

# Appendix

**Table 0.1 Top 100 Sequences of the 6223-Humlib Incubation with the AF6 PDZ Domain.**

Spot	Acc.No.	SP.en.	Sequence	Protein description
53	P41595	5H2B	GDKTEEQVSYV	5-hydroxytryptamine 2B receptor
116	O95477	ABC1	LQDEKVKESYV	ATP-binding cassette, sub-family A, member 1
131	Q12979	ABR	KRNTLYFSTDV	active breakpoint cluster region-related protein.
220	P50052	AG22	SSLREMETFVS	type-2 angiotensin II receptor
237	Q92667	AKA1	AQWVDSYYTSL	A kinase anchor protein 1
328	Q02410	APB1	LLTAQEQPVYI	amyloid beta A4 precursor protein-binding family a member 1
329	Q99767	APB2	LLTGQETPLYI	amyloid beta A4 precursor protein-binding family a member 2
330	O96018	APB3	LLTGQEQPVYL	amyloid beta A4 precursor protein-binding family a member 3
409	P11245	ARY2	VKPGDGSITI	arylamine n-acetyltransferase 2
441	P23634	ATCS	DSSLQSLETSV	calcium-transporting atpase plasma membrane, isoform 4
481	Q9UKP5	ATS6	SSCNLAKETLL	adam-ts 6 precursor
511	Q13072	BAGE	PEDGTALCFIF	B melanoma antigen
542	P11274	BCR	KRQSILFSTEV	breakpoint cluster region protein
668	P16581	C3AR	NVISERNSTTV	C3A anaphylatoxin chemotactic receptor
699	P05997	CA25	FGVEIGPVCFV	collagen alpha 2(V) chain precursor
775	P05814	CASB	PLAPVHNPISV	beta casein precursor
793	P43234	CATO	GIADSVSSIFV	cathepsin o precursor
826	O00257	CBX4	LTVTFKEYVTV	chromobox protein homolog 4
907	P01732	CD8A	GDKPSLSARYV	t-cell surface glycoprotein cd8 alpha chain precursor
1027	P35499	CIN4	TVRPGVKESLV	sodium channel protein, skeletal muscle alpha-subunit
1028	Q14524	CIN5	PSPDRDRESIV	sodium channel protein, cardiac muscle alpha-subunit
1050	P35523	CLC1	TDEEDEDELIL	chloride channel protein, skeletal muscle
1060	P57739	CLD2	EFNSYSLTGYV	claudin-2
1062	O14493	CLD4	AARSAAASNYV	claudin-4
1066	P56748	CLD8	SPSVYSRSQYV	claudin-8
1068	P78369	CLDA	PSKQFDKNAYV	claudin-10
1257	P34998	CRF1	SFHSIKQSTAV	corticotropin releasing factor receptor 1 precursor
1323	Q9UKL4	CXA9	GRTQSSDSAYV	gap junction alpha-9 protein.
1324	P78310	CXAR	IPAQSKDGSIV	coxsackievirus and adenovirus receptor precursor
1351	P33402	CYG4	IGTMFLRETSI	guanylate cyclase soluble, alpha-2 chain
1409	P11926	DCOR	RAACASASINV	ornithine decarboxylase
1442	P18282	DEST	SLIVAFEGCPV	destrin
1506	Q09019	DMWD	QPGNSPSGTVV	dystrophia myotonica-containing WD repeat motif protein
1551	O60469	DSCA	NNPYAKSYTLV	down syndrome cell adhesion molecule precursor
1611	O00341	EAT5	TIQISELETNV	excitatory amino acid transporter 5
1659	P19957	ELAF	GSCGMACFVPQ	elafin precursor
1702	Q15375	EPA7	MLHLHGTGIQV	ephrin type-A receptor 7 precursor
1703	P29322	EPA8	MENGSLDTFLR	ephrin type-A receptor 8
1706	P54753	EPB3	LQMNQTLVPQV	ephrin type-B receptor 3 precursor
1708	O15197	EPB6	QHLRQQGSVEV	ephrin type-B receptor 6 precursor
1953	Q12951	FXI1	GVLYPREGTEV	forkhead box protein I1
1954	Q92949	FXJ1	LQDWASVGAFI	forkhead protein J1
2019	P47211	GALR	DTPPSTNCTHV	galanin receptor type 1
2156	P04921	GLPC	AGDSSRKEYFI	glycophorin C
2207	P46089	GPR3	IPFRSRSPSDV	probable G protein-coupled receptor GPR3
2209	P46095	GPR6	VPFRSRSPSEV	probable g protein-coupled receptor GPR6
2213	P47775	GPRC	LAQRARSPSDV	probable g protein-coupled receptor GPR12
2217	Q15760	GPRJ	PINSNPPNTFV	probable g protein-coupled receptor GPR19
2250	P30968	GRHR	FDPLIYGYFSL	gonadotropin-releasing hormone receptor

Spot	Acc.No.	SP.en.	Sequence	Protein description
2257	P30550	GRPR	INGNICHERYV	gastrin-releasing peptide receptor
2271	P36969	GSHH	LVIEKDLPHYF	phospholipid hydroperoxide glutathione peroxidase
2340	O60229	HAPP	LGPGDPFSTYV	huntingtin-associated protein-interacting protein
2536	P01765	HV3D	WGEGLTVTVSS	IG heavy chain V-III region TIL
2545	P01774	HV3M	FAHYGQGTLVT	IG heavy chain V-III region POM
2546	P01775	HV3N	FAHWGQGTLVT	IG heavy chain V-III region LAY
2547	P01776	HV3O	FDVFGQGTLVT	IG heavy chain V-III region WAS
2548	P01777	HV3P	SAVWGQGTLVT	IG heavy chain V-III region TEI
2549	P01778	HV3Q	SDVWGQGLVLS	IG heavy chain V-III region ZAP
2550	P01779	HV3R	FDVWGQGTKVS	IG heavy chain V-III region TUR
2638	P42574	ICE3	SMLTKELYFYH	apopain precursor
2648	Q02556	ICSB	SFFRENQQITV	interferon consensus sequence binding protein
2653	P98153	IDD	RHSRSSLNTVV	integral membrane protein DGCR2/IDD precursor
2665	Q16666	IF16	SSMETSPPDFFF	gamma-interferon-inducible protein IFI-16
2881	Q14624	ITH4	GVEISCWSVEL	inter-alpha-trypsin inhibitor heavy chain H4 precursor
2891	Q9Y624	JAM1	GEFKQTSSFLV	junctional adhesion molecule precursor
3051	P05771	KPC1	SYTNPEFVINV	protein kinase C, beta-1 type
3072	P10398	KRAA	ACLLSAARLVP	a-Raf proto-oncogene serine/threonine-protein kinase
3130	Q03252	LAM2	PRTTSRGCYVM	lamin B2
3264	P01704	LV2A	FGGGTYVTVLR	IG lambda chain V-II region TOG
3492	Q9ULZ9	MM17	ALWTAAQALTL	matrix metalloproteinase-17 precursor
3532	Q99549	MPP8	DENSGEFGIIL	m-phase phosphoprotein 8
3796	P26718	NKGD	PNTYICMQRTV	NKG2-D type II integral membrane protein
3859	Q02297	NRG1	SVIANQDPIAV	pro-neuregulin-1
3927	P49146	NY2R	PNDSFTEATNV	neuropeptide y receptor type 2
4269	Q15147	PIB4	AEMDRRPATVV	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 4
4451	P48556	PSD8	IEYARQLEMIV	26S proteasome regulatory subunit S14
4475	P08118	PSSP	KKTCSVSEWII	prostate secreted seminal plasma protein precursor
4480	P49753	PTE2	GGREGTIPSKV	peroxisomal acyl-coenzyme a thioester hydrolase 2
4509	P23470	PTPG	SDPAESMESLV	protein-tyrosine phosphatase gamma precursor
4516	P23471	PTPZ	GNIAESLESILV	protein-tyrosine phosphatase zeta precursor
4554	P40429	R13A	TEVLKTHGLLV	60s ribosomal protein l13A
4701	O14924	RGSC	PKTSAHHATFV	regulator of G-protein signaling 12
4898	P34925	RYK	TEFHAALGAYV	tyrosine-protein kinase RYK precursor
5136	Q9UBP0	SPAS	RWNKDFGDTTV	spastin
5141	Q13813	SPCN	YVEFTRSLFVN	spectrin alpha chain, brain
5298	Q15046	SYK	TLESTTVGSSV	lysyl-tRNA synthetase
5454	P01135	TGFA	RTACCHSETVV	transforming growth factor alpha precursor
5524	P50591	TN10	EASFFGAFLVG	tumor necrosis factor ligand superfamily member 10
5551	O95985	TP3B	DKMSALAAAYFV	DNA topoisomerase III beta-1
5574	Q15643	TR11	GLGPGGPGIFF	thyroid receptor interacting protein 11
5771	P30039	ULA4	PIFIADAFNVR	unknown protein from 2D-PAGE of liver tissue
5945	Q14135	Y121	SYRRPPSATCV	hypothetical protein KIAA0121
6010	O60299	Y552	SRLERIESTEI	hypothetical protein kiaa0552
6015	Q9Y2G5	Y958	SGHFHTVCLLV	hypothetical protein kiaa0958
6025	Q9UPW0	YA41	IQDDFDWDSIV	putative fork head domain protein KIAA1041
6142	O94822	Z294	STCPLCRETFF	zinc finger protein 294
6161	Q15915	ZIC1	ALSSNFNEWYV	zinc finger protein zic 1
6162	O95409	ZIC2	GLSSNFNEWYV	zinc finger protein zic2
6163	O60481	ZIC3	GLPPNFNEWYV	zinc finger protein zic3
6222	P98168	ZXDA	LITVTGSSFLV	zinc finger X-linked protein ZXDA

**Footnotes:** Spot: the spot-ID of the sequence in the library. Acc.no.: SWISS-PROT database accession number. SP.en.: SWISS-PROT database protein entry name with the ‘\_HUMAN’ suffix omitted. The sequences are listed in alphabetical order of the SWISS-PROT entry name.

**Table 0.2 Top 100 Sequences of the 6223-Humlib Incubation with the ERBIN PDZ Domain.**

Spot	Acc.No.	SP.en.	Sequence	Protein description
23	P00973	25A1	QAEDWTCTIL	(2'-5')oligoadenylate synthetase 1
71	P25100	A1AD	ADYSNLRETDI	alpha-1D adrenergic receptor
75	Q10567	A1B1	VYQAYETILKN	adapter-related protein complex 1 beta 1 subunit
102	P12814	AAC1	FSTALYGESDL	alpha-actinin 1, cytoskeletal isoform
103	P35609	AAC2	FSSALYGESDL	alpha-actinin 2, skeletal muscle isoform
116	O95477	ABC1	LQDEKVKESYV	ATP-binding cassette, sub-family A, member 1
131	Q12979	ABR	KRNTLYFSTDV	active breakpoint cluster region-related protein
220	P50052	AG22	SSLREMETFVS	type-2 angiotensin II receptor
237	Q92667	AKA1	AQWVDSYYTSL	A kinase anchor protein 1
278	P19961	AMYC	PFTAIHAESKL	alpha-amylase 2B precursor
336	P25054	APC	RHSGSYLVTSV	adenomatous polyposis coli protein
407	O00192	ARVC	DAKQPVDSSWV	armadillo repeat protein deleted in velo-cardio-facial syndrome
431	Q04656	AT7A	GDFREDDDTAL	copper-transporting ATPase 1
438	P20020	ATB1	GSPLHSLETSL	calcium-transporting ATPase plasma membrane, isoform 1B
439	Q01814	ATB2	GSPIHSLETSL	calcium-transporting atpase plasma membrane, isoform 2
441	P23634	ATCS	DSSLQSLETSL	calcium-transporting ATPase plasma membrane, isoform 4
481	Q9UKP5	ATS6	SSCNLAKETLL	ADAM-TS 6 precursor
489	P27037	AVR2	NVDFPPKESSL	activin receptor type II precursor
490	Q13705	AVRB	NVDLPPKESSI	activin receptor type IIB precursor
494	P08588	B1AR	CRPGFASESKV	beta-1 adrenergic receptor
505	O75531	BAF	GCLREWCD AFL	barrier-to-autointegration factor
513	O60241	BAI2	EPPDGDGFQTEV	brain-specific angiogenesis inhibitor 2 precursor
514	O60242	BAI3	DVQEGDGFQTEV	brain-specific angiogenesis inhibitor 3 precursor
542	P11274	BCR	KRQSILFSTEV	breakpoint cluster region protein
681	P02452	CA11	FGFDVGPVCFLL	collagen alpha 1(I) chain precursor
756	P21941	CAMA	KRLAILENTVV	cartilage matrix protein precursor
757	P49069	CAMG	ELLDYWGSEVP	calcium-signal modulating cyclophilin ligand
788	P08311	CATG	FKLLDQMETPL	cathepsin G precursor
834	Q13936	CCAC	LQDSRVYVSSL	voltage-dependent l-type calcium channel alpha-1c subunit
875	P28906	CD34	ARQHVVADTEL	hematopoietic progenitor cell antigen CD34 precursor
962	P13569	CFTR	ETEEEVQDTRL	cystic fibrosis transmembrane conductance regulator
1017	P22459	CIK4	CSNAKAVETDV	voltage-gated potassium channel protein Kv1.4
1018	P22460	CIK5	LCCLDTSRETDL	voltage-gated potassium channel protein Kv1.5
1027	P35499	CIN4	TVRPGVKESLV	sodium channel protein, skeletal muscle alpha-subunit
1099	Q99527	CML2	EQSDVRFSSAV	chemokine receptor-like 2
1168	P53618	COPB	KINLSQKETS I	coatamer beta subunit
1223	P10635	CPD6	PSPYELCAVPR	cytochrome p450 2D6
1253	P23508	CRCM	NSRPHTNETSL	colorectal mutant cancer protein
1284	O14936	CSKP	APQWVPVSWVY	peripheral plasma membrane protein CASK
1300	P35222	CTNB	SNQLAWFD TDL	beta-catenin
1351	P33402	CYG4	IGTMFLRETSL	guanylate cyclase soluble, alpha-2 chain
1611	O00341	EAT5	TIQISELETNV	excitatory amino acid transporter 5
1668	Q00013	EM55	SPQWVPVSWVY	55 kDa erythrocyte membrane protein
1703	P29322	EPA8	MENGLD TFLR	ephrin type-A receptor 8
1776	Q92800	EZH1	YVGIERETDVL	enhancer of zeste homolog 1
1958	O43524	FXO3	KQASSQSWVPG	forkhead protein O3A
2054	P50150	GBG4	FREKKFFCTIL	guanine nucleotide-binding protein g(i)/g(s)/g(o) gamma-4 subunit
2549	P01778	HV3Q	SDVWGQGT LVS	IG heavy chain V-III region ZAP
2550	P01779	HV3R	FDVWGQGT KVS	IG heavy chain V-III region TUR

Spot	Acc.No.	SP.en.	Sequence	Protein description
2627	P22692	IBP4	DCHQLADSFRE	insulin-like growth factor binding protein 4 precursor
2646	P31944	ICEE	QSTLRKRLYLQ	caspase-14 precursor
2977	P49619	KDGG	FSLRRKSRSKD	diacylglycerol kinase, gamma
3214	P07942	LMB1	SQKVAVYSTCL	laminin beta-1 chain precursor
3340	P27816	MAP4	TLDSQIQETSI	microtubule-associated protein 4
3371	P33993	MCM7	VNASRTRITFV	DNA replication licensing factor MCM7
3372	P15529	MCP	ETHREVKFTSL	membrane cofactor protein precursor
3387	P51608	MEC2	DSRTPVTERVS	methyl-CPG-binding protein 2
3388	Q02078	MEFA	VKRMMDAWVT	myocyte-specific enhancer factor 2A
3408	P55082	MFA3	YKDGAYENCQL	microfibril-associated glycoprotein 3 precursor
3420	Q9Y5V3	MGD1	NFGAIGFFWVE	melanoma-associated antigen D1
3454	P53778	MK12	LGARVSKETPL	mitogen-activated protein kinase 12
3466	Q16048	MLC2	LGRVYQSCWQV	pro-MCH variant
3486	P24347	MM11	FGCAEPANTFL	stromelysin-3 precursor
3495	Q9Y5R2	MM24	TYYKRPVQEWV	matrix metalloproteinase-24 precursor
3506	P53985	MOT1	EGGPKKEESEPV	monocarboxylate transporter 1
3507	O60669	MOT2	QSVTSERETNI	monocarboxylate transporter 2
3508	O15427	MOT3	GEVVHTPETSU	monocarboxylate transporter 3
3528	Q14168	MPP2	EPQWVPVSWVY	MAGUK p55 subfamily member 2
3529	Q13368	MPP3	DTHWVPVSWVR	MAGUK p55 subfamily member 3
3547	O15439	MRP4	PSTLTIFETAL	multidrug resistance-associated protein 4
3777	O75438	NINM	ELQPSEEVTWK	NADH-ubiquinone oxidoreductase MNLL subunit
3807	Q14957	NME3	WRRISSLESEV	glutamate [NMDA] receptor subunit epsilon 3 precursor
3843	Q06495	NPT2	ALPAHNNATRL	renal sodium-dependent phosphate transport protein 2
3848	Q9Y466	NR21	LLSDMYKSSDI	orphan nuclear receptor NR2E1
3882	P48065	NTBE	GLIAGEKETHL	sodium- and chloride-dependent betaine transporter
3927	P49146	NY2R	PNDSFTEATNV	neuropeptide Y receptor type 2
4011	O43929	ORC4	RQWATSSLSWL	origin recognition complex subunit 4
4045	Q15363	P24	LKRFFFEVRRV	cop-coated vesicle membrane protein p24 precursor
4068	P47900	P2YR	PEFKQNGDTSL	P2Y purinoceptor 1
4156	Q13258	PD2R	CSNSTNMESL	prostaglandin D2 receptor
4232	P16234	PGDS	DSSDLVEDSFL	alpha platelet-derived growth factor receptor precursor
4267	Q9NQ66	PIB1	DIPGKEFDTP	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 1
4268	Q00722	PIB2	IAKADAQESRL	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 2
4301	Q13393	PLD1	KEAIVPMEVWT	phospholipase D1
4459	Q00889	PSG6	PNTWFQEILL	pregnancy-specific beta-1-glycoprotein 6 precursor
4525	P22234	PUR6	QADKKIRECNL	multifunctional protein ADE2
4711	P25800	RHM1	QLNGTFESQVQ	rhombotin-1
4781	O60896	RMP3	VWRSKRTDTLL	receptor activity-modifying protein 3 precursor
4939	Q13228	SBP1	PGGDCSSDIWI	selenium-binding protein 1
4995	O00141	SGK	FSYAPPTDSFL	serine/threonine-protein kinase SGK
5016	O95343	SIX3	SVTSSDSECDV	homeobox protein six3
5027	Q92911	SL55	DGGRDQQETNL	sodium/iodide cotransporter
5028	Q9Y289	SL56	SSTCILQETSL	sodium-dependent multivitamin transporter
5106	P18583	SON	VYIVYLSDFV	SON protein
5136	Q9UBP0	SPAS	RWNKDFGDTTV	spastin
5446	P10646	TFPI	IAYEEIFVKNM	tissue factor pathway inhibitor precursor
5840	P41587	VIPS	QSFLQTETSVI	vasoactive intestinal polypeptide receptor 2 precursor
5956	Q14155	Y142	MNDPAWDETNL	hypothetical protein kiaa0142
5990	Q92558	Y269	DSEFDEVDWLE	hypothetical proline-rich protein kiaa0269
6026	P46937	YA65	KLDKESFLTWL	65 kDa YES-associated protein

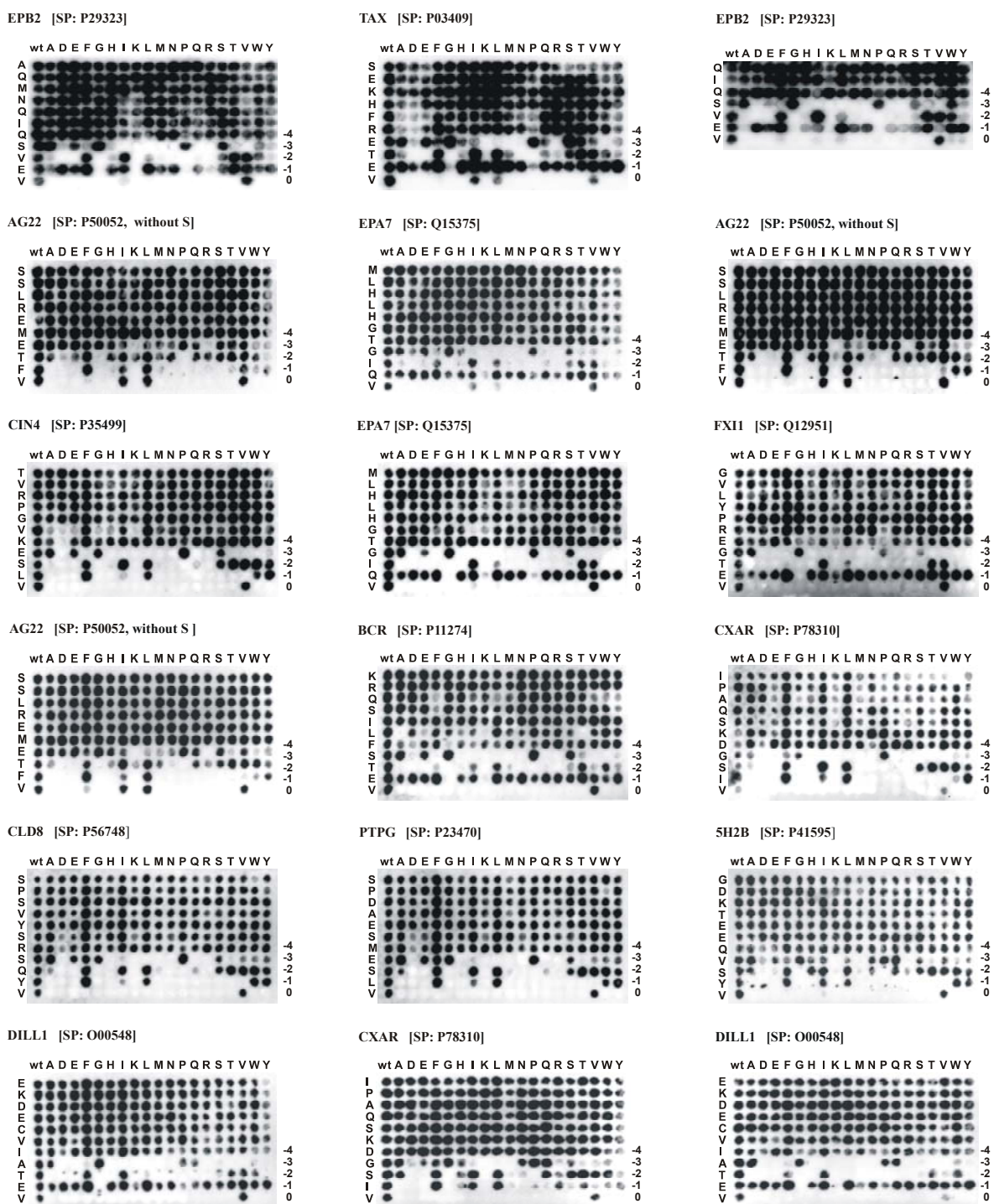
**Footnotes:** Spot: the spot-ID of the sequence in the library. Acc.no.: SWISS-PROT database accession number. SP.en.: SWISS-PROT database protein entry name with the ‘\_HUMAN’ suffix omitted. The sequences are listed in alphabetical order of the SWISS-PROT entry name.

**Table 0.3 Top 100 Sequences of the 6223-Humlib Incubation with the SNA1 PDZ Domain.**

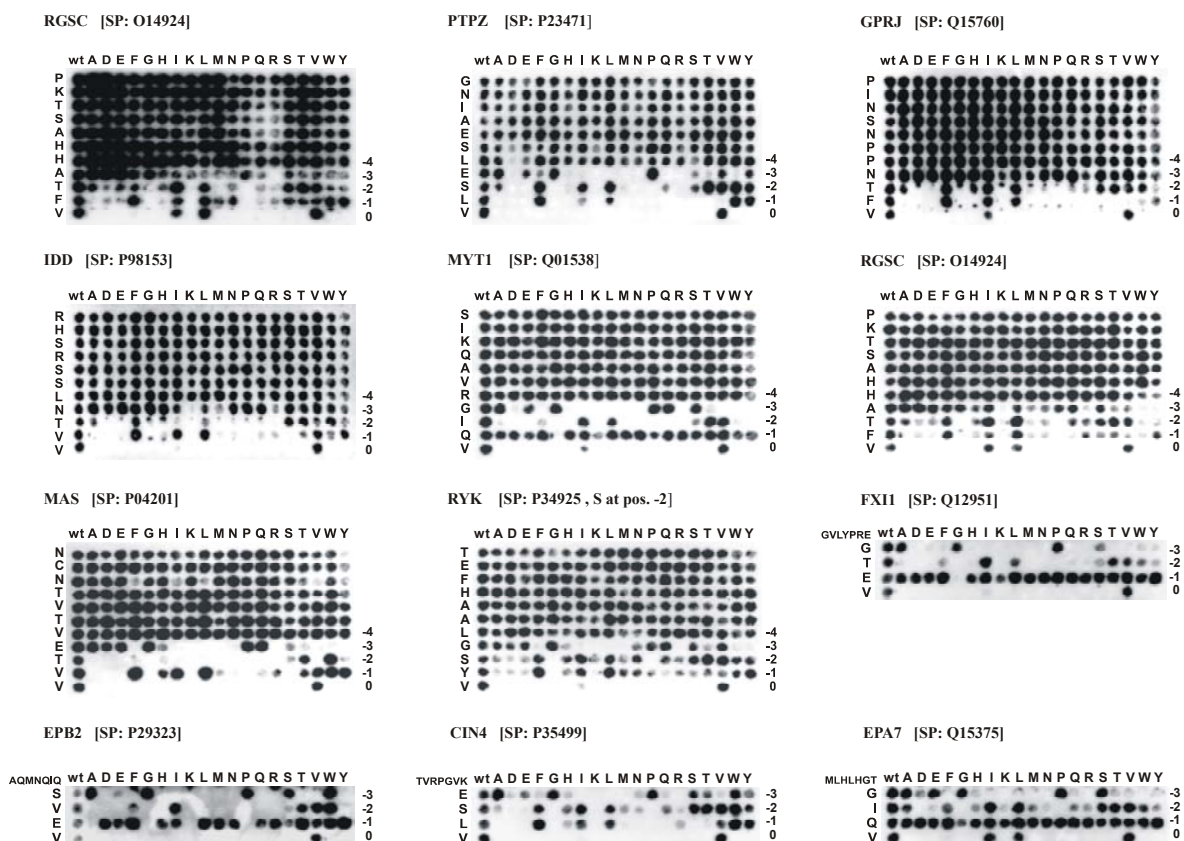
Spot	Acc.No.	SP.en.	Sequence	Protein description
23	P00973	25A1	QAEEDWTCTIL	(2'-5')oligoadenylate synthetase 1
54	P28335	5H2C	SSVVSERISSV	5-hydroxytryptamine 2c receptor
65	O95336	6PGL	LTVPFEKHSTL	6-phosphogluconolactonase
131	Q12979	ABR	KRNTLYFSTDV	active breakpoint cluster region-related protein
220	P50052	AG22	SSLREMETFVS	type-2 angiotensin II receptor
336	P25054	APC	RHSGSYLVTSV	adenomatous polyposis coli protein
439	Q01814	ATCQ	GSPIHSLETSL	calcium-transporting ATPase plasma membrane, brain isoform 2
441	P23634	ATCS	DSSLQSLETSV	calcium-transporting ATPase plasma membrane, isoform 4
481	Q9UKP5	ATS6	SSCNLAKETLL	ADAM-TS 6 precursor
494	P08588	B1AR	CRPGFASESKV	beta-1 adrenergic receptor
513	O60241	BAI2	EPPDGDGFQTEV	brain-specific angiogenesis inhibitor 2 precursor
514	O60242	BAI3	DVQEGDFQTEV	brain-specific angiogenesis inhibitor 3 precursor
542	P11274	BCR	KRQSILFSTEV	breakpoint cluster region protein
624	P35070	BTC	INEDIEETNIA	betacellulin precursor
668	Q16581	C3AR	NVISERNSTTV	C3A anaphylatoxin chemotactic receptor
756	P21941	CAMA	KRLAILENTVV	cartilage matrix protein precursor
788	P08311	CATG	FKLLDQMETPL	cathepsin g precursor
849	O60359	CCG3	NNPANRRTPV	voltage-dependent calcium channel gamma-3 subunit
850	Q9UBN1	CCG4	VSMLNRRTPV	voltage-dependent calcium channel gamma-4 subunit
1027	P35499	CIN4	TVRPGVKESLV	sodium channel protein, skeletal muscle alpha-subunit
1028	Q14524	CIN5	PSPDRDRESIV	sodium channel protein, cardiac muscle alpha-subunit
1099	Q99527	CML2	EQSDVRFSSAV	chemokine receptor-like 2
1106	P09543	CN37	KGGALQSCCTII	2',3'-cyclic nucleotide 3'-phosphodiesterase
1118	P20694	CNBP	LARECTIEATA	cellular nucleic acid binding protein
1168	P53618	COPB	KINLSQKETSII	coatamer beta subunit
1180	P81408	COTE	SLNGGSRETGL	cote1 protein
1261	P11844	CRGA	VGSLRRVTDLY	gamma crystallin A
1351	P33402	CYG4	IGTMFLRETSL	guanylate cyclase soluble, alpha-2 chain
1432	P12838	DEF4	VSFTYCCTRV	neutrophil defensin 4 precursor
1506	Q09019	DMWD	QPGNSPSGTVV	dystrophia myotonica-containing WD repeat motif protein
1532	Q14195	DPY3	PGGRSNITSL	dihydropyrimidinase related protein-3
1567	Q05923	DUS2	LLQFETQVLCH	dual specificity protein phosphatase 2
1611	O00341	EAT5	TIQISELETNV	excitatory amino acid transporter 5
1776	Q92800	EZH1	YVGIERETDVL	enhancer of zeste homolog 1
1787	P23610	F8I2	LHLVLQETISP	factor VIII intron 22 protein
1790	P00748	FA12	YLAWIREHTVS	coagulation factor XII precursor
1980	P06744	G6PI	FIKQQREARVQ	glucose-6-phosphate isomerase
2117	Q08379	GG95	DENDEVKITVI	golgin-95
2153	O95838	GLP2	TMEEILEESEI	glucagon-like peptide 2 receptor precursor
2167	Q9UI32	GLSL	ALSKENLESMV	glutaminase, liver isoform, mitochondrial precursor
2181	Q09327	GNT3	PARGKLDEAEV	beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyl-transferase
2207	P46089	GPR3	IPFRSRSPSDV	probable G protein-coupled receptor GPR3
2212	P49683	GPRA	HGQNMTPSVVI	probable G protein-coupled receptor GPR10
2217	Q15760	GPRJ	PINSNPNTFV	probable G protein-coupled receptor GPR19
2296	P11169	GTR3	IEPAKETTTNV	glucose transporter type 3, brain
2303	Q9Y2T3	GUAD	GKQVVPFSSV	guanine deaminase
2340	O60229	HAPP	LGPGDPFSTYV	huntingtin-associated protein-interacting protein
2547	P01776	HV3O	FDVFGQGLVLT	IG heavy chain V-III region WAS
2550	P01779	HV3R	FDVWGQGTKVS	IG heavy chain V-III region TUR

Spot	Acc.No.	SP.en.	Sequence	Protein description
2556	O43711	HX1M	SSKVPAVTSLV	homeobox protein HOX-11L2
2628	P24593	IBP5	QCHTFDSSNVE	insulin-like growth factor binding protein 5 precursor
2653	P98153	IDD	RHSRSSLNTVV	integral membrane protein DGCR2/IDD precursor
2744	P25025	IL8B	GSSSGHTSTTL	high affinity interleukin-8 receptor B
2829	P48049	IRK2	EPRPLRRESEI	inward rectifier potassium channel 2
2831	P48050	IRK4	DNISYRRESAI	inward rectifier potassium channel 4
2833	P48051	IRK6	DVANLENESKV	G protein-activated inward rectifier potassium channel 2
2835	Q92806	IRK9	CLPPPESESKV	G protein-activated inward rectifier potassium channel 3
2836	P78508	IRKA	GSALSVRISNV	ATP-sensitive inward rectifier potassium channel 10
2838	Q14500	IRKC	EQRPYRRESEI	ATP-sensitive inward rectifier potassium channel 12
2839	Q99712	IRKF	LRLLLLQQSNV	ATP-sensitive inward rectifier potassium channel 15
2967	Q13555	KCCG	SKPIHTTILNP	calcium/calmodulin-dependent protein kinase type II gamma chain
3066	P11801	KPSH	VDPGARM TALQ	putative serine/threonine-protein kinase H1
3256	P01699	LV1A	FGGGTKVTVLG	IG lambda chain V-I region VOR
3262	P06887	LV1H	FGTGTKVTVLR	IG lambda chain V-I region MEM
3265	P01705	LV2B	FGGGTRVTVLS	IG lambda chain V-II region NEI
3275	P06318	LV6D	VFGGTRLTVLG	IG lambda chain V-VI region WLT
3348	P04201	MAS	NCNTVTVETVV	MAS proto-oncogene
3371	P33993	MCM7	VNASRTRITFV	DNA replication licensing factor MCM7
3454	P53778	MK12	LGARVSKETPL	mitogen-activated protein kinase 12
3507	O60669	MOT2	QSVT SERETNI	monocarboxylate transporter 2
3508	O15427	MOT3	GEVVHTPETS	monocarboxylate transporter 3
3585	Q13613	MTR1	SHSATS VHTSV	myotubularin-related protein 1
3586	Q13614	MTR2	AQCVPVQTVV	myotubularin-related protein 2
3807	Q14957	NME3	WRRISSESEV	glutamate [NMDA] receptor subunit epsilon 3 precursor
3842	Q14916	NPT1	DWAKEKQHTRL	renal sodium-dependent phosphate transport protein 1
3843	Q06495	NPT2	ALPAHNNATRL	renal sodium-dependent phosphate transport protein 2
3845	O00476	NPT4	EWAKERKLTRL	sodium-dependent phosphate transport protein 4
3874	O60591	NS2D	NALEEPKGTRL	nitric oxide synthase, inducible IID
3882	P48065	NTBE	GLIAGEKETHL	sodium- and chloride-dependent betaine transporter
4027	O43613	OX1R	VVLTSVTTVLP	orexin receptor type 1
4087	Q29459	PA1B	ETPEEKQTTIA	platelet-activating factor acetylhydrolase IB beta subunit
4121	P51888	PARG	MCFRLLQSVVI	prolargin precursor
4631	Q06330	RBJK	SVTSSTATVVS	J kappa-recombination signal binding protein
4711	P25800	RHM1	QLNGTFESQVQ	rhombotin-1
4718	O00212	RHOD	RRITQGFVVT	rho-related GTP-binding protein rhod
4721	Q15669	RHOH	RLFSINECKIF	rho-related GTP-binding protein rhoh
5181	P30872	SSR1	NGTCTSRITTL	somatostatin receptor type 1
5454	P01135	TGFA	RTACCHSETVV	transforming growth factor alpha precursor
5573	Q15642	TR10	VPTS YLRVTLN	thyroid receptor interacting protein 10
5658	P04436	TVA1	IFGSGTRLSIR	t-cell receptor alpha chain V region HPB-MLT precursor
5659	P04437	TVA2	FGTGTRLQVTL	t-cell receptor alpha chain v region CTL-I17 precursor
5660	P01733	TVB1	TFGSGTRLTVV	t-cell receptor beta chain V region YT35 precursor
5661	P04435	TVB2	HFGDGTRLSIL	t-cell receptor beta chain V region CTL-I17 precursor
5662	P03979	TVC	LFSGGTLLVVT	t-cell receptor gamma chain V region PT-gamma-1/2 precursor
5667	Q9UMR3	TX20	FRDSSRLTDIE	TBX20 protein
5728	P40818	UBP8	SLGPRVTDVAT	ubiquitin carboxyl-terminal hydrolase 8
5766	P49289	UHA4	TAGAIMETNLK	unknown protein from 2D-page of heart
5799	P47901	V1BR	DGEGTAETIIF	vasopressin V1B receptor
5820	Q99437	VATO	ILQTSRVKMGD	vacuolar ATP synthase 21 kDa proteolipid subunit
5840	P41587	VIPS	QSFLQTETSVI	vasoactive intestinal polypeptide receptor 2 precursor

**Footnotes:** Spot: the spot-ID of the sequence in the library. Acc.no.: SWISS-PROT database accession number. SP.en.: SWISS-PROT database protein entry name with the ‘\_HUMAN’ suffix omitted. The sequences are listed in alphabetical order of the SWISS-PROT entry name.

**Figure 0.1** Substitutional Analyses used for Profile Definition Incubated with the AF6 PDZ Domain.





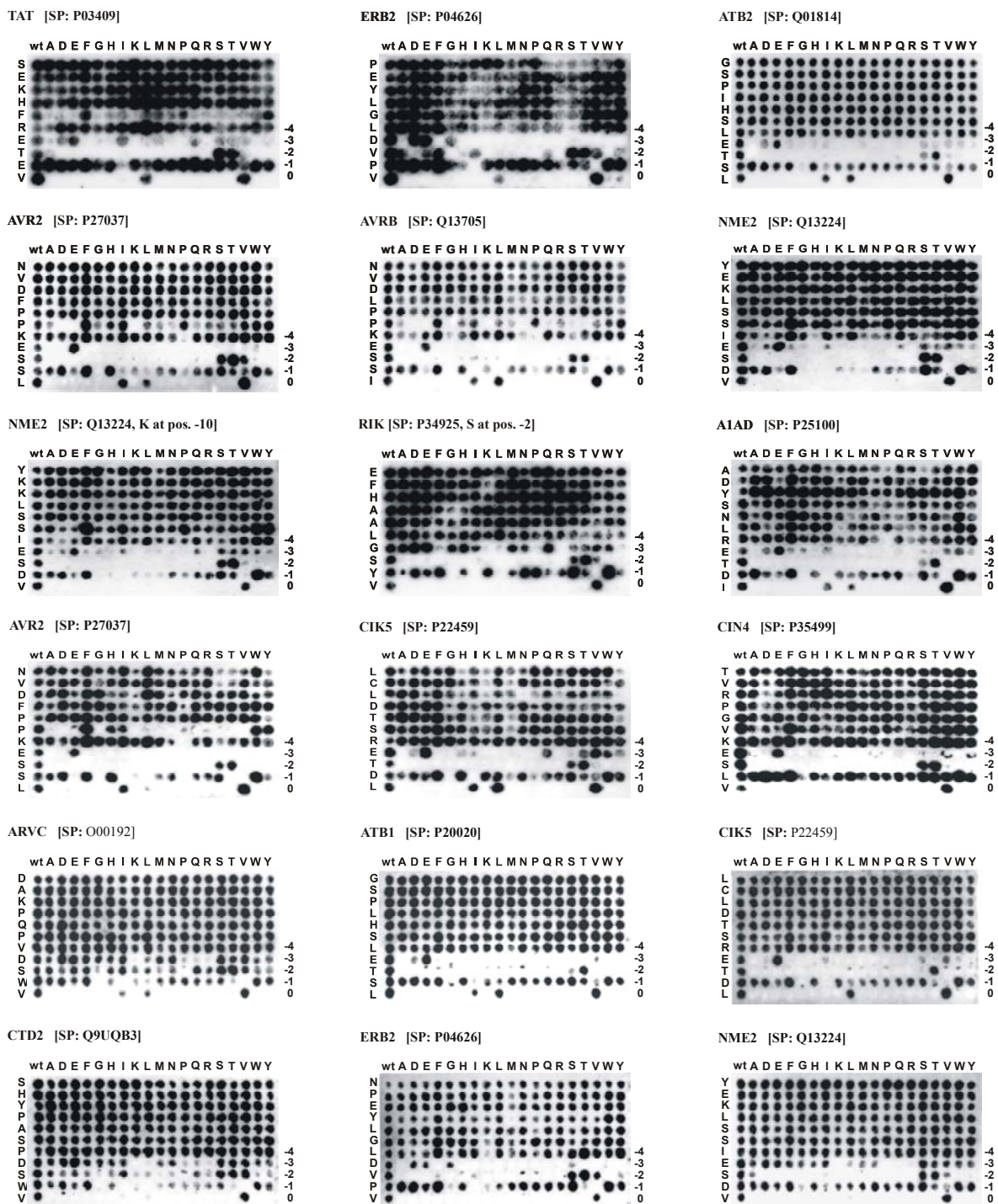
#### Footnotes: Characterization of the Ligand/AF6 PDZ Domain Interaction.

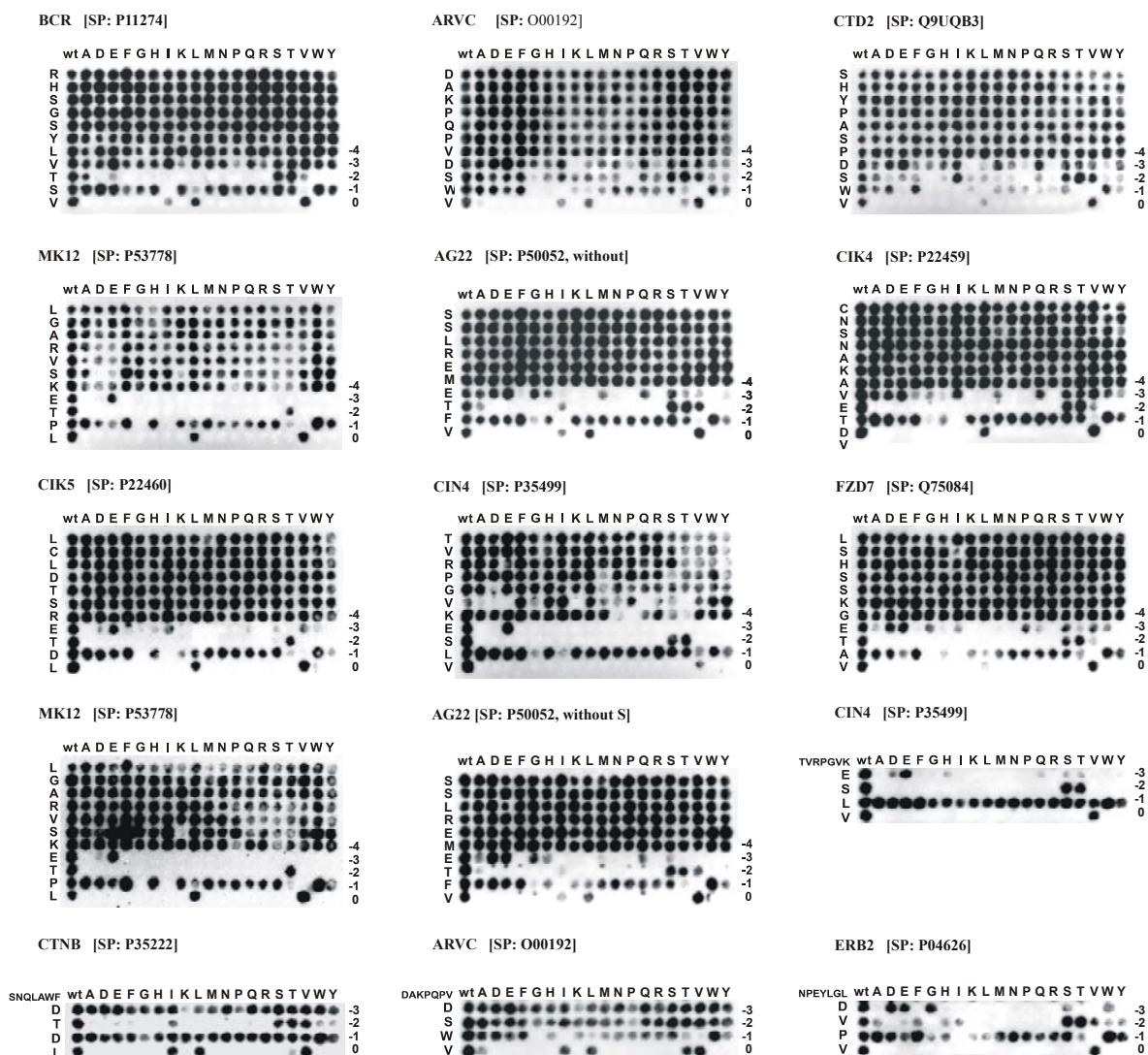
The substitutional analyses of the AF6 PDZ domain revealed a similar pattern of the essential amino acids, which is mainly characterized by the last four C-terminal residues. Furthermore, a class-specific substitution pattern is not observable.

All spots in the left hand columns are identical and represent the wild type (wt) peptide. All other spots represent the substitution of one amino acid against the amino acid in the respective column. Hence, each spot bears a single substitution compared to the sequence of the wild type. For example, V in position 0 can only be substituted by itself and in some cases by I and L. The last four or five C-terminal ligand positions are numbered to the right of each substitutional analysis.



**Figure 0.2 Substitutional Analyses used for Profile Definition Incubated with the ERBIN PDZ Domain.**



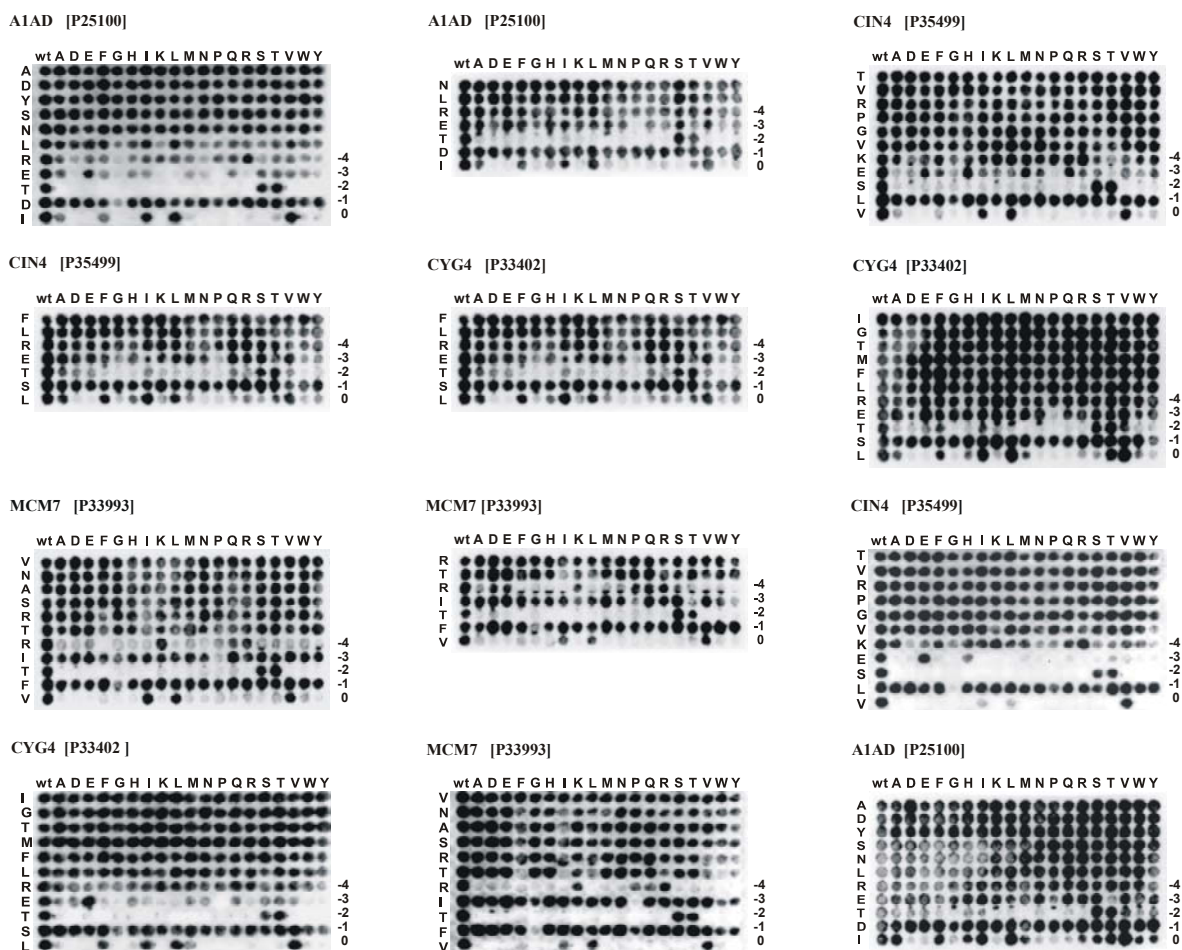


### Footnotes: Characterization of the Ligand/ERBIN PDZ Domain Interaction.

The substitutional analyses of the ERBIN PDZ domain revealed a similar pattern of the essential amino acids, which is mainly characterized by the last four C-terminal residues. Furthermore, a class-specific substitution pattern is not observable.

All spots in the left hand columns are identical and represent the wild type (wt) peptide. All other spots represent the substitution of one amino acid against the amino acid in the respective column. Hence, each spot bears a single substitution compared to the sequence of the wild type. For example, V in position 0 can only be substituted by itself and in some cases by I and L. The last four or five C-terminal ligand positions are numbered to the right of each substitutional analysis.

**Figure 0.3 Substitutional Analyses used for Profile Definition Incubated with the SNA1 PDZ Domain.**



**Footnotes: Characterization of the Ligand/AF6 PDZ Domain Interaction.**

The substitutional analyses of the AF6 PDZ domain revealed a similar pattern of the essential amino acids, which is mainly characterized by the last four C-terminal residues. Furthermore, a class-specific substitution pattern is not observable.

All spots in the left hand columns are identical and represent the wild type (wt) peptide. All other spots represent the substitution of one amino acid against the amino acid in the respective column. Hence, each spot bears a single substitution compared to the sequence of the wild type. For example, V in position 0 can only be substituted by itself and in some cases by I and L. The last four or five C-terminal ligand positions are numbered to the right of each substitutional analysis.

## Publications

**Boisguérin, P.**, Leben, R., Ay, B., Radziwill, G., Moelling, K., Dong, L., and Volkmer-Engert, R. (2004). An Improved Method for the Synthesis of Cellulose Membrane-Bound Peptides with Free C-Termini Useful for PDZ Domain Binding Studies. *Chemistry & Biology* 11, 449-559.

**Wiedemann U.\***, **Boisguérin P.\***, Leben R., Leitner D., Krause G., Moelling K., Volkmer-Engert R. and Oschkinat H.

Quantification of PDZ Domain Specificity, Prediction of Ligand Affinity and Rational Design of Super-Binding Peptides. *Accepted to Journal of Molecular Biology*.

(\* contributed equally to this work)

Dong L., **Boisguérin P.**, Schneider-Mergener J. and Volkmer-Engert R.

Generation of Cellulose Membran-Bound Peptides with Free C-Termini: a Useful Approach for PDZ Binding Studies. *Poster, 17<sup>th</sup> American Peptide Symposium*, San Diego (USA). In: Lebl, M & Houghten, R.A. (Ed.s) *Peptides 2001 Proceedings of the 2<sup>th</sup> International and the 17<sup>th</sup> American Peptide Symposium*.

**Boisguérin P.**, Kretschmar I., Volkmer-Engert R., Schneider-Mergener J. and Oschkinat H.

Specificity of PDZ Interaction Investigated by NMR Spectroscopy and Synthetic Peptide Libraries. *Poster, 27<sup>th</sup> European Peptide Symposium*, Sorrento (Italy). In: Benedetti, C. & Pedone, C. (Eds) *Peptides 2002 Proceedings of the 28<sup>th</sup> European Peptide Symposium*.

**Boisguérin P.**, Leben R., Volkmer-Engert R., Schneider-Mergener J. and Oschkinat H.

Specificity of PDZ Interaction using NMR Spectroscopy and Spot Synthesis. *Poster, 18<sup>th</sup> American Peptide Symposium*, Boston (USA). In: Chorev, M. & Sawyer, T.K. (Eds). *Peptides 2003 Proceedings of the 18<sup>th</sup> American Peptide Symposium*.

# Curriculum Vitae

## Personal Details

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## School Education

1979-1981 Elementary School: Ecole de l'amitié  
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1981-1984 Elementary School: Ecole Victor Hugo  
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1984-1985 Secondary School: Collège Voltaire  
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Supervised by Prof. Dr. H. Oschkinat

## **Declaration of Honesty (Eidesstattliche Versicherung)**

Hereby I declare that I have written this thesis by myself, marked the sources of any quotations or content obtained otherwise and mentioned any personal help by name.

(Ich erkläre hiermit, dass ich die vorliegende Doktorarbeit selbständig verfasst, die wörtlich oder inhaltlich anderen Quellen entnommenen Stellen als solche kenntlich gemacht und die

Inanspruchnahme persönlicher Hilfe namentlich aufgeführt habe.)

Berlin

Prisca Boisguérin