**Table 12.1: Peptides synthesized on membranes shown in Fig. 6.7**

Binding of CD2BP2-GYF to peptides derived from splicing factors, containing the reduced motif PPG. A protein description is given in column ‘Description’. Protein names and Swiss-Prot entry names are listed in the column ‘Protein’. Binding classification: (–): < 5 x background [BLU] (Boehringer Light Units); (+): 5–25 x background [BLU]; (++) 25–125 x background [BLU]; (+++): > 125 x background [BLU].

SPOT-number	Description	Sequence	Binding	Protein
1	CD2BP2 interaction partner	SHRPPPPGHR	+++	Human CD2
2		LGSGLPPPGMPPGSF	+	
3		PPPGMPPPGFPPPVP	–	
4		FPPPVPPPGALPPGIP	+	
5	Part of the U2 snRNP	PPPGALPPGIPPPAMPP	–	Splicing factor 3B subunit 4 (Q15427)
6		MPPPPMPPPGAAGHGPP	–	
7		GHPHAGPPGSGGQPPP	–	
8		QPPPRPPPGMHPGPP	+	
9	Associates with	HDFRSPPPGMGLNQNR	+++	
10	U4/U6•U5 tri-snRNP	PPTSGAPPGSGPPTP	–	Pro- and Glu-rich (P23246)
11		PAVTSAPPGAPPPTPP	+	
12	Vertebrate homolog to <i>Drosophila melanogaster</i> splicing regulator, suppressor-of-white-apricot	YCLAPPPPGIDVTTYY	–	Splicing factor, Arg/Ser-rich 8 (Q12872)
13		TTTAPPPPGTTPPPP	–	
14		GAPTQYPPLGLGPPPM	–	
15		MGRGAPPPGMMGPPPG	+	
16	Close homolog to SmB	PGMMGPPPGMRPPMGP	+	SNRPB protein (Q15182)
17		FLTGPPPPGMRRPPR	+++	
18		GMPTVIIPPGLTREQER	++	
19		MNQGPHPPGHGPPPM	–	
20	Mammalian branch-point binding protein BBP, interacts with U1 snRNA	GVQPPPLPPGAPPPPPP	+	SF1-Bo isoform (Q15637-2)
21		PPPPPPPPGSAGMMIP	–	
22		MNQGPHPPGHGPPPM	–	
23		GVQPPPLPPGAPPPPPP	+	(Q15637-1)
24		PPPPPPPPGSAGMMYA	–	
25		VGRATPPPGIMAPPPG	+	
26	Human SNRPN gene with novel exon 3	PGIMAPPPGMRPPMGP	+	RT-LI (Q9BPU5)
27		TPIGMPPPGMRPPPG	++	
28		PGMRPPPPGIRGEAFL	++	
29		MGRGAPPPGMMGPPPG	+	
30		PGMMGPPPGMRPPMGP	+	
31	Core snRNP protein	TPPMGMPGGMRPPPG	+	SmB/B' (P14678)
32		PGMRPPPPGMRPPPG	+++	
33		GMRGPPPPGMRPPR	++	
34		VGRATPPPGIMAPPPG	+	
35	Tissue-specific splicing protein	PGIMAPPPGMRPPMGP	+	
36		TPIGMPPPGMRPPPG	++	Sm-D (SNRPN) (P14648)
37		PGMRPPPPGIRGPPPP	+++	
38		GIRGPPPPGMRPPR	+++	
39		QPPYMPPPGMIPPPGL	+	
40	Part of the U1 snRNP	PPGMIPPPGILAPGQIP	–	U1 small nuclear ribonucleoprotein A (P09012)
41		LAPGQIPPGAMPPQQL	–	

**Table 12.2: Peptides synthesized on membranes shown in Fig. 8.3**

List of peptides, synthesized on the membranes, shown in Fig. 8.3. The membranes were incubated with CD2BP2-GYF GST-fusion protein. The first column refers to the numbers in Fig. 8.3. The column ‘Sequence’ and ‘Accession Number/Description’ give the sequence of each peptide and the identifier in Swiss-Prot, EMBL, and TrEMBL databases of the corresponding proteins or a description of the peptide, respectively. Lists of peptides on different membranes are separated by rows indicating the motif applied for the database search.

SPOT-number	Sequence	Accession Number/Description	
<b>PPG[AEFHILMSTWY] x (0,40) PPG[AEFHILMSTWY]</b>			
1	SHRPPPPGHR	Control	
2	SQAPSHRPPPPGHDRVQ		
3	ATSQHPPPPGHSQQA		
4	VMQKRSRAIHSSDEGE		
5	NIPYSVPHDSTQ	Negative Control	
6	PSSGDAPPAGPLALTA	A1AD_HUMAN	
7	PDPDPPEPPGTPEMQAP	A1AD_HUMAN	
8	AYPGQAPPGAYPGQAP	AAH53667	
9	AYPGQAPPGAYHGAPG		
10	PQLPPGPGGAPKPPPA	AAM20739	
11	MGGQQAPPGLGPILED		
12	QGTAQPPPAGAPQGPPG		
13	PGAPQGPPGAASGPPP		
14	SLHHLQPPGAPALLPP		
15	ELPDGAPPGHPPGSGG	AAO92063	
16	GAPHPGPGSGGAESA		
17	ELAGEMPPGLNFDLDA	AAP35525	
18	ALNLSGPPGASGEQCL		
19	MVPPPGEESQTVI	AAP35537	
20	SQTVILPPGWQSYLSP		
21	GGAPTQPPGLRPQTQT	AAP35632	
22	DVNLPRLPPPGALCEQKR		
23	PGAPGMPPGIPPLMPG	AAP36029	
24	PVMPGMPPGLHHQRKY		
25	PLMPGMPPGMPPVPVR		
26	PVETPLPPGLRSAGEE	AIRE_HUMAN	
27	GEEVRGPPGEPLAGMD		
28	EYVCCPPGTPDPSTGT	APP1_HUMAN	
29	PSTRSWPPGSRVVEGAE		
30	SHRPPPPGHR	Control	
31	VMQKRSRAIHSSDEGE		
32	NIPYSVPHDSTQ	Negative Control	
33	VGRATPPPVGIMAPPNG	CAA34288	
34	PGIMAPPGMRPPMGP		
35	TPIGMPPGMRRPPPG		
36	PGMRPPPPGIRGPPP		
37	GIRGPPPPGMRPPR		
38	CGNPGSPPGALKQFLP	CAD60192	
39	ALKQFLPPGTTGAAAS		
40	SQHPPPPGHSQAPS	CD2_HUMAN	
41	PSHRPPPPGHRVQHQP		
42	SRMFQAPPGAPPHPQ	DRPL_HUMAN	
43	NNASASPPGLQAQPLP		
44	GNSGPPPPGAFPHPLE		
45	AYKTATPPGYKPGSPP		
46	SFRTGTPPGYRGTSPP		
47	LALQPGPPGHLFPFHF		
48	LHPVPPPGMALPYNP	DVL2_HUMAN	
49	VPPAVQPPPAPPVRDL		
50	SFRDCCPPGLAVGMDG	FBN2_HUMAN	
51	SYSCTCPPGYVFRTET		
52	SFRCICCPPGYEVKSEN		
53	GFQCLCPPGFVLSDNG		
54	TFMCICCPPGMARRPDG		
55	GFTCKCAPPGFTQHHTA		
56	GYLCGPPGYYRVGQG		
57	RRLPPPGEQPPSGS	FZD8_HUMAN	
58	GSGHGRPPGARPPHRG		
59	SHYGGVPPGAGPPGLG	HAN2_HUMAN	
60	VPPGAGPPGLGGPRPV		
61	PGEDRTPPGLAAEPER	HCN4_HUMAN	
62	AAIFRPPPGSGLGNLG		
63	SSSSSPPPPGACGSPSA		
64	AQPSAPPAGARGGLGL		
65	PGQLGQPPGELSLGLA		
66	PRGGLSPPGHSPGPPR		
67	SHRPPPPGHR	Control	
68	VMQKRSRAIHSSDEGE		
69	NIpYSVPHDSTQ	Negative Control	
70	HPALPLPPGPHPHPGP	KLF4_HUMAN	
71	HYQELMPPGSCMPEEP		
72	AYPGQAPPGAYPGQAP	LEG3_HUMAN	
73	AYPGQAPPGAYHGAPG		
74	PVTTQNPPGAPPNVWL	MGD1_HUMAN	
75	PLAWQNPPGQWTPPGW		
76	PPGWQTTPGWQTPPGW		
77	PPGWQTTPGWQGPPDW		
78	AQSLVPPPPGPGSSTP	MK07_HUMAN	
79	GVLPYFPPGLPPPDAG		
80	EAACLCPGPGVGERCQ	NTC3_HUMAN	
81	RFLCSCPYPGQGRSCR		
82	RAICTCPPGFTGGACD		
83	GFRCLCPGSLPLCL		
84	SFTCTCPGYYGGFHCE		
85	GAYCLCPGWSGRLCD		
86	RYLCSCPPTGLVLC		
87	GFRCTCPPGTYGLRCE		
88	GPRCACPPGLSGPSCR		
89	RSFPGSPPGASNASC		
90	LGPLLCPGAFPLGLK		
91	QIQCHCAPPGEFGHACE		
92	FHLCLCPGFIGPDCE	NTC4_HUMAN	
93	SFNCLCPGTYGTRCE		
94	TFHCLCPGLEGQLCE		
95	SYFCHCAPPGFQGSLCQ		
96	GFHCACPPGFVGLRCE		
97	HGALWLPPGFTRRPRT		
98	SHRPPPPGHR	Control	
99	VMQKRSRAIHSSDEGE		
100	NIpYSVPHDSTQ	Negative Control	
101	QCLNKMPGEIKVDDA	NUCM_HUMAN	
102	TEGYQVPPGATYTAIE		
103	CGQDDGPPGSEDERD	NXP3_HUMAN	
104	LLGLLAPPGEAWGILG		
105	MSSMPPPPGMMFPPGM	O14776	
106	PPGMMFFPPGMPVTAP		
107	MHRAVDPPGARAAREA	O15054	
108	SEQTGLPPGLPLPPP		
109	PAYTAHPPGHLVPA		
110	PGPGPRPPGAESHGCL		
111	CLPATRPPGSDLRESR		
112	PYAPSRRPPGLPGTTTS		
113	VTQAPLPPGWEQRVDQ	O43584	
114	DRPEPLPPGWERRVDN		
115	DPLGPLPPGWEKRTDS		
116	IQGPPGPPGEKGDRGP	O60505	
117	FPGPIGPPGLKGDRGA		
118	PPPPGGPPGALAVRPS	O60630	
119	PAEPAPPAPPGAPPSPG		
120	HAAPPPPGEHSGIPF	O75048	
121	TPPPPPPPGEHSSSGG		
122	RLAVQLPPGEDLNDWV	O75249	
123	QVRHLEPPGEGPPSRA		

124	TPTPLSPPGLGMSPAA		199	HIREHEPPGALTELDL	Q86YC3
125	TDGCVCPGTVLIDER	O75851	200	NQLLGVPVPGFANARN	
126	MEARTLPPGMAAVTVV		201	YCLAPPPPGLDVTYY	Q8IV81
127	LPGCRCPPGLLLHDTR		202	TTTAPPPPPTTPPPP	
128	APGCTCPPGLFLHNAS		203	DNPRRSPPGAGGSPPG	Q8IVC6
129	EQAQELPPGTVLTRNC		204	PGAGGSPPGAVALPSA	
130	CQGEIVPPGETWQQVA		205	LLLLLPPPGSEPPGL	Q8IVL6
131	NIALPPPPGIAPPPIP	O95607	206	PPGSPEPPGLTQLSPG	
132	GIAPPNGFGPHMFH		207	KQDLSAPPYGLTENV	Q8IWA9
133	SHRPPPPGHR	Control	208	RQAAHGPPGLHSDSHS	
134	VMQKRSRAIHSSDEGE		209	PPGPMGPPGETPCPPG	Q8IWL1
135	NIpYSVPHDSTQ	Negative Control	210	EAGERGPPGLPAHLDE	
136	GREPGGPPGSFLTSRR	O95785	211	PPGPMGPPGEMPCPPG	Q8IWL2
137	DAHLGLPPGLAKKSSS		212	EPGERGPPGLPAHLDE	
138	NKAIKSPPPGFSAKGLG		213	PPFPFFFFPAGMFGASR	Q8IX92
139	AKKLPPPPGSPLGHSP		214	FASARSPPGAGAPASG	
140	RPLAASPPGTVKAEHH		215	AYPGQAPPGAYPGQAP	Q8IXB9
141	TALPTAPPGLLGPYTA	PCB4_HUMAN	216	AYPGQAPPGAYPGAPG	
142	PASPGPPGLAAYTAK		217	HCVNTCPPLGHADCA	Q8IXF3
143	GLPNRLPPGAVPPGAR	PSMF1_HUMAN	218	RAPSPPPPGSEAAPSP	
144	LPPGAVPPGARFDLPG		219	RDPTPRPGLPSEEATA	
145	NPDHLPPPGYDDMYL		220	SHRPPPPGHR	Control
146	PRGEAGPPGSGEKGER	Q02802	221	VMQKRSRAIHSSDEGE	
147	VPGPPGPPGAMGPPGP		222	NIpYSVPHDSTQ	Negative Control
148	AMGPPGPPGAPGPAGP		223	LIGPALPPGFKARGTA	Q8IXQ4
149	PPGPRGPPGEGLPGPP		224	FFGPALPPGFKQDDDS	
150	LPGPPGPPGSFLSNSE		225	IIGPALPPGFIKSTQK	
151	PPGPPGPPGSISSSGQ		226	PVTTQNPPGAPPNVLW	Q8IZ84
152	PRGPPGPPGASGDGSL		227	PLAWQNPPGWQTTPGW	
153	LPGPPGPPGLPGTSYE		228	PPGWQTTPGWQTTPGW	
154	PPGPPGPPGIPGNVWS		229	PPGWQTTPGWQGPPDW	
155	QPGQGQPPGISKVFS		230	SPAALGPPGYLHSAPG	Q8IZJ4
156	DRGPAGPPGHPGPPGP		231	APGEGPPPPGTVLEPQS	
157	VQLSAPPGEETSQW	Q07912	232	GLPNRLPPGAVPPGAR	Q8N1D6
158	TPSPLVPPGSSPLPPR		233	LPPGAVPPGARFDLPG	
159	GAPTYQPPGLPPPPM	Q15182	234	NPDHLPPPGYDDMYL	
160	MGRGAPPGMMGPPPG		235	NECGYQPPGAPPGLGS	Q8N5L8
161	PGMMGPPPGMRPPMGP		236	YQPPGAPPGLGSMPPSS	
162	FLTGPPPPGMRPPRP		237	FGVPPPPGIGHYQHLM	Q8N684
163	SYSCSCPFGHFWDQT	Q86SJ5	238	PHLAVPPPGAIAPPALH	
164	SYKCQCPGHELAKG		239	LPHNSLPPGSGLGTFS	Q8NEZ4
165	SFQCECPPGYHLSEHT		240	QDPYSQPPGTPRPPVVD	
166	SFRICICPPGFQVQSDH		241	TDPYSQPPGTPRPTTV	
167	SFQCLCSCPFGVLSNDG		242	SDPYAHPPGTPRPGIS	
168	TFACVCPPGMRPLPGS		243	RLPFSAPPGSVVEASS	
169	AFTCRCPPGFTQHHQA		244	LLLRRGPPPGSANPPRL	
170	SHRPPPPGHR	Control	245	PCSLGLPPGHALQDIL	Q8NF26
171	VMQKRSRAIHSSDEGE		246	VLALLAAPPGSTAEEAAR	
172	NIpYSVPHDSTQ	Negative Control	247	LPATVPPPGMPVMPVMP	Q8NF45
173	PELPGPPGLPSPPLP	Q86TR4	248	LPTSVPPPGMPVPSLSS	
174	GQDGARPPGEGSSTGA		249	LSSATPPPGIIPPPGV	
175	GASPESSPPGAEAVPEA		250	RPGMYPPPGSYRPPPP	
176	GQGAEGPPGTPRRTGK		251	PPPMGKPPGSIVRPSA	
177	AVPPHPPPGLGLPPAS	Q86U16	252	IIPPPGLQPEPGY	Q8NFX5L
178	VPPPPIPPIPPGMPPVGGL		253	REPGYTPPGAGQNPP	
179	TTLWQCPPGEEPDLDP	Q86V34	254	GAGNQNPPGMYPVTGP	
180	TLCRPCPGTFSAAWG		255	ELAGEMPPGLNFDLDA	Q8NI97
181	SRMFQAPPGAPPHPQ	Q86V38	256	ALNLSGPPGASGEQCL	
182	NNASASPPGLGAQPLP		257	QPPPAPPGSQIPIPT	Q8TAQ2
183	GNSGPPPPGAFPHPLE		258	PAGSGAPPGLGPSEQ	
184	AYKTATPPGYKPGSPP		259	PQLPPGPPGAPKPPPA	Q8TB55
185	SFRGTTPPGYRGTSPP		260	MGGQQAPPGLGPILED	
186	LALQPGPPGLHPFPFH		261	QGTAQPPPGAPQGPPG	
187	HDFRSPPPGMGLNQNR	Q86VG2	262	PGAPQGPPGAASGPPP	
188	PPTSGAPPGSGPGPTP		263	SLHHLQPPGAPALLPP	
189	PAVTSAPPGAPPPTP		264	SHRPPPPGHR	Control
190	PTRPPGMNGPSSL	Q86WW5	265	VMQKRSRAIHSSDEGE	
191	NSNTLTGGAGMLGFP		266	NIpYSVPHDSTQ	Negative Control
192	HAAPPPPGEHSGIPF	Q86XD2	267	PRGPPGPPGFPKGPKGM	Q8TEJ5
193	TPPPPPPPGEHSSGG		268	QPGPAGPPGFSRMGKA	
194	PPPPGPPPGALAVRPS	Q86Y01	269	RMGKAGPPGLPGKVGP	
195	PAEPAPPNGAPPNSP		270	LRGPPGPPGLPGPSGI	
196	LPATVPPPGMPPVMP	Q86YA8	271	AQGVPGPPGFQCEPGP	
197	LPTSVPPPGMPPSLSS		272	QGGAPGPPGLPGPAGL	
198	LSSATPPPGIIPPPGV		273	EPGTRGPPGLIGPTGY	

274	PQGLGGPPGLPGSAGL		349	TFACVCPPGMRPLPGS	
275	EPGLPGPPGEGRAGEP		350	AFTCRCPPGFTQHHQA	
276	PPGPBPGPPGAPGAFDE	Q8TEJ5	351	YCEELCPPGSHGAHCE	Q96KG6
277	DCSQPCPPGHGENCA	Q8TEK2	352	TGECACPPGWTGAVCA	
278	TGACVCPPGHSGAPCR		353	VCAQPCPPGTFGQNCS	Q96KG6
279	GSQPPLPPGLPPGHYD		354	LCQRICPPGFYGHGCA	
280	PLPPGLPPGHYDSPKN		355	DCSQACPPGFWGPACF	
281	GKPPGSALARGT	Q8TEN0	356	SADPERPPGATCPESP	Q96RK0
282	PVTTQNPPGAPPNVSG		357	EEEASGPPGPEPRLDSE	
283	PLAWQNPPGWTPPGW		358	GPLRPPPPGAGGPATP	
284	PPGWQTTPPGWTPPGW		359	SIRFTLPPGTSTNGKV	
285	PPGWQTTPPGWQGPPDW		360	ATPTEQPPGAEALPV	
286	PELPSGPPGLSPPLP	Q8TER5	361	KMVSMSKPPGFQASLAR	Q96RR9
287	GQDGARPPGEGSSTGA		362	PGVPPPHPPGPKSAASH	
288	GASEFESPPGAEAVPEA		363	SQHPPPPPGRHSQAPS	Q96TE5
289	GQGAEGPPGTPRRTGK		364	PSHRPPPPGHRVQHQP	
290	AGPGRGPPGLCGLSLG	Q8TET1	365	PRGEAGPPGSGEKGER	Q99018
291	TQQEPEPPGSDSALDS		366	VPGPPGPPGAMGPPGP	
292	KMVSMSKPPGFQASLAR		367	AMGPPGPPGAPGPAGP	
293	PGVPPHPPGPKSAASH		368	VGRATPPGIMAPPPG	Q9BPU5
294	GSSPRPPPGLWYLATA		369	PGIMAPPPGMRRPMGP	
295	LPLPPPPPGEPSAPPG	Q8WX45	370	TPIGMPPPGMRPPPG	
296	PGEESAPPGTCGPRYS		371	PGMRPPPPGIRGEAFL	
297	DLMSSLPPPGESEEEEE	Q8WX64	372	PPTSGAPPGSGPGPTP	Q9BSV4
298	PAIAAPPGFRDNSSD		373	PAVTSAPPGAPPPTPP	
299	TGQSPGPGGARRKLPQ		374	DYLNQNAPPFFPRLGV	Q9BUR5
300	GAATEHPPGSPTSATV		375	IKKLVYPPGMGLAAS	
301	PVTTQNPPGAPPNVLW	Q8WY92	376	VTQAPLPPGWEQRVDQ	Q9BY75
302	PLAWQNPPGWTPPGW		377	DRPEPLPPGWERRVDN	
303	PPGWQTTPPGWTPPGW		378	DPLGPLPPGWEKRTDS	
304	PPGWQTTPPGWQGPPDW		379	TALPTAPPGLLGT PYA	Q9C064
305	KSPGEVPPGTSPACIL	Q8WYN6	380	PASP GPPPGGLAAYTAK	
306	CILATWPPGLLVLWLWQ		381	TALPTAPPGLLGT PYA	Q9GZT1
307	GERYSTPPGETLERYS	Q8WZ53	382	PASP GPPPGGLAAYTAK	
308	LERYSTPPGETLERYS		383	PAVMQPPPGLPPLPAD	Q9H305
309	LERYSTPPGETLERYS		384	GPPPYEPPGHPMPQPG	
310	LERYSTPPGETLERYS		385	ADGTYMPPGFYPPPGP	
311	LERYSTPPGETLERYS		386	VTQAPLPPGWEQRVDQ	Q9H451
312	LERYSTPPGEALERYS		387	DRPEPLPPGWERRVDN	
313	QHLKSSPPGFQANQNP	Q92576	388	DPLGPLPPGWEKRTDS	
314	PPPLLPPPFGFGFAQNP		389	SEDPLLPPGWSVDWTM	Q9H4B6
315	GMPTVI PPPGLTREQER	Q92744	390	LEREGLPPGWERVESS	
316	MNQGPHPGGHGGPPPM		391	PPPTTCPPGALQAPEA	Q9H7J3
317	GVQPPPLPPGAPP PPP		392	RSAPKEPPGLPRLPLGS	
318	PPPPPPPPGSAGMMIP		393	PPRMPPPPGFSAVVLL	
319	GMPTVI PPPGLTREQER	Q92745	394	GTPPPPPPGLVPPISK	
320	MNQGPHPGGHGGPPPM		395	PPISKPPPGFSLPLPS	
321	GVQPPPLPPGAPP PPP		396	SHRPPPPGHR	Control
322	PPPPPPPPGSAGMMYA		397	VMQKRSRAIHSSDEGE	
323	QPPPALPPGSQPIPPT	Q92923	398	NIpYSVPHDSTQ	Negative Control
324	PAGSGAPPGLGPSEQ		399	QGDGARPPGEGSSTGA	Q9H7L6
325	DYAYI PPPGLQPEPGY	Q93052	400	GASPESPPGAEAVPEA	
326	REPGYTPPGAGQNQNP		401	GQGAEGPPGTPRRTGK	
327	GAGNQNPPGMYPVTGP		402	TQQEPEPPGSDSALDS	Q9H7P7
328	SHRPPPPGHR	Control	403	KMVSMSKPPGFQASLAR	
329	VMQKRSRAIHSSDEGE		404	PGVPPHPPGPKSAASH	
330	NIpYSVPHDSTQ	Negative Control	405	GSSPRPPPGLWYLATA	
331	PPGPAGPPGSKGDRGQ	Q96A83	406	PQLPPGPPGAPKPPPA	Q9HB34
332	EKGPGAGPPGLLGP GP		407	MGGQQAPPGLGPILED	
333	PRGPPGPPGTPGSQGL		408	QGTAQPPPAGQGPPG	
334	TALPTAPPGLLGT PYA	Q96AH7	409	PGAPQGPPGAASGPPP	
335	PASP GPPPGLAAYTAK		410	SLHHLQPPGAPALLPP	
336	VTQAPLPPGWEQRVDQ	Q96F66	411	TALPTAPPGLLGT PYA	Q9HCU2
337	DRPEPLPPGWERRVDN		412	PASP GPPPGGLAAYTAK	Q9NPY0
338	DPLGPLPPGWEKRTDS		413	PSSGDAPPGLALTA	
339	KPPFPFPGAPPTHLP	Q96F80	414	PDPDPEPPGTPEMQAP	
340	APPLI PPPGF PPPGA		415	QHLKSSPPGFQANQNP	Q9NQ16
341	PPGFPPPPGAPPSSLI		416	PPPLLPPPGFGFAQNP	
342	AQSLVPPPGLPGSSTP	Q96G51	417	LPHNSLPPGSGLGTFS	Q9NR13
343	GVLPYFPPGLPPPDAG		418	QDPYSQPPGTPR PVVD	
344	SYSCSCP GFGHF FWQDT	Q96JP8	419	TDPYSQPPGTPRPTTV	
345	SYKCQCPCP GHETAKG		420	SDPYAHPPGTPRPGIS	
346	SFQCEC PPGYH LSEHT		421	RLPFSAPP GS VVEASS	
347	SFRICCP PGF QVQSDH		422	LLL RGPPPG SANP RPL	
348	SFQCLC PPGF VL SDNG		423	PAVMQPPPGLPPLPAD	Q9P112

424	GPPPYEPPGHPMPQPG		499	SHRPPPPGHR	Control
425	ADGYTYPFGYPPPBP		500	VMQKRSRAIHSSDEGE	
426	LPHNSLPPGSGLTFS	Q9P222	501	NIpYSVPHDSTQ	Negative Control
427	QDPYSQPPGTPRVVD		502	IQQQQPPGEEKKKPKE	SYV2_HUMAN
428	TDPYSQPPGTPRPTV		503	TYDLPTPGEKKDVSG	
429	SDPYAHPPGTPRPGIS		504	VSDPAVPPGEGEDPDGRY	
430	RLPFSAAPPGSVVVEASS	Q9P222	505	TAPAWPPPGEDEPGTTP	T13C_HUMAN
431	PRGEAGPPGSGEKGER	Q9UC14	506	EDPGTTPPGHGVVPVA	
432	VGPGPPGPGAMGPPGP		507	LPVPPPPIPGEPSAPPG	TED_HUMAN
433	AMGPPGPGGAPGPAGP		508	PGEPSAPPCTCGPRYS	
434	QHLKSSPPGFPPGP	Q9UI45	509	ANFKIEPPLFLGRGRN	TOP1_HUMAN
435	PPPLLPPPGFGFAQNP		510	AKVPSPPPGHKWKEVR	
436	TPMGMPPPGMRPPPPG	Q9UIS4	511	LVCAQCPCPGTFVQRPC	TR6B_HUMAN
437	PGMRPPPPGMGRGPPP		512	LEHASCPPGAGVIAPG	
438	GMRGPPPPGMRPPRP		513	TQCQPCPCPGTSASSS	
439	TPIGMPPPGMRRPPP	Q9UKR4	514	SGVEEIPPGIVNKELI	TRIO_HUMAN
440	PGMRPPPPGIRGPPP		515	PGPSLPPPGAAPEAGP	
441	GIRGPPPPGMRPPRP		516	SAPSRRPPGADAEKGSE	
442	PPGEFGPPGSPGPSPG	Q9UM16	517	TTLWQCPCGEEDPLDP	TRLT_HUMAN
443	EPGIQGPPGLPGLPPGP		518	TLCRPCPCPGTFSAAWG	
444	LPGPPGPPGSQSFY		519	PGFCICCPGFYGVNCD	WIF1_HUMAN
445	GLPPGPPPGAPPFLRP	Q9Y2W2	520	PGKCICCPGLEGEQCE	
446	APPFLRPPGMGLRGP		521	TWERPLPPLPPGWEKRTDP	WWP2_HUMAN
447	GPPPGPPPGLPPGPPP		522	DPLGPLPPLPPGWEKRQDN	
448	RLPPPAPPGIPPPRPG		523	IQEPALPPGWEWKYTS	
449	PPLPGPAPPGLFPAPL		524	PGAPGMPPGIPPLMPG	Z207_HUMAN
450	RLSEAPPGGSSSSLKP	Q9Y5L9	525	PVMPGMPPGMMMPGGM	
451	LKPLTVPPGTYTFFPAA		526	PLMPGMPPGMPMPVPR	
452	AGQGGHPPGTYTSLASR	Q9Y6C2	527	GLPLGLPPLGMLGPGP	Z409_HUMAN
453	EAGPPGPPGLQGPPGP		528	GPGPPPPPGATPTSSP	
454	PPGPGAGPPGSPGKDQ		529	HHQRDGPPGLVPMLE	ZAP3_HUMAN
455	FGPPIPPPGLGGAFC	RBMC_HUMAN	530	PESPPVPPGCSYMPPSQ	
456	PGSLGGPPGFGSGPPG		531	IQATTTPPGIPPPGVP	
457	PGFGSGPPGLGSAPGH		532	RPGMYPPPGSYRPPP	
458	PIHIGGPPGFASSSGK		533	PPPMGKPPGSIVRPSA	
459	VSMVPVPPGFSPIPP	RBMG_HUMAN	534	SHRPPPPGHR	Control
460	FNPSQPPGFMPVV		535	-	-
461	MGRGAPPGMGMPGPG	RSMB_HUMAN	536	-	
462	PGMMPGPPGMRPPMP		537	-	
463	TPMGMPPPGMRRPPP		538	-	
464	PGMRPPPPGMRPPPP		539	-	
465	GMRGPPPPGMRPPRP		540	-	
466	VGRATPPPGIMAPPNG	RSMN_HUMAN	541	-	
467	PGIMAPPPGMRPPMP		542	-	
468	TPIGMPPPGMRRPPP		543	-	
469	PGMRPPPPGIRGPPP		544	-	
470	GIRGPPPPGMRPPRP		545	-	
471	QPPYMPPPGMIPPPGL	RU1A_HUMAN	546	-	
472	PPGMIPPPGLAPGQIP		547	-	
473	LAPGQIPPGAMPQQL		548	-	
474	YSYPSLPPGYQNTTPP	S24A_HUMAN	549	-	
475	GYQNTTPPGATGVPPS		550	-	
476	LGSLPPPGMPPGSF	S3B4_HUMAN			
477	PPPGMPPGSFPPPPV				
478	FPPPVPPPGALPPGIP		1	SHRPPPPGHR	Control
479	PPPGALPPGIPPPAMPP		2	SQAPSHRPPPPGHRVQ	
480	MPPPPMPPGAAHGPP		3	ATSQHPPPPGHRSQAA	
481	GHPHAGPPGSQQPPP		4	VMQKRSRAIHSSDEGE	
482	QPFRPPPGMPHPGPP		5	NIzSVPHDSTQ	Negative Control
483	HDFRSPPPGMGLNQNR	SFPQ_HUMAN	6	HAMVAKPPGWSAVA	AAH07078
484	PPTSGAPPGSGPPTP		7	HAMVAKPPGWSAVA	AAH08386
485	PAVTSAAPPGPPTPP		8	MADQVLPPGQEEQAI	AAH14093
486	YCLAPPGGIDVTTYY	SFR8_HUMAN	9	PSELTCPGPGWEWDDA	AAH52617
487	TTTAPPGGTTTPPP		10	GSPGPPPGVWRDPRL	AAK83389
488	PPLGIPPPGFPGVPP	SRA4_HUMAN	11	CVGMSCPPGWHLDAT	AAL11095
489	FNPMHLPPGFLPPGPP		12	DELGPLPPGWEVRSTV	AAM90910
490	LIPLQRPPGMPPPHLQ		13	SQTVLPPGWQSYLSP	AAP35537
491	HCNVTCPPGLHGADCA	SRC2_HUMAN	14	LLWALRPPGWLQWHC	AAP35670
492	RAPSPPPGSEAAPSP		15	QTDPLPPGWRKVSIDI	ABB2_HUMAN
493	RDPTPRPPGLPEEATA		16	EVEAGLPPGWRKIHDA	ABB3_HUMAN
494	NITLGEPPPGFLHSWWC	SSB3_HUMAN	17	EWGLDTPPGPWAAEPA	ABD4_HUMAN
495	MPGGPIPPGFFQGPPG		18	MADQVLPPGQEEQAI	ABP_HUMAN
496	PGFFQGPPGSQSPSPA		19	TTRGMTPPGWLQYILP	AD29_HUMAN
497	PPGGGGPPGTPIMPSP		20	VPDSEAPPGWDRADSG	BAA20769
498	ISGISNPPGTPRDDGE		21	CVGMSCPPGWHLDAT	BAB69487

22	EVEAGLPPGWRKIHD A	BAC22578	97	NDLGPLPPGWEERIHL	
23	GDRDPLPPGWEIKIDP	BAG3_HUMAN	98	HAMVAKPPGWSAVA	Q8WUX5
24	CVGMSCPPGWGHLDAT	CAC83682	99	PLAWQNPPGWTPPPWW	Q8WY92
25	CVGMSCPPGWGHLDAT	CAD12729	100	PPGWQTTPGWQTPPGW	
26	PYQCDCPPGWTGSRCH	CAD97901	101	PPGWQTTPGWQGPPDW	
27	PYQCDCPPGWTGSRCH	CAD97988	102	HTDSEGPPGKGDPSP	Q8WY94
28	SQTVILPPGWQSYLSP	GAS7_HUMAN	103	ELEPEEPPGRELVPP	Q92888
29	TFRCACPPGKGSTCA	JAG2_HUMAN	104	ELEPEEPPGRELVPP	Q96BF4
30	PLAWQNPPGWTPPPWW	MGD1_HUMAN	105	SHRPPPPGHR	Control
31	PPGWQTTPGWQGPPDW	MGD1_HUMAN	106	VMQKRSRAIHSSDEGE	
32	PPGWQTTPGWQGPPDW	MYOF_HUMAN	107	NIZSVPHDSTQ	Negative Control
33	PSELTCPPGWEWEDDA	Control	108	EVEAGLPPGWRKIHD A	Q96DX9
34	SHRPPPPGHR		109	KWGLDTPPGPAAEPA	Q96E75
35	VMQKRSRAIHSSDEGE		110	ELEPEEPPGRELVPP	Q96F17
36	NIZSVPHDSTQ	Negative Control	111	VTQAPLPPGWQRVDQ	Q96F66
37	PTQVPVPPGWNQLPSG	NCO6_HUMAN	112	DRPEPLPPGWERRVDN	
38	QEPLSPLPPGWEERQDI	NED4_HUMAN	113	DPLGPLPPGWEKRTDS	
39	PTSSGLPPGEEKWQDE		114	PWYARNPPGSQLFLG	Q96GJ1
40	NDLGPLPPGWEERTH T		115	LLWALRPPGWLQPWHC	Q96HI4
41	LLWALRPPGWLQPWHC	NMT1_HUMAN	116	HAMVAKPPGWSAVA	Q96HL5
42	LLWALRPPGWLQWHD	NMT2_HUMAN	117	VPDSEAPPGWDRADSG	Q96HP1
43	GSPGGPPPGWVRDPR L	NOS3_HUMAN	118	WEPPAVPPGWTGVSSY	Q96ID2
44	EYKRCPPGWSKGSCQ	NTC1_HUMAN	119	PWYARNPPGSQLFLG	Q96IH9
45	EAAACLCPPGWGVERC Q	NTC3_HUMAN	120	TGECACPPGWTGAVCA	Q96KG6
46	GAYCLCPCPGWSGRLCD		121	DSEDELPPGWEERTTK	Q96KM3
47	ELEPEEPPGRELVPP	O00513	122	CVGMSCPPGWGHLDAT	Q96L37
48	WEPPAVPPGWTGVSSY	O15034	123	SAPFPDPPGWRDIEPE	Q96MJ8
49	TALLSPPPGWGGLSPL	O3A4_HUMAN	124	ESGSAPPGWRGPWWS	Q96NH1
50	LPPPPLPPGEEKVDN	O43165	125	LPPPPLPPGEEKVDN	Q96PU5
51	VTQSFLPPGWEEMRIAP		126	VTQSFLPPGWEEMRIAP	
52	NDLGPLPPGWEERIHL		127	NDLGPLPPGWEERIHL	
53	VTQAPLPPGWEQRVDQ	O43584	128	EVEAGLPPGWRKIHD A	Q96Q18
54	DRPEPLPPGWERRVDN		129	SSGVILPPGWPGYKD	Q96QU9
55	DPLGPLPPGWEKRTDS		130	DSEDELPPGWEERTTK	Q96RF2
56	PPEPARPPGQGAREG	O60432	131	SSGVILPPGWPGYKD	Q96RM4
57	STPARWPPGPWPLPPCS	O76032	132	VTPRTRPPGWEEDYWTA	Q96RZ4
58	CNQFDCCPPGWHIE	P82987	133	YNGSYVPPGWEVGL	Q96SG2
59	ADEEKLPPGWEKRM SR	PIN1_HUMAN	134	MRQLGYPPGWLKEAEL	Q96SK7
60	ADEEKLPPGWEKRM SR	PINL_HUMAN	135	RVRRALPPGWTQQAEE	Q96T57
61	YNGSYIPPGWREWLGL	Q86YV8	136	WESKPPPPGWRPKGLL	Q99570
62	EVEAGLPPGWRKIHD A	Q86Z13	137	ELEPEEPPGRELVPP	Q9BSB1
63	LSVIKSPPPGWEVGVYA	Q8IV01	138	SAPFPDPPGWRDIEPE	Q9BSE2
64	AGSPPVPPGWNPNSSS	Q8IYB2	139	DSEDELPPGWEERTTK	Q9BTT8
65	RGCPVSPPGWEELSPSP	Q8IYL2	140	GTRPSPPGWRLLRTG	Q9BUS0
66	RKYGGPPPGWVGSPPP	Q8IYX4	141	VPDSEAPPGWDRADSG	Q9BV84
67	PLAWQNPPGWTPPPWW	Q8IZ84	142	LPPPPLPPGEEKVDN	Q9BW58
68	PPGWQTTPGWQTPPGW		143	VTQSFLPPGWEEMRIAP	
69	PPGWQTTPGWQGPPDW		144	NDLGPLPPGWEERIHL	
70	MRQLGYPPGWLKEAEL	Q8N2K5	145	VTQAPLPPGWEQRVDQ	Q9BY75
71	VPDSEAPPGWDRADSG	Q8N347	146	DRPEPLPPGWERRVDN	
72	TDELPLPPGWEMTFTA	Q8N3P2	147	DPLGPLPPGWEKRTDS	
73	ELEPEEPPGRELVPP	Q8N4J4	148	EVEAGLPPGWRKIHD A	Q9BYD4
74	LPPPPLPPGEEKVDN	Q8N5A7	149	TDELPLPPGWEMTFTA	Q9GZV5
75	VTQSFLPPGWEEMRIAP		150	LPPPPLPPGEEKVDN	Q9H2W4
76	NDLGPLPPGWEERIHL		151	VTQSFLPPGWEEMRIAP	
77	QGSCSCP GWMGTICS	Q8N780	152	NDLGPLPPGWEERIHL	
78	LSLGPLPPGWLFAVL	Q8N819	153	ETREKEPPGQGQGE	Q9H2Y3
79	YPCMPPPPGWMVPGST	Q8N9P2	154	ETREKEPPGQGQGE	Q9H3B3
80	RGCPVSPPGWEELSPSP	Q8NA95	155	TRPQGVPPGWEELALS	Q9H407
81	LSRGLSPPGWTGRSLL	Q8NAQ8	156	VTQAPLPPGWEQRVDQ	Q9H451
82	EVLSVLPPGWPQDPEV	Q8NAY9	157	DRPEPLPPGWERRVDN	
83	PEKENRPPGWERTRKR	Q8NB13	158	DPLGPLPPGWEKRTDS	
84	PYQCDCPPGWTGSRCH	Q8NBT9	159	SEDLPLPPGWSVDWTM	Q9H4B6
85	LGNLGIPPGWFSGLGG	Q8ND23	160	LEREGLPPGWERVESS	
86	SGEAAGPPGQGCPDE	Q8NDF7	161	GSCTLCPPGWSYIQQS	Q9H5G4
87	ADEEKLPPGWEKRM SR	Q8NFL2	162	LWLHCHPPGWKNI	Q9H8T2
88	RKYGGPPPGWEGPHPQ	Q8NI52	163	SEDLPLPPGWSVDWTM	Q9H949
89	SGEAAGPPGQGCPDE	Q8TBE0	164	LEREGLPPGWERVESS	
90	RKFGGPPPGWEGPPP P	Q8TBY0	165	PWYARNPPGSQLFLG	Q9H9K2
91	GPPGRGPPGWRREEL	Q8TC11	166	SEDLPLPPGWSVDWTM	Q9HAK9
92	PLAWQNPPGWTPPPWW	Q8TEN0	167	LEREGLPPGWERVESS	
93	PPGWQTTPGWQTPPGW		168	ETREKEPPGQGQGE	Q9HAW0
94	PPGWQTTPGWQGPPDW		169	MADQVLPPGQEEQAI	Q9HBM7
95	LPPPPLPPGEEKVDN		170	DSEDELPPGWEERTTK	Q9NPC9
96	VTQSFLPPGWEEMRIAP	Q8WUU9	171	RKYGGPPPGWDAPPE	Q9NQ93

172	RKYGGPPPGWDAAPPE	Q9NQ94	199	HSPSQLPPGWTIRSTF	Q9Y2Y4
173	RKYGGPPPGWDAAPPE	Q9NQX8	200	ITGPGSPPGWATLQIQ	Q9Y405
174	RKYGGPPPGWDAAPPE	Q9NQX9	201	DELGPLPPGWEVRSTV	SUF1_HUMAN
175	DSEDELPPGWEERTTK	Q9NRF4	202	EELGPLPPGWEIRNTA	SUF2_HUMAN
176	DSEDELPPGWEERTTK	Q9NRF5	203	DQRRTLPPGVSLGRA	TPP1_HUMAN
177	DSEDELPPGWEERTTK	Q9NRF6	204	ERPQPLPPGWERVDD	WWP1_HUMAN
178	MRQLGYPPGWLKEAEL	Q9NSS2	205	DPYGPLPPGWEKRVDS	WWP2_HUMAN
179	MRQLGYPPGWLKEAEL	Q9NSS3	206	TWERPLPPGWEKRTDP	
180	LPPPLPPGEEKVDN	Q9NT88	207	DPLGPLPPGWEKRQDN	
181	VTQSFLPPGWEEMRIAP		208	IQEPALPPGDEMKYTS	
182	NDLGLLPPGWEERIHL		209	VPDSEAPPGWRADSG	Y310_HUMAN
183	GPPGRGPPGWRREEL	Q9NTV3	210	SHRPPPPGHR	Control
184	ETREKEPPPGWGQQGGE	Q9NUY6	211	VMQKRSRAIHSSDEGE	
185	SHRPPPPGHR	Control	212	NIZSVPHDSTQ	Negative Control
186	VMQKRSRAIHSSDEGE	Control	213	-	-
187	NIZSVPHDSTQ	Negative Control	214	-	
188	RKYGGPPPGWEGHPQ	Q9NXG3	215	-	
189	DSEDELPPGWEERTTK	Q9NZC5	216	-	
190	DSEDELPPGWEERTTK	Q9NZC7	217	-	
191	RKYGGPPPGWDAAPPE	Q9NZD3	218	-	
192	ARHRSHPPGWAASARP	Q9P0U7	219	-	
193	MDCPALPPGWKKEEVI	Q9UBB5	220	-	
194	MDCPALPPGWKKEEVI	Q9UIS8	221	-	
195	YNGSYVPPGKWEVGL	Q9ULH3	222	-	
196	CNQFDCPPGWHIEEWQ	Q9ULI7	223	-	
197	YNGSYIPPGWREWLGL	Q9UPSS5	224	-	
198	SGEAAGPPGWQGCPDE	Q9Y2F4	225	-	

**Table 12.3: Viral peptides synthesized on the membrane depicted in Fig. 8.6**

List of peptides, synthesized on the membrane, depicted in Fig. 8.6. Columns are as in Table 12.2.

SPOT-number	Sequence	Accession Number/Description			
<b>PPG[AEFHILMSTVWY]</b>					
1	SHRPPPPGHRV	Control	37	FFIGLVPPGYKYLGP	COAT_MEVA
2	SHRPPPPGHRV		38	MVPPGYKYLGP	COAT_MUMIM
3	-	-	39	SIPMSHPPGTIFIKLA	COAT_PAVBO
4	-		40	LAALIVPPGIEPVESP	COAT_SMSV1
5	-		41	TFSSLKPPGSLLKHGS	
6	-		42	LAALLVPPGVEPIESV	COAT_SMSV4
7	-		43	TFALLKPPGSLIKHGS	
8	-		44	IIVCCVPPGFTSSSLT	COAT_SOUV3
9	-		45	ISQPSTPPGTIDINLWE	
10	-		46	LAPPVFPPGFGEALVY	
11	-		47	PPGPPGPGLPGLFVT	COLL_HVSC
12	-		48	PTTPVPPGYLIQHEE	CORA_HPBDU
13	-		49	LCCLSCPCTGYASRLC	CRMB_CAMPS
14	-		50	IFPNGKPPGSNQPNPQ	DNBI_HV11
15	-		51	LFPNGKPPGSNDNPNPQ	DNBI_HV2B2
16	-		52	LFPRGHPPGIDTPNPQ	DNBI_HSVEB
17	-		53	EDHQPNPPGEGLKFPPL	DPOL_ADE02
18	-		54	YVLIAAPPGSSKNVNPN	DPOL_GPCMV
19	-		55	LKMQGVPPFGFRVIQR	DPOL_RHCM6
20	-		56	AYDTIAPPGERQLIKT	DUT_VACCC
21	HPVHAGIAPGQMREP	HIV I GAG-protein (trans)	57	DGEPDVPPGAIEQGP	EBN1_EBV
22	HPVAAGIAPGQMREP		58	AAPAQPPPVGINDQQL	EBN2_EBV
23	HPVAMGIAPGQMREP	HIV I GAG-protein (cis)	59	LPFGCNPPGSIDVSCY	ENV_AVISN
24	HPPAMGPLPPGQIREP		60	LTRLCPPGHVFCGN	
25	KKHQKEPPFLWLMGYEL	HIV-Po1	61	VAMVTSPPGYRIVNDT	ENV_BIV06
26	DPTKAGPPGEGLRKPV	ABL_MLVAB	62	RPPQPPPPTASIVPE	ENV_FRSFB
27	PQSTAKPPGTPTSPVS		63	RFRYCAPPFGFALLRCN	ENV_HV2BE
28	RIRPFHPPGPSWPANRP	BRL1_EBV	64	RPFSSPPPGYIQLQIHI	
29	SEFDLLPPGSRIVECN	COAT_DSDNV	65	RFRYCAPPFGFAILRCN	ENV_HV2CA
30	LAAIVVPPGIDPVQST	COAT_FCVC6	66	KFRYCAPPFGFALLRCN	ENV_HV2D1
31	KFHLLKPPGSMLTHGS		67	RFRYCAPPFGFLLRCN	ENV_HV2D2
32	LAAIVVPPGVDPVQST	COAT_FCVF4	68	KFRYCAPPFGYALLRCN	ENV_HV2G1
33	KFHLLKPPGSVLTNGS		69	RFRYCAPPGLCLLRCN	ENV_HV2KR
34	ARRGLVPPGYKYLGP	COAT_FPV	70	RPVFSSPPPGYIQLQIHI	
35	SEFDLLPPGSRVVECN	COAT_GMDNV	71	RFRYCAPPFGYALLRCN	ENV_HV2RO
36	QLVNYEPPGAFDPISN	COAT_IRV16	72	RFRYCAPPFGVLLRCN	ENV_HV2SB
			73	RPPQPPPAGAASIVPE	ENV_MCFF
			74	RCRYCAPPFGYALLRCN	ENV_SIVM1
			75	RPLQPPPAGAASIVPE	ENV2_FRSFV
			76	RLRVCIPPGYFGRFLA	EXXK_ADE02

77	NGLQEKKPGVLSLKYT	FIB1_ADE40	152	-	
78	DGLQENPPGVLAALKYT	FIB2_ADE40	153	-	
79	DGLQEKKPGVLAALKYT	FIB2_ADE41	154	-	
80	NGFQESPPGVLSLRVS	FIBP_ADE02	155	-	
81	NGFQESPPGVLSLRLS	FIBP_ADE05	156	-	
82	NGFQNFPVGVLKLA	FIBP_ADE08	157	-	
83	DGFQNFPVGVLKLA	FIBP_ADE09	158	-	
84	NGLQEKKPGVLAALNYK	FIBP_ADE12	159	-	
85	NAFQEKKPGVLSLNYK	FIBP_ADE31	160	-	
86	QGLTESPPGTLAVNVS	FIBP_ADECT	161	-	
87	CFPILHPPGAPSARHP	GAG_HTLV2	162	-	
88	FPVAQAPPGLIPTAPP	GAG_HV2G1	163	-	
89	MAGLDPPPFPSSKH	GAG_JSrv	164	-	
90	AWRAIPPPGVKTVLA	GAG_MMTVB	165	-	
91	KGSKRAPPGLCPRCKK		166	-	
92	GQGGDTPPGAEQSRAE	GAG_RSVP	167	-	
93	DKQAQFPVPLTQIQS	GAG_SMRVH	168	-	
94	FRLTDPGFTGGTTN	HELI_HSVEB	169	-	
95	PIYSFTPVGNCNSKGK	HEMA_MUMP1	170	-	
96	KTRIIINPPGSSRDWVH	HEMA_PI4HA	171	-	
97	VERIIINPPGVLDVWAT	HEMA_SV5	172	-	
98	YWSVLTPPGEADDPLP	HEPA_HS2H	173	-	
99	NPHWLPPPFGYTGGFE	HEX3_ADE02	174	-	
100	NPHWLPPPFGYTGEFD	HEX3_ADE12	175	-	
101	NKHWTPPPFGYTGDDE	HEX3_ADEM1	176	-	
102	FNPFSGPPGHYPDQFI	HEX8_ADE02	177	-	
103	FQPFSGPPGSYPDFI	HEX8_ADEB2	178	-	
104	INPFSGPPGTYPDQFI	HEX8_ADEP3	179	-	
105	NQEVIIPPGIKFTVVT	HLIK_ASFB7	180	-	
106	AATRPAPPAGPRSSSS	ICP0_HS2H	181	SHRPPPPGHRV	Control
107	PRPRPRPPGVGPGGGA	ICP3_HS2H	182	SHRPPPPGHRV	
108	PRPRSPPPGAGPGGGA	ICP3_HS1D	183	-	-
109	GALPPAPPGIRWASAT	ICP4_HS2H	184	-	
110	PGGGLLPPGARILEYL	ICP4_HSVEB	185	-	
111	I PRVMWPFGAAETV	ICP4_VZVD	186	-	
112	GKRRHLPPGARAPRAP	IE63_EBV	187	-	
113	RVEPRGPPGAPSSGN	IRS1_HCMVA	188	-	
114	RDPCCRPPGTSSFPRG	J1L_HCMVA	189	-	
115	ALIPPTPPGTNLILGT	KITH_HS2H	190	-	
116	MAACVPPGEAPRSAS	KITH_HSVE4	191	LLLAYSPPGASVPTSR	POLG_EC05N
117	DMSPAAPPGLLFTLPA	KITH_VZV4	192	LLLAYSPPGASVPKAR	POLG_EC09H
118	FTLPAEPPGTNLVVCT	KR1_HS2H	193	FLLAYAPPGANPKNR	POLG_EC11G
119	PPCGASPPGIRRRSRD	KR2_PRVN3	194	FLLAYAPPGANPKSR	POLG_EC12T
120	LFAALLPPGSGPSAEA	MYC_AVIM2	195	QTSLVVPGAPATCGV	
121	RAPRAAPPGANPAALL	MYC_AVIME	196	FLIAYAPPAGVPGSR	POLG_EC30B
122	PLGRRGPPGAGPAALL	NCAP_CVBF	197	FLIAYTPPGAGKPTSR	POLG_EMcv
123	AIPPTRFPPTVLPQGY	NCAP_IBVG	198	YMVAYIPPGVETPPDT	POLG_FMDV1
124	YCKRTIIPPYKVQDFV	NCAP_IBV	199	YMVAYIPPGVETPPET	POLG_FMDVA
125	DAGVNNPPGAEYKWYD	PEN3_ADEG1	200	YMVAYAPPGMEPKTP	POLG_FMDVO
126	DLEKLSPPGTFQET	PIV2_ADEG1	201	YMVAYVPPGVETPPDT	POLG_FMDVZ
127	IWAQSLPPGTSQAQKAE	POL_BAEVM	202	VLATATPPGSVTPHP	POLG_HCV1
128	STGLPYPPGIKECEHL	POL_BIV06	203	LVGWPKPPGARSLTPC	POLG_HCVBK
129	LLQGHYPGPGKQYKY	POL_SFV1	204	VLATATPPGSVTVSHP	POLG_HCVH
130	FYFEKLPPGAYKELTT	POL1_GFLV	205	LVGWPSPPGTKSLEPC	POLG_HCVJ6
131	GYTTSGPPGSMEPYIY	POL2_TRSVR	206	VLATATPPGSVTTPH	
132	QTNMVIPPGFPNTAGI	POLG_BOVEV	207	LVGWPSPPGTKSLDPC	POLG_HCVJ8
133	YQVMYVPPGAPVPSNQ	POLG_CXA16	208	VLATATPPGTVTPHS	
134	LQYMYVPPGAPRPTSR	POLG_CXA21	209	LVGWPAPPGARSMTPC	POLG_HCVJA
135	LLLSYSPPGAKPKPTNR	POLG_CXA24	210	VLATATPPGSITVPH	
136	DQIMYIIPPGAPRPTSW	POLG_CXA24	211	LVGWHAPPGARSLTPC	POLG_HCVJT
137	ILLSYSPPGAKPKPTTR	POLG_CXA24	212	VAAQLAPPGAASAFVG	POLG_HCVTW
138	YQLMYIIPPGAPRPTAW	POLG_CXA24	213	LQYMFVPPGAPKPDTR	POLG_HE71B
139	FLIAYSPPGANPPKTR	POLG_CXA9	214	LQYMFVPPGAPKPESR	POLG_HE71M
140	QTGMIVPPGTPNSSI	POLG_CXA9	215	LILAYTPPGAGPKQDR	POLG_HRV14
141	FLLAYSPPGAGVKPNR	POLG_CXB1J	216	VQAMYVPPGAPNPKEW	
142	FLLAYSPPGAGAPTTR	POLG_CXB3N	217	VLLAYTPPGIGKPRSR	POLG_HRV16
143	FLLAYSPPGAGAPDSR	POLG_CXB4E	218	MQYMYVPPGAPIPTTR	
144	FLLAYSPPGAGAPTTR	POLG_CXB5P	219	AVMIHGPPGTTGKSITT	
145	DSFYQGPPGEAVERAI		220	LLLAYTPPGIDKPATR	POLG_HRV1B
146	IFMTATPPGSVEAFPQ	POLG_DEN1S	221	MQYMYVPPGAPIPKTR	
147	IFMTATPPGSRDPFPQ	POLG_DEN26	222	LLLAYTPPGIAEPTTR	POLG_HRV2
148	IFMTATPPGATDAFPQ	POLG_DEN3	223	MQYMYVPPGAPVPSNR	
149	IFMTATPPGATDPFPQ	POLG_DEN4	224	AIVIHGPPGAGKSITT	
150	FLLSYAPPGAGAKTR	POLG_ECO1F	225	LLIAYTPPGVGKPKSR	POLG_HRV89
151	-	-	226	LQFMYVPPGAPVPEKR	

227	IFMTATPPGTTDPFPD	POLG_JAEV1	302	IVDPGCPPGVAPSIPV	TEGU_HCMVA
228	IFMTATPPGTSDFPPE	POLG_KUNJM	303	TRRSPEPPGADLAQLF	TEGU_HSV11
229	IYLSATPPGHAPDTGS	POLG_MCFA	304	PFKFTGPPGYTIPVHG	TEGU_HSVEB
230	LLVSYAPPGADPPKKR	POLG_POL1M	305	PWQLSPPPGVKANVDA	TEGU_VZVD
231	YQIMYVPPGAPVPEKW		306	GPEPLPPGARPRHRF	TERM_ADE02
232	LLVSYAPPGAEAPKSR	POLG_POL2L	307	GPEPLPPGARPRRRF	TERM_ADE12
233	YQIMYIAPPGAPIPGKW		308	NIVSSLPPGSEGVIYV	U120_HSVMG
234	LLVSYAPPGAKAPESR	POLG_POL2W	309	SSVAGDPPGADGPYVT	UL03_HSV2H
235	YQIMYIAPPGAPIPGKR		310	KPARDDPPGAGS	UL06_EBV
236	LLVAYAPPGAQPPTSR	POLG_POL32	311	DGVVQVPVPGLLNGLR	UL07_VZVD
237	YQIMYIAPPGAPTPKSW		312	TPTPTGPPGAPAAPLS	UL14_HSV11
238	ILVAYAPPGAQPPTSR	POLG_POL3L	313	GSLYPRPPGSGLAKHP	UL16_HCMVA
239	LKVSAATPPGHEVDFKT	POLG_PPVD	314	PLAPPGPPGTLPRPDS	UL16_HSV11
240	LKVSAATPPGHEVEFKT	POLG_PPVNA	315	DLGSLCPGGSRARHLG	
241	LKVSAATPPGVEVDFKT	POLG_PPVSK	316	TYDELLPPGTRYGADS	UL17_HSVEB
242	DNFFQGPPGEVVERAI	POLG_SDVH	317	SVVCDGPPGSPTDSAR	UL24_HCMVA
243	DNFFQGPPGEVMGRAI	POLG_SDVU	318	VLPVVWPPGWNVLQE	
244	FIIAYTTPGAGKPTTR	POLG_TMEVG	319	FMLTYPGTELRLCN	
245	FRIAYTTPGAGKPTTR	POLG_TMEVG	320	LLARTLPPGSGEIVLA	UL24_HSVE1
246	ILMTATPPGTSDFPH	POLG_YEFV1	321	LLAKTLPPGSGEILLA	UL24_HSVE4
247	ISLVSNPNGVNVRVITR	POLN_EEV3	322	NRQAAYPPGTfadNKI	UL25_EBV
248	TSLVSNPNGVNVRVITR		323	GGDGGAPPGLAVAEME	UL25_HSV11
249	TSLVSTPPGVNRVITR	POLN_EEVV	324	MATSPPGVLASVAV	UL32_HSV11
250	PPEVLLPPPPTYRTASY	POLN_HEVBU	325	AAKDLPPPGYRVGRG	UL41_HCMVA
251	PPEVLLPPPPTYRTSSY	POLN_HEVME	326	VGVLLCPGSGTGRSG	UL43_HSV11
252	SSTAPLPPGTYEPAYL	POLN_LORDV	327	CLEVELPPGERCACGR	UL49_EBV
253	NPMVVDPGTTGPTTS	POLN_MANCV	328	PAAQAHPPGEAGGGFS	
254	IIASVIPPVGDPSSIR		329	PPRPRAPPGANAVASG	UL49_HSVC
255	LVRAVIPPGIEIGPGL	POLN_RHDV	330	DSPKRAPPAGAIASG	UL49_VZVD
256	AGARPRPPGHRRARG	POLN_RUBVT	331	LPFGDAPPGFDDPRNF	UL52_PRVKA
257	VHSFYRPPGTQTSVKV	POLN_SINDO	332	STIPSNPNGFDELSNF	UL52_VZVD
258	VHSFYRPPGTQTCVKV	POLN_SINDV	333	EIDLGLPPGVQVGDLL	UL71_EBV
259	RVKDDSPGEGQVKWSA	POLN_SOUV3	334	EIEIAQPPGVFVGDI	UL71_HSVSA
260	VIMMCPPGIGTKAA		335	RSRSALPPGVPRPDFIF	UL87_HSV6U
261	SSPEPLPPGVYEPAYL		336	KRPCGLPPGVRLVPPA	UNG_PRVIF
262	DEIGLYPPGYLTLLQM	POLR_ASGVP	337	PCPGGLPPGAPCAIL	US02_HSVBS
263	QYTSDKPPGFYWNHHG	POLS_EEEV	338	GAITRPPGAGAIASG	US15_HCMVA
264	FILAKCOPGEFLQVSI	POLS_SFV	339	GTVIYVPPGIQETRLA	
265	EGRYRYPGPGVLTYDS	PRTP_HSV11	340	SLPISAPPGRWLDFVE	US26_HCMVA
266	HVFKSAPPGLYAVSEL	PRTP_HSVB2	341	PPPSVAPPGEKKELPA	US29_HCMVA
267	PLFGTTPPGTDFPLAL	RIR2_HSVBC	342	PRSACAPPGTLMARVR	V120_HSV11
268	EDTIKIPPGIANSQNA	RPO1_FOWPV	343	YIWPWAPPFGSLPGAS	V18K_MLVAB
269	SEYVEGPGSGKTFHL	RPOA_EAV	344	LRPQLKPPGLPKPQPI	V51K_BWYVF
270	SKFIVGPPGSGKTTWL	RPOA_LELV	345	LTPQLKPPGLPKPQPI	V51K_BWYVG
271	SEYIVCPGTDQEAIS	RRP2_THOGV	346	QCCNRCPGEGFAKVR	VA53_VACCC
272	STRGPPLPPGTNLGSE	RRP3_THOGV	347	AAPNRDPPGYRYAAAM	VCAP_HSV11
273	VTFVMPGPPGTGKTTFV	RRPB_BEV	348	EYQFKRPPGSEMTQD	VCAP_VZVD
274	YCTVQGPPGTGKSHLA	RRPB_CVMA5	349	TETSTVPPGTAVLLPA	VCOM_ADEB2
275	KAARAPPGEQFKHLI		350	KSPCAKPPGVHREQRV	VE1 HPV70
276	KAARAPPGEQFKHLV	RRPB_CVMJH	351	LKHVPLPPGMNISGFT	VE2_BPV1
277	RTTVQGPPGSGKSHFA	RRPB_IBVB	352	LSTVKVPPGIVQVILGH	VE2 HPV03
278	PVNSKAPPGEQFNHLR		353	PVTSSTPPGSPGGQAD	VE2 HPV05
279	EGQRPDPPGEFLNRVK	RRPL_EBOSM	354	PVTSSTPPGSPGGQAD	VE2 HPV08
280	LGNSDRPPGLDNLNQSN		355	LNVVKVPPGIVQVILGY	VE2 HPV10
281	KLYDЛЛPPGELRKAIC	RRPL_MABVP	356	PVTSSTPPGSPGQRDP	VE2 HPV12
282	HCDIEIAPPGSNQSLLD	RRPL_NDVB	357	IKIMKLPPGVWDWSLG	VE2 HPV15
283	DDYTKLPPGLIESVVM	RRPO_NM	358	IQKMKLPPGVWDWSLG	VE2 HPV17
284	RTTVRGPPGFKNPFTQ	RRPO_P1AMV	359	LANVKIPPGMQAHLG	VE2 HPV29
285	EVIKTAPPGSFVYRAL	RRPO_PMMVJ	360	LSTVKLPPGPIKSCIGY	VE2 HPV32
286	DEMQLYPPGYFDLVVS	RRPO_PVMR	361	LKTMKLPPGVWDWSLG	VE2 HPV37
287	DDYSKLPPGYIEALIC	RRPO_PVX	362	PVTSSTPPGSPGGQTD	VE2 HPV47
288	DDYSKLPPGYIEALVS	RRPO_PVXCP	363	PVTSSTPPGSPGRQAD	VE2 HPV5B
289	DDYSKLPPGYIEALVC	RRPO_PVXX3	364	IDHQVVPGTTSKAKA	VE2 HPV70
290	EVHKTAPPGSFVYKCI	RRPO_TMOB	365	LQQVPLPPGMSAHGVT	VE2_PAPVD
291	EVHKTAPPGSFVYKSL	RRPO_TMV	366	LKRPVPLPPGMRAQALT	VE2_PAPV
292	LGKGSIPPGVTAVLTS	RRPP_PI2H	367	TPAAAAPPGVPKPEHG	VG02_HSVI1
293	LGKNTIIPGVTLGLLTN	RRPP_SV5	368	LPKRDPPPGVPTDEM	VG09_VACCC
294	YRAVGAPPGEAAAAAQ	SPLR_NPVOP	369	IRKCCDPPGIGFPNP	VG11_HSVI1
295	KVSQIFPPGIITMNYY	TALA_BFDV	370	SGSRSGPPGTVTSLYV	VG11_HSVA
296	KRTQIFPPGLVTMNEY	TALA_POVBA	371	ALECTIPPGSMEIFIL	
297	KVTQIFPPGIVTCNEY	TALA_POVBO	372	MIPPGIPVQVQLS	VG17_HSVI1
298	KRTQVFPPGIVTMNEY	TALA_POVJC	373	DFPWPFPPGVEIPWET	VG27_BPMD2
299	KKTQIFPPGIVTSNEY	TALA_POVMK	374	APQEPPPPGTSAPTLE	VG28_HSVI1
300	KRTQIFPPGIVTMNEF	TALA_SV40	375	KFGKTVPPGEGLRAFN	VG39_HSVI1
301	HQKMNSPPGIPIPPPP	TAMI_POVHA	376	DVPEGRPPGFYFEFR	VG42_BPMD2

377	NLLYAI <sup>P</sup> PGSTIPGMR	VG59_HSVI1	414	AQAQPPPPGTQAPEAH	VP40_EBV
378	KSMETVPPGAYSEVFL	VG63_HSVI1	415	VPAATAPPGATVAGAS	VP40_HCMVA
379	DLPPLDLP <sup>P</sup> GAYE <sup>P</sup> PD <sup>L</sup>	VG65_HSVI1	416	PESTDIPPGSIAAPQ	VP40_HSV11
380	DLPRLDLP <sup>P</sup> GAYE <sup>P</sup> PD <sup>L</sup>		417	PGYGFPPPGLESQIMA	VP40_HSVBC
381	PTTAVI <sup>P</sup> PGTHSVPA	VG72_HSVI1	418	PYVPLPPP <sup>P</sup> GAMPFAPP	VP40_HSVE2
382	CILEAY <sup>P</sup> PGAGPVSAI	VG75_HSVI1	419	LVRYDEPPGEAELFLP	VP40_SCMVC
383	PNPTPPPGASANASV	VGLB_HSV11	420	TGGYGC <sup>P</sup> PGHFGGPYG	VP40_VZVD
384	GGLES <sup>P</sup> PGAPGLHRR	VGLB_MCMVS	421	GVFGPLPPGTVGLLL <sup>G</sup>	VPRT_JSRV
385	IVRH <sup>F</sup> Y <sup>P</sup> PGSVVVSWR	VGLC_HSVMB	422	GPPPPPPPGLV	VPX_HV2BE
386	LDQLTD <sup>P</sup> PGVRVYHI	VGLD_HSV11	423	GPPPPPPPGLA	VPX_HV2D2
387	PDRLTDP <sup>P</sup> PGVRVYHI	VGLD_HSV1A	424	PGPPPPP <sup>P</sup> GLV	VPX_HV2KR
388	LDQLTD <sup>P</sup> PGVKRVYHI	VGLD_HSV2	425	GRPGRVPPGLD	VPX_SIVA1
389	TCRCAD <sup>P</sup> PGIISQNYG	VGLF_NDVA	426	GRAGRVP <sup>P</sup> GLD	VPX_SIVAG
390	TCRCVN <sup>P</sup> PGIISQNYG	VGLF_NDVB	427	GGAPP <sup>P</sup> PGLA	VPX_SIVAI
391	TCRSAD <sup>P</sup> PGIISQNYG	VGLF_NDVU	428	GRANRVP <sup>P</sup> GLE	VPX_SIVAT
392	HGPADAPP <sup>P</sup> GAPP <sup>P</sup> P	VGLG_HSV2H	429	PVGPVF <sup>P</sup> PGMNWTDLI	VS06_ROTBR
393	PIRPTL <sup>P</sup> PGILGPLAP		430	PVGPVF <sup>P</sup> PGMNWTEI	VS06_ROTRE1
394	TDFPPCPGTTIQTAV	VGLG_SIGMA	431	EESPTGP <sup>P</sup> PGSIRTWFO	VSGP_EBOSB
395	DPADENPPGALPGPPG	VGLH_HSV11	432	LCCTSCP <sup>P</sup> GSYASRLC	VT2_MYXVL
396	GDPKPQ <sup>P</sup> PGVNHEPPS	VGLI_HSV11	433	LFYHCEPPGS <sup>P</sup> AVLYPF	VTER_HSV11
397	RPAPGSP <sup>P</sup> GIPEYAED	VGLM_HSV11	434	FKNHRFP <sup>P</sup> GH <sup>L</sup> WTMQL	VU1_HSV6U
398	LATLATPPGALLLGAL	VGLM_HSVBC	435	TRMEFMP <sup>P</sup> GTQPNLTI	VU54_HSV6U
399	HDAITTP <sup>P</sup> PGIMTPIAI	VHS_HSVEB	436	LGKGSVP <sup>P</sup> GTIAVLTN	VV_SV41
400	SEAISTPPGVLTPIAI	VHS_PRVKA	437	LNYGGVP <sup>P</sup> GHVMCCPR	Y054_NPVAC
401	PSIISTPPGV <sup>P</sup> TVAV	VHS_VZVD	438	LSYGGAPP <sup>P</sup> GHLMCCPR	Y054_NPVOP
402	CVEDK <sup>P</sup> PPGSC <sup>P</sup> PIEL	VL1_HPV14	439	MDYFGAPP <sup>P</sup> GARPAGI	
403	CATDN <sup>P</sup> PPGSC <sup>P</sup> IEL	VL1_HPV21	440	NVPLIEP <sup>P</sup> GEIVT <sup>P</sup> GN	Y119_NPVOP
404	EAYYL <sup>P</sup> KPGEMELKMP	VL1_PAPVD	441	ASIHP <sup>P</sup> PG <sup>P</sup> LIDGSV	YAL4_ICMV
405	FTIPTI <sup>P</sup> PG <sup>P</sup> GLR <sup>I</sup> YV	VL2_HPV04	442	FANELL <sup>P</sup> PGFSITTPK	YBL2_SFV1
406	MIMPTI <sup>P</sup> PGVALKLF <sup>I</sup>	VL2_HPV60	443	LRLCKWP <sup>P</sup> GTNYSTPG	YG36_BPMV4
407	FSIPTI <sup>P</sup> PG <sup>P</sup> GLR <sup>I</sup> YV	VL2_HPV65	444	QQTRRL <sup>P</sup> PGWGQRTAP	YHL1_EBV
408	RASG <sup>P</sup> PP <sup>P</sup> GA <sup>P</sup> R <sup>S</sup> TA <sup>K</sup>	VMAT_MEASY	445	AQRGH <sup>P</sup> PP <sup>P</sup> GA <sup>P</sup> R <sup>S</sup> PG	YHL1_EBV
409	NKLISRPPG <sup>P</sup> GLVEPIHM	VNCS_AEDEB	446	TVAQSFP <sup>P</sup> GE <sup>P</sup> ALR <sup>D</sup> E	YHL4_HCMVA
410	RIFDRM <sup>P</sup> PGFQPSKHL	VP10_RDVA	447	QT <sup>V</sup> WVTP <sup>P</sup> PG <sup>S</sup> TS <sup>V</sup> SSV	YOR3_SOUV3
411	RVAVL <sup>P</sup> PGWENDNL <sup>S</sup>	VP18_NPVOP	448	NLAIYI <sup>P</sup> PGSDFYIF	YORM_TTV1
412	LDGTDAPP <sup>P</sup> GALT <sup>P</sup> NNDD	VP19_HSV11	449	SHR <sup>P</sup> PPP <sup>P</sup> GH <sup>R</sup> V	Control
413	LGVAPL <sup>P</sup> PGAFIQNTG	VP23_HSVEB	450	SHR <sup>P</sup> PPP <sup>P</sup> GH <sup>R</sup> V	

**Table 12.4: Peptides synthesized on membranes shown in Fig. 9.3**

List of peptides, synthesized on the membranes, depicted in Fig. 9.3. Columns are as in Table 12.2. Peptides on different membranes are separated by rows, indicating the GST-GYF domain fusion constructs used for incubation and the motif, applied for the database search. Note that the peptide membrane for the relaxed consensus sequence of PERQ2 is identical to the membrane shown in Fig. 8.3, incubated with CD2BP2-GYF GST-fusion protein. Sequences and identifiers or descriptions of these peptides are listed in Table 12.2 and are omitted here. Peptides with identifiers in italicized letters were synthesized onto the membranes for other reasons and are stated here just for completeness.

SPOT-number	Sequence	Accession Number/Description			
	<b>PERQ2</b>				
	<b>PPG[AEFHILMSTWY] x (0,40) PPG[AEFHILMSTWY]</b>				
	-Sequences listed in Table 12.2-				
	<b>PERQ2</b>				
	<b>PPGL</b>				
1	SHR <sup>P</sup> PPP <sup>P</sup> GH <sup>R</sup>	Control			
2	SQAPSHR <sup>P</sup> PP <sup>P</sup> GH <sup>R</sup> VQ				
3	ATSQH <sup>P</sup> PPP <sup>P</sup> GH <sup>R</sup> SQ <sup>A</sup>				
4	VMQKRSRAIHSSDEGE				
5	NI <sup>P</sup> YSVPH <sup>D</sup> TQ	Negative Control	10	LLIL <sup>P</sup> PPV <sup>P</sup> NPSPTLR	
6	SITSPP <sup>P</sup> SPAL <sup>P</sup> KYKL	O75137	11	VPFSPGP <sup>P</sup> APP <sup>P</sup> PHMGEL	
7	PILQEEPL <sup>P</sup> PLALVPF		12	PQQQQQQQQQQQQQQP	
8	ERWRPHSPDGR <sup>P</sup> SAGW		13	VASPPPSP <sup>P</sup> AMPKYKLA	
9	VQKEPI <sup>P</sup> EQEMDFRP		14	GSITSPPPSPALPKYK	Q6Y7W9:
			15	SHR <sup>P</sup> PPP <sup>P</sup> GH <sup>R</sup>	Control
			16	SQAPSHR <sup>P</sup> PP <sup>P</sup> GH <sup>R</sup> VQ	
			17	ATSQH <sup>P</sup> PPP <sup>P</sup> GH <sup>R</sup> SQ <sup>A</sup>	
			18	VMQKRSRAIHSSDEGE	
			19	NI <sup>P</sup> YSVPH <sup>D</sup> TQ	Negative Control
			20	KGVPCEP <sup>P</sup> PG <sup>P</sup> GLDDPLAQ	AA2A_HUMAN
			21	YLDKAPP <sup>P</sup> GLPAETIK	AAB50213
			22	GSGPQ <sup>P</sup> PP <sup>P</sup> GLV <sup>P</sup> CGA	AAH06132
			23	MLVIP <sup>P</sup> GLSEEEEA	AAH25235
			24	QPPLNC <sup>P</sup> PG <sup>P</sup> LEYLSQI	AAH32718
			25	SMDRSI <sup>P</sup> PG <sup>P</sup> LVNGLAL	AAH33634
			26	HDHSP <sup>P</sup> PG <sup>P</sup> GLQPASSA	AAH36093
			27	PPG <sup>P</sup> PP <sup>P</sup> PG <sup>P</sup> GLPPSGVP	AAH38224
			28	AHNKAL <sup>P</sup> PG <sup>P</sup> LSKEQAP	AAH40207
			29	ARYGVE <sup>P</sup> PG <sup>P</sup> LIKLEKE	AAH40470
			30	PPPPS <sup>P</sup> PP <sup>P</sup> GLLPLLPP	AAH52968
			31	PSEN <sup>P</sup> MP <sup>P</sup> GLSTPTAS	AAH52983

32	DSAMHIPPGLKPHPER	AAK2_HUMAN	107	GAMDGAPPGLGAPLGA	NK24_HUMAN
33	MGGQQAPPGLGPILED	AAM20739	108	LSPPPPPPGLYFSPSA	NK61_HUMAN
34	ELAGEMPPGLNFSDLDA	AAP35525	109	GPRCACPPGLSGPSCR	NTC3_HUMAN
35	SGVPGRPPGLEEELTL	AAP35630	110	TFHCLCPGLEGQLCE	NTC4_HUMAN
36	EEYAWVPPGLKPEQVY	AAP36091	111	TKVAVTPPGLAREDWK	NUAM_HUMAN
37	AGPPPAPPGLPAGADC	AAP36093	112	IQRGQWPPGLPBPSTY	O00443
38	KLLDRPPPGLQRPEDR	AAP41133	113	SPPPQIPPPGLRPFCA	O15446
39	AGPPPAPPGLPAGADC	AAP44001	114	GSLQPRPAGLSSDPST	O43263
40	ETLSSPPPGLEKGADR	AAP46636	115	SHRPPIPPGHR	Control
41	YQDRVAPPGLTQIPQI	ATNB_HUMAN	116	VMQKRSRAIHSSDEGE	
42	VPSWPAPPGLGPFLLL	BAA74450	117	NIpYSVPHDSTQ	Negative Control
43	LNPQGQPPGLGDPGSL	BAC06168	118	GSLQPLPPGLKRFSCSCL	O60448
44	YKRGNFPPGLLVIAPG	BAC65211	119	FPGPIGPPGLKGDRGA	O60505
45	ELPSSPPPGLEPVAPD	BAC77376	120	CNPAWPPPGLAPHLTH	O60623
46	RPEERPPGGLPLPPPP	BAT2_HUMAN	121	PSSPAQPPGLTQSQNL	O75359
47	PDLYDVPPPGLRRPGPG	BCA1_HUMAN	122	VVPAAPPGLPGEGAE	O75808
48	PVSTAMPGLAKSSSE	BRD2_HUMAN	123	GTAQPPPPGLQPHAEV	O76022
49	VALLCGPGLGKTTLA	CAB53056	124	RAVQGPPGLPRLPRPL	O95364
50	KFLVRWPGLAEEVVL	CABI_HUMAN	125	GDQDGPPPGGLGRVIGE	O95714
51	MAPQVHPPGLALNAV	CAD92588	126	DAHLGLPPGLAKKSSS	O95785
52	RSPPPSPPGLEPLDG	CCAI_HUMAN	127	GLSQSGPPGGLLPSPSF	P121_HUMAN
53	PGEGLQPPGLYPSSH	CCB1_HUMAN	128	WEHRSPPPGLSKFELC	P285_HUMAN
54	YLDKAAPPGLPAETIK	CDK4_HUMAN	129	TALPTAPPGLLGTPTYA	PCB4_HUMAN
55	SWSGLPPPGLSSPPSRP	CG1_HUMAN	130	PASPQGPPGLAAYTAK	
56	SHRPPPPGHR	Control	131	ETLSSPPPGLEKGADR	PCN2_HUMAN
57	VMQKRSRAIHSSDEGE		132	TWAGKPPPPGLHLDVVK	PPR8_HUMAN
58	NIpYSVPHDSTQ	Negative Control	133	DPPPPPPPGLGPCSGAL	PRDD_HUMAN
59	QLRISFPFPGLCWGDRM	CHD3_HUMAN	134	YLQARRPPGLLEYCYNP	Q02063
60	QRPGPRPPGGLPARPEA	CLR3_HUMAN	135	QPRHLAPPGLHPVPGG	Q12996
61	ICVQWDPPGLAEQHG	CLR3_HUMAN	136	GAPTCYPPGLGPPPM	Q15182
62	RLLRSLLPPGLLRRVSS	CN3A_HUMAN	137	GMPTVIPPGLTREQER	Q15913
63	RSTMSLPPGGLGNWSG	DF5L_HUMAN	138	GNFKIEPPGLFRGRGD	Q86V82
64	QLMAPTPPGLRNSLNR	DOC6_HUMAN	139	ARDPMRPPGLVRNLQV	Q86VF2
65	NNASAPGLAQPLP	DRPL_HUMAN	140	KKVRKVPPGLPSSVYA	Q86VM2
66	LALQPGPGLHPFPFH		141	ELPSSPPPGLEPVAPD	Q86XP8
67	GPAPTPPPGLSYSGSF	EGR4_HUMAN	142	GVSQEGPPGLPPQPPP	Q86YS8
68	QDLERVPPGLLALDNM	ELM3_HUMAN	143	IDQLLLEPPGLGARCDH	Q8IUH1
69	PPPPSPPPGLLPLLPP	EPB3_HUMAN	144	PVTPLRPPGLGSASLH	Q8IVH2
70	YLNQARRPPGLYEYCYNP	FGR1_HUMAN	145	PPGSPEPPGLTQLSPG	Q8IVL6
71	FLRARRPPGLDYSFDT	FGR3_HUMAN	146	PSENNSMPGGLSTPTAS	Q8IVS9
72	LSVQNFPFPGLYCKTS	FMR2_HUMAN	147	KSKPELPPGLSPEATA	Q8IXJ8
73	APETRQPPGLLCDLDA	FXH1_HUMAN	148	SMDRSIPPPGLVNGLAL	Q8IY86
74	PLLGCPPPGLGSGPPI	FXN1_HUMAN	149	NGLEVAPPGLITNFSL	Q8N5S7
75	LTTTAPPPGLQPGAGG	FZD2_HUMAN	150	SRLPELPPGLHLPLQLK	Q8N6C4
76	PRADPEPPGLAAGLVQ	GAK_HUMAN	151	KKVRKVPPGLPSSVYA	Q8NEH3
77	NGLEVAPPGLITNFSL	GP17_HUMAN	152	LPGLPRPPGLPAAPWL	Q8NET5
78	GLIAAPPGLGVRLRG	GP62_HUMAN	153	TAPSRRPPGLTGQKPP	Q8NEZ0
79	TSWPACPPGLVHTLGN	HAIR_HUMAN	154	RSPPSSPPGLEELPLDG	Q8NFX6
80	NLASYLPPGLALRPLE	HAIR_HUMAN	155	ISVRGGPPGLRSARSG	Q8NG09
81	VPPGAGPGLGGPRPV	HAN2_HUMAN	156	LRFRGAPPGLHALTSR	Q8NGZ7
82	PGEDRTTPGLAAEPE	HCN4_HUMAN	157	EILKAVPPGLVHLCIC	Q8NI35P
83	KKVRKVPPGLPSSVYA	HTF4_HUMAN	158	KRSRVAAPPGLSS	Q8NI38
84	QGADFQPPGLYPRPDF	HXD4_HUMAN	159	ELAGEMPPGLNFDLDA	Q8NI97
85	MERPPGLRPGAGG	IKKA_HUMAN	160	GLLAAPPGLGRVRLG	Q8TAM0
86	AREGRLPPGLSASPQP	IPF1_HUMAN	161	RTFTPQPPGLERLWL	Q8TAY0
87	QLDLHFPPGLSFRKVE	ITAL_HUMAN	162	TIRVIAPPGLGTFAFN	Q8WW91
88	KKVRKVPPGLPSSVYA	ITF2_HUMAN	163	VRRDPAPPGLRELCIQ	Q8WWV8
89	DPYRGRGPPGLQGQSVS		164	DYAYIPPPGLQPEPGY	Q93052
90	SHIQIPPPGLTELLQG	KAP2_HUMAN	165	LGLYPPPPGLTEIPPG	Q96BC6
91	MAEKAPPGLNRKTSR	KCB2_HUMAN	166	GPQCPGPPGLPAQARA	Q96DV1
92	PGEPTPPPGLLLFPSC	KFC1_HUMAN	167	MLVIPPLSEEAAA	Q96F56
93	ASEAGRPPGLETYGFP	LGR6_HUMAN	168	AQSLVPPPGLPGSSTP	Q96G51
94	SLSWHLPPGLSAKMLS	LH2A_HUMAN	169	GVLPYFPFPGLPPPDAG	
95	CQVILPPLPGLLTHAQ	LMA5_HUMAN	170	PSRTAVPPGLSSLPLT	Q96L91
96	TGRCNCPPGLSGERC		171	QPRHLAPPGLHPVPGG	Q96QD6
97	TKKSAVPPGLPVYLDL	MAPB_HUMAN	172	SHRPPIPPGHR	Control
98	LFATQNPPGLYGRKV	MDN1_HUMAN	173	VMQKRSRAIHSSDEGE	
99	PSENSMPGGLSTPTAS	MICA_HUMAN	174	NIpYSVPHDSTQ	Negative Control
100	GNQGLPPPGLTISNSC	MITF_HUMAN	175	SLCVALPPGLAVSVLK	Q96RK5
101	EEHVLAPPGLQPPHCP	MYF6_HUMAN	176	LEGLPLPPGLKQVLHN	Q96RY2
102	ESPGEPPPGLELFRWQ	NAH5_HUMAN	177	ASGPAPPGLAAGPGP	Q96S59
103	PNTVTKPPGLTDLEV	NCO6_HUMAN	178	TSGPSTPPGLVLPVHTE	Q96T58
104	VMASPPPPGLPAGSGP	NCR2_HUMAN	179	ESDHEYPPGLVVAFSA	Q9BRQ5
105	QMLAPPAPPGLPRLALP	NFIC_HUMAN	180	SFGGGGPPGLGGLFQA	Q9BU37
106	MDLELPPPGLPSQDM	NFL2_HUMAN	181	GTAQPPPPGLQPHAEV	Q9BUJ2

182	PPPPPPPPGLGLGFP	Q9BWD2	3	QSSQPPPPGLSGSQGD	Q6QTF1
183	PPQKRPPPGLSDPWGA	Q9BXM8	4	SVPLLPPPGIPSNESE	
184	NGLKLNPGLREFPSG	Q9BYX3	5	QPDVHPPPGMLRFPPP	
185	PGPPQAPPGLPGQASL	Q9BZJ5	6	RCPVSAPPGVSVPTPS	Q6RF52
186	FDPAPPPPGLGSSRPS	Q9GZM8	7	TPSRPPPPGFSNNGRD	
187	TALPTAPPGLLGTPYA	Q9GZT1	8	PQGYMPPPGVPQMMAP	Q84VV2
188	PASPGPPPGLAAYTAK		9	QNGILRPPGMAPIPGQ	
189	EPRTPGPPPGLTTTAP	Q9H1C2	10	PGQGGGPPGMAPIPGQ	
190	GAWGSLPPGLTFQNKL	Q9H2I5	11	GNIPLMPPGGLPPPPP	Q8GUK8
191	GMMGGYPPGLPLQGP	Q9H2T5	12	QGPTFQPPGIMYYGAP	
192	TALPTAPPGLLGTPYA	Q9HCU2	13	PPESYPPPGYQSHYPP	Q940Z6
193	PASPGPPPGLAAYTAK		14	YQSHYPPPGYPSAPP	
194	SDTPSPPPGLSKSNPV	Q9NPQ1	15	YPSAPPNGYPSPPSH	
195	SDTPSPPPGLSKSNPV	Q9NZN6	16	HQEVAWPPGVVEPGAA	Q941Q3
196	NYSNWGPGLGPMSMLS	Q9UBG0	17	SAVEPLPPGVKRTSEA	
197	PGEGLQPPGGLYPSSHP	Q9UD79	18	YAPPVYPPGVPPGYPF	Q9CAQ5
198	QQQPPPPGGLVRQNS	Q9UGY9	19	VYPPGYPGPFSYPT	
199	LGLYPPPPGLTEIPPG	Q9UHB4	20	LLEEKSPPGIVDKFGW	Q9FND9
200	QVMQT1PPGLFWRFQI	Q9UKZ4	21	LVDGGCPGPGLVLIDDG	
201	EGPIQGPPGLPGPPGP	Q9UM16	22	RPQVSAPPFGSAPNRL	Q9LSS9
202	SPPPQ1PPGGLRPRFCA	Q9UPF6	23	APNRLPPPGFSSHERV	
203	GPPPGPPPGLPPGPPP	Q9Y2W2	24	SAVEPLPPGVKRTSEG	Q9LTW6
204	PPLGAPPGLFPAPL		25	RTQVSAPPFGSAPNRL	Q9M1E4
205	SFPFTFPGLFARYSV	Q9Y4C4	26	APNRLPPPGFSSHQRG	
206	FGPP1PPPGGLGGAFG	RBMC_HUMAN	27	NPRSMGPFGFPGIGGP	Q9SGW9
207	PGFGSGPPGLGSAPGH		28	FPGIGGPPGPFGPTFVG	
208	GSLQRPNGLSDPST	RED1_HUMAN	29	PPPVTTPGGLLPPITT	Q9SXE7
209	KLKQSLPPGLAVKELK	RL38_HUMAN	30	LPPITTPGGLLPPVTT	
210	PSFCPNPPLGEALSPN	RON_HUMAN	31	LPPVTTTPGGLLPPVTT	
211	GKMNSGPPGLGGKRKG	RRS1_HUMAN	32	LPPVTTTPGGLLPPIIN	
212	PPGM1PPPGLAPGQIP	RU1A_HUMAN	33	GLMITQPPGMLTVPVG	WRK3_ARATH
213	PPPPPPPPGLGLGFP	S3B2_HUMAN	34	PGMFTVPPGGLSPATLL	
214	LLLSPPPPGLPSLHSL	SIX2_HUMAN	35	-	-
215	MGTPGGLQTDCEA	SNC1_HUMAN	36	-	
216	KLKEFMPGGLQELIPF	SYS_HUMAN	37	-	
217	NGLKLNPGLREFPSG	T2AZ_HUMAN	38	-	
218	FLREPGPGLSHQLMS	TAU_HUMAN	39	-	
219	KKVRKVPPGLPSSVYP	TFE2_HUMAN			
220	ANFKIEPPGLFRGRGN	TOP1_HUMAN			
221	LEGCFPPGGLYMDERG	VWF_HUMAN			
222	SFGGGGGPGLGLFQA	WAIP_HUMAN			
223	PPGPPPPPGLPSDGDH	WASL_HUMAN	1	GHPQATPPGFGHQIN	ARRC_ARATH
224	PGKC1CPPGLEGEQCE	WIF1_HUMAN	2	WNPAMPPPFGYPPPGY	BF2A_ARATH
225	HHQRDGPPGLVPMELE	ZAP3_HUMAN	3	QQQPPSPPGFPIIGNL	C729_ARATH
226	MAPQVHPPGLALNAVG	ZEP1_HUMAN	4	YRQFPCPPGFFIIGNL	C72W_ARATH
227	SHRPPPPGHR	Control	5	QRKPPSPGFPIIGNL	C72X_ARATH
228	VMQKRSRAIHSSDEGE		6	CFYNCNGPPGFF	LC12_ARATH
229	NIpYSPVHDSTQ	Negative Control O75420	7	VQGLCVPPGPFDIDQA	LC28_ARATH
230	SAPHPGPMQKGPKEPI		8	PPQPNLPPGPFRFHPTD	NA18_ARATH
231	RVPFAPGPSPPPLLGN		9	LTQLSLPPGPFRFYPTD	NA19_ARATH
232	LGLDLTTPPPPPPQQQQ		10	MVEAKLPPGFRFHPTD	NA22_ARATH
233	QLQALKPSSRSAEKW		11	TSQSTLPPGPFRFHPTD	NA29_ARATH
234	RQLHKQPPPPREPARAQ		12	SELLQLPPGPFRFHPTD	NAC2_ARATH
235	QLRTASLPAIPNPFPPE	Pepscan of GRB10_MOUSE	13	WRWKIRPPGFIQL	NUCC_ARATH
236	TASLPAIPNPFPPELTG		14	GDSQYLPPGPFRFHPTD	O04017
237	SLPAIPNPFPPELTGAA		15	DVPDIRPPGPVKEPLS	O04254
238	GAAPGSPPSVAPSSL		16	ASPVLKPPGPSTPRVS	O04535
239	VAPSSLPPPPSQPPAK		17	DPLTFLPPGPFLERTKK	O04622
240	PPPPSQQPAKHFPPGF		18	PGHPHLPPGPFRFHPTD	O22734
241	PPSQPPAKHFPPGFQL		19	RGVLRLPPGPFRFHPTD	O22798
242	PPAKHFPPGFQLSKLT		20	SEESKLPPGPFLETVDK	O22820
243	PQRKGLPPP FNAPMRS		21	SKGCKCPGPFIGDGLK	O22925
244	LPPP FNAPMRS VSENS		22	RFLWTAPPFGARLLW	O23306
245	-		23	EVYMAQPPGFIDKDRP	O23529
246	-		24	FWMPQAPPGVSLGCV	O23557
247	-		25	FWRPHPPPGFASLDY	O23558
248	-		26	EVYVTQPPGVFDKDNa	O49143
249	-		27	SLTGP1PPGFQNLTS	O49318
250	-		28	MGSSCLPPGPFRFHPTD	O49697
			29	AFKISFPPGPFRPNASY	O64539
			30	STPPPPPPGFSNNQRG	O64642
			31	VCSKQLPPGPQC	O65369
			32	KDKYEFPPGPFGNCVASG	O65405
			33	ILSVPQPPGVFPVNPK	O65472
			34	TLPVPLPPGFFFNRNGP	O65477

**GYN4**  
**PPG[FILMVWY] x (0,40) PPG[FILMVWY]**

1	WNPAMPPPFGYPPPGY	BF2A_ARATH
2	PPGFYPPPGYPPMFYP	

35	ALAEPRPPGFFFRSKQ	O65478	110	DEQMDLPPGFRFHPTD	Q9FLR3
36	ALAVPRPPGFFLRSKQ	O65479	111	RAKSGPPPGFTGAKQN	Q9FMM3
37	TLPVPQPQPGFFRERS	O65480	112	STQRFIPPGFSQLAR	Q9FN44
38	TLHVPQPQPGFVFRVRF	O65483	113	FRQNSPPPGFTELASE	Q9FNJ2
39	RKFPIPPGFLKIEDL	O65500	114	KGEASVPPGFEKIWTP	Q9FNQ6
40	DQSCSVPNGFGRFHPTD	O65508	115	DDLPSVPPGFEFYATF	Q9FRS3
41	RPPMPRPPGFPVPGSF	O65671	116	NSFSHVPPGFRFHPTD	Q9FWX2
42	DVQDDLPPGFSPPCTD	O80663	117	TVYMYEPPGFDVNKNP	Q9FX18
43	SVKCECPGPFGKGDGTK	O80977	118	EVYMQFDPGFRGDKT	Q9FXB7
44	SVKCECPGPFGKGDGVK	O80979	119	PSDDNLPPGFGGGPFSA	Q9FXI4
45	NGQSQVEPPGFRFHPTE	O81033	120	NGVLRLPPGFRFHPTD	Q9FY93
46	SLIMSCKPPGFKYKSGQ	O81211	121	TSGCRCPPGFKGDGLK	Q9FYH7
47	SYPPLKPPGFTQQPNY	O81495	122	EVYVTQPPGFIDPDRP	Q9FZK7
48	TVFMTQPPGFEDPSRP	O82493	123	YQPQLPPPGBTQQQQQ	Q9FZN9
49	YKKHGYPGPFGKGLPE	O82607	124	TLPVPRPPGFFFNRNP	Q9LDM5
50	YQQPNPPPGFTQQPQQ	O82610	125	TLPVPRPPGFFFNRNS	Q9LDS6
51	TLDDNTVPPGFDATNQN	PRH_ARATH	126	TLNVPQPPGFFFNRNP	Q9LDT0
52	PFSILMPPGFDIDMHQ		127	LPPLQFPPGFGHQLNPN	Q9LEZ9
53	VWQEGLPPGFGVHRVTI	Q67XH7	128	SSGVQAPPGFLEEFFK	Q9LF41
54	MAPMSLPPGFRFHPTD	Q67Z40	129	DSDNSRPPGFETASPK	Q9LFC0
55	SFVVNFPPPGFKIGKYF	Q689D6	130	EVYIEQPPGFIEEKEE	Q9LH44
56	RCPVSAAPPGSVPTPS	Q6RF52	131	NCGKNPPPGFKCPA	Q9LIE8
57	TPSRP PPPGFSNGRD		132	EDES LMP PGFRFHPTD	Q9LIL8
58	NYQPPPPPFGFTQQNQ	Q7FZN4	133	HRPIPPGPFGPIIGNL	Q9LIP7
59	NYQQQPPPGFAPQQNQ	Q7FZS4	134	QEIVQNPPGFDTPEPVP	Q9LJ94
60	PMSGGLPPGFRPMGGG	Q84WQ1	135	AELGSPPPGFPSSKVA	Q9LJA6
61	PSFVYYPGPFRQILNY	Q8GRX1	136	SEKIDLPPGFRFHPTD	Q9LJW3
62	MNLPPGFRFFFPTD	Q8GWK6	137	DDIVFIPPGFEVSTEQ	Q9LK46
63	VPVVDPPPGFSLPFEI	Q8H1K9	138	RSRQLPPPGBTQQQQQ	Q9LKR9
64	ELDEELPPGFEESLAR	Q8L3P4	139	NYHQPPP PGPFGAPQQNQ	Q9LKT2
65	EVYMRLLPPGFKCSDPS	Q8L700	140	ATRENVP PGFGEQKAP	Q9LMB7
66	TLPVQPPP GFGFRNRP	Q8L710	141	RQALSPPPGPFGQAVFPQ	Q9LMB8
67	MDTISAPPGFVSQTSF	Q8L7T6	142	QPALQKPPGPFRDQQNQ	Q9LMN2
68	YGHSGPPGPFGNPMYGA	Q8L9T4	143	LQIPKPPPFGFASDQKP	Q9LMS9
69	TVSVE TPGFNIQVTP	Q8LAE1	144	GRFYVDP PGFVERLNS	Q9LN29
70	VPSGNLPPGFDPSTCR	Q8LAP3	145	EEDPELPPGFG	Q9LN96
71	VVVF TAPP GPFKPPEPK	Q8LAP7	146	RMPRESPPGFNDDELKI	Q9LNS2
72	LLDFTGPPGFGVHQVSP	Q8LAY7	147	YQQQLPPPGBTQQQQQ	Q9LPB1
73	DIGSKLPPGFRFHPSD	Q8LB22	148	NGQSKVPPGFRFHPTE	Q9LP17
74	MDLPPGFRFHPTD	Q8LF13	149	LGMLFPPGPFDYT YPL	Q9LQ02
75	QSLNSMPPGF DQRKQH	Q8LPN4	150	IPSGNLP PGFDPSTCR	Q9LQ19
76	RADYTFPPGPFTGEQKR	Q8RWJ1	151	MVGSLFPPGPFRFYPTD	Q9LQK5
77	SGSVSVPGPFGSSDYCY	Q8RXD9	152	RPPLWIPPGFYSNILI	Q9LR50
78	QKQNFPPGPFTQQPQQ	Q8S8J9	153	MEENLPPGFRFHPTD	Q9LS50
79	SRDILDPPGFSRASQE	Q93VE6	154	MAPVGLP PGF RHFPTD	Q9LSH5
80	RFLCTVPPGF GARRIW	Q93ZZ1	155	MVEANLPPGFRFHPRD	Q9LSI1
81	TLGILKPPGPFE EYRTS	Q940V3	156	RPQVSAPP GF SAPP NRL	Q9LSS9
82	YSRNDFPPGPFGSGT	Q94A86	157	APNRLPPGPFGSSHERV	
83	PRGPDLPPGPFGEGNHYA	Q94C33	158	QSTYEKPPGPFGEPDK	Q9LT25
84	QQHQLQPPGPFTNVHAV	Q94C89	159	ISGSIPPPGPFGAPRASA	Q9LVG3
85	PVYMLQPPGPFGDQEKP	Q94KV0	160	FRQIGIPPGFDVNHLG	Q9LVP1
86	EVYMAQPPGPFDVKDRP	Q94LA8	161	NRGLVKPPGPFSLLELN	Q9LW32
87	SPDLSGPPGFQSLPAS	Q94AUB4	162	TIAYVLP PGFKFMPND	Q9LXY4
88	ALAVPQPPGFFRFSNH	Q9C5S8	163	AADDVPPGPFGPVASR	Q9LYE6
89	DERCEPPPGFDNSVVA	Q9C6G0	164	RRPHTTP PGF CRHQGR	Q9LYL7
90	LTLISLPPGPFDISKIP	Q9C6G8	165	APRPLVPPG FFASTILE	Q9M140
91	GGVGGAPPGPFRPLN A	Q9C7H2	166	RTQVSAPP GF SAPP NRL	Q9M1E4
92	RLSGPLPPGFLSALDQ	Q9C7S5	167	APNRLPPGPFGSSHQRG	
93	SSNGGVPGPFRFHPTD	Q9C878	168	PPPSSAPP GF SENNNI	Q9M1Q0
94	DIYMKPPPGFKTTDPS	Q9C8F4	169	QRFVLRPPGPFGQNKCV	Q9M342
95	SSFVYYPGPFRQILNY	Q9C8J9	170	LPNGECPPGPFLGFAVN	Q9M3A7
96	IMQSSMPPGF RHFPTD	Q9C8W9	171	TIAYVLP PGFKFVPND	Q9M3C9
97	GADLQFPPGPFGFRFHPTD	Q9CAR0	172	RHKAQI PPGFFV	Q9M912
98	PNQYALP PGPFGEQPQYK	Q9FF62	173	MAPVSLP PGF RHFPTD	Q9M9N8
99	FGASDKP PGPFSYTMES	Q9FFW9	174	GGQLSVP PGF RHFPTD	Q9MA17
100	GRSMRKLPPGFRFDPD	Q9FGQ1	175	RNERGLP PGF RHFPTD	Q9S851
101	DYSCS1PPGPFRFHPTD	Q9FH59	176	SKFENVPPGPFGFNSTT	Q9S9Q3
102	KVASNLPPGFEATDYA	Q9FH61	177	TGF WPTPPGPFGGGT	Q9SFZ3
103	EVYIKFPPGPFGSDDNR	Q9FIC5	178	NPRSMGPPGPFGIGGP	Q9SGW9
104	ALYVTKPPGPFGKYKSGM	Q9FJD6	179	FPGIGGPPGPFGTPFG	
105	EELVLDLPPGPFRFHPTD	Q9FK44	180	RLSGPLP PGFFSTLDQ	Q9SHI3
106	EEHIDLPPGPFRFHPTD	Q9FKA0	181	GNYQQQPPGPFGAPPQHQ	Q9SHM3
107	HQQPPPPPGFYRLPAP	Q9FKP8	182	NSFSQVPPGPFGFRHPTD	Q9SI80
108	EVYVSQPPGPFI DRDRP	Q9FLA4	183	YKKHGFP PGFTPKGKS	Q9SIM3
109	EEQMDLPPGPFRFHPTD	Q9FLJ2	184	FRVRDFPPGPFLDNIAR	Q9SJN9

185	NYQPQPPPGFAPQQNQ	Q9SJS1	22	QHQQPPILPPPGLMYT	CLG1
186	TPSRPPPPGFSSNGRD	Q9SK04	23	DLGYSVVSQPPPGYEQ	YHL002W
187	FEDHPLPPGFGSNICK	Q9SK31	24	TSTSMPPPGVPMSGNN	RRD1
188	YQQQQPPPGFTPHQQQ	Q9SKR9	25	NHITAPPGGFWDDAS	IME2
189	DKLDLAPPGFDSGSHV	Q9SL27	26	QENEGPPPPGYMCYRC	YKL059C
190	DDSSSSPPGFFDGGGV	Q9SL38	27	PAPPBPPPPPPGAFST	VRP1
191	MESCSVEPPGFRFHPTD	Q9SL41	28	PNRNSI PPPGMNP NAN	CST9
192	EVYMKLPPGEFAHPN	Q9SLF0	29	NMSLKLPPIQODDHS	VIP1
193	DPSYPPIPFGQFDKLP	Q9SL14	30	DLIEARRPPGIFAA MN	MYO5
194	MSLPPGFRFHPTD	Q9SLK1	31	HSKKPAPPPGMQNKA	
195	DPRSSLPPGFRFHPTD	Q9SQQ5	32	RNGEILPPPPGFETM	YMR171C
196	QEVDLPPGFRFHPTD	Q9SQQ6	33	LAQNRRIPPPGFSQNI	INP53
197	HSSPLEPPGFQLNAST	Q9SQW9	34	NVGNQPPPPIGIESQWK	YPL105C
198	RNWNRIRPPGFSSDEFK	Q9SR71	35	NAQMRFPPPGILTGVK	NEW1
199	FNQPPSPPGFWISFLR	Q9SRR0	36	VTILAPPGDAYLLVQ	MUP1
200	MAPVSMPGPFRFHPTD	Q9SRZ8	37	KNKPNPPGSDDCYCT	ZAP1
201	RPRVNRRPPGFMRFISN	Q9SSM2	38	SQYAPPGP PPPMAYN	YOR197W
202	CGADYPPGFCRENE	Q9SUV8	39	PYYPPP PPEHMGRP	NOP3
203	TVYMYQPPGFENQDRP	Q9SV56	40	FSGTVPPPGRTKAARP	RRPW_YEAST
204	GHQNQQPPGFRQAQQL	Q9SVV7	41	TSTSMP PGVPPSGNN	YIP3_YEAST
205	ILYLRIPPGFRIILRG	Q9SW29	42	STPPPPPGLIAHQGP	YKU4_YEAST
206	EFGHKDPPGFETYLAD	Q9SW43	43	AQNVTPTPPGGLTSS	MSL5 as Positive Control
207	DVYMSQPPGFIDKDRP	Q9SXQ3	44	SSIAPPGLSGPPGFS	
208	ELYMSQPPGFVDKDRP	Q9SXQ5	45	INKPTPPGLQGPPGL	
209	LPSGNLPPGFDTTCR	Q9SY4	46	VMQKRSRAIHSSDEGE	
210	LAQLSLPPGFRTFYPTD	Q9SZR8	47	NIpYSVPHDSTQ	Negative Control
211	YQQQNNSPPGFTQQPQP	Q9XH31	48	IICFVGPPGVGKTSIG	PIM1
212	YKKHGFPFGFTPKGKA	Q9XI17	49	RLYETTPGVVMGLAW	
213	YKKHGFPFGFTPDKDV	Q9XI18	50	RGVLLHGGPGCGKTSI	YLL034C
214	YQQQQPPPGFTPQQYQ	Q9ZQ08	51	VLLWGPPGCGKTLAK	
215	KEEALPPGFRFHPTD	Q9ZQ25	52	PQSLRAVKPPGLFARF	DRS2
216	EVYVTQPPGFVIEGKE	Q9ZQE9	53	MSPMVAAPGAQSQFTQ	YBL005W-A
217	NYQQQTTPPGFAPQHQK	Q9ZQJ9	54	SVAVQAPPGYGKTEL F	YBL111C
218	AYDKRAPPGFVRKSEQ	Q9ZRE3	55	GLYDYGPPGCAFQNNI	YBR121C/GRS1
219	KQPQDYPPGFHV	Q9ZT57	56	STSPTISVPPGVTRTV	YBR130C/SHE3
220	EVYMSQPPGFVDKDRP	Q9ZT94	57	TRKYFSAGNYKLPPGI	YBR205W/KTR3
221	DVYVAQPPGFINPDRP	Q9ZUJ1	58	ETEMVFPPIFYEFAS	YBR229C/ROT2
222	EVYMKLPPGFRSHSPD	Q9ZW00	59	LPGEGENILPPGVSLPN	YBR251W/MRPS5
223	RSLFSMPGPFEAGKPG	Q9ZW02	60	HIQTNNNNMPGVQKNF	YBR260C/RGD1
224	RSLFSMPGPFEGEKTG	Q9ZW07	61	LLIPPGFPTKNYPPGT	YCL010C
225	LTGAVTPPGFRVVTS	QORL_ARATH	62	IYVKQPPGFVNERNPD	YCL074W
226	PPFGFPFPGFSSFYPF	SUV1_ARATH	63	FLVKEKPPGVNVNSSV	YCR007C
227	RELIEPPPGFKDNRVS	SUV2_ARATH	64	KAKTIVWNGPPGVFEEF	YCR012W/PGK1
228	-	-	65	RLHLPFPGLPSYMEG	YCR068W/CVT17
229	-	-	66	APRREDMPPGWPMPGSK	YCR076C
230	-	-	67	QSAQPPGVNVNPQGG	YCR093W/CDC39
231	-	-	68	SYSRPSAPPGYETAS	YDL012C
232	-	-	69	IFMLGRIFPPGCTVTA	YDL052C/SLC1
233	-	-	70	KFKLIQQVPPGGLDALV	YDL132W/CDC53
234	-	-	71	TQPLHVYYPPGSPD	YDL183C
SMY2 and SYH1					
PPG[ACFGILMVWY]					
1	AQNVTPTPPGGLTSS	MSL5 as Positive Control	72	VFPPGVNDDELPIRGQ	YDR069C/DOA4
2	SSIAPPGLSGPPGFS		73	ANDFDGVPPGVNDDE	
3	INKPTPPGLQGPPGL		74	RSIYEIFGPPGIGKTN	YDR076W/RAD55
4	VMQKRSRAIHSSDEGE		75	MTLSLNTPPGVHCQPL	YDR133C
5	NIpYSVPHDSTQ	Negative Control	76	AQNVTPTPPGGLTSS	MSL5 as Positive Control
6	MSGLPPPPGFEEDSD	PRP8	77	SSIAPPGLSGPPGFS	
7	DNALPPPPPPPGYEI		78	INKPTPPGLQGPPGL	
8	DFTLPPPPPPGLDEL		79	VMQKRSRAIHSSDEGE	
9	ETSTPPPPPPGLIAHQ	EAP1	80	NIpYSVPHDSTQ	Negative Control
10	FPQRMMPPPPGLVQFQ		81	PYQMSPMYAPPQAQSQ	YDR170W-A
11	QYMPPPPPPGFMPH		82	QMSPMYAPPQAQSQFT	
12	QAQNVTPTPPGGLTSS	MSL5	83	DIDQYTIPPGGLDLLPT	
13	EQPKFSLPPPGMTTV		84	RMVLIGPPGAKGKTQA	YDR200C
14	SSIAPPGLSGPPGFS		85	RTINAFFPGACSEYSG	YDR226W/ADK1
15	MNQLTGIPPPGLMNNS	CCR4	86	SRLIGAPPGYLSESG	YDR245W/MNN10
16	NTTVRPPPPGVIVYRL	SUL1	87	DLVKIYPPGMKIWIVS	YDR258C/HSP78
17	SQFAPPFFFFGVNVNM	PAT1	88	KLTNEDPGMLYMLKAF	YDR403W/DIT1
18	YSRPSAPPGYETASR	YDL012C	89	SVAVQAPPGYGKTEL F	YDR443C/SSN2
19	NEAPPQTRKFQPPPGF	SMB1	90	RTHRYLPPGYLEGEPV	YDR545W/YRF1-1
20	PLNVSTPPPGIFGPQH	MOT2	91	THRSSGKLPPIFEIVS	YEL032W/MCM3
21	TWPRPKGPPPGVNNEK	YFL010C	92	PSVAVQAPPGYGKTEL	YEL047C
			93	MAASVPPGGQRLQKR	YEL077C
			94	PPLNVSTPPPGIFGPQ	YER019C-A/SB2
			95	DQYGRLLPPGWERRTDN	YER068W/MOT2
			96	GHFDHYPPGYDPTDPN	YER125W/RSP5
					YER166W

97	SVAVQAPPGYGYKTEF	YER190W/YRF1-2	149	HRSSGKLPPGFEIVQA	YJR051W/OSM1
98	EEIELPPGVKKPLNLL	YFL004W/VTC2	150	PSVAVQAPPGYGYKTEL	YJL225C
99	GTTWPRPKGPPPGVNN	YFL010C	151	GAITTVVPPGFIDAST	YJR074W/MOG1
100	EKSSRQQADQAPPPYS		152	AGIEHVKPPGFIKTGR	YJR095W/SFC1
101	QLSFFIAPPMSLEAKM	YFL025C/BST1	153	VFGQMNEPPGARARVA	YJR121W/ATP2
102	PSVAVQAPPGYGYKTEL	YFL066C	154	VRGMYSSPPGYGSRVV	YKL106W/AAT1
103	RMKEDAPPGVASPLP	YGL058W/RAD6	155	ITSLTLSPPGGEYTII	YKL121W
104	ASSTNLPPGFSISLQP	YGL083W/SCY1	156	DLIEAKNPPGILAAMN	YKL129C/MYO3
105	GNNKQPLRKPGFFDE	YGL139W	157	DELVKRLPPGLSMILGS	YKL157W/APE2
106	CIVDGVPGMSTLEAD	YGL148W/ARO2	158	MSTLYFKPPGIFHNAI	YKR037C/SPC34
107	HPMNVVGGPIPGANDV	YGL173C/KEM1	159	VEEIGSRRPPGVLVVGK	YKR069W/MET1
108	NDVADVGLPYNIPPGF		160	PSVAVQAPPGYGYKTEL	YLL066C
109	GLPYNIPPGFMTHPNG		161	LERQFSVPPGLLIMM	YLR072W
110	ANDVGLPYNIPPGFMT	YGL173C	162	EVGVFHVPVPPGLMSKLG	YLR092W/SUL2
111	RNRSKSPPGFGRLDFP	YGL175C/SAE2	163	LLFATQNPPGIYGGRK	YLR106C
112	KNIQAPPGAISPILLY	YGL206C/CHC1	164	SKLSDGPPGASDARG	YLR129W/DIP2
113	NSNTLSPPGFEGNSS	YGL231C	165	RLEIKSLPPGFIKSAL	YLR152C
114	EDKVYAPPGYEQYARP	YGR009C/SEC9	166	YFIVNKPPIGIPSQPD	YLR165C/PUS5
115	PSGVLLYGPPICGKTM	YGR028W/MSP1	167	QQQAQGPPIGWDFNVQI	YLR207W/HRD3
116	RIVPGVPPGAAKKTIP	YGR054W	168	SGEYHLHPPGYTTNGS	YLR219W/MSC3
117	ESNETDPPGFLGEWLV	YGR099W/TEL2	169	AENSRRQSPPGYYVIR	YLR311C
118	ASKIVIPPGMGRGNRS	YGR162W/TIF4631	170	KGVLLYGPPIGCSKLT	YLR397C/AFG2
119	QDTANKKAPPGYVIDS	YGR196C/FYV8	171	PSVAVQAPPGYGYKTEL	YLR466W
120	KEQYLSKKPPGIVGNT	YGR206W	172	AQNVTPTPPPGLTSS	MSL5 as Positive Control
121	AQNVTPTPPPGLTSS	MSL5 as Positive Control	173	SSIAPPGLSGPPGFS	
122	SSIAPPGLSGPPGFS		174	INKPTPPGLQGPGL	
123	INKPTPPGLQGPGL		175	VMQKRSRAIHSSDEGE	
124	VMQKRSRAIHSSDEGE		176	NIpYSPVHDSTQ	Negative Control
125	NIpYSPVHDSTQ	Negative Control	177	SASNTPQPPGLDDEDA	YML114C/TAF65
126	WDPKITTTPPGIYILGL	YGR227W/DIE2	178	PSVAVQAPPGYGYKTEL	YML133C
127	PSVAVQAPPGYGYKTEL	YGR296W/YRF1-3	179	SGDLLLPPGIYHRFT	YMR009W
128	DLCGYSVVSQPPPGYEQ	YHL002W	180	QQLIKDSSPGIVAGPK	YMR022W/QRI8
129	HSLRSPPPGVFPVRGMG	YHL008C	181	QMSPMYAPPQAQSQFT	YMR045C
130	SVAVQAPPGYGYKTEL	YHL050C	182	PAQPLHLPWGWKINTM	YMR070W/MOT3
131	PFEEKYPPGFYTGADD	YHR104W/GRE3	183	KILLLHGPPGIGKTSV	YMR078C/CTF18
132	RRAQQFPPGVDSLADV	YHR150W	184	CKIHQKLPPGAILVFL	YMR128W/ECM16
133	SLADVIPPTGWSFDPN		185	LIKKAGFPFGVVNVIP	YMR169C/ALD3
134	LSDATWPPLRSSEIF	YHR202W	186	LIKKAGFPFGVVNVIP	YMR170C/ALD2
135	SVAVQAPPGYGYKTEL	YHR218W	187	KFFHVDVPPGAQRNYM	YMR214W/SCJ1
136	IMPQYLYPPGMGPQAQ	YIL122W	188	RGDEFSSPPGFEPSSRA	YMR264W/CUE1
137	PSVAVQAPPGYGYKTEL	YIL177C	189	PSMILWGPPIPGVGTSL	YNL218W/MGS1
138	DAPKYYPPGPIPTNDT	YJL020C/BBC1	190	SLYGRLSPPGWDPRVH	YNL240C/NAR1
139	TNSKTLVPPGIISNEK	YJL076W/NET1	191	PSVAVQAPPGYGYKTEL	YNL339C/YRF1-6
140	ISVSISTPPGIEMSD	YJL088W/ARG3	192	KKPTSNNNPPGIFTNGT	YNR051C/BRE5
141	LKNNSNLMPPGISSVQY	YJL091C	193	PVSVASLPPGLNVLQQ	YNR052C/POP2
142	QVKTVDPPGIFAVNI	YJL093C/TOK1	194	AQNVTPTPPPGLTSS	MSL5 as Positive Control
143	NTNPELKPPGLVECPF	YJL099W/CHS6	195	SSIAPPGLSGPPGFS	MSL5 as Positive Control
144	TNHITAPPPGGFWDDA	YJL106W/IME2	196	INKPTPPGLQGPGL	
145	FQDSFLIPPGVETKKI	YJL112W/MDV1	197	VMQKRSRAIHSSDEGE	
146	ARRAVKLPPGMSLKM	YJL128C/PBS2	198	NIpYSPVHDSTQ	Negative Control
147	DLRRVRLPPGWEIIHE	YJL168C/SET2	199	-	-
148	PSVAVQAPPGYGYKTEL	YJL225C	200	-	

## 12.2 NMR Backbone Assignment of the SMY2-GYF Domain

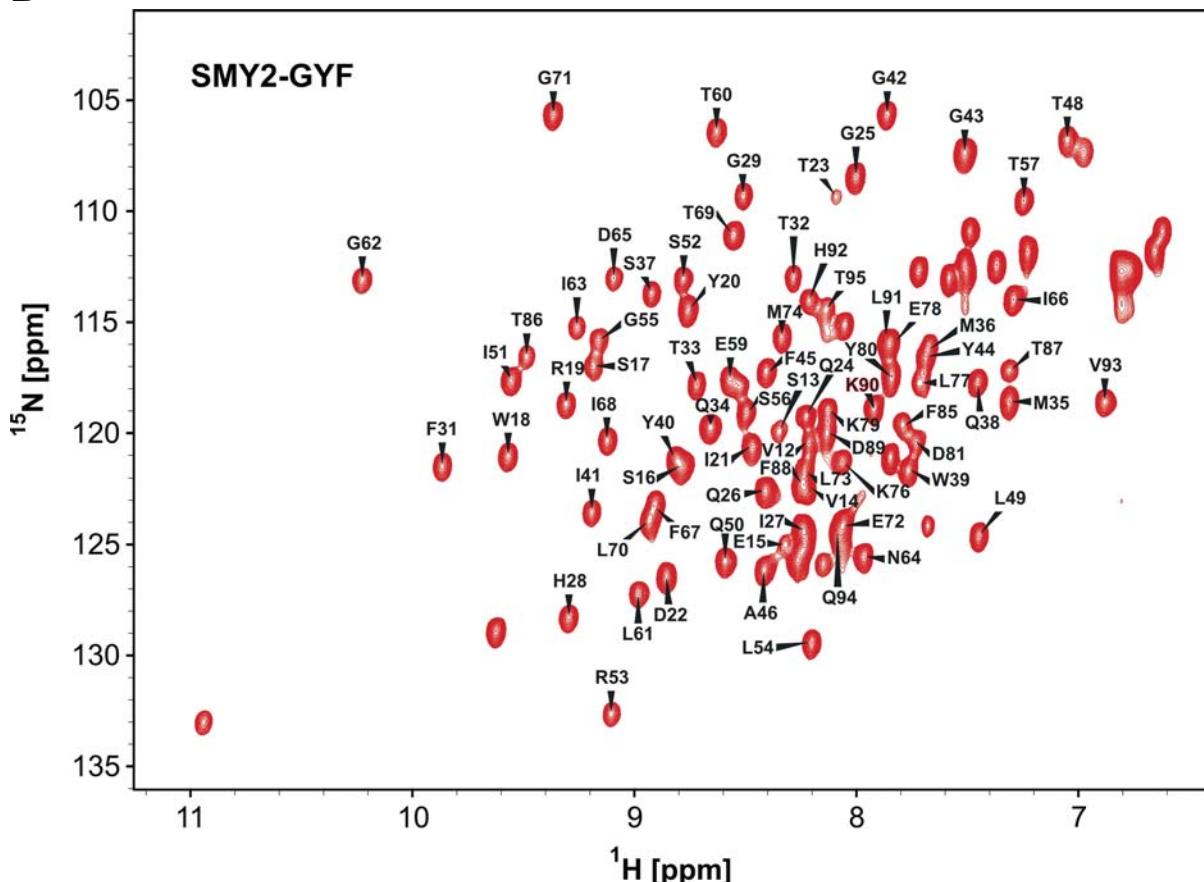
**Table 12.5: List of chemical shifts of the backbone NH groups in SMY2-GYF**

The backbone assignment was obtained by standard triple resonance experiments with SMY2-GYF. Chemical shifts of carbon atoms are omitted. Proline residues are devoid of an amide-proton and cannot be observed in HSQC spectra (denoted by –). Residues marked by an asterisk could not be assigned unambiguously (ND: not determined).

SMY2 Residue	H <sup>N</sup> [ppm]	N <sup>H</sup> [ppm]			
Val 12	120.452	8.213	Leu 54	129.421	8.206
Ser 13	119.913	8.347	Gly 55	115.812	9.163
Val 14	122.445	8.219	Ser 56	119.081	8.495
Glu 15	124.999	8.319	Thr 57	109.527	7.245
Ser 16	121.480	8.786	Pro 58	–	–
Ser 17	116.975	9.187	Glu 59	117.576	8.570
Trp 18	121.034	9.569	Thr 60	106.381	8.630
Arg 19	118.692	9.308	Leu 61	127.209	8.983
Tyr 20	114.446	8.758	Gly 62	113.077	10.226
Ile 21	120.631	8.468	Ile 63	115.230	9.259
Asp 22	126.411	8.855	Asn 64	125.544	7.965
Thr 23	109.359	8.092	Asp 65	113.014	9.093
Gln 24	119.239	8.227	Ile 66	113.980	7.292
Gly 25	108.436	8.002	Phe 67	123.267	8.910
Gln 26	122.583	8.409	Ile 68	120.334	9.124
Ile 27	124.408	8.237	Thr 69	111.051	8.554
His 28	128.289	9.295	Leu 70	123.870	8.931
Gly 29	109.277	8.510	Gly 71	105.641	9.365
Pro 30	–	–	Glu 72	124.149	8.062
Phe 31	121.470	9.866	Leu 73	121.815	8.229
Thr 32	112.967	8.283	Met 74	115.655	8.337
Thr 33	117.811	8.718	Thr 75*	ND	ND
Gln 34	119.751	8.657	Lys 76	121.277	8.062
Met 35	118.587	7.311	Leu 77	117.732	7.713
Met 36	116.249	7.679	Glu 78	115.976	7.832
Ser 37	113.687	8.923	Lys 79	118.971	8.128
Gln 38	117.705	7.453	Tyr 80	117.450	7.841
Trp 39	121.656	7.766	Asp 81	120.158	7.731
Tyr 40	121.125	8.820	Thr 82*	ND	ND
Ile 41	123.528	9.192	Asp 83*	ND	ND
Gly 42	105.641	7.861	Pro 84	–	–
Gly 43	107.367	7.512	Phe 85	119.618	7.791
Tyr 44	116.539	7.687	Thr 86	116.550	9.485
Phe 45	117.213	8.406	Thr 87	117.170	7.310
Ala 46	126.147	8.416	Phe 88	122.200	8.252
Ser 47*	ND	ND	Asp 89	119.998	8.132
Thr 48	106.778	7.050	Lys 90	118.888	7.921
Leu 49	124.603	7.448	Leu 91	115.705	7.867
Gln 50	125.739	8.591	His 92	114.028	8.213
Ile 51	117.636	9.555	Val 93	118.584	6.881
Ser 52	113.049	8.780	Gln 94	124.381	8.085
Arg 53	132.638	9.105	Thr 95	114.450	8.137

**A**

1	11	21	31	41		
193	G S N G M S Q L P A	P V S V E S S W R Y	I D T Q G Q I H G P	F T T Q M M S Q W Y	I G G Y F A S T L Q	240
241	<i>I S R L G S T P E T</i>	<i>L G I N D I F I T L</i>	<i>G E L M T K L E K Y</i>	<i>D T D P F T T F D K</i>	<i>L H V Q T T S S D S</i>	290

**B**

**Fig. 12.1: Sequence of the SMY2-GYF construct and assignment of its  $^1\text{H}$ - $^{15}\text{N}$ -HSQC spectrum**

(A) Sequence of the SMY2-GYF construct, used for the backbone assignment. Italicised residues do not belong to the cognate SMY2 protein. Flanking numbers indicate the position of residues within full-length SMY2. (B) Assignment of NH resonances in the  $^1\text{H}$ - $^{15}\text{N}$ -HSQC spectrum of SMY2-GYF according to the chemical shifts in Table 12.5. Resonances are labeled with amino acid type and residue number according to (A). The spectrum was recorded at 299 K with a 1.2 mM protein sample, buffered in PBS.