#### 6. Anhang

# 6.1. Biochemische Bestimmung der Enzymaktivität von Pim-1 nach Substratbehandlung

In diesem Experiment wurde die Inhibition der Pim-1-WT-GST Enzymaktivität durch verschiedene Substanzen untersucht. Es wurden fünf unterschiedliche, potentielle Pim-1 Inhibitoren in einem HTRF-Assay (<u>homogeneous time resolved fluoreszenz</u>) getestet (Informationen zum HTRF-Methode siehe: www.htrf-assays.com/technology/htrftheory/htrf\_chemistry/).

Die Phosphorylierung eines Substratpeptids diente als Maß für die Enzymaktivität von Pim-1 und reziprok für die Wirkung des Inhibitors. Die Substratphosphorylierung korrelierte indirekt zur Intensität des Fluoreszenzsignals. Es wurde ein Antikörper verwendet, der das phosphorylierte Epitop auf dem Substratpeptid erkannte. An diesem Primärantikörper war ein Donorfluorophor, Europium-Kryptat, (CisBio) gekoppelt. Ein Sekundärantikörper, der den Primärantikörper erkannte, trug das entsprechende Akzeptorfluorophor XL665 (CisBio). Nach Fluoreszenzanregung emittiert das Europium-Kryptat (Donor) eine lang anhaltende Fluoreszenz bei 620 nm, während der Akzeptor XL665 ein kurzlebiges Signal bei 665 nm produziert. Das Emissionsspektrum des Donors und das Absorptionsspektrum des Akzeptors überlappen sich, so dass ein Energietransfer zwischen beiden stattfinden kann, wenn sie sich in direkter räumlicher Nähe zueinander befinden (phosphoryliertes Substratpeptid/Primärantikörper/Sekundärantikörper-Komplex). Als Folge des Energietransfers emittiert der Akzeptor XL665 ebenfalls eine lang anhaltende Fluoreszenz von 665 nm. Das Verhältnis zwischen der kurzlebigen und der lang anhaltenden Fluoreszenz des Akzeptors (665nm zu 620nm) kann mit einem Fluoreszenzmeßgerät ermittelt werden und dient indirekt als Maß für die Substratphosphorylierung.

Die Experimente zur biochemischen Bestimmung der Enzymaktivität von Pim-1-WT-GST nach Substratbehandlung wurden von der Arbeitsgruppe von Dr. M. Husemann, Abteilung AD-HTS, Schering AG, Berlin durchgeführt.



#### Abb. 52 Test von potentiellen Pim-1 Inhibitoren im HTRF-Assay

In einem HTRF-Assay wurden die Wirkungen von fünf ausgewählten Substanzen auf die Pim-1-GST Enzymaktivität untersucht. Als Maß für die Enzymaktivität diente die Phosphorylierung des Substratpeptids. Der bekannte Kinaseinhibitor Staurosporin zeigte eine starke Inhibition der Enzymaktivität von Pim-1-GST. Es wurde ein IC<sub>50</sub>-Wert von 2,4nM ermittelt. Die Substanz A ergab einen IC<sub>50</sub>-Wert von 170nM und war damit der wirksamste der vier getesteten, potentiellen Pim-1 Inhibitoren. Bei der Substanz B konnte noch ein IC<sub>50</sub>-Wert von 1,1 $\mu$ M ermittelt werden. Die Substanzen C und D zeigten keine inhibitorische Wirkung im eingesetzten Konzentrationsbereich. Für beide konnten keine IC<sub>50</sub>-Werte bestimmt werden.

#### 6.2. Sequenzen

6.2.1.	p21-WT-Sec	quenz des	pOTB7 Ex	pressionsvektors
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+1	Met	Ser	Glu	Pro	Ala	Gly	Asp	Val	Arg	Gln	Asn	Pro	Cys	Gly	Ser	Lys
1	ATG	TCA	GAA	CCG	GCT	GGG	GAT	GTC	CGT	CAG	AAC	CCA	TGC	GGC	AGC	AAG
+1	Ala	Cys	Arg	Arg	Leu	Phe	Gly	Pro	Val	Asp	Ser	Glu	Gln	Leu	Arg	Arg
49	GCC	TGC	CGC	CGC	CTC	- TTC	GGC	CCA	GTG	GAC	AGC	GAG	CAG	CTG	- AGA	CGC
+1	Asp	Cys	Asp	Ala	Leu	Met	Ala	Gly	Cys	lle	Gln	Glu	Ala	Arg	Glu	Arg
97	GAC	TGT	- GAT	GCG	CTA	- ATG	GCG	GGC	- TGC	- ATC	CAG	GAG	GCC	- CGT	GAG	CGA
+1	Trp	Asn	Phe	Asp	Phe	Val	Thr	Glu	Thr	Pro	Leu	Glu	Gly	Asp	Phe	Ala
145	TGG	AAC	TTC	GAC	TTT	GTC	ACC	GAG	ACA	CCA	CTG	GAG	GGT	GAC	TTC	GCC
+1	Trp	Glu	Arg	Val	Arg	Gly	Leu	Gly	Leu	Pro	Lys	Leu	Tyr	Leu	Pro	Thr
193	TGG	GAG	CGT	GTG	CGG	GGC	CTT	GGC	CTG	CCC	AAG	CTC	- TAC	CTT	CCC	ACG
+1	Gly	Pro	Arg	Arg	Gly	Arg	Asp	Glu	Leu	Gly	Gly	Gly	Arg	Arg	Pro	Gly
241	GGG	CCC	CGG	CGA	GGC	CGG	GAT	GAG	TTG	GGA	GGA	GGC	AGG	CGG	CCT	GGC
+1	Thr	Ser	Pro	Ala	Leu	Leu	Gln	Gly	Thr	Ala	Glu	Glu	Asp	His	Val	Asp
289	ACC	- TCA	CCT	- GCT	CTG	CTG	CAG	- GGG	ACA	GCA	GAG	- GAA	GAC	CAT	GTG	GAC
+1	Leu	Ser	Leu	Ser	Cys	Thr	Leu	Val	Pro	Arg	Ser	Gly	Glu	Gln	Ala	Glu
337	CTG	- TCA	CTG	- TCT	- TGT	ACC	CTT	- GTG	CCT	CGC	- TCA	GGG	GAG	CAG	GCT	GAA
+1	Gly	Ser	Pro	Gly	Gly	Pro	Gly	Asp	Ser	Gln	Gly	Arg	Lys	Arg	Arg	Gln
385	GGG	TCC	CCA	GGT	GGA	CCT	GGA	GAC	TCT	CAG	GGT	CGA	AAA	CGG	CGG	CAG
+1	Thr	Ser	Met	Thr	Asp	Phe	Tyr	His	Ser	Lys	Arg	Arg	Leu	lle	Phe	Ser
433	ACC	AGC	ATG	ACA	- GAT	TTC	TAC	CAC	TCC	AAA	CGC	CGG	CTG	ATC	TTC	тсс
+1	Lys	Arg	Lys	Pro	***			*****		*****						
481	AAG	AGG	AAG	CCC	TAA											

Abb. 53 p21-WT-Sequenz des pOTB7 Expressionsvektors In dieser Abb. ist die p21-WT-Sequenz des pOTB7 Expressionsvektors dargestellt (Ausgangssequenz siehe 2.1.1.).

+1	Ala	Ala	Met	Glu	Gln	Lys	Leu	lle	Ser	Glu	Glu	Asp	Leu	Ala	Arg	Ala
1	GCC	GCC	ATG	GAG	CAG	AAA	СТС	ATC	TCT	GAA	GAG	GAT	CTG	GCC	CGG	GCG
+1	Asp	Pro	Glu	Gln	Lys	Leu	lle	Ser	Glu	Glu	Asp	Leu	Gly	Cys	Arg	Asn
49	GAT	CCC	GAG	CAG	AAA	CTC	ATC	TCT	GAA	GAG	GAT	CTG	GGC	TGC	AGG	AAT
+1	Ser	Met	Leu	Leu	Ser	Lys	lle	Asn	Ser	Leu	Ala	His	Leu	Arg	Ala	Ala
97	TCG	ATG	CTC	TTG	TCC	AAA	ATC	AAC	TCG	CTT	GCC	CAC	CTG	CGC	GCC	GCG
+1	Pro	Cys	Asn	Asp	Leu	His	Ala	Thr	Lys	Leu	Ala	Pro	Gly	Lys	Glu	Lys
145	CCC	TGC	AAC	GAC	CTG	CAC	GCC	ACC	AAG	CTG	GCG	CCC	GGC	AAG	GAG	AAG
+1	Glu	Pro	Leu	Glu	Ser	Gln	Tyr	Gln	Val	Gly	Pro	Leu	Leu	Gly	Ser	Gly
193	GAG	CCC	CTG	GAG	TCG	CAG	TAC	CAG	GTG	GGC	CCG	CTA	CTG	GGC	AGC	GGC
+1	Gly	Phe	Gly	Ser	Val	Tyr	Ser	Gly	lle	Arg	Val	Ser	Asp	Asn	Leu	Pro
241	GGC	TTC	GGC	TCG	GTC	TAC	TCA	GGC	ATC	CGC	GTC	TCC	GAC	AAC	TTG	CCG
+1	Val	Ala	lle	Lys	His	Val	Glu	Lys	Asp	Arg	lle	Ser	Asp	Trp	Gly	Glu
289	GTG	GCC	ATC	AAA	CAC	GTG	GAG	AAG	GAC	CGG	ATT	TCC	GAC	TGG	GGA	GAG
+1	Leu	Pro	Asn	Gly	Thr	Arg	Val	Pro	Met	Glu	Val	Val	Leu	Leu	Lys	Lys
337	CTG	CCT	AAT	GGC	ACT	CGA	GTG	CCC	ATG	GAA	GTG	GTC	CTG	CTG	AAG	AAG
+1	Val	Ser	Ser	Gly	Phe	Ser	Gly	Val	lle	Arg	Leu	Leu	Asp	Trp	Phe	Glu
385	GTG	AGC	TCG	GGT	TTC	TCC	GGC	GTC	ATT	AGG	CTC	CTG	GAC	TGG	TTC	GAG
+1	Arg	Pro	Asp	Ser	Phe	Val	Leu	lle	Leu	Glu	Arg	Pro	Glu	Pro	Val	Gln
433	AGG	CCC	GAC	AGT	TTC	GTC	CTG	ATC	CTG	GAG	AGG	CCC	GAG	CCG	GTG	CAA
+1	Asp	Leu	Phe	Asp	Phe	lle	Thr	Glu	Arg	Gly	Ala	Leu	Gln	Glu	Glu	Leu
481	GAT	CTC	TTC	GAC	TTC	ATC	ACG	GAA	AGG	GGA	GCC	CTG	CAA	GAG	GAG	CTG
+1	Ala	Arg	Ser	Phe	Phe	Trp	Gln	Val	Leu	Glu	Ala	Val	Arg	His	Cys	His
529	GCC	CGC	AGC	TTC	TTC	TGG	CAG	GTG	CTG	GAG	GCC	GTG	CGG	CAC	TGC	CAC
+1	Asn	Cys	Gly	Val	Leu	His	Arg	Asp	lle	Lys	Asp	Glu	Asn	lle	Leu	lle
577	AAC	TGC	GGG	GTG	CTC	CAC	CGC	GAC	ATC	AAG	GAC	GAA	AAC	ATC	CTT	ATC
+1	Asp	Leu	Asn	Arg	Gly	Glu	Leu	Lys	Leu	lle	Asp	Phe	Gly	Ser	Gly	Ala
625	GAC	CTC	AAT	CGC	GGC	GAG	CTC	AAG	CTC	ATC	GAC	TTC	GGG	TCG	GGG	GCG
+1	Leu	Leu	Lys	Asp	Thr	Val	Tyr	Thr	Asp	Phe	Asp	Gly	Thr	Arg	Val	Tyr
673	CTG	CTC	AAG	GAC	ACC	GTC	TAC	ACG	GAC	TTC	GAT	GGG	ACC	CGA	GTG	TAT
+1	Ser	Pro	Pro	Glu	Trp	lle	Arg	Tyr	His	Arg	Tyr	His	Gly	Arg	Ser	Ala
721	AGC	CCT	CCA	GAG	TGG	ATC	CGC	TAC	CAT	CGC	TAC	CAT	GGC	AGG	TCG	GCG
+1	Ala	Val	Trp	Ser	Leu	Gly	lle	Leu	Leu	Tyr	Asp	Met	Val	Cys	Gly	Asp
769	GCA	GTC	TGG	TCC	CTG	GGG	ATC	CTG	CTG	TAT	GAT	ATG	GTG	TGT	GGA	GAT
+1	lle	Pro	Phe	Glu	His	Asp	Glu	Glu	lle	lle	Arg	Gly	Gln	Val	Phe	Phe
817	ATT	CCT	TTC	GAG	CAT	GAC	GAA	GAG	ATC	ATC	AGG	GGC	CAG	GTT	TTC	TTC
+1	Arg	Gln	Arg	Val	Ser	Ser	Glu	Cys	Gln	His	Leu	lle	Arg	Trp	Cys	Leu
865	AGG	CAG	AGG	GTC	TCT	TCA	GAA	TGT	CAG	CAT	CTC	ATT	AGA	TGG	TGC	TTG
+1	Ala	Leu	Arg	Pro	Ser	Asp	Arg	Pro	Thr	Phe	Glu	Glu	lle	Gln	Asn	His
913	GCC	CTG	AGA	CCA	TCA	GAT	AGG	CCA	ACC	TTC	GAA	GAA	ATC	CAG	AAC	CAT
+1	Pro	Ггр	Met	Gln	Asp	Val	Leu	Leu	Pro	Gln	Glu	Гhr •	Ala	Glu	lle	His
961	CCA	TGG	ATG	CAA	GAT	GTT	CTC	CTG	CCC	CAG	GAA	ACT	GCT	GAG	ATC	CAC
+1	Leu	His	Ser	Leu	Ser	Pro	Gly	Pro	Ser	Lys	***	Pro	Ser	Thr	Ser	Arg
1009	CTC	CAC	AGC	CTG	TCG	CCG	GGG	CCC	AGC	AAA	TAG	CCG	TCG	ACC	TCG	AGG
+1	Gly	Gly	Pro	Val	Pro	***	Leu	-								

1057 GGG GGC CCG GTA CCT TAA TTA AT

#### Abb. 54 c-Myc-Pim-1-WT-Sequenz des pCMV-tag3 Expressionsvektors

In dieser Abb. ist die Myc-Pim-1-WT-Sequenz des pCMV-tag3 Expressionsvektors (Ausgangsplasmid, siehe 2.1.1.) dargestellt. Violette Zeichen geben das Ausmaß der KOZAK-Sequenz an. Grüne Zeichen kennzeichnen das Ausmaß der zwei Myc-tags. Rote Zeichen geben das Ausmaß der Pim-1-WT-Sequenz an.

#### 6.2.3. p21-WT-CFP-Sequenz

+1	Asp Leu Glu Leu Lys Leu Ala Met Ser Glu Pro Ala Gly Asp Val Arg Gln Asn Pro Cys
1	GATCTCGAGCTCAAGCTTGCCATGTCAGAACCGGCTGGGGATGTCCGTCAGAACCCATGC
+1	Giy Ser Lys Ala Cys Arg Arg Leu Phe Giy Pro Val Asp Ser Giu Gin Leu Arg Arg Asp
61	GGCAGCAAGGCCTGCCGCCGCCTCTTCGGCCCAGTGGACAGCGAGCAGCTGAGACGCGAC
+1	Cys Asp Ala Leu Met Ala Gly Cys lle Gin Glu Ala Arg Glu Arg Trp Asn Phe Asp Phe
121	TGTGATGCGCTAATGGCGGGCTGCATCCAGGAGGCCCGTGAGCGATGGAACTTCGACTTT
+1	Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala Trp Glu Arg Val Arg Gly Leu Gly Leu
181	GTCACCGAGACACCACTGGAGGGTGACTTCGCCTGGGAGCGTGTGCGGGGCCTTGGCCTG
+1	Pro Lys Leu Tyr Leu Pro Thr Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Gly Arg
241	CCCAAGCTCTACCTTCCCACGGGGGCCCGGGCGAGGCCGGGATGAGTTGGGAGGAGGCAGG
+1	Arg Pro Gly Thr Ser Pro Ala Leu Leu Gin Gly Thr Ala Glu Glu Asp His Val Asp Leu
301	CGGCCTGGCACCTCACCTGCTGCTGCAGGGGGACAGCAGGGAGGACACCATGTGGACCTG
+1	Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gin Ala Glu Gly Ser Pro Gly Gly
361	TCACTGTCTTGTACCCTTGTGCCTCGCTCAGGGGAGCAGGCTGAAGGGTCCCCAGGTGGA
+1	Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln Thr Ser Met Thr Asp Phe Tyr His Ser
421	CCTGGAGACTCTCAGGGTCGAAAACGGCGGCAGACCAGCATGACAGATTTCTACCACTCC
+1	Lys Arg Arg Leu lle Phe Ser Lys Arg Lys Pro Lys Pro Ser Thr Val Pro Arg Ala Arg
481	AAACGCCGGCTGATCTTCTCCAAGAGGAAGCCCAAACCGTCGACGGTACCGCGGGCCCGG
+1	Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr
541	GATCCACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACC

#### Abb. 55 p21-WT-CFP-Sequenz

In dieser Abb. ist die p21-WT-CFP-Sequenz dargestellt. Das Start- und das modifizierte "Stopkodon" des p21-WT-Gens ist durch rote Buchstaben gekennzeichnet. Blaue Zeichen geben das Startkodon des CFP-Gens an.

#### 6.2.4. p21-WT-YFP-Sequenz

+1	Asp Leu	Glu	Leu	Lys	Leu	Ala	Mət	Ser	Glu	Pro	Ala	Gly	Asp	Val	Arg	GIn	Asn	Pro	Cys
1	GATCTC	GAG	CTC	AAG	CTT	GCC	ATG	TCA	GAA	CCG	GCT	GGG	GAT	GTC	CGT	CAG	AAC	CCA	TGC
+1	Gly Ser	Lys	Ala	Cys	Arg	Arg	Leu	Phe	Gly	Pro	Val	Asp	Ser	Glu	GIn	Leu	Arg	Arg	Asp
61	GGCAGC	AAGO	GCC	rgc	CGC	CGC	СТС	TTC	GGC	CCA	GTG	GAC	AGC	GAG	CAG	CTG	AGA	CGC	GAC
+1	Cys Asp	Ala	Leu	Mət	Ala	Gly	Cys	lle	GIn	Glu	Ala	Arg	Glu	Arg	Тгр	Asn	Phe	Asp	Phe
121	TGTGAT	GCG	CTA	ATG	GCG	GGC	TGC	ATC	CAG	GAG	GCC	CGT	GAG	CGA	TGG	AAC	TTC	GAC	TTT
+1	Val Thr	Glu	Thr	Pro	Leu	Glu	Gly	Asp	Phe	Ala	Тгр	Glu	Arg	Val	Arg	Gly	Leu	Gly	Leu
181	GTCACC	GAGI	ACA	CCA	CTG	GAG	GGT	GAC	TTC	GCC	TGG	GAG	CGT	GTG	CGG	GGC	CTT	GGC	CTG
+1	Pro Lys	Leu	Tyr	Leu	Pro	Thr	Gly	Pro	Arg	Arg	Gly	Arg	Asp	Glu	Leu	Gly	Gly	Gly	Arg
241	CCCAAG	стст	FAC	стт	ccc	ACG	GGG	ccc	CGG	CGA	GGC	CGG	GAT	GAG	TTG	GGA	GGA	GGC	AGG
+1	Arg Pro	Gly	Thr	Ser	Pro	Ala	Leu	Leu	GIn	Gly	Thr	Ala	Glu	Glu	Asp	HIS	Val	Asp	Leu
301	CGGCCT	GGCI	ACCI	<b>FCA</b>	CCT	GCT	CTG	CTG	CAG	GGG	ACA	GCA	GAG	GAA	GAC	CAT	GTG	GAC	CTG
+1	Ser Leu	Ser (	Cys	Thr	Leu	Val	Pro	Arg	Ser	Gly	Glu	GIn	Ala	Glu	Gly	Ser	Pro	Gly	Gly
361	TCACTG	TCTI	rgt <i>i</i>	ACC	CTT	GTG	CCT	CGC	TCA	GGG	GAG	CAG	GCT	GAA	GGG	TCC	CCA	GGT	GGA
+1	Pro Gly	Asp	Ser	GIn	Gly	Arg	Lys	Arg	Arg	GIn	Thr	Ser	Mət	Thr	Asp	Phe	Tyr	HIS	Ser
421	CCTGGA	GACI	<b>FCT</b>	CAG	GGT	CGA	ААА	CGG	CGG	CAG	ACC	AGC	ATG	ACA	GAT	TTC	TAC	CAC	TCC
+1	Lys Arg	Arg	Leu	llə	Phe	Ser	Lys	Arg	Lys	Pro	Lys	Pro	Ser	Thr	Val	Pro	Arg	Ala	Arg
481	AAACGC	CGGC	CTGI	ATC	TTC	TCC	AAG	AGG	AAG	ccc	ААА	CCG	TCG	ACG	GTA	CCG	CGG	GCC	CGG
+1	Asp Pro	Pro	Val	Ala	Thr	Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr				
541	GATCCA	ccd	TCO	GCC	ACC	ATG	GTG	AGC	AAG	GGC	GAG	GAG	CTG	TTC	ACC				

#### Abb. 56 p21-WT-YFP-Sequenz

In dieser Abb. ist die p21-WT-YFP-Sequenz dargestellt. Das Start- und das modifizierte "Stopkodon" des p21-WT-Gens ist durch rote Buchstaben gekennzeichnet. Blaue Zeichen geben das Startkodon des YFP-Gens an.

#### 6.2.5. p21-T145A-CFP-DNA-Sequenz

+1	Asp Leu Giu Leu Lys Leu Ala Met Ser Giu Pro Ala Giy Asp Val Arg Gin Asn Pro Cys
1	GATCTCGAGCTCAAGCTTGCCATGTCAGAACCGGCTGGGGATGTCCGTCAGAACCCATGC
+1	Gly Ser Lys Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser Glu Gln Leu Arg Arg Asp
61	GGCAGCAAGGCCTGCCGCCGCCTCTTCGGCCCAGTGGACAGCGAGCAGCTGAGACGCGAC
+1	Cys Asp Ala Leu Met Ala Gly Cys lle Gin Glu Ala Arg Glu Arg Trp Asn Phe Asp Phe
121	TGTGATGCGCTAATGGCGGGCTGCATCCAGGAGGCCCGTGAGCGATGGAACTTCGACTTT
+1	Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala Trp Glu Arg Val Arg Gly Leu Gly Leu
181	GTCACCGAGACACCACTGGAGGGTGACTTCGCCTGGGAGCGTGTGCGGGGCCTTGGCCTG
+1	Pro Lys Leu Tyr Leu Pro Thr Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Gly Arg
241	CCCAAGCTCTACCTTCCCACGGGGGCCCCGGCGAGGCCGGGATGAGTTGGGAGGAGGCAGG
+1	Arg Pro Gly Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu Glu Asp His Val Asp Leu
301	CGGCCTGGCACCTCACCTGCTGCTGCAGGGGGACAGCAGAGGAAGACCATGTGGACCTG
+1	Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gln Ala Glu Gly Ser Pro Gly Gly
361	TCACTGTCTTGTACCCTTGTGCCTCGCTCAGGGGAGCAGGCTGAAGGGTCCCCAGGTGGA
+1	Pro Gly Asp Ser Gin Gly Arg Lys Arg Arg Gin Ala Ser Met Thr Asp Phe Tyr His Ser
421	CCTGGAGACTCTCAGGGTCGAAAACGGCGGCAGGCCAGCATGACAGATTTCTACCACTCC
+1	Lys Arg Arg Leu lie Phe Ser Lys Arg Lys Pro Lys Pro Ser Thr Val Pro Arg Ala Arg
481	AAACGCCGGCTGATCTTCTCCAAGAGGAAGCCCAAACCGTCGACGGTACCGCGGGCCCGG
+1	Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr
541	GATCCACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACC

#### Abb. 57 p21-T145A-CFP-Sequenz

In dieser Abb. ist die p21-T145A-CFP-Sequenz dargestellt. Das Start- und das modifizierte "Stopkodon" des p21-WT-Gens ist durch rote Buchstaben und die Mutation T145A durch grüne Buchstaben gekennzeichnet. Blaue Zeichen geben das Startkodon des YFP-Gens an.

#### 6.2.6. Pim-1-WT-CFP-Sequenz

+1	Asp Leu Glu Leu Lys Leu Ala Ala Met Glu Gln Lys Leu lle Ser Glu Glu Asp Leu Ala
1	GATCTCGAGCTCAAGCTTGCCGCCATGGAGCAGAAACTCATCTCTGAAGAGGATCTGGCC
+1	Arg Ala Asp Pro Glu Gin Lys Leu lle Ser Glu Glu Asp Leu Gly Cys Arg Asn Ser Met
61	CGGGCGGATCCCGAGCAGAAACTCATCTCTGAAGAGGATCTGGGCTGCAGGAATTCGATG
+1	Leu Leu Ser Lys lie Asn Ser Leu Ala His Leu Arg Ala Ala Pro Cys Asn Asp Leu His
121	CTCTTGTCCAAAATCAACTCGCTTGCCCACCTGCGCGCGC
+1	Ala Thr Lys Leu Ala Pro Gly Lys Glu Lys Glu Pro Leu Glu Ser Gln Tyr Gln Val Gly
181	GCCACCAAGCTGGCGCCCGGCAAGGAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTGGGC
+1	Pro Leu Leu Gly Ser Gly Gly Phe Gly Ser Val Tyr Ser Gly lle Arg Val Ser Asp Asn
241	CCGCTACTGGGCAGCGGCGGCGTCTCGGCTCGGTCTACTCAGGCATCCGCGTCTCCGACAAC
+1	Leu Pro Val Ala lle Lys His Val Giu Lys Asp Arg lle Ser Asp Trp Giy Giu Leu Pro
301	${\tt TTGCCGGTGGCCATCAAACACGTGGAGAAGGACCGGATTTCCGACTGGGGAGAGCTGCCT$
+1	Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val Ser Ser Gly Phe Ser
361	AATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCGGGTTTCTCC
+1	Gly Val lle Arg Leu Leu Asp Trp Phe Glu Arg Pro Asp Ser Phe Val Leu lle Leu Glu
421	GGCGTCATTAGGCTCCTGGACTGGTTCGAGAGGCCCGACAGTTTCGTCCTGATCCTGGAG
+1	Arg Pro Glu Pro Val Gin Asp Leu Phe Asp Phe Ile Thr Glu Arg Gly Ala Leu Gin Glu
481	AGGCCCGAGCCGGTGCAAGATCTCTTCGACTTCATCACGGAAAGGGGAGCCCTGCAAGAG
+1	Glu Leu Ala Arg Ser Phe Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn Cys
541	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC
+1	Gly Val Leu His Arg Asp lie Lys Asp Glu Asn lie Leu lie Asp Leu Asn Arg Gly Glu
601	GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG
+1	Leu Lys Leu lle Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe
661	CTCAAGCTCATCGACTTCGGGTCGGGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC
+1	Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp lle Arg Tyr His Arg Tyr His Gly Arg
721	GATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAGG
+1	Ser Ala Ala Val Trp Ser Leu Gly lle Leu Leu Tyr Asp Met Val Cys Gly Asp lle Pro
781	TCGGCGGCAGTCTGGTCCCTGGGGGATCCTGCTGTATGATATGGTGTGTGGAGATATTCCT
+1	Phe Glu His Asp Glu Glu lie lie Arg Gly Gin Val Phe Phe Arg Gin Arg Val Ser Ser
841	TTCGAGCATGACGAAGAGATCATCAGGGGGCCAGGTTTTCTTCAGGCAGAGGGTCTCTTCA
+1	Glu Cys Gin His Leu lie Arg Trp Cys Leu Ala Leu Arg Pro Ser Asp Arg Pro Thr Phe
901	GAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGGCCAACCTTC
+1	Glu Glu lle Gin Asn His Pro Trp Met Gin Asp Val Leu Leu Pro Gin Giu Thr Ala Glu
961	GAAGAAATCCAGAACCATCCATGGATGCAAGATGTTCTCCTGCCCCAGGAAACTGCTGAG
+1	lle His Leu His Ser Leu Ser Pro Gly Pro Ser Lys Lys Pro Ser Thr Val Pro Arg Ala
1021	ATCCACCTCCACAGCCTGTCGCCGGGGGCCCAGCAAAAAGCCGTCGACGGTACCGCGGGGCC
+1	Arg Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr
1091	CGGGATCCACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACC

#### Abb. 58 Pim-1-WT-CFP-Sequenz

In dieser Abb. ist die Pim-1-WT-CFP-Sequenz dargestellt. Das Start- und das modifizierte "Stopkodon" des Pim-1-WT-Gens ist durch rote Buchstaben gekennzeichnet. Blaue Zeichen geben das Startkodon des CFP-Gens an.

#### 6.2.7. Pim-1-WT-GFP-Sequenz

+1	Asp Leu Giu Leu Lys Pro Ala Ala Met Giu Gin Lys Leu lle Ser Giu Giu Asp Leu Ala
1	GATCTCGAGCTCAAGCCTGCCGCCATGGAGCAGAAACTCATCTCTGAAGAGGATCTGGCC
+1	Arg Ala Asp Pro Glu Gin Lys Leu lie Ser Glu Glu Asp Leu Gly Cys Arg Asn Ser Met
61	CGGGCGGATCCCGAGCAGAAACTCATCTCTGAAGAGGATCTGGGCTGCAGGAATTCGATG
+1	Leu Leu Ser Lys lle Asn Ser Leu Ala His Leu Arg Ala Ala Pro Cys Asn Asp Leu His
121	CTCTTGTCCAAAATCAACTCGCTTGCCCACCTGCGCGCCGCGCCCTGCAACGACCTGCAC
+1	Ala Thr Lys Leu Ala Pro Gly Lys Glu Lys Glu Pro Leu Glu Ser Gln Tyr Gln Val Gly
181	GCCACCAAGCTGGCGCCCGGCAAGGAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTGGGC
+1	Pro Leu Leu Gly Ser Gly Gly Phe Gly Ser Val Tyr Ser Gly lle Arg Val Ser Asp Asn
241	CCGCTACTGGGCAGCGGCGGCGCCTCGGCTCGGCTCTACTCAGGCATCCGCGTCTCCGACAAC
+1	Leu Pro Val Ala lle Lys His Val Giu Lys Asp Arg lle Ser Asp Trp Giy Giu Leu Pro
301	TTGCCGGTGGCCATCAAACACGTGGAGAAGGACCGGATTTCCGACTGGGGAGAGCTGCCT
+1	Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val Ser Ser Gly Phe Ser
361	AATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCGGGTTTCTCC
+1	Gly Val lie Arg Leu Leu Asp Trp Phe Glu Arg Pro Asp Ser Phe Val Leu lie Leu Glu
421	GGCGTCATTAGGCTCCTGGACTGGTTCGAGAGGCCCGACAGTTTCGTCCTGATCCTGGAG
+1	Arg Pro Glu Pro Val Gin Asp Leu Phe Asp Phe Ile Thr Glu Arg Gly Ala Leu Gin Glu
481	AGGCCCGAGCCGGTGCAAGATCTCTTCGACTTCATCACGGAAAGGGGAGCCCTGCAAGAG
+1	Glu Leu Ala Arg Ser Phe Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn Cys
541	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC
541 +1	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCCGTGCGGCACTGCCACAACTGC Gly Val Leu His Arg Asp lie Lys Asp Glu Asn lie Leu lie Asp Leu Asn Arg Gly Glu
541 +1 601	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Gly Val Leu His Arg Asp lie Lys Asp Glu Asn lie Leu lie Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG
541 +1 601 +1	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Gly Val Leu His Arg Asp lie Lys Asp Glu Asn lie Leu lie Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG Leu Lys Leu lie Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe
541 +1 601 +1 661	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Gly Val Leu His Arg Asp IIe Lys Asp Glu Asn IIe Leu IIe Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG Leu Lys Leu IIe Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe CTCAAGCTCATCGACTTCGGGTCGGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC
541 +1 601 +1 661 +1	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Gly Val Leu His Arg Asp lie Lys Asp Glu Asn lie Leu lie Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG Leu Lys Leu lie Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe CTCAAGCTCATCGACTTCGGGGTCGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp lie Arg Tyr His Arg Tyr His Gly Arg
541 +1 601 +1 661 +1 721	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Gly Val Leu His Arg Asp lie Lys Asp Glu Asn lie Leu lie Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGGGGGGG
541 +1 601 +1 661 +1 721 +1	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Gly Val Leu His Arg Asp lie Lys Asp Glu Asn lie Leu lie Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG Leu Lys Leu lie Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe CTCAAGCTCATCGACTTCGGGTCGGGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp lie Arg Tyr His Arg Tyr His Gly Arg GATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAGG Ser Ala Ala Val Trp Ser Leu Gly lie Leu Leu Tyr Asp Met Val Cys Gly Asp lie Pro
541 +1 601 +1 661 +1 721 +1 781	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Gly Val Leu HIs Arg Asp IIe Lys Asp Glu Asn IIe Leu IIe Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG Leu Lys Leu IIe Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe CTCAAGCTCATCGACTTCGGGTCGGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp IIe Arg Tyr HIs Arg Tyr HIs Gly Arg GATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAGG Ser Ala Ala Val Trp Ser Leu Gly IIe Leu Leu Tyr Asp Met Val Cys Gly Asp IIe Pro TCGGCGGCAGTCTGGTCCCTGGGGATCCTGCTGTATGATATGGTGTGTGGAGATATTCCT
541 +1 601 +1 661 +1 721 +1 781 +1	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Gly Val Leu His Arg Asp lie Lys Asp Glu Asn lie Leu lie Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG Leu Lys Leu lie Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe CTCAAGCTCATCGACTTCGGGTCGGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp lie Arg Tyr His Arg Tyr His Gly Arg GATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAGG Ser Ala Ala Val Trp Ser Leu Gly lie Leu Leu Tyr Asp Met Val Cys Gly Asp lie Pro TCGGCCGCCAGTCTGGTCCCTGGGGGATCCTGCTGTATGATATGGTGTGTGGAGATATTCCT Phe Glu His Asp Glu Glu lie lie Arg Gly Gln Val Phe Phe Arg Gln Arg Val Ser Ser
541 +1 601 +1 661 +1 721 +1 781 +1 841	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe Leu IIe Asp Leu Asn Arg Giy Giu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe CTCAAGCTCATCGACTTCGGGTCGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC Asp Giy Thr Arg Val Tyr Ser Pro Pro Giu Trp IIe Arg Tyr His Arg Tyr His Giy Arg GATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAGG Ser Ala Ala Val Trp Ser Leu Giy IIe Leu Leu Tyr Asp Met Val Cys Giy Asp IIe Pro TCGGCGGCAGTCTGGTCCCTGGGGGATCCTGCTGTATGATATGGTGTGTGGAGATATTCCT Phe Giu His Asp Giu Giu IIe IIe Arg Giy Gin Val Phe Phe Arg Gin Arg Val Ser Ser TTCGAGCATGACGAAGAGAGATCATCAGGGGCCCAGGTTTTCTTCAGGCAGAGAGGGTCTCTTCA
541 +1 601 +1 661 +1 721 +1 781 +1 841 +1	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Gly Val Leu HIS Arg Asp IIe Lys Asp Glu Asn IIe Leu IIe Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG Leu Lys Leu IIe Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe CTCAAGCTCATCGACTTCGGGTCGGGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp IIe Arg Tyr HIS Arg Tyr HIS Gly Arg GATGGGACCCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAGG Ser Ala Ala Val Trp Ser Leu Gly IIe Leu Leu Tyr Asp Met Val Cys Gly Asp IIe Pro TCGGCGGCAGTCTGGTCCCTGGGGGATCCTGCTGTATGATATGGTGTGTGGGAGATATTCCT Phe Glu HIS Asp Glu Glu IIe IIe Arg Gly Gln Val Phe Phe Arg Gln Arg Val Ser Ser TTCGAGCATGACGAAGAGATCATCAGGGGCCAGGTTTTCTTCAGGCAGAGGGTCTCTTCA Glu Cys Gln HIS Leu IIe Arg Trp Cys Leu Ala Leu Arg Pro Ser Asp Arg Pro Thr Phe
541 +1 601 +1 661 +1 721 +1 781 +1 841 +1 901	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGGCACTGCCACAACTGC Gly Val Leu His Arg Asp IIe Lys Asp Glu Asn IIe Leu IIe Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG Leu Lys Leu IIe Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe CTCAAGCTCATCGACTTCGGGTCGGGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp IIe Arg Tyr His Arg Tyr His Gly Arg GATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAGG Ser Ala Ala Val Trp Ser Leu Gly IIe Leu Leu Tyr Asp Met Val Cys Gly Asp IIe Pro TCGGCGGCAGTCTGGTCCTGGGGGATCCTGCTGTATGATATGGTGTGGGAGATATTCCT Phe Glu His Asp Glu Glu IIe IIe Arg Gly Gln Val Phe Phe Arg Gln Arg Val Ser Ser TTCGAGCATGACGAAGAGATCATCAGGGGCCAGGTTTTCTTCAGGCAGAGGGTCTCTTCA Glu Cys Gln His Leu IIe Arg Trp Cys Leu Ala Leu Arg Pro Ser Asp Arg Pro Thr Phe GAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGGCCAACCTTC
541 +1 601 +1 661 +1 721 +1 781 +1 841 +1 901 +1	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Gly Val Leu His Arg Asp IIe Lys Asp Glu Asn IIe Leu IIe Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGGCGAG Leu Lys Leu IIe Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe CTCAAGCTCATCGACTTCGGGTCGGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC Asp Gly Thr Arg Val Tyr Ser Pro Pro Giu Trp IIe Arg Tyr His Arg Tyr His Gly Arg GATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAGG Ser Ala Ala Val Trp Ser Leu Gly IIe Leu Leu Tyr Asp Met Val Cys Gly Asp IIe Pro TCGGCGGCAGTCTGGTCCCTGGGGGATCCTGCTGTATGATATGGTGTGGGAGATATTCCT Phe Glu His Asp Glu Glu IIe IIe Arg Gly Gln Val Phe Phe Arg Gin Arg Val Ser Ser TTCGAGCATGACGAAGAGATCATCAGGGGCCAGGTTTTCTTCAGGCAGAGGGGTCTCTTCA Glu Cys Gln His Leu IIe Arg Trp Cys Leu Ala Leu Arg Pro Ser Asp Arg Pro Thr Phe GAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGGCCAACCTTC Glu Glu IIe Gin Asn His Pro Trp Met Gin Asp Val Leu Leu Pro Gin Glu Thr Ala Glu
541 +1 601 +1 661 +1 721 +1 781 +1 841 +1 901 +1 961	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Gly Val Leu His Arg Asp IIe Lys Asp Glu Asn IIe Leu IIe Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG Leu Lys Leu IIe Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe CTCAAGCTCATCGACTTCGGGTCGGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp IIe Arg Tyr His Arg Tyr His Gly Arg GATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAGG Ser Ala Ala Val Trp Ser Leu Gly IIe Leu Leu Tyr Asp Met Val Cys Gly Asp IIe Pro TCGGCGGCAGTCTGGTCCCTGGGGGATCCTGCTGTATGATATGGTGTGGAGATATTCCT Phe Glu His Asp Glu Glu IIe IIe Arg Gly Gln Val Phe Phe Arg Gln Arg Val Ser Ser TTCGAGCATGACGAAGAGATCATCAGGGGCCAGGTTTTCTTCAGGCAGAGGGGTCTCTTCA Glu Cys Gln His Leu IIe Arg Trp Cys Leu Ala Leu Arg Pro Ser Asp Arg Pro Thr Phe GAATGTCAGCATCTCATTAGATGGTGCTGGAGACCATCAGATAGGCCAACCTTC Glu Glu IIe Gin Asn His Pro Trp Met Gin Asp Val Leu Leu Pro Gin Glu Thr Ala Glu GAAGAAATCCAGGAACCATCCATCGAGAGGCCAAGATGTTCTCCTGCCCCAGGAAACTGCTGAG
541 +1 601 +1 661 +1 721 +1 781 +1 841 +1 901 +1 961 +1	GAGCTGGCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGGCACTGCCACAACTGC Gly Val Leu His Arg Asp lie Lys Asp Glu Asn lie Leu lie Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGGGGGG Leu Lys Leu lie Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe CTCAAGCTCATCGACTTCGGGTCGGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp lie Arg Tyr His Arg Tyr His Gly Arg GATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAGG Ser Ala Ala Val Trp Ser Leu Gly lie Leu Leu Tyr Asp Met Val Cys Gly Asp lie Pro TCGGCGGCAGTCTGGTCCCTGGGGATCCTGCTGTATGATATGGTGTGTGGGAGATATTCCT Phe Glu His Asp Glu Glu lie lie Arg Gly Gln Val Phe Phe Arg Gln Arg Val Ser Ser TTCGAGCATGACGAAGAGATCATCAGGGGCCCGCGGGGCCTGCTGAGGAGAGGGTCTCTTCA Glu Cys Gln His Leu lie Arg Trp Cys Leu Ala Leu Arg Pro Ser Asp Arg Pro Thr Phe GAATGTCAGCATCTCATTAGGTGCCTTGGCCCTGAGACCATCAGGATAGGCCAACCTTC Glu Glu lie Gln Asn His Pro Trp Met Gln Asp Val Leu Leu Pro Gin Glu Thr Ala Glu GAAGAAATCCAGAACCATCCATGGATGCAAGATGTTCTCTGGCCCCAGGAAACTGCTGAG
541 +1 601 +1 661 +1 721 +1 781 +1 841 +1 901 +1 961 +1 1021	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC   Gly Val Leu His Arg Asp IIIe Lys Asp Glu Asn IIIe Leu IIIe Asp Leu Asn Arg Gly Glu   GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG   Leu Lys Leu IIIe Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe   CTCAAGCTCATCGACTTCGGGTCGGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC   Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp IIIe Arg Tyr His Arg Tyr His Gly Asp IIIe Pro   GATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAGG   Ser Ala Ala Val Trp Ser Leu Gly IIIe Leu Leu Tyr Asp Met Val Cys Gly Asp IIIe Pro   TCGGCGGCAGTCTGGTCCCTGGGGGACCCAGCGTTTTCTTCAGGTGTGGGAGATATTCCT   Phe Glu His Asp Glu Glu IIIe IIIe Arg Gly Gln Val Phe Phe Arg Gln Arg Val Ser Ser   TTCGAGCATGACGAAGAGATCATCAGGGGCCCAGGTTTTCTTCAGGCAGAGGGTCTCTTCA   Glu Cys Gln His Leu IIIe Arg Trp Cys Leu Ala Leu Arg Pro Ser Asp Arg Pro Thr Phe   GAU Cys Gln Asn His Pro Trp Met Gln Asp Val Leu Leu Pro Gln Glu Thr Ala Glu   GAAGAAATCCAAGAACCATCCATGGATGCCAGGTTCTCTCCTGCCCAGGAAACTGCTGAG   IIIe His Leu His Ser Leu Ser Pro Gly Pro Ser Lys Lys Pro Ser Thr Val Pro Arg Ala   ATCCACCTCCACAGCCTGTCGCCGGGGCCCAGCAAAAAGCCGTCGACGTACCGCGGGCCCAGGTACCGCGGGCCCAGCAGACGTACCGCGGGGCCCAGGTACCGCGGGGCCCAGCACAGGTACCGCGCGGGGCCCAGGTACCGCGGGGCCCAGCCAG
541 +1 601 +1 661 +1 721 +1 781 +1 841 +1 901 +1 961 +1 1021 +1	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC Gly Val Leu His Arg Asp lie Lys Asp Glu Asn lie Leu lie Asp Leu Asn Arg Gly Glu GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGGGGGG Leu Lys Leu lie Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe CTCAAGCTCATCGACTTCGGGTCGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp lie Arg Tyr His Arg Tyr His Gly Arg GATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGCAGG Ser Ala Ala Val Trp Ser Leu Gly lie Leu Leu Tyr Asp Met Val Cys Gly Asp lie Pro TCGGCGGCAGTCTGGTCCCTGGGGGATCCTGCTGTATGATATGGTGTGTGGAGATATTCCT Phe Glu His Asp Glu Glu lie lie Arg Gly Gln Val Phe Phe Arg Gln Arg Val Ser Ser TTCGAGCATGACGAAGAGATCATCAGGGGGCCTGGCTGAGACCATCAGGAGAGGGTCTCTTCA Gliu Cys Glin His Leu lie Arg Trp Cys Leu Ala Leu Arg Pro Ser Asp Arg Pro Thr Phe GAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGGCCAACCTTC Gliu Glu lie Gln Asn His Pro Trp Met Glin Asp Val Leu Leu Pro Glin Glu Thr Ala Glu GAAGAAATCCAGAACCATCCATGGAGGATGCTGCTGGCGCAGAGACCATCAGGAAACTGCTGAG Ile His Leu His Ser Leu Ser Pro Gly Pro Ser Lys Lys Pro Ser Thr Val Pro Arg Ala ATCCACCTCCACAGCCTGCCGCGGGGCCCAGCAAAAAGCCCGTCGACGGTACCGCGGGCC Arg Asp Pro

#### Abb. 59 Pim-1-WT-GFP-Sequenz

In dieser Abb. ist die Pim-1-WT-GFP-Sequenz dargestellt. Das Start- und das modifizierte "Stopkodon" des Pim-1-WT-Gens ist durch rote Buchstaben gekennzeichnet. Blaue Zeichen geben das Startkodon des GFP-Gens an.

#### 6.2.8. Pim-1-K67M-GFP-Sequenz

+1	Asp Pro Leu Ala Leu Pro Asp Ser Asp Leu Glu Leu Lys Leu Ala Ala Met Glu Gin Lys
1	GATCCGCTAGCGCTCCCGGACTCAGATCTCGAGCTCAAGCTTGCCGCCATGGAGCAGAAA
+1	Leu lle Ser Glu Glu Asp Leu Ala Arg Ala Asp Pro Glu Gln Lys Leu lle Ser Glu Glu
61	CTCATCTCTGAAGAGGATCTGGCCCGGGCGGATCCCGAGCAGAAACTCATCTCTGAAGAG
+1	Asp Leu Gly Cys Arg Asn Ser Met Leu Leu Ser Lys lle Asn Ser Leu Ala His Leu Arg
121	GATCTGGGCTGCAGGAATTCGATGCTCTTGTCCAAAATCAACTCGCTTGCCCACCTGCGC
+1	Ala Ala Pro Cys Asn Asp Leu His Ala Thr Lys Leu Ala Pro Gly Lys Glu Lys Glu Pro
181	GCCGCGCCCTGCAACGACCTGCACGCCACCAAGCTGGCGCCCGGCAAGGAGAAGGAGCCC
+1	Leu Glu Ser Gin Tyr Gin Val Gly Pro Leu Leu Gly Ser Gly Gly Phe Gly Ser Val Tyr
241	${\tt CTGGAGTCGCAGTACCAGGTGGGCCCGCTACTGGGCAGCGGCGGCTTCGGCTCGGTCTAC}$
+1	Ser Gly lle Arg Val Ser Asp Asn Leu Pro Val Ala lle Met His Val Glu Lys Asp Arg
301	TCAGGCATCCGCGTCTCCGACAACTTGCCGGTGGCCATCATGCACGTGGAGAAGGACCGG
+1	lle Ser Asp Trp Gly Glu Leu Pro Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu
361	ATTTCCGACTGGGGAGAGCTGCCTAATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTG
+1	Lys Lys Val Ser Ser Gly Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg Pro
421	AAGAAGGTGAGCTCGGGTTTCTCCGGCGTCATTAGGCTCCTGGACTGGTTCGAGAGGCCC
+1	Asp Ser Phe Val Leu Ile Leu Glu Arg Pro Glu Pro Val Gin Asp Leu Phe Asp Phe Ile
481	GACAGTTTCGTCCTGATCCTGGAGAGGCCCGAGCCGGTGCAAGATCTCTTCGACTTCATC
+1	Thr Glu Arg Gly Ala Leu Gin Glu Glu Leu Ala Arg Ser Phe Phe Trp Gin Val Leu Glu
541	ACGGAAAGGGGAGCCCTGCAAGAGGAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAG
+1	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp lie Lys Asp Giu Asn lie
601	GCCGTGCGGCACTGCCACAACTGCGGGGTGCTCCACCGCGACATCAAGGACGAAAACATC
+1	Leu lle Asp Leu Asn Arg Gly Glu Leu Lys Leu lle Asp Phe Gly Ser Gly Ala Leu Leu
661	CTTATCGACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGTCGGGGGGGCGCTGCTC
+1	Lys Asp Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp Ile
721	AAGGACACCGTCTACACGGACTTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATC
+1	Arg Tyr His Arg Tyr His Giy Arg Ser Ala Ala Val Trp Ser Leu Giy lie Leu Leu Tyr
781	CGCTACCATCGCTACCATGGCAGGTCGGCGGCAGTCTGGTCCCTGGGGGATCCTGCTGTAT
+1	Asp Met Val Cys Gly Asp lie Pro Phe Glu His Asp Glu Glu lie lie Arg Gly Gin Val
841	GATATGGTGTGTGGGGGATATTCCTTTCGAGCATGACGAAGAGATCATCAGGGGCCAGGTT
+1	Phe Phe Arg Gin Arg Val Ser Ser Giu Cys Gin His Leu lie Arg Trp Cys Leu Ala Leu
901	TTCTTCAGGCAGAGGGTCTCTTCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTG
+1	Arg Pro Ser Asp Arg Pro Thr Phe Giu Giu ile Gin Asn His Pro Trp Met Gin Asp Val
961	AGACCATCAGATAGGCCAACCTTCGAAGAAATCCAGAACCATCCAT
+1	Leu Leu Pro Gin Giu Thr Ala Giu Ile His Leu His Ser Leu Ser Pro Giy Pro Ser Lys
1021	CTCCTGCCCCAGGAAACTGCTGAGATCCACCTCCACAGCCTGTCGCCGGGGCCCAGCAAA
+1	Lys Pro Ser Thr Val Pro Arg Ala Arg Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly
1081	AAGCCGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGGTGAGCAAGGGA
+1	Lys Giu Leu Phe Thr
1141	AAGGAGCTGTTCACC

Abb. 60 Pim-1-K67M-GFP-Sequenz

In dieser Abb. ist die Pim-1-K67M-GFP-Sequenz dargestellt. Das Start- und das modifizierte "Stopkodon" des Pim-1-K67M-Gens ist durch rote Buchstaben und die Mutation K67M durch grüne Buchstaben gekennzeichnet

#### 6.2.9. Pim-1-WT-YFP-Sequenz

+1	Asp Pro Leu Ala Leu Pro Asp Ser Asp Leu Glu Leu Lys Leu Ala Ala Met Glu Gln Lys
1	GATCCGCTAGCGCTACCGGACTCAGATCTCGAGCTCAAGCTTGCCGCCATGGAGCAGAAA
+1	Leu lle Ser Glu Glu Asp Leu Ala Arg Ala Asp Pro Glu Gln Lys Leu lle Ser Glu Glu
61	CTCATCTCTGAAGAGGATCTGGCCCGGGCGGATCCCGAGCAGAAACTCATCTCTGAAGAG
+1	Asp Leu Gly Cys Arg Asn Ser Met Leu Leu Ser Lys lle Asn Ser Leu Ala His Leu Arg
121	GATCTGGGCTGCAGGAATTCGATGCTCTTGTCCAAAATCAACTCGCTTGCCCACCTGCGC
+1	Ala Ala Pro Cys Asn Asp Leu His Ala Thr Lys Leu Ala Pro Giy Lys Giu Lys Giu Pro
181	GCCGCGCCCTGCAACGACCTGCACGCCACCAAGCTGGCGCCCGGCAAGGAGAAGGAGCCC
+1	Leu Glu Ser Gin Tyr Gin Val Gly Pro Leu Leu Gly Ser Gly Gly Phe Gly Ser Val Tyr
241	CTGGAGTCGCAGTACCAGGTGGGCCCGCTACTGGGCAGCGGCGGCTTCGGCTCGGTCTAC
+1	Ser Gly lle Arg Val Ser Asp Asn Leu Pro Val Ala lle Lys His Val Glu Lys Asp Arg
301	TCAGGCATCCGCGTCTCCGACAACTTGCCGGTGGCCATCAAACACGTGGAGAAGGACCGG
+1	lle Ser Asp Trp Gly Glu Leu Pro Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu
361	ATTTCCGACTGGGGAGAGCTGCCTAATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTG
+1	Lys Lys Val Ser Ser Gly Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg Pro
421	AAGAAGGTGAGCTCGGGTTTCTCCGGCGTCATTAGGCTCCTGGACTGGTTCGAGAGGCCC
+1	Asp Ser Phe Val Leu IIe Leu Glu Arg Pro Glu Pro Val Gln Asp Leu Phe Asp Phe IIe
481	GACAGTTTCGTCCTGATCCTGGAGAGGCCCGAGCCGGTGCAAGATCTCTTCGACTTCATC
+1	Thr Glu Arg Gly Ala Leu Gin Glu Glu Leu Ala Arg Ser Phe Phe Trp Gin Val Leu Glu
541	ACGGAAAGGGGAGCCCTGCAAGAGGAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAG
+1	Ala Val Arg His Cys His Asn Cys Gly Val Leu His Arg Asp lie Lys Asp Glu Asn lie
+1 601	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGTGCTCCACCGCGACATCAAGGACGAAAACATC
+1 601 +1	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGTGCTCCACCGCGACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Giy Giu Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu
+1 601 +1 661	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGGGGGCGCCCCACCGCGACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Giy Giu Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGTCGGGGGGGG
+1 601 +1 661 +1	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGGGGCGCCCCACCGCGACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Giy Giu Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGTCGGGGGGGCGCTGCTC Lys Asp Thr Val Tyr Thr Asp Phe Asp Giy Thr Arg Val Tyr Ser Pro Pro Giu Trp IIe
+1 601 +1 661 +1 721	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGTGCTCCACCGCGACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Giy Giu Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGTCGGGGGGGCGCTGCTC Lys Asp Thr Val Tyr Thr Asp Phe Asp Giy Thr Arg Val Tyr Ser Pro Pro Giu Trp IIe AAGGACACCGTCTACACGGACTTCGATGGGACCCCGAGTGTATAGCCCTCCAGAGTGGATC
+1 601 +1 661 +1 721 +1	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGTGCTCCACCGCGACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Giy Giu Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGTCGGGGGGGG
+1 601 +1 661 +1 721 +1 781	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGTGCTCCACCGCGACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Giy Giu Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGTCGGGGGGCGCTGCTC Lys Asp Thr Val Tyr Thr Asp Phe Asp Giy Thr Arg Val Tyr Ser Pro Pro Giu Trp IIe AAGGACACCGTCTACACGGACTTCGATGGGACCCCGAGTGTATAGCCCTCCAGAGTGGATC Arg Tyr His Arg Tyr His Giy Arg Ser Ala Ala Val Trp Ser Leu Giy IIe Leu Leu Tyr CGCTACCATCGCTACCATGGCAGGTCGGCGGCGCCGCTGCTC
+1 601 +1 661 +1 721 +1 781 +1	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGGGGCGCCCCACCGCGACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Giy Giu Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGGGGGGGCGAGCTCAAGCTCATCGACTTCGGGGTCGGGGGGGG
+1 601 +1 661 +1 721 +1 781 +1 841	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCCGGGGGTGCTCCACCGCGACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Giy Giu Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGTCGGGGGGGCGCTGCTC Lys Asp Thr Val Tyr Thr Asp Phe Asp Giy Thr Arg Val Tyr Ser Pro Pro Giu Trp IIe AAGGACACCGTCTACACGGACTTCGATGGGACCCCGAGTGTATAGCCCTCCAGAGTGGATC Arg Tyr His Arg Tyr His Giy Arg Ser Ala Ala Val Trp Ser Leu Giy IIe Leu Leu Tyr CGCTACCATCGCTACCATGGCAGGTCGGCGGCGGCGGCGCTGCTGTAT Asp Met Val Cys Giy Asp IIe Pro Phe Giu His Asp Giu Giu IIe IIe Arg Giy Gin Val GATATGGTGTGTGGGAGATATTCCTTTCGAGCATGACGAAGAGAACATCATCAGGGGCCAGGTT
+1 601 +1 661 +1 721 +1 781 +1 841 +1	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCCGGGGGTGCTCCACCGCGACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Giy Giu Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGTCGGGGGGGG
+1 601 +1 661 +1 721 +1 781 +1 841 +1 901	Ala Val Arg His Cys His Asn Cys Gly Val Leu His Arg Asp IIe Lys Asp Glu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGTGCTCCACCGCGACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Gly Glu Leu Lys Leu IIe Asp Phe Gly Ser Gly Ala Leu Leu CTTATCGACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGGTCGGGGGGGCGCTGCTC Lys Asp Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp IIe AAGGACACCGTCTACACGGACTTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATC Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala Val Trp Ser Leu Gly IIe Leu Leu Tyr CGCTACCATCGCTACCATGGCAGGTCGGCGGCAGTCTGGTCCTGGGGGATCCTGCTGTAT Asp Met Val Cys Gly Asp IIe Pro Phe Glu His Asp Glu Glu IIe IIe Arg Gly Gln Val GATATGGTGTGTGGAGATATTCCTTTCGAGCATGACGAAGAGATCATCAGGGGCCAGGTT Phe Phe Arg Gln Arg Val Ser Ser Glu Cys Gln His Leu IIe Arg Trp Cys Leu Ala Leu TTCTTCAGGCAGAGGGTCTCTTCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTG
+1 601 +1 661 +1 721 +1 781 +1 841 +1 901 +1	Ala Val Arg His Cys His Asn Cys Gly Val Leu His Arg Asp IIe Lys Asp Glu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGTGCTCCACCGCGCACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Gly Glu Leu Lys Leu IIe Asp Phe Gly Ser Gly Ala Leu Leu CTTATCGACCTCAATCGCGGGGGGGGCGCAGCTCAAGCTCATCGACTTCGGGGTCGGGGGGGCGCTGCTC Lys Asp Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu Trp IIe AAGGACACCGTCTACACGGACTTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATC Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala Val Trp Ser Leu Gly IIe Leu Leu Leu Tyr CGCTACCATCGCTACCATGGCAGGTCGGCGGCGGCGGCGGCGCTGCTGTAT Asp Met Val Cys Gly Asp IIe Pro Phe Glu His Asp Glu Glu IIe IIe Arg Gly Gln Val GATATGGTGTGTGGGAGATATTCCTTTCGAGCATGACGAAGAGATCATCAGGGGGCCAGGTT Phe Phe Arg Gln Arg Val Ser Ser Glu Cys Gln His Leu IIe Arg Trp Cys Leu Ala Leu TTCTTCAGGCAGAGGGTCTCTTCCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTG Arg Pro Ser Asp Arg Pro Thr Phe Glu Glu IIe Gln Asn His Pro Trp Met Gln Asp Val
+1 601 +1 661 +1 721 +1 781 +1 841 +1 901 +1 901	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGTGCTCCACCGCGACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Giy Giu Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGTCGGGGGGCGCTGCTC Lys Asp Thr Val Tyr Thr Asp Phe Asp Giy Thr Arg Val Tyr Ser Pro Pro Giu Trp IIe AAGGACACCGTCTACACGGACTTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATC Arg Tyr His Arg Tyr His Giy Arg Ser Ala Ala Val Trp Ser Leu Giy IIe Leu Leu Tyr CGCTACCATCGCTACCATGGCAGGTCGGCGGCAGTCTGGTCCTGGGGATCCTGCTGTAT Asp Met Val Cys Giy Asp IIe Pro Phe Giu His Asp Giu Giu IIe IIe Arg Giy Gin Val GATATGGTGTGTGGAGATATTCCTTTCGAGCATGACGAAGAGATCATCAGGGGGCCAGGTC Phe Phe Arg Gin Arg Val Ser Ser Giu Cys Gin His Leu IIe Arg Trp Cys Leu Ala Leu TTCTTCAGGCAGAGGGTCTCTTCCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTG Arg Pro Ser Asp Arg Pro Thr Phe Giu Giu IIe Gin Asn His Pro Trp Met Gin Asp Val AGACCATCAGATAGGCCAACCTTCGAAGAAATCCAGAACCATCCAT
+1 601 +1 661 721 +1 781 +1 841 +1 901 +1 961 +1	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGTGCTCCACCGCGCACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Giy Giu Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGGGGGGGCGAGCTCAAGCTCATCGACTTCGGGTCGGGGGGGG
+1 601 +1 661 721 +1 781 +1 841 +1 901 +1 961 +1 1021	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp lie Lys Asp Giu Asn lie GCCGTGCGGCACTGCCACAACTGCGGGGGTGCTCCACCGCGACATCAAGGACGAAAACATC Leu lie Asp Leu Asn Arg Giy Giu Leu Lys Leu lie Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGGTCGGGGGGCGCTGCTC Lys Asp Thr Val Tyr Thr Asp Phe Asp Giy Thr Arg Val Tyr Ser Pro Pro Giu Trp lie AAGGACACCGTCTACACGGACTTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATC Arg Tyr His Arg Tyr His Giy Arg Ser Ala Ala Val Trp Ser Leu Giy lie Leu Leu Tyr CGCTACCATCGCTACCATGGCAGGTCGGCGGCGGCAGTCTGGTCCTGGGGGATCCTGCTGTAT Asp Met Val Cys Giy Asp lie Pro Phe Giu His Asp Giu Giu lie lie Arg Giy Gin Val GATATGGTGTGTGGGAGATATTCCTTTCGAGCATGACGAAGAGATCATCAGGGGCCCAGGTT Phe Phe Arg Gin Arg Val Ser Ser Giu Cys Gin His Leu lie Arg Trp Cys Leu Ala Leu TTCTTCAGGCAGAGGGTCTCTTCGAAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTG Arg Pro Ser Asp Arg Pro Thr Phe Giu Giu lie Gin Asn His Pro Trp Met Gin Asp Val AGACCATCAGATAGGCCAACCTTCGAAGAAATCCCAGAACCATCCAT
+1 601 +1 661 721 +1 781 +1 841 +1 901 +1 961 +1 1021 +1	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp IIe Lys Asp Giu Asn IIe GCCGTGCGGCACTGCCACAACTGCGGGGGTGCTCCACCGCGGACATCAAGGACGAAAACATC Leu IIe Asp Leu Asn Arg Giy Giu Leu Lys Leu IIe Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGCGAGGCTCAAGCTCATCGACTTCGGGTCGGGGGGCGCTGCTC Lys Asp Thr Val Tyr Thr Asp Phe Asp Giy Thr Arg Val Tyr Ser Pro Pro Giu Trp IIe AAGGACACCGTCTACACGGACTTCGATGGGGACCCGAGTGTATAGCCCTCCAGAGTGGATC Arg Tyr His Arg Tyr His Giy Arg Ser Ala Ala Val Trp Ser Leu Giy IIe Leu Leu Tyr CGCTACCATCGCTACCATGGCAGGTCGGCGGCAGTCTGGTCCCTGGGGATCCTGCTGTAT Asp Met Val Cys Giy Asp IIe Pro Phe Giu His Asp Giu Giu IIe IIe Arg Giy Gin Val GATATGGTGTGTGGGAGATATTCCTTTCGAGCATGACGAAGAGATCATCAGGGGCCCAGGTT Phe Phe Arg Gin Arg Val Ser Ser Giu Cys Gin His Leu IIe Arg Trp Cys Leu Ala Leu TTCTTCAGGCAGAGGGTCTCTTCGAAGAAATCCAGGAACCATCCAT
+1 601 +1 661 721 71 781 +1 841 41 901 +1 901 +1 1021 +1 1021 +1 1081	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp lie Lys Asp Giu Asn lie GCCGTGCGGCACTGCCACAACTGCGGGGGTGCTCCACCGCGGACATCAAGGACGAAAACATC Leu lie Asp Leu Asn Arg Giy Giu Leu Lys Leu lie Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGGGGAGCTCAAGCTCATCGACTTCGGGTCGGGGGGGG
+1 601 +1 661 721 +1 781 +1 841 +1 901 +1 901 +1 1021 +1 1081 +1	Ala Val Arg His Cys His Asn Cys Giy Val Leu His Arg Asp lie Lys Asp Giu Asn lie GCCGTGCGGCACTGCCACAACTGCGGGGGGTGCTCCACCGCGGACATCAAGGACGAAAACATC Leu lie Asp Leu Asn Arg Giy Giu Leu Lys Leu lie Asp Phe Giy Ser Giy Ala Leu Leu CTTATCGACCTCAATCGCGGGGGGGGGCTCAAGCTCAGGACTCGGGGGGGG

#### Abb. 61 Pim-1-WT-YFP-Sequenz

In dieser Abb. ist die Pim-1-WT-YFP-Sequenz dargestellt. Das Start- und das modifizierte "Stopkodon" des Pim-1-WT-Gens ist durch rote Buchstaben gekennzeichnet. Blaue Zeichen geben das Startkodon des YFP-Gens an.

#### 6.2.10. Pim-1-K67M-YFP-Sequenz

+1	Asp Leu Glu Leu Lys Leu Ala Ala Met Glu Gln Lys Leu lle Ser Glu Glu Asp Leu Ala
1	GATCTCGAGCTCAAGCTTGCCGCCATGGAGCAGAAACTCATCTCTGAAGAGGATCTGGCC
+1	Arg Ala Asp Pro Glu Gin Lys Leu lie Ser Glu Glu Asp Leu Gly Cys Arg Asn Ser Met
61	CGGGCGGATCCCGAGCAGAAACTCATCTCTGAAGAGGATCTGGGCTGCAGGAATTCGATG
+1	Leu Leu Ser Lys lle Asn Ser Leu Ala His Leu Arg Ala Ala Pro Cys Asn Asp Leu His
121	CTCTTGTCCAAAATCAACTCGCTTGCCCACCTGCGCGCCGCGCCCTGCAACGACCTGCAC
+1	Ala Thr Lys Leu Ala Pro Gly Lys Glu Lys Glu Pro Leu Glu Ser Gln Tyr Gln Val Gly
181	GCCACCAAGCTGGCGCCCGGCAAGGAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTGGGC
+1	Pro Leu Leu Gly Ser Gly Gly Phe Gly Ser Val Tyr Ser Gly lle Arg Val Ser Asp Asn
241	CCGCTACTGGGCAGCGGCGGCGCCTCGGCTCGGTCTACTCAGGCATCCGCGTCTCCGACAAC
+1	Leu Pro Val Ala lle Met His Val Giu Lys Asp Arg lle Ser Asp Trp Giy Giu Leu Pro
301	TTGCCGGTGGCCATCATGCACGTGGAGAAGGACCGGATTTCCGACTGGGGAGAGCTGCCT
+1	Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val Ser Ser Gly Phe Ser
361	AATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCGGGTTTCTCC
+1	Gly Val lle Arg Leu Leu Asp Trp Phe Glu Arg Pro Asp Ser Phe Val Leu Ile Leu Glu
421	GGCGTCATTAGGCTCCTGGACTGGTTCGAGAGGCCCGACAGTTTCGTCCTGATCCTGGAG
+1	Arg Pro Glu Pro Val Gin Asp Leu Phe Asp Phe Ile Thr Glu Arg Gly Ala Leu Gin Glu
481	AGGCCCGAGCCGGTGCAAGATCTCTTCGACTTCATCACGGAAAGGGGAGCCCTGCAAGAG
+1	Glu Leu Ala Arg Ser Phe Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn Cys
541	GAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAACTGC
+1	Giy Val Leu His Arg Asp Ile Lys Asp Giu Asn Ile Leu Ile Asp Leu Asn Arg Giy Giu
601	GGGGTGCTCCACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAG
+1	Leu Lys Leu lle Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp Thr Val Tyr Thr Asp Phe
661	CTCAAGCTCATCGACTTCGGGTCGGGGGGGCGCTGCTCAAGGACACCGTCTACACGGACTTC
+1	Asp Gly Thr Arg Val Tyr Ser Pro Ile Ala Leu Gln Ser Gly Ser Ala Thr Ile Ala Thr
721	GATGGGACCCGAGTGTATAGCCCTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACC
+1	Met Ala Gly Arg Arg Gin Ser Gly Pro Trp Gly Ser *** Leu Tyr Asp Met Val Cys Gly
781	ATGGCAGGTCGGCGGCAGTCTGGTCCCTGGGGGATCCTAGCTGTATGATATGGTGTGTGGA
+1	Asp lie Pro Phe Giu His Asp Giu Giu lie lie Arg Giy Gin Val Phe Phe Arg Gin Arg
841	GATATTCCTTTCGAGCATGACGAAGAGATCATCAGGGGGCCAGGTTTTCTTCAGGCAGAGG
+1	Val Ser Ser Glu Cys Gin His Leu lie Arg Trp Cys Leu Ala Leu Arg Pro Ser Asp Arg
901	GTCTCTTCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGG
+1	Pro Thr Phe Glu Glu Ile Gin Asn His Pro Trp Met Gin Asp Val Leu Leu Pro Gin Glu
961	
	CCAACCIICGAAGAAAICCAGGAACCAICCAIGGAIGCAAGAIGIICIICCIGCCCCAGGAA
+1	Thr Ala Glu lie His Leu His Ser Leu Ser Pro Gly Pro Ser Lys Lys Pro Ser Thr Val
+1 1021	Thr Ala Glu lie His Leu His Ser Leu Ser Pro Gly Pro Ser Lys Lys Pro Ser Thr Val ACTGCTGAGATCCACCTCCACAGCCTGTCGCCGGGGGCCCAGCAAAAAGCCGTCGACGGTA
+1 1021 +1	Thr Ala Glu lie His Leu His Ser Leu Ser Pro Gly Pro Ser Lys Lys Pro Ser Thr Val ACTGCTGAGATCCACCTCCACAGCCTGTCGCCGGGGGCCCAGCAAAAAGCCGTCGACGGTA Pro Arg Ala Arg Asp Pro Pro Val Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr

#### Abb. 62 Pim-1-K67M-YFP-Sequenz

In dieser Abb. ist die Pim-1-K67M-YFP-DNA-Sequenz dargestellt. Das Start- und das modifizierte "Stopkodon" des Pim-1-K67M-Gens ist durch rote Buchstaben und die Mutation K67M durch grüne Buchstaben gekennzeichnet. Blaue Zeichen geben das Startkodon des YFP-Gens an.

# 6.3. Listen 6.3.1. Chemikalien und Reagenzien Agarose-Beads Agarose NA ATP $[\gamma^{33}]$ -ATP ATP Big Dye v1.1 Cycle Sequencing kit biotinyliertes Histon-H3 Peptid **BSA** Dimethylsulfoxid (DMSO) Dithiothreitol (DTT) Dulbecco's Medium **FDTA** EndoFree Plasmid Maxi kit Ethanol fötales Kälberserum FuGENE 6 Transfektionsreagenz Geneticin Glutamin Ham's F12 Medium Hepes, pH 7,0 HindIII spezifischer Puffer B Hoechst 33342 Immunglobulin Insulin Isopropanol Kanamycin MES-Laufpuffer MnCl<sub>2</sub> MgCl<sub>2</sub> Na-Orthovanadat NuPage LDS 4x Probenpuffer

NuPage 10x Reducing Agent

Becton Dickinson, Heidelberg Amersham/GE Healthcare, Braunschweig Amersham/GE Healthcare, Braunschweig Perkin Elmer, Rodgau - Jügesheim Sigma, Deisenhofen Applied Biosystems, Darmstadt Upstate, Lake Placid (USA) Sigma, Deisenhofen Sigma, Deisenhofen Merck, Darmstadt Gibco, Eggenstein Sigma, Deisenhofen QIAGEN, Hilden Merck, Darmstadt PAA, Cölbe Roche, Penzberg Gibco, Eggenstein Gibco, Eggenstein PAA, Cölbe **Biochrom KG**, Berlin Roche, Penzberg Invitrogen, Karlsruhe Dianova, Hamburg Sigma, Deisenhofen Merck, Darmstadt Sigma, Deisenhofen Invitrogen, Karlsruhe Sigma, Deisenhofen Sigma, Deisenhofen Sigma, Deisenhofen Invitrogen, Karlsruhe Invitrogen, Karlsruhe

Östradiol **Opti-MEM-I** Medium Paraformaldehyd PBS PCR SuperMix Penicillin und Streptomycin Pim-1-GST Platinum Pfx DNA Polymerase kit Proteaseinhibitorcocktail Tablette (complete Mini, EDTA-free) Proteaseinhibitorcocktail Protein-G-Agarose-Beads QIAquik extraction kit **QIAquick PCR purification kit** QIAprep Spin Miniprep kit QuickChange XL Site-Directed Mutagenesis kit Restriktionsenzym HindIII Restriktionsenzym Sall **RIPA-Puffer** Sall spezifischer Puffer H sequence reaction cleanup kit Staurosporin Triton-X-100 Trypsin T4 DNA Ligase T4 DNA-Ligase Puffer (10x) Tween 20 WesternBreeze Immunodetection kit XL1-Blue superkompetente E.coli Zellen

Sigma, Deisenhofen Gibco, Eggenstein Sigma, Deisenhofen Gibco, Eggenstein Invitrogen, Karlsruhe Gibco, Eggenstein Upstate, Lake Placid (USA) Invitrogen, Karlsruhe Roche, Penzberg

Sigma, Deisenhofen KPL, Gaithersburg (USA) QIAGEN, Hilden QIAGEN, Hilden QIAGEN, Hilden Stratagene, La Jolla (USA)

Roche, Penzberg Roche, Penzberg Upstate, Lake Placid (USA) Roche, Penzberg Milipore, Eschborn Sigma, Deisenhofen Merck, Darmstadt Gibco, Eggenstein New England BioLabs, Ipswich (USA) New England BioLabs, Ipswich (USA) Sigma, Deisenhofen Invitrogen Stratagene, La Jolla (USA)

# 6.3.2. Laborgeräte und Materialien

Axiovert-200 Fluoreszenzmikroskop	Zeiss, Oberkochen
Axiovert-25 Mikroskop	Zeiss, Oberkochen
Brutschrank	Hereaus, Osterode
Discovery-1 (Fluoreszenzmikroskop)	Molecular Devices
Inkubationsschüttler	Ecotron, Bad Aibling
Mikrotiterplatte 384-Well	Greiner, Frickenhausen
Mikrotiterplatte 96-Well (µclear Platte)	Greiner, Frickenhausen
Mikrotiterplatten 96-Well (sensoplate)	Greiner, Frickenhausen
Mini submarine Elektrophorese unit	Amersham/GE Healthcare, Braunschweig
Hoefer HE33	
Nitrozellulosemembran	Invitrogen, Karlsruhe
NuPage-Novex 4-12%-ige Bis-Tris	Invitrogen, Karlsruhe
Gradientengele	
PCR-Maschine "Mastercycler"	Eppendorf, Hamburg
Plastikröhrchen: 15ml, 50ml	TPP, Trasadingen (Schweiz)
Plastikröhrchen: 1,5ml, 2ml	Eppendorf, Hamburg
310 Genetic Analyser	Applied Biosystems, Darmstadt
(Sequenziermaschine)	
Streptavidin FlashPlate HTA-Plus	Perkin Elmer, Rodgau - Jügesheim
Thermomixer 5436	Eppendorf, Hamburg
Tischzentrifuge BioFuge-fresco	Heraeus, Osterode
TopCount-NXT	Perkin Elmer, Rodgau - Jügesheim
Wasserbad Julabo TW8	Julabo, Seelbach
XCell II Blot Module	Invitrogen, Karlsruhe
XCell SureLock Mini Cell	Invitrogen, Karlsruhe
Elektrophoresekammer	
Zellkulturflaschen	Corning, Schiphol-Rijk (Niederlande)
Zentrifuge RC5C	Sorvall Instruments, Langenselbold

### 6.3.3. Antikörper

monoklonaler anti c-myc Antikörper Klon 9E10 aus der Maus #M 4439, Sigma, Deisenhofen monoklonaler anti-p21 Antikörpermix aus der Maus

#05-345, Upstate, Lake Placid (USA)	
monoklonaler anti-p21 Antikörpermix aus der Maus	
#05-345, Upstate, Lake Placid (USA)	
polyklonaler anti-p-p21-Thr145 Antikörper aus dem Kaninchen	
#sc-20220-R, Santa Cruz Bio., Santa Cruz (USA)	
polyklonaler anti-p-p21-Ser146 Antikörper aus der Ziege	
#sc-12902, Santa Cruz Bio., Santa Cruz (USA)	
monoklonaler anti-c-myc Antikörper aus der Maus	
#4439, Sigma, Deisenhofen	
monoklonaler anti-α-Tubulin Antikörper aus der Maus, FITC konjugiert	
#2168, Sigma, Deisenhofen	
monoklonaler anti-γ-Tubulin Antikörper aus der Maus	
#6557, Sigma, Deisenhofen	
polyklonaler anti-phospho-Histon-H3 (Ser10) Antikörper aus dem Kaninchen	
#06-570, Upstate, Lake Placid (USA)	

Sekundär Antikörper Cy2, Cy3 oder Cy5 konjugiert

Jackson ImmunResearch, Soham (England)

#### 6.3.4. Expressionsplasmide

pECFP-N1(Klonierungsvektor)	Becton Dickinson, Heidelberg
pEGFP-N1(Klonierungsvektor)	Becton Dickinson, Heidelberg
pEYFP-N1(Klonierungsvektor)	Becton Dickinson, Heidelberg
c-Myc-Pim-1-WT-	Frau Dr. L. Toschi, Schering AG, Berlin
Expressionsplasmid (pCMV-tag3)	
p21-WT-Expressionsplasmid	RZPD, Berlin
(pOTB7, Klon ID: IRALp962C169)	

### 6.3.5. Computerprogramme

Vector NTI	Invitrogen, Karlsruhe
Excell	Microsoft, (USA)
Programms GraFit 5.0.6	Erithacus software Limited, Surrey (England)
Programms MetaMorph 6.2	Molecular Devices, Downingtown (USA)

# 6.3.6. Abkürzungen

AFP	autofluoreszierende Proteine
BSA	Rinderserumalbumin
CAK	CDK activating kinases
CDK	cyclin dependent kinase
CFP	blau (cyan) fluoreszierendes Proteinen
DMSO	Dimethylsulfoxid
GFP	grün fluoreszierendes Proteinen
Cpm	counts pro Minute
HCA	High Content Analysis
IP	Immunpräzipitation
MCS	multiple cloning site
MG	Molekulargewicht
NLS	nuclear localisation signal
NuMA	nuclear mitotic apparatus protein
PCNA	proliferting cell nuclear antigen
PCR	Polymerase-Kettenreaktion
PFA	Paraformaldehydlösung
Pim-1	proviral integration site for murine leukemia virus
Rb	Retinoblastoma Protein
RT-PCR	Reverse Transkriptase- Polymerase-Kettenreaktion
SDS	Sodiumdodecylsulfat
STAT	signal transducers and activators of transcription
WT	Wildtyp
YFP	gelb fluoreszierendes Proteinen

# 7. Verzeichnes der Abbildungen

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