Novel peptides and combination of peptides for use in immunotherapy against Hepatocellular carcinoma (HCC) and other cancers

The present invention relates to peptides, proteins, nucleic acids and cells for use in immunotherapeutic methods. In particular, the present invention relates to the immunotherapy of cancer. The present invention furthermore relates to tumor-associated T-cell peptide epitopes, alone or in combination with other tumor-associated peptides that can for example serve as active pharmaceutical ingredients of vaccine compositions that stimulate anti-tumor immune responses, or to stimulate T cells *ex vivo* and transfer into patients. Peptides bound to molecules of the major histocompatibility complex (MHC), or peptides as such, can also be targets of antibodies, soluble T-cell receptors, and other binding molecules. In particular, the present invention relates to several novel peptide sequences and their variants derived from HLA class I and class II molecules of human tumor cells that can be used in vaccine compositions for eliciting anti-tumor immune responses or as targets for the development of pharmaceutically / immunologically active compounds and cells.

Background of the invention

Hepatocellular carcinoma (HCC) is one of the most common tumors in the world and accounts for about 6% of all new cancer cases diagnosed worldwide. In 2012 about 782,000 new cases of HCC occurred in the world, making it the fifth most common cancer in men (554,000 cases) and the ninth in women (228,000 cases) (http://globocan.iarc.fr). HCC is the most common primary liver malignancy accounting for over 80% of all adult primary liver cancers.

The distribution of HCC varies geographically, and rates of incidence depend on gender. The age-standardized incidence rate (ASR) of HCC in men is highest in Eastern Asia (31.9) and South-Eastern Asia (22.2), intermediate in Southern Europe (9.5) and Northern America (9.3) and lowest in Northern Europe (4.6) and South-Central

Asia (3.7). Incident rates of HCC in women are lower than male ASRs. The highest ASR in women occurs in Eastern Asia (10.2) and Western Africa (8.1), the lowest in Northern Europe (1.9) and Micronesia (1.6).

The overall prognosis for patients with HCC is poor. The 5-year relative survival rate (5Y-RSR) from HCC is about 15%, depending on the stage at the time of diagnosis. For localized HCC, where the cancer is still confined to the liver, the 5Y-RSR is about 28%. For regional and distant HCC, were the cancer has grown into nearby or distant organs, 5Y-RSRs are 7% and 2%, respectively.

The incidence of HCC is related to several risk factors, cirrhosis being the most important one. Cirrhosis often occurs alongside alcohol abuse or HBV or HCV infections, but can also be caused by metabolic diseases like type II diabetes. As a result, healthy liver tissue gets replaced by scar tissue, which increases the risk of cancer development.

Disease management depends on the tumor stage at the time of diagnosis and the overall condition of the liver. If possible, parts of the liver (partial hepatectomy) or the whole organ (liver resection) is removed by surgery. Especially patients with small or completely resectable tumors are qualified to receive a liver transplant.

If surgery is not a treatment option, different other therapies are available at hand. For tumor ablation, a probe is injected into the liver and the tumor is destroyed by radio or microwaves or cryotherapy. In embolization procedures, the blood supply of the tumor is blocked by mechanical or chemical means. High energy radio waves can be used to destroy the tumor in radiation therapy.

Chemotherapy against HCC includes combinations of doxorubicin, 5-fluorouracil and cisplatin for systemic therapy and doxorubicin, floxuridine and mitomycin C for hepatic artery infusions. However, most HCC show a high resistance to chemotherapeutics (Enguita-German and Fortes, 2014).

Therapeutic options in advanced non-resectable HCC are limited to Sorafenib, a multi-tyrosine kinase inhibitor (Chang et al., 2007; Wilhelm et al., 2004). Sorafenib is the only systemic drug confirmed to increase survival by about 3 months and currently represents the only experimental treatment option for such patients (Chapiro et al., 2014; Llovet et al., 2008).

Lately, a limited number of immunotherapy trials for HCC have been conducted. Cytokines have been used to activate subsets of immune cells and/or increase the tumor immunogenicity (Reinisch et al., 2002; Sangro et al., 2004). Other trials have focused on the infusion of Tumor-infiltrating lymphocytes or activated peripheral blood lymphocytes (Shi et al., 2004a; Takayama et al., 1991; Takayama et al., 2000).

So far, a small number of therapeutic vaccination trials have been executed. Butterfield et al. conducted two trials using peptides derived from alpha-fetoprotein (AFP) as a vaccine or DCs loaded with AFP peptides *ex vivo* (Butterfield et al., 2003; Butterfield et al., 2006). In two different studies, autologous dendritic cells (DCs) were pulsed *ex vivo* with autologous tumor lysate (Lee et al., 2005) or lysate of the hepatoblastoma cell line HepG2 (Palmer et al., 2009). So far, vaccination trials have only shown limited improvements in clinical outcomes.

Summary of the invention

In a first aspect of the present invention, the present invention relates to a peptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 300 or a variant sequence thereof which is at least 80%, preferably at least 90%, homologous (preferably at least 80% or at least 90% identical) to SEQ ID NO: 1 to SEQ ID NO: 300, wherein said variant binds to MHC and/or induces T cells cross-reacting with said peptide, or a pharmaceutical acceptable salt thereof, wherein said peptide is not the underlying full-length polypeptide.

The present invention further relates to a peptide of the present invention comprising a sequence that is selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 300 or a variant thereof, which is at least 80%, preferably at least 88%, homologous (preferably at least 80% or at least 88% identical) to SEQ ID NO: 1 to SEQ ID NO: 300, wherein said peptide or variant thereof has an overall length of between 8 and 100, preferably between 8 and 30, and most preferred of between 8 and 14 amino acids.

The following tables show the peptides according to the present invention, their respective SEQ ID NOs, and the prospective source (underlying) genes for these peptides. All peptides in Table 1 bind to HLA-A*02, peptides in Table 2 bind to HLA-A*24 alleles. The peptides in Table 3 have been disclosed before in large listings as results of high-throughput screenings with high error rates or calculated using algorithms, but have not been associated with cancer at all before. They bind to HLA-A*02. The peptides in Table 4 are additional peptides that may be useful in combination with the other peptides of the invention. Peptides bind A*02 or, where indicated, A*24. The peptides in Table 5 are furthermore useful in the diagnosis and/or treatment of various malignancies that involve an over-expression or over-presentation of the respective underlying polypeptide.

Table 1: HLA-A*02 peptides according to the present invention - S* = phosphoserine

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
1	VMAPFTMTI	338	APOB
2	KLQAGTVFV	10840	ALDH1L1
3	ILDDNMQKL	79611	ACSS3
4	KLQDFSDQL	338	APOB
5	ALVEQGFTV	338	APOB
6	KLSPTVVGL	8313	AXIN2
7	ALVDTLKFV	338	APOB
8	KLLEEATISV	54808	DYM
9	ALANQKLYSV	23195	MDN1
10	SLLEEFDFHV	8615	USO1
11	SLSQELVGV	24149	ZNF318
12	FLAELAYDL	2719	GPC3

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
13	GLIDTETAMKAV	3290	HSD11B1
14	ALADLTGTVV	23385	NCSTN
15	LLYGHTVTV	347734	SLC35B2
16	SLLGGNIRL	2181	ACSL3
17	RVAS*PTSGV	8660	IRS2
18	ALYGKTEVV	57513	CASKIN2
19	FLEETKATV	338	APOB
20	KLSNVLQQV	338	APOB
21	QLIEVSSPITL	338	APOB
22	RIAGIRGIQGV	23167	EFR3A
23	RLYDPASGTISL	23456	ABCB10
24	SLAEEKLQASV	2194	FASN
25	SLDGKAALTEL	338	APOB
26	SLLHTIYEV	85407	NKD1
27	TLPDFRLPEI	338	APOB
28	TLQDHLNSL	338	APOB
29	YIQDEINTI	338	APOB
30	YLGEGPRMV	5704	PSMC4
31	YQMDIQQEL	338	APOB
32	ALNAVRLLV	9368	SLC9A3R1
33	LLHGHIVEL	57678	GPAM
34	SLAEGTATV	540	ATP7B
35	SLQESILAQV	23644	EDC4
36	ILNVDGLIGV	47	ACLY
37	LLLPLLPPLSP	347252	IGFBPL1
38	ALADVVHEA	26873	OPLAH
39	ALDPKANFST	10188	TNK2
40	ALLAEGITWV	54499	TMCO1
41	ALLELDEPLVL	2158	F9
42	ALLGGNVRMML	2182	ACSL4
43	ALLGVWTSV	444	ASPH
44	ALQDAIRQL	51268	PIPOX
45	ALQDQLVLV	183	AGT
46	AMAEMKVVL	11283, 4051, 57834, 66002, 8529	CYP4F8,CYP4F3,CYP4F11,CYP4F12,CYP4F2
47	FLDTPIAKV	85407	NKD1
48	FLLEQPEIQV	5345	SERPINF2
49	FLYPEKDEPT	338	APOB
50	FTIPKLYQL	338	APOB
51	GLAEELVRA	5091	PC

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
52	GLFNAELLEA	3929	LBP
53	GLIHLEGDTV	81494	CFHR5
54	GLLDPNVKSIFV	79033	ERI3
55	GLYGRTIEL	55908	C19orf80
56	GVLPGLVGV	162515	SLC16A11
57	HLTEAIQYV	6097	RORC
58	ILADLNLSV	55705	IPO9
59	ILADTFIGV	222223	KIAA1324L
60	ILSPLSVAL	5345	SERPINF2
61	KIADFELPTI	338	APOB
62	KIAGTNAEV	2752	GLUL
63	KIDEKNFVV	5887	RAD23B
64	KILEETLYV	8443	GNPAT
65	KLFSGDELLEV	8777	MPDZ
66	KLHEEIDRV	1571	CYP2E1
67	KLKETIQKL	338	APOB
68	KLLAATVLLL	336	APOA2
69	KLLDEVTYLEA	1573	CYP2J2
70	KLLDLETERILL	2803	GOLGA4
71	KLLDNWDSV	335	APOA1
72	KLSEAVTSV	55258	THNSL2
73	KLTLVIISV	8647	ABCB11
74	KLYDLELIV	570	BAAT
75	KQMEPLHAV	284111	SLC13A5
76	LLADIGGDPFAA	3268	AGFG2
77	LLHEENFSV	6942	TCF20
78	LLIDDEYKV	23065	EMC1
79	LLLSTGYEA	23556	PIGN
80	LLYEGKLTL	440107	PLEKHG7
81	NLASFIEQVAV	5092	PCBD1
82	NVFDGLVRV	338	APOB
83	QLHDFVMSL	8647	ABCB11
84	QLTPVLVSV	1244	ABCC2
85	RILPKVLEV	10840	ALDH1L1
86	RLAAFYSQV	91289	LMF2
87	RLFEENDVNL	5053	PAH
88	RLIDRIKTV	60560	NAA35
89	RLIEEIKNV	347051	SLC10A5
90	RLLDVLAPLV	80781	COL18A1
91	RLPDIPLRQV	55656	INTS8

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
92	RLPPDTLLQQV	5986	RFNG
93	RLYTMDGITV	1571	CYP2E1
94	RMSDVVKGV	113251	LARP4
95	SICNGVPMV	54575, 54576, 54577, 54578, 54579, 54600, 54657, 54658, 54659	UGT1A10,UGT1A8,UGT1A7, UGT1A6,UGT1A5,UGT1A9,UGT1A4,UGT1A1,UGT1A3
96	SLLEEPNVIRV	4703	NEB
97	SLLPQLIEV	338	APOB
98	SLLSPEHLQYL	7512	XPNPEP2
99	SLSAFLPSL	54757	FAM20A
100	SLVGDIGNVNM	1401	CRP
101	SLWEGGVRGV	411	ARSB
102	SLWSVARGV	57678	GPAM
103	SMGDHLWVA	2752	GLUL
104	SVWFGPKEV	28982	FLVCR1
105	SVYDGKLLI	5445	PON2
106	TLAAIIHGA	5243	ABCB1
107	TLGQFYQEV	3700, 375346	ITIH4,TMEM110
108	TLLKKISEA	84675	TRIM55
109	TLYALSHAV	338	APOB
110	TVGGSEILFEV	1401	CRP
111	TVMDIDTSGTFNV	26063, 4833	DECR2,NME4
112	VLGEVKVGV	122622	ADSSL1
113	VLMDKLVEL	338	APOB
114	VLSQVYSKV	338	APOB
115	VVLDDKDYFL	100292290, 3336	HSPE1
116	WVIPAISAV	1528	CYB5A
117	YAFPKSITV	6566	SLC16A1
118	YLDDEKNWGL	5005	ORM2
119	YLDKNLTVSV	100293534, 720, 721	C4A,C4B
120	YLGEEYVKA	7018	TF
121	YLITGNLEKL	1314	COPA
122	YLSQAADGAKVL	2584	GALK1
123	YLWDLDHGFAGV	832	CAPZB
124	LLIDVVTYL	338	APOB
125	ALYGRLEVV	23294	ANKS1A
126	TLLDSPIKV	338	APOB
127	VLIGSNHSL	9919	SEC16A

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
128	GLAFSLNGV	81502	HM13
129	SQADVIPAV	55034	MOCOS
130	ALDAGAVYTL	10840	ALDH1L1
131	ALDSGAFQSV	55907	CMAS
132	ALHEEVVGV	1593	CYP27A1
133	ALLEMDARL	54512	EXOSC4
134	ALLETNPYLL	1209	CLPTM1
135	ALLGKIEKV	2590	GALNT2
136	ALLNQHYQV	2058	EPRS
137	ALPTVLVGV	5351	PLOD1
138	ALSQVTLLL	392636	AGMO
139	ALSSKPAEV	256987	SERINC5
140	ALTSISAGV	392636	AGMO
141	AMGEKSFSV	57720	GPR107
142	AVIGGLIYV	366	AQP9
143	FILPDSLPLDTL	6632	SNRPD1
144	FIQLITGV	477, 478	ATP1A2,ATP1A3
145	FLIAEYFEHV	23743, 635	BHMT2,BHMT
146	FLWTEQAHTV	3953	LEPR
147	GLAPGGLAVV	58525	WIZ
148	GLFAPLVFL	6566	SLC16A1
149	GLLSGLDIMEV	383	ARG1
150	GLSNLGIKSI	122553	TRAPPC6B
151	HLAKVTAEV	6184	RPN1
152	KLDNNLDSV	80232	WDR26
153	KLIEVNEEL	100507203	SMLR1
154	KLTDHLKYV	3250	HPR
155	LLEPYKPPSAQ	439	ASNA1
156	LLFPHPVNQV	8518	IKBKAP
157	QLLPNLRAV	5092	PCBD1
158	RIISGLVKV	101060372, 2330	FMO5
159	RLFPDGIVTV	152831	KLB
160	RLLAKIICL	3075	CFH
161	RLLDEQFAV	9026	HIP1R
162	RLMSALTQV	9462	RASAL2
163	RLTESVLYL	368	ABCC6
164	RMLIKLLEV	6710, 6711	SPTB,SPTBN1
165	RVIEHVEQV	3034	HAL
166	SILDIVTKV	130132	RFTN2
167	SLAESSFDV	54658	UGT1A1

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
168	SLAVLVPIV	1361	CPB2
169	SLFEWFHPL	2519	FUCA2
170	SLHNGVIQL	1314	COPA
171	SLIPAVLTV	57462	KIAA1161
172	SLLNFLQHL	2968	GTF2H4
173	SLTSEIHFL	55755	CDK5RAP2
174	TLAELGAVQV	2875	GPT
175	TLFEHLPHI	2888	GRB14
176	TLGQIWDV	1778	DYNC1H1
177	VLDEPYEKV	100034743, 5174, 728939	PDZK1P2,PDZK1,PDZK1P1
178	YIFTTPKSV	22862	FNDC3A
179	YIHNILYEV	160518	DENND5B
180	YLGPHIASVTL	81671	VMP1
181	YLLEKFVAV	1663, 440081, 642846	DDX11,DDX12P
182	YLLHFPMAL	1109	AKR1C4
183	YLYNNEEQVGL	1109	AKR1C4
184	VVLDGGQIVTV	6506	SLC1A2
185	ALFPALRPGGFQA	8878	SQSTM1
186	VLLAQIIQV	89797	NAV2

Table 2: HLA-A*24 peptides according to the present invention with SEQ ID numbers - S* = phosphoserine

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
187	SYPTFFPRF	6596	HLTF
188	RYSAGWDAKF	8630	HSD17B6
189	AFSPDSHYLLF	3679	ITGA7
190	RYNEKCFKL	54800	KLHL24
191	KYPDIISRI	3978	LIG1
192	SYITKPEKW	79694	MANEA
193	IYPGAFVDL	51360	MBTPS2
194	QYASRFVQL	10733	PLK4
195	RYAPPPSFSEF	29066	ZC3H7A
196	AYLKWISQI	60561	RINT1
197	RWPKKSAEF	100132742, 100526842, 6139, 645296, 645441	RPL17P7, RPL17-C18orf32, RPL17, RPL17P39, RPL17P6
198	LYWSHPRKF	6235, 648343	RPS29, RPS29P9
199	KFVTVQATF	718	C3

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
200	AYLLQPSQF	732	C8B
201	AYVNTFHNI	1201	CLN3
202	AYGTYRSNF	9919	SEC16A
203	YYGILQEKI	10237	SLC35B1
204	KYRLTYAYF	2266	FGG
205	VYGLQRNLL	57159, 84675, 84676	TRIM54, TRIM55, TRIM63
206	KWPETPLLL	55757	UGGT2
207	IYLERFPIF	51096	UTP18
208	SYNPAENAVLL	1314	COPA
209	VFHPRQELI	1314	COPA
210	AYPAIRYLL	7818	DAP3
211	IYIPSYFDF	27042	DIEXF
212	VYGDVISNI	8893	EIF2B5
213	YYNKVSTVF	8661	EIF3A
214	IYVTSIEQI	55879	GABRQ
215	IYTGNISSF	8836	GGH
216	IYADVGEEF	100302182, 11052	MIR1279, CPSF6
217	DYIPYVFKL	338	APOB
218	VYQGAIRQI	338	APOB

Table 3: Additional peptides according to the present invention with no prior known cancer association - S* = phosphoserine

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
219	GVMAGDIYSV	123	PLIN2
220	SLLEKELESV	1819	DRG2
221	ALCEENMRGV	1938	EEF2
222	LTDITKGV	1938	EEF2
223	FLFNTENKLLL	3422	IDI1
224	ALASVIKEL	28981	IFT81
225	KMDPVAYRV	5859	QARS
226	AVLGPLGLQEV	79178	THTPA
227	ALLKVNQEL	25813	SAMM50
228	YLITSVELL	2182	ACSL4
229	KMFESFIESV	5576	PRKAR2A
230	VLTEFTREV	55705	IPO9
231	RLFNDPVAMV	10195	ALG3
232	KLAEIVKQV	8550	MAPKAPK5
233	ALLGKLDAI	5876	RABGGTB
234	YLEPYLKEV	727947,7381	UQCRB

235	KLFEEIREI	255394	TCP11L2
236	ALADKELLPSV	84883	AIFM2
237	ALRGEIETV	10128	LRPPRC
238	AMPPPPPQGV	5885	RAD21
239	FLLGFIPAKA	5976	UPF1
240	FLWERPTLLV	79922	MRM1
241	FVLPLLGLHEA	55161	TMEM33
242	GLFAPVHKV	6249	CLIP1
243	GLLDNPELRV	26263	FBXO22
244	KIAELLENV	9100	USP10
245	KLGAVFNQV	23450	SF3B3
246	KLISSYYNV	84928	TMEM209
247	KLLDTMVDTFL	100527963,11243	PMF1-BGLAP,PMF1
248	KLNDLIQRL	1314	COPA
249	LLLGERVAL	23475	QPRT
250	NLAEVVERV	26263	FBXO22
251	RLFADILNDV	64755	C16orf58
252	RTIEYLEEV	3030	HADHA
253	RVPPPPQSV	6464	SHC1
254	RVQEAIAEV	57678	GPAM
255	SLFGQDVKAV	26036	ZNF451
256	SLFQGVEFHYV	3930	LBR
257	SLLEKAGPEL	54625	PARP14
258	SLMGPVVHEV	5116	PCNT
259	TLITDGMRSV	29894	CPSF1
260	TLMDMRLSQV	24148	PRPF6
261	VLFQEALWHV	2194	FASN
262	VLPNFLPYNV	10299	MARCH6
263	VLYPSLKEI	50717,5824	DCAF8,PEX19
264	VMQDPEFLQSV	266971,5710	PIPSL,PSMD4
265	WLIEDGKVVTV	10726	NUDC
266	SLLESNKDLLL	6520	SLC3A2
267	ALNENINQV	80025	PANK2
268	KLYQEVEIASV	5976	UPF1
269	YLMEGSYNKV	5714	PSMD8
270	SVLDQKILL	9875	URB1
271	LLLDKLILL	85440	DOCK7
272	QQLDSKFLEQV	6772	STAT1
273	AILETAPKEV	6238	RRBP1
274	ALAEALKEV	55164	SHQ1
275	ALIEGAGILL	10440	TIMM17A

276	ALLEADVNIKL	6729	SRP54
277	ALLEENSTPQL	83933	HDAC10
278	ALTSVVVTL	1021	CDK6
279	ALWTGMHTI	51479	ANKFY1
280	ATLNIIHSV	51542	VPS54
281	GLLAGDRLVEV	9368	SLC9A3R1
282	GQFPSYLETV	54919	HEATR2
283	ILSGIGVSQV	3703	STT3A
284	KLDAFVEGV	528	ATP6V1C1
285	KLLDLSDSTSV	6093	ROCK1
286	KVLDKVFRA	375056	MIA3
287	LIGEFLEKV	8731	RNMT
288	LLDDSLVSI	25824	PRDX5
289	LLLEEGGLVQV	7353	UFD1L
290	NLIDLDDLYV	57187	THOC2
291	QLIDYERQL	11072	DUSP14
292	RIPAYFVTV	7407	VARS
293	FLASESLIKQI	4736	RPL10A
294	RLIDLHTNV	23256	SCFD1
295	SLFSSPPEI	252983	STXBP4
296	SLLSGRISTL	51133,92799	KCTD3,SHKBP1
297	TLFYSLREV	80233	C17orf70
298	TMAKESSIIGV	1429	CRYZ
299	ALLRVTPFI	401505	TOMM5
300	TLAQQPTAV	4802	NFYC

Table 4: Peptides useful for e.g. personalized cancer therapies - S* = phosphoserine

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
301	VLADFGARV	114899,23600	C1QTNF3,AMACR
302	KIQEILTQV	10643	IGF2BP3
303	GVYDGEEHSV	4113	MAGEB2
304	SLIDQFFGV	9097	USP14
305	GVLENIFGV	399909	PCNXL3
306	KLVEFDFLGA	10460	TACC3
307	AVVEFLTSV	29102	DROSHA
308	ALLRTVVSV	2590	GALNT2
309	GLIEIISNA	23020	SNRNP200
310	SLWGGDVVL	157680	VPS13B
311	FLIPIYHQV	31	ACACA

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
312	RLGIKPESV	1466	CSRP2
313	LTAPPEALLMV	79050	NOC4L
314	YLAPFLRNV	23019	CNOT1
315	KVLDGSPIEV	29974	A1CF
316	LLREKVEFL	4779	NFE2L1
317	KLPEKWESV	26156	RSL1D1
318	KLNEINEKI	1373	CPS1
319	KLFNEFIQL	10885	WDR3
320	GLADNTVIAKV	6897	TARS
321	GVIAEILRGV	10528	NOP56
322	ILYDIPDIRL	10667	FARS2
323	KIIDEDGLLNL	5981	RFC1
324	RLFETKITQV	100293534,720,721	C4A,C4B
325	RLSEAIVTV	51249	TMEM69
326	ALSDGVHKI	55179	FAIM
327	GLNEEIARV	10403	NDC80
328	RLEEDDGDVAM	10482	NXF1
329	SLIEDLILL	64754	SMYD3
330	SMSADVPLV	5111	PCNA
331	SLLAQNTSWLL	7070	THY1
332	AMLAVLHTV	60673	C12orf44
333	GLAEDIDKGEV	1938	EEF2
334	SILTIEDGIFEV	100287551,3306,3312	HSPA8P8,HSPA2,HSPA8
335	SLLPVDIRQYL	6773	STAT2
336	YLPTFFLTV	54898	ELOVL2
337	TLLAAEFLKQV	100288772,10574	CCT7P2,CCT7
338	KLFDSDPITVTV	1191	CLU
339	RLISKFDTV	1977	EIF4E
340	KVFDEVIEV	8908	GYG2
341	YLAIGIHEL	3034	HAL
342	AMSSKFFLV	7474	WNT5A
343	LLLPDYYLV	27044	SND1
344	VYISSLALL (A*24)	10213	PSMD14
345	SYNPLWLRI (A*24)	259266	ASPM
346	LYQILQGIVF (A*24)	983	CDK1
347	ALNPADITV	51497	TH1L
348	AYKPGALTF	84883	AIFM2

The present invention furthermore generally relates to the peptides according to the present invention for use in the treatment of proliferative diseases, such as, for

example, pancreatic cancer, colon or rectal cancer, kidney cancer, brain cancer, and/or leukemias.

Particularly preferred are the peptides – alone or in combination - according to the present invention selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 300. More preferred are the peptides – alone or in combination - selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 124 (see Table 1), preferably for A*02 binding, and from the group consisting of SEQ ID NO: 187 to SEQ ID NO: 218 (see Table 2) preferably for A*24 binding, and their uses in the immunotherapy of HCC, brain cancer, kidney cancer, pancreatic cancer, colon or rectal cancer or leukemia, and preferably HCC.

As shown in the following tables 5A and B, many of the peptides according to the present invention can also be used in the immunotherapy of other indications. The tables show, for selected peptides on which additional tumor types they were found showing over-presentation (including specific presentation) on more than 5% of the measured tumor samples, or presentation on more than 5% of the measured tumor samples with a ratio of geometric means tumor vs normal tissues being larger than 3. Over-presentation is defined as higher presentation on the tumor sample as compared to the normal sample with highest presentation. Normal tissues against which over-presentation was tested were: adipose tissue, adrenal gland, blood cells, blood vessel, bone marrow, brain, cartilage, esophagus, eye, gallbladder, heart, kidney, large intestine, liver, lung, lymph node, nerve, pancreas, parathyroid gland, peritoneum, pituitary, pleura, salivary gland, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, ureter, urinary bladder.

Table 5A: Peptides according to the present invention and their specific uses in other proliferative diseases, especially in other cancerous diseases - S* = phosphoserine

SEQ ID No.	Sequence	Other relevant organs / diseases
1	VMAPFTMTI	Pancreas

SEQ ID No.	Sequence	Other relevant organs / diseases
6	KLSPTVVGL	Colon, Rectum
10	SLLEEFDFHV	Kidney
14	ALADLTGTVV	Kidney, Brain, Pancreas
15	LLYGHTVTV	Kidney, Brain, Colon, Rectum, Pancreas
16	SLLGGNIRL	Brain, Colon, Rectum
17	RVAS*PTSGV	Brain
22	RIAGIRGIQGV	Kidney, Colon, Rectum
26	SLLHTIYEV	Colon, Rectum
30	YLGEGPRMV	Colon, Rectum, CLL
34	SLAEGTATV	Colon, Rectum
36	ILNVDGLIGV	Kidney, Brain, Colon, Rectum
39	ALDPKANFST	Kidney, Brain
41	ALLELDEPLVL	Pancreas
43	ALLGVWTSV	Pancreas
47	FLDTPIAKV	Brain, Colon, Rectum
51	GLAEELVRA	Brain
54	GLLDPNVKSIFV	Kidney, Brain
55	GLYGRTIEL	Kidney
58	ILADLNLSV	Pancreas
59	ILADTFIGV	Colon, Rectum, Pancreas
60	ILSPLSVAL	Kidney, Pancreas
65	KLFSGDELLEV	Brain, Colon, Rectum
69	KLLDEVTYLEA	Colon, Rectum
70	KLLDLETERILL	Colon, Rectum
72	KLSEAVTSV	Kidney
77	LLHEENFSV	Kidney, Colon, Rectum
80	LLYEGKLTL	Colon, Rectum
81	NLASFIEQVAV	Kidney, Colon, Rectum, Pancreas
88	RLIDRIKTV	Brain, Colon, Rectum
90	RLLDVLAPLV	Kidney
96	SLLEEPNVIRV	Kidney
101	SLWEGGVRGV	Brain
112	VLGEVKVGV	Kidney
116	WVIPAISAV	Kidney
119	YLDKNLTVSV	Kidney
121	YLITGNLEKL	Kidney, Colon, Rectum, Pancreas
123	YLWDLDHGFAGV	Brain, Colon, Rectum
125	ALYGRLEVV	Brain, Colon, Rectum
127	VLIGSNHSL	Colon, Rectum

SEQ ID No.	Sequence	Other relevant organs / diseases
133	ALLEMDARL	Kidney, Brain, Colon, Rectum
134	ALLETNPYLL	Brain
135	ALLGKIEKV	Brain, Pancreas
137	ALPTVLVGV	Kidney, Brain, Colon, Rectum
138	ALSQVTLLL	Kidney
139	ALSSKPAEV	Colon, Rectum, Pancreas
141	AMGEKSFSV	Brain
144	FIQLITGV	Pancreas
147	GLAPGGLAVV	Brain
148	GLFAPLVFL	Kidney
161	RLLDEQFAV	Brain
166	SILDIVTKV	Brain
169	SLFEWFHPL	Kidney, Brain, Colon, Rectum
170	SLHNGVIQL	Kidney
172	SLLNFLQHL	Kidney, Colon, Rectum, CLL
173	SLTSEIHFL	CLL
176	TLGQIWDV	Brain, Colon, Rectum, Pancreas
177	VLDEPYEKV	Kidney
179	YIHNILYEV	Brain
181	YLLEKFVAV	Colon, Rectum
184	VVLDGGQIVTV	Brain
186	VLLAQIIQV	Kidney, Brain, Colon, Rectum
187	SYPTFFPRF	Kidney, Brain
189	AFSPDSHYLLF	Kidney, Brain
191	KYPDIISRI	Brain
192	SYITKPEKW	Kidney, Brain
193	IYPGAFVDL	Brain
194	QYASRFVQL	Brain
195	RYAPPPSFSEF	Brain
196	AYLKWISQI	Brain
197	RWPKKSAEF	Kidney, Brain
198	LYWSHPRKF	Kidney
199	KFVTVQATF	Brain
203	YYGILQEKI	Kidney, Brain
206	KWPETPLLL	Kidney, Brain
208	SYNPAENAVLL	Brain
214	IYVTSIEQI	Brain
219	GVMAGDIYSV	Kidney
220	SLLEKELESV	Brain

SEQ ID No.	Sequence	Other relevant organs / diseases
221	ALCEENMRGV	Kidney, Brain, Colon, Rectum
223	FLFNTENKLLL	Colon, Rectum
224	ALASVIKEL	Brain
229	KMFESFIESV	Kidney, Brain, Colon, Rectum
230	VLTEFTREV	Kidney, Brain, Colon, Rectum
231	RLFNDPVAMV	Brain, Colon, Rectum
232	KLAEIVKQV	Colon, Rectum
233	ALLGKLDAI	Kidney, Colon, Rectum
234	YLEPYLKEV	Kidney, Brain, Colon, Rectum
236	ALADKELLPSV	Kidney, Colon, Rectum, Pancreas
237	ALRGEIETV	Colon, Rectum
238	AMPPPPPQGV	Brain, Colon, Rectum
239	FLLGFIPAKA	Brain
240	FLWERPTLLV	CLL
244	KIAELLENV	Brain, Colon, Rectum
245	KLGAVFNQV	Brain
247	KLLDTMVDTFL	Colon, Rectum
248	KLNDLIQRL	Pancreas
249	LLLGERVAL	Colon, Rectum
250	NLAEVVERV	Brain, Colon, Rectum, CLL
251	RLFADILNDV	Brain, Colon, Rectum
255	SLFGQDVKAV	Kidney, Brain, Colon, Rectum
258	SLMGPVVHEV	Brain
259	TLITDGMRSV	Brain
260	TLMDMRLSQV	Kidney, Brain, Colon, Rectum
261	VLFQEALWHV	Colon, Rectum
266	SLLESNKDLLL	Colon, Rectum
268	KLYQEVEIASV	Brain
269	YLMEGSYNKV	Brain, Colon, Rectum
270	SVLDQKILL	Kidney, Brain
271	LLLDKLILL	Brain, Colon, Rectum
272	QQLDSKFLEQV	Kidney, Brain
274	ALAEALKEV	Colon, Rectum
275	ALIEGAGILL	Kidney, Colon, Rectum, Pancreas
276	ALLEADVNIKL	Pancreas
277	ALLEENSTPQL	Kidney
278	ALTSVVVTL	Kidney, Brain
279	ALWTGMHTI	Kidney, Brain
281	GLLAGDRLVEV	Kidney

SEQ ID No.	Sequence	Other relevant organs / diseases
282	GQFPSYLETV	Kidney, Brain, Colon, Rectum
283	ILSGIGVSQV	Pancreas
285	KLLDLSDSTSV	Kidney, Colon, Rectum
286	KVLDKVFRA	Pancreas
287	LIGEFLEKV	CLL
288	LLDDSLVSI	Pancreas
289	LLLEEGGLVQV	Kidney, Colon, Rectum, Pancreas
290	NLIDLDDLYV	Brain, Colon, Rectum, Pancreas
291	QLIDYERQL	Kidney, Colon, Rectum, Pancreas
292	RIPAYFVTV	Kidney
293	FLASESLIKQI	Brain, Colon, Rectum
295	SLFSSPPEI	Kidney, Brain
296	SLLSGRISTL	Kidney
297	TLFYSLREV	Kidney, Brain, Colon, Rectum
299	ALLRVTPFI	CLL
300	TLAQQPTAV	Pancreas
301	VLADFGARV	Kidney, Colon, Rectum
302	KIQEILTQV	Kidney, Brain, Colon, Rectum, Pancreas, CLL
304	SLIDQFFGV	Brain, Colon, Rectum, Pancreas
305	GVLENIFGV	Kidney, Brain
306	KLVEFDFLGA	Brain, Colon, Rectum
308	ALLRTVVSV	Kidney, Pancreas
309	GLIEIISNA	Brain
310	SLWGGDVVL	Brain, Colon, Rectum
311	FLIPIYHQV	Kidney, Brain
312	RLGIKPESV	Brain
313	LTAPPEALLMV	Kidney, Brain, Colon, Rectum, Pancreas
315	KVLDGSPIEV	Kidney
316	LLREKVEFL	Kidney, Brain, Colon, Rectum, Pancreas
317	KLPEKWESV	Brain, Colon, Rectum, Pancreas
319	KLFNEFIQL	Kidney, Brain, Colon, Rectum
321	GVIAEILRGV	Kidney, Brain
324	RLFETKITQV	Kidney
325	RLSEAIVTV	Brain, Pancreas
326	ALSDGVHKI	Pancreas
327	GLNEEIARV	Brain, Colon, Rectum
328	RLEEDDGDVAM	Kidney, Brain, Colon, Rectum
329	SLIEDLILL	Kidney, Brain, Colon, Rectum, Pancreas
330	SMSADVPLV	Brain, Colon, Rectum

SEQ ID No.	Sequence	Other relevant organs / diseases
331	SLLAQNTSWLL	Brain, Colon, Rectum, Pancreas
332	AMLAVLHTV	Brain, Colon, Rectum
333	GLAEDIDKGEV	Kidney, Brain
334	SILTIEDGIFEV	Kidney, Brain, Colon, Rectum, Pancreas, CLL
335	SLLPVDIRQYL	Kidney, CLL
336	YLPTFFLTV	Kidney, Brain
337	TLLAAEFLKQV	Brain
338	KLFDSDPITVTV	Brain
339	RLISKFDTV	Brain
340	KVFDEVIEV	Brain
342	AMSSKFFLV	Brain, Colon, Rectum, Pancreas
343	LLLPDYYLV	Brain, Pancreas
344	VYISSLALL (A*24)	Brain
345	SYNPLWLRI (A*24)	Brain
346	LYQILQGIVF (A*24)	Kidney
347	ALNPADITV	Brain

Table 5B: Peptides according to the present invention and their specific uses in other proliferative diseases, especially in other cancerous diseases - S* = phosphoserine

SEQ ID NO.	Sequence	Additional Entities
189	AFSPDSHYLLF	NSCLC, PrC
273	AILETAPKEV	Esophageal Cancer
236	ALADKELLPSV	NSCLC, SCLC, GC, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer, NHL
14	ALADLTGTVV	NSCLC, SCLC, BRCA, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, PC
38	ALADVVHEA	BRCA, OC
274	ALAEALKEV	BRCA, MCC, Melanoma, OC, Uterine Cancer, AML
9	ALANQKLYSV	NSCLC, CRC, MCC, OC, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer, PC
224	ALASVIKEL	SCLC, PC, Melanoma
221	ALCEENMRGV	NSCLC, SCLC, MCC, Melanoma
131	ALDSGAFQSV	CRC, Melanoma, Gallbladder Cancer, Bile Duct

		Cancer
185	ALFPALRPGGF QA	Gallbladder Cancer, Bile Duct Cancer
275	ALIEGAGILL	SCLC, MCC, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, NHL
276	ALLEADVNIKL	Gallbladder Cancer, Bile Duct Cancer, OC
277	ALLEENSTPQL	SCLC, CLL, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, NHL
133	ALLEMDARL	NSCLC, SCLC, BRCA, MCC, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, AML, NHL
134	ALLETNPYLL	Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer
135	ALLGKIEKV	NSCLC, SCLC, BRCA, OC, Gallbladder Cancer, Bile Duct Cancer
233	ALLGKLDAI	CLL, OC, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer, AML, NHL
43	ALLGVWTSV	SCLC, Brain Cancer, CLL, BRCA, PC
227	ALLKVNQEL	Melanoma, Uterine Cancer
136	ALLNQHYQV	BRCA, OC
299	ALLRVTPFI	NHL, OC
32	ALNAVRLLV	SCLC
267	ALNENINQV	SCLC, Brain Cancer, MCC, Melanoma, Esophageal Cancer, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer
137	ALPTVLVGV	NSCLC, GC, BRCA, Melanoma, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, PC
45	ALQDQLVLV	SCLC, Brain Cancer
237	ALRGEIETV	SCLC, BRCA, OC, Esophageal Cancer, Urinary bladder cancer, NHL
139	ALSSKPAEV	PrC, OC, Uterine Cancer
278	ALTSVVVTL	NSCLC, SCLC, GC, Esophageal Cancer, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer, AML, NHL
279	ALWTGMHTI	Esophageal Cancer, Urinary bladder cancer, PC
125	ALYGRLEVV	BRCA, MCC, Melanoma, OC, Urinary bladder cancer, Uterine Cancer
141	AMGEKSFSV	Melanoma
238	AMPPPPPQGV	NSCLC, SCLC, BRCA, MCC, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer, NHL
342	AMSSKFFLV	NSCLC, GC, PrC, BRCA, Melanoma, OC,

		Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, PC
280	ATLNIIHSV	Urinary bladder cancer
226	AVLGPLGLQEV	PrC, Melanoma, OC
202	AYGTYRSNF	NSCLC
196	AYLKWISQI	NSCLC
210	AYPAIRYLL	NSCLC, GC
144	FIQLITGV	NSCLC, Brain Cancer, Urinary bladder cancer
293	FLASESLIKQI	NSCLC, PrC, MCC, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, NHL, PC
47	FLDTPIAKV	NSCLC, GC, Esophageal Cancer
223	FLFNTENKLLL	Melanoma, Urinary bladder cancer, NHL
145	FLIAEYFEHV	SCLC
239	FLLGFIPAKA	Urinary bladder cancer, AML, NHL
128	GLAFSLNGV	Melanoma, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
147	GLAPGGLAVV	NSCLC, SCLC, PrC, BRCA, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer
148	GLFAPLVFL	Esophageal Cancer, Gallbladder Cancer, Bile Duct Cancer, NHL
242	GLFAPVHKV	Urinary bladder cancer
52	GLFNAELLEA	SCLC
281	GLLAGDRLVEV	NSCLC, SCLC, OC, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, NHL
243	GLLDNPELRV	Urinary bladder cancer
54	GLLDPNVKSIFV	NSCLC, SCLC, OC, Urinary bladder cancer
149	GLLSGLDIMEV	SCLC
150	GLSNLGIKSI	Urinary bladder cancer, NHL
55	GLYGRTIEL	SCLC
282	GQFPSYLETV	NSCLC, CLL, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, NHL
219	GVMAGDIYSV	SCLC, Gallbladder Cancer, Bile Duct Cancer, PC
151	HLAKVTAEV	SCLC, OC, Urinary bladder cancer
57	HLTEAIQYV	NHL
58	ILADLNLSV	BRCA
59	ILADTFIGV	NSCLC, SCLC, GC, OC, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer, NHL
36	ILNVDGLIGV	NSCLC, SCLC, PrC, Melanoma, OC, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, NHL, PC

283	ILSGIGVSQV	NSCLC, PrC, BRCA, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, NHL, PC
216	IYADVGEEF	NSCLC, GC, PrC
211	IYIPSYFDF	NSCLC, Brain Cancer, GC
207	IYLERFPIF	NSCLC, GC
193	IYPGAFVDL	NSCLC
214	IYVTSIEQI	NSCLC, RCC
244	KIAELLENV	NSCLC, SCLC, PrC, CLL, BRCA, Melanoma, OC, Uterine Cancer, AML, NHL
62	KIAGTNAEV	BRCA
63	KIDEKNFVV	SCLC, Brain Cancer, Urinary bladder cancer, Uterine Cancer
64	KILEETLYV	Esophageal Cancer, Urinary bladder cancer, Uterine Cancer
302	KIQEILTQV	NSCLC, SCLC, GC, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, AML, NHL, PC
232	KLAEIVKQV	NSCLC, SCLC, BRCA, Melanoma, OC, Urinary bladder cancer
284	KLDAFVEGV	BRCA, OC
152	KLDNNLDSV	BRCA, Melanoma
235	KLFEEIREI	NSCLC, CRC, Melanoma, Urinary bladder cancer
245	KLGAVFNQV	NSCLC, SCLC, RCC, PrC, BRCA, Melanoma, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer
246	KLISSYYNV	OC
69	KLLDEVTYLEA	Urinary bladder cancer
70	KLLDLETERILL	OC, Uterine Cancer
285	KLLDLSDSTSV	SCLC, Uterine Cancer
247	KLLDTMVDTFL	NSCLC, SCLC, RCC, Brain Cancer, CLL, BRCA, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, AML, NHL
8	KLLEEATISV	SCLC, MCC, Melanoma, Urinary bladder cancer, Uterine Cancer
248	KLNDLIQRL	GC, Uterine Cancer
20	KLSNVLQQV	SCLC
6	KLSPTVVGL	CLL, OC
154	KLTDHLKYV	SCLC
268	KLYQEVEIASV	CRC, MCC, Melanoma, Urinary bladder cancer
225	KMDPVAYRV	CRC, PrC, BRCA, Urinary bladder cancer, Uterine Cancer
229	KMFESFIESV	NSCLC, SCLC, PrC, OC, Urinary bladder cancer

286	KVLDKVFRA	CRC, Gallbladder Cancer, Bile Duct Cancer
206	KWPETPLLL	GC
191	KYPDIISRI	NSCLC, GC
287	LIGEFLEKV	SCLC, RCC, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, NHL
288	LLDDSLVSI	Melanoma, Urinary bladder cancer, AML
156	LLFPHPVNQV	NSCLC, SCLC, OC, Esophageal Cancer, Urinary bladder cancer
77	LLHEENFSV	NSCLC, SCLC, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, NHL
78	LLIDDEYKV	Esophageal Cancer, Urinary bladder cancer, PC
271	LLLDKLILL	CLL, Melanoma, OC, Urinary bladder cancer, Uterine Cancer
289	LLLEEGGLVQV	NSCLC, SCLC, PrC, Melanoma, OC, Urinary bladder cancer, NHL
249	LLLGERVAL	OC
37	LLLPLLPPLSP	SCLC, PC, MCC, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
80	LLYEGKLTL	OC
15	LLYGHTVTV	NSCLC, SCLC, BRCA, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, NHL, PC
222	LTDITKGV	BRCA, NHL
346	LYQILQGIVF	NSCLC, Brain Cancer, GC
198	LYWSHPRKF	NSCLC
250	NLAEVVERV	NSCLC, SCLC, PrC, BRCA, MCC, OC, Gallbladder Cancer, Bile Duct Cancer
81	NLASFIEQVAV	SCLC, PrC, OC, Uterine Cancer, NHL
290	NLIDLDDLYV	SCLC, PrC, MCC, OC, Urinary bladder cancer, Uterine Cancer
291	QLIDYERQL	NSCLC, SCLC, Brain Cancer, BRCA, Melanoma, Esophageal Cancer, Urinary bladder cancer, NHL, PC
157	QLLPNLRAV	RCC
272	QQLDSKFLEQV	MCC, OC, NHL
194	QYASRFVQL	NSCLC, GC
22	RIAGIRGIQGV	NSCLC, PrC, BRCA, OC, NHL
292	RIPAYFVTV	GC, BRCA, Melanoma, NHL
86	RLAAFYSQV	AML
251	RLFADILNDV	NSCLC, SCLC, PrC, Melanoma, Urinary bladder cancer, Uterine Cancer
231	RLFNDPVAMV	NSCLC, SCLC, MCC, Melanoma, OC, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer

294	RLIDLHTNV	Esophageal Cancer
88	RLIDRIKTV	NSCLC, SCLC, OC, AML, NHL
89	RLIEEIKNV	SCLC
161	RLLDEQFAV	SCLC, BRCA
90	RLLDVLAPLV	BRCA
91	RLPDIPLRQV	NSCLC, CLL, Urinary bladder cancer, NHL
92	RLPPDTLLQQV	Urinary bladder cancer
23	RLYDPASGTISL	CLL, Melanoma, NHL
164	RMLIKLLEV	SCLC, CRC
94	RMSDVVKGV	BRCA, OC
252	RTIEYLEEV	Melanoma
17	RVAJPTSGV	AML
197	RWPKKSAEF	NSCLC
195	RYAPPPSFSEF	NSCLC
190	RYNEKCFKL	NSCLC
95	SICNGVPMV	Urinary bladder cancer
166	SILDIVTKV	SCLC, CLL, MCC, Melanoma, Urinary bladder cancer, AML
24	SLAEEKLQASV	PrC, BRCA, Urinary bladder cancer
169	SLFEWFHPL	NSCLC, Gallbladder Cancer, Bile Duct Cancer
255	SLFGQDVKAV	NSCLC, SCLC, CLL, BRCA, MCC, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, NHL, PC
256	SLFQGVEFHYV	CRC, CLL, MCC, NHL
295	SLFSSPPEI	NSCLC, SCLC, CRC, PrC, BRCA, Melanoma, OC, Urinary bladder cancer, Uterine Cancer
170	SLHNGVIQL	NSCLC, Urinary bladder cancer, Uterine Cancer, NHL
331	SLLAQNTSWLL	NSCLC, RCC, GC, BRCA, Melanoma, Esophageal Cancer, Urinary bladder cancer
10	SLLEEFDFHV	NSCLC, BRCA, OC, Esophageal Cancer, Uterine Cancer
96	SLLEEPNVIRV	Melanoma, Gallbladder Cancer, Bile Duct Cancer
257	SLLEKAGPEL	CLL, Melanoma, OC
220	SLLEKELESV	NSCLC, SCLC, PrC, CLL, BRCA, OC, Esophageal Cancer, Urinary bladder cancer, NHL
266	SLLESNKDLLL	SCLC, MCC, Uterine Cancer
16	SLLGGNIRL	GC, PrC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, PC
26	SLLHTIYEV	PrC, BRCA, Esophageal Cancer, NHL
172	SLLNFLQHL	AML
97	SLLPQLIEV	SCLC

296	SLLSGRISTL	BRCA, Urinary bladder cancer
258	SLMGPVVHEV	SCLC, MCC, Melanoma, OC, Urinary bladder cancer, NHL
35	SLQESILAQV	NSCLC, SCLC, PrC, MCC, Melanoma, Urinary bladder cancer, AML
99	SLSAFLPSL	OC, Esophageal Cancer, Gallbladder Cancer, Bile Duct Cancer, NHL
11	SLSQELVGV	Brain Cancer, Melanoma, Uterine Cancer, NHL
173	SLTSEIHFL	Uterine Cancer, NHL
101	SLWEGGVRGV	Melanoma
103	SMGDHLWVA	BRCA, Urinary bladder cancer, NHL
330	SMSADVPLV	NSCLC, SCLC, BRCA, MCC, Melanoma, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, AML, NHL
129	SQADVIPAV	Urinary bladder cancer
270	SVLDQKILL	Melanoma, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, NHL
104	SVWFGPKEV	SCLC, Melanoma, Urinary bladder cancer, PC
192	SYITKPEKW	NSCLC
208	SYNPAENAVLL	NSCLC
345	SYNPLWLRI	NSCLC, RCC, GC
187	SYPTFFPRF	NSCLC, PrC
300	TLAQQPTAV	Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, NHL
297	TLFYSLREV	BRCA, Uterine Cancer, AML
176	TLGQIWDV	NSCLC, GC, Melanoma, Urinary bladder cancer, PC
259	TLITDGMRSV	RCC, CRC, OC, Esophageal Cancer, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer, PC
260	TLMDMRLSQV	SCLC, PrC, CLL, OC, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
298	TMAKESSIIGV	SCLC, Gallbladder Cancer, Bile Duct Cancer
110	TVGGSEILFEV	SCLC, Gallbladder Cancer, Bile Duct Cancer
111	TVMDIDTSGTFNV	SCLC, CRC, CLL, Melanoma, OC, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer, NHL
209	VFHPRQELI	NSCLC
261	VLFQEALWHV	Urinary bladder cancer
127	VLIGSNHSL	PC, BRCA, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, AML
186	VLLAQIIQV	Melanoma, OC, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
262	VLPNFLPYNV	NSCLC, SCLC, Brain Cancer, GC, BRCA, MCC, Melanoma, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile

		Duct Cancer, NHL, PC
114	VLSQVYSKV	SCLC
230	VLTEFTREV	NSCLC, SCLC, CLL, BRCA, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, NHL
263	VLYPSLKEI	RCC, BRCA, Uterine Cancer
1	VMAPFTMTI	SCLC, Melanoma, NHL
264	VMQDPEFLQSV	SCLC, CRC, PC, CLL, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer, NHL
115	VVLDDKDYFL	CLL
344	VYISSLALL	NSCLC, GC, CRC
265	WLIEDGKVVTV	Melanoma
117	YAFPKSITV	PC
178	YIFTTPKSV	AML
179	YIHNILYEV	CLL, NHL
341	YLAIGIHEL	SCLC
234	YLEPYLKEV	NSCLC, SCLC, BRCA, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, AML, NHL, PC
30	YLGEGPRMV	NSCLC, Melanoma, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
180	YLGPHIASVTL	Melanoma
121	YLITGNLEKL	NSCLC, CLL, BRCA, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer, NHL, PC
228	YLITSVELL	OC, NHL
181	YLLEKFVAV	NSCLC, SCLC, CLL, OC, Urinary bladder cancer, AML, NHL
269	YLMEGSYNKV	NSCLC, SCLC, PrC, BRCA, MCC, Melanoma, OC, Esophageal Cancer, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer
123	YLWDLDHGFAGV	NSCLC, SCLC, PrC, BRCA, Melanoma, OC, Esophageal Cancer, AML, NHL
31	YQMDIQQEL	SCLC
203	YYGILQEKI	NSCLC
213	YYNKVSTVF	NSCLC

NSCLC= non-small cell lung cancer, SCLC= small cell lung cancer, RCC= kidney cancer, CRC= colon or rectum cancer, GC= stomach cancer, HCC= liver cancer, PC= pancreatic cancer, PrC= prostate cancer, leukemia, BRCA=breast cancer, MCC=

Merkel cell carcinoma, OC= ovarian cancer, NHL= non-Hodgkin lymphoma, AML= acute myeloid leukemia, CLL= chronic lymphocytic leukemia.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 1, 14, 15, 41, 43, 58, 59, 60, 81, 121, 135, 139, 144, 176, 236, 248, 275, 276, 283, 286, 288, 289, 290, 291, 300, 302, 304, 308, 313, 316, 317, 325, 326, 329, 331, 334, 342, and 343 for the – in one preferred embodiment combined - treatment of pancreatic cancer.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to SEQ ID No. 6, 15, 16, 22, 26, 30, 34, 36, 47, 59, 65, 69, 70, 77, 80, 81, 88, 121, 123, 125, 127, 133, 137, 139, 169, 172, 176, 181, 186, 221, 223, 229, 230, 231, 232, 233, 234, 236, 237, 238, 244, 247, 249, 250, 251, 255, 260, 261, 266, 269, 271, 274, 275, 282, 285, 289, 290, 291, 293, 297, 301, 302, 304, 306, 310, 313, 316, 317, 319, 327, 328, 329, 330, 331, 332, 334, and 342 for the - in one preferred embodiment combined - treatment of colon cancer or renal cancer.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to SEQ ID No. 10, 14, 15, 22, 36, 39, 54, 55, 60, 72, 77, 81, 90, 96, 112, 116, 119, 121, 133, 137, 138, 148, 169, 170, 172, 177, 186, 187, 189, 192, 197, 198, 203, 206, 219, 221, 229, 230, 233, 234, 236, 255, 260, 270, 272, 275, 277, 278, 279, 281, 282, 285, 289, 291, 292, 295, 296, 297, 301, 302, 305, 308, 311, 313, 315, 316, 319, 321, 324, 328, 329, 333, 334, 335, 336, and 346 for the - in one preferred embodiment combined - treatment of kidney cancer.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to SEQ ID No. 14, 15, 16, 17, 36, 39, 47, 51, 54, 65, 88, 101, 123, 125, 133, 134, 135, 137, 141, 147, 161, 166, 169, 176, 179, 184, 186, 187, 189, 191, 192, 193, 194, 195, 196, 197, 199, 203, 206, 208, 214, 220, 221, 224, 229, 230, 231, 234, 238, 239, 244, 245, 250, 251, 255, 258, 259, 260, 268,

269, 270, 271, 272, 278, 279, 282, 295, 297, 302, 304, 305, 306, 309, 310, 311, 312, 313, 316, 317, 319, 321, 325, 327, 328, 329, 330, 331, 332, 333, 334, 336, 337, 338, 339, 340, 342, 343, 344, 345, and 347 for the - in one preferred embodiment combined - treatment of brain cancer.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to SEQ ID No. 172, 173, 240, 250, 287, 299, 302, 334, and 335 for the - in one preferred embodiment combined - treatment of CLL.

Similarly, the peptides as listed in Table 5B as above can form the basis for the - in one preferred embodiment combined - treatment of the diseases as indicated.

Thus, another aspect of the present invention relates to the use of the peptides according to the present invention for the - preferably combined - treatment of a proliferative disease selected from the group of HCC, brain cancer, kidney cancer, pancreatic cancer, colon or rectal cancer, and leukemia.

The present invention furthermore relates to peptides according to the present invention that have the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I or - in an elongated form, such as a length-variant - MHC class -II.

The present invention further relates to the peptides according to the present invention wherein said peptides (each) consist or consist essentially of an amino acid sequence according to SEQ ID NO: 1 to SEQ ID NO: 300.

The present invention further relates to the peptides according to the present invention, wherein said peptide is modified and/or includes non-peptide bonds.

The present invention further relates to the peptides according to the present invention, wherein said peptide is part of a fusion protein, in particular fused to the N-terminal

amino acids of the HLA-DR antigen-associated invariant chain (Ii), or fused to (or into the sequence of) an antibody, such as, for example, an antibody that is specific for dendritic cells.

The present invention further relates to a nucleic acid, encoding the peptides according to the present invention. The present invention further relates to the nucleic acid according to the present invention that is DNA, cDNA, PNA, RNA or combinations thereof.

The present invention further relates to an expression vector capable of expressing and/or expressing a nucleic acid according to the present invention.

The present invention further relates to a peptide according to the present invention, a nucleic acid according to the present invention or an expression vector according to the present invention for use in the treatment of diseases and in medicine, in particular in the treatment of diseases including cancer and autoimmune / inflammatory / immune pathological diseases.

The present invention further relates to antibodies against the peptides according to the present invention or complexes of said peptides according to the present invention with MHC, and methods of making these.

The present invention further relates to T-cell receptors (TCRs), in particular soluble TCR (sTCRs) and cloned TCRs engineered into autologous or allogeneic T cells, and methods of making these, as well as NK cells or other cells bearing said TCR or cross-reacting with said TCRs.

The antibodies and TCRs are additional embodiments of the immunotherapeutic use of the peptides according to the invention at hand.

The present invention further relates to a host cell comprising a nucleic acid according to the present invention or an expression vector as described before. The present invention further relates to the host cell according to the present invention that is an antigen presenting cell, and preferably is a dendritic cell.

The present invention further relates to a method for producing a peptide according to the present invention, said method comprising culturing the host cell according to the present invention, and isolating the peptide from said host cell or its culture medium.

The present invention further relates to said method according to the present invention, wherein the antigen is loaded onto class I or II MHC molecules expressed on the surface of a suitable antigen-presenting cell or artificial antigen-presenting cell by contacting a sufficient amount of the antigen with an antigen-presenting cell.

The present invention further relates to the method according to the present invention, wherein the antigen-presenting cell comprises an expression vector capable of expressing or expressing said peptide containing SEQ ID No. 1 to SEQ ID No.: 300, preferably containing SEQ ID No. 1 to SEQ ID No. 124, and SEQ ID No. 187 to SEQ ID No.: 218 or a variant amino acid sequence.

The present invention further relates to activated T cells, produced by the method according to the present invention, wherein said T cell selectively recognizes a cell which expresses a polypeptide comprising an amino acid sequence according to the present invention.

The present invention further relates to a method of killing target cells in a patient which target cells aberrantly express a polypeptide comprising any amino acid sequence according to the present invention, the method comprising administering to the patient an effective number of T cells as produced according to the present invention.

The present invention further relates to the use of any peptide as described, the nucleic acid according to the present invention, the expression vector according to the present invention, the cell according to the present invention, the activated T lymphocyte, the T cell receptor or the antibody or other peptide- and/or peptide-MHC-binding molecules according to the present invention as a medicament or in the manufacture of a medicament. Preferably, the medicament is active against cancer.

Preferably, said medicament is for a cellular therapy, a vaccine or a protein based on a soluble TCR or antibody.

The present invention further relates to a use according to the present invention, wherein said cancer cells are HCC, brain cancer, kidney cancer, pancreatic cancer, colon or rectal cancer or leukemia, and preferably HCC cells.

The present invention further relates to particular marker proteins and biomarkers based on the peptides according to the present invention, herein called “targets” that can be used in the diagnosis and/or prognosis of HCC. The present invention also relates to the use of these novel targets in the context of cancer treatment.

There are two classes of MHC-molecules, MHC class I and MHC class II. MHC molecules are composed of an alpha heavy chain and beta-2-microglobulin (MHC class I receptors) or an alpha and a beta chain (MHC class II receptors), respectively. Their three-dimensional conformation results in a binding groove, which is used for non-covalent interaction with peptides. MHC class I molecules can be found on most nucleated cells. They present peptides that result from proteolytic cleavage of predominantly endogenous proteins, defective ribosomal products (DRIPs) and larger peptides. MHC class II molecules can be found predominantly on professional antigen presenting cells (APCs), and primarily present peptides of exogenous or transmembrane proteins that are taken up by APCs during endocytosis, and are subsequently processed. Complexes of peptide and MHC class I are recognized by CD8-positive T cells bearing the appropriate TCR (T-cell receptor), whereas complexes

of peptide and MHC class II molecules are recognized by CD4-positive-helper-T cells bearing the appropriate TCR. It is well known that the TCR, the peptide and the MHC are thereby present in a stoichiometric amount of 1:1:1.

CD4-positive helper T cells play an important role in inducing and sustaining effective responses by CD8-positive cytotoxic T cells. The identification of CD4-positive T-cell epitopes derived from tumor associated antigens (TAA) is of great importance for the development of pharmaceutical products for triggering anti-tumor immune responses (Gnjatic S, et al. Survey of naturally occurring CD4+ T cell responses against NY-ESO-1 in cancer patients: correlation with antibody responses. Proc Natl Acad Sci U S A. 2003 Jul 22;100(15):8862-7). At the tumor site, T helper cells, support a cytotoxic T cell-(CTL-) friendly cytokine milieu Mortara L, et al. CIITA-induced MHC class II expression in mammary adenocarcinoma leads to a Th1 polarization of the tumor microenvironment, tumor rejection, and specific antitumor memory. Clin Cancer Res. 2006 Jun 1;12(11 Pt 1):3435-43) and attract effector cells, e.g. CTLs, NK cells, macrophages, granulocytes (Hwang ML, et al. Cognate memory CD4+ T cells generated with dendritic cell priming influence the expansion, trafficking, and differentiation of secondary CD8+ T cells and enhance tumor control. J Immunol. 2007 Nov 1;179(9):5829-38).

In the absence of inflammation, expression of MHC class II molecules is mainly restricted to cells of the immune system, especially professional antigen-presenting cells (APC), e.g., monocytes, monocyte-derived cells, macrophages, dendritic cells. In cancer patients, cells of the tumor have been found to express MHC class II molecules (Dengjel J, et al. Unexpected abundance of HLA class II presented peptides in primary renal cell carcinomas. Clin Cancer Res. 2006 Jul 15;12(14 Pt 1):4163-70).

Elongated (longer) peptides of the invention can act as MHC class II active epitopes. T-helper cells, activated by MHC class II epitopes, play an important role in orchestrating the effector function of CTLs in anti-tumor immunity. T-helper cell epitopes that trigger a T-helper cell response of the TH1 type support effector functions of CD8-positive killer T

cells, which include cytotoxic functions directed against tumor cells displaying tumor-associated peptide/MHC complexes on their cell surfaces. In this way tumor-associated T-helper cell peptide epitopes, alone or in combination with other tumor-associated peptides, can serve as active pharmaceutical ingredients of vaccine compositions that stimulate anti-tumor immune responses.

It was shown in mammalian animal models, e.g., mice, that even in the absence of CD8-positive T lymphocytes, CD4-positive T cells are sufficient for inhibiting manifestation of tumors via inhibition of angiogenesis by secretion of interferon-gamma (IFNγ).

There is evidence for CD4 T cells as direct anti-tumor effectors (Braumuller et al., 2013; Tran et al., 2014).

Since the constitutive expression of HLA class II molecules is usually limited to immune cells, the possibility of isolating class II peptides directly from primary tumors was not considered possible. However, Dengjel et al. were successful in identifying a number of MHC Class II epitopes directly from tumors (WO 2007/028574, EP 1 760 088 B1).

The antigens that are recognized by the tumor specific cytotoxic T lymphocytes, that is, the epitopes thereof, can be molecules derived from all protein classes, such as enzymes, receptors, transcription factors, etc. which are expressed and, as compared to unaltered cells of the same origin, usually up-regulated in cells of the respective tumor.

Since both types of response, CD8 and CD4 dependent, contribute jointly and synergistically to the anti-tumor effect, the identification and characterization of tumor-associated antigens recognized by either CD8+ T cells (ligand: MHC class I molecule + peptide epitope) or by CD4-positive T-helper cells (ligand: MHC class II molecule + peptide epitope) is important in the development of tumor vaccines.

For an MHC class I peptide to trigger (elicit) a cellular immune response, it also must bind to an MHC-molecule. This process is dependent on the allele of the MHC-molecule and specific polymorphisms of the amino acid sequence of the peptide. MHC-class-I-binding peptides are usually 8-12 amino acid residues in length and usually contain two conserved residues ("anchors") in their sequence that interact with the corresponding binding groove of the MHC-molecule. In this way each MHC allele has a “binding motif” determining which peptides can bind specifically to the binding groove.

In the MHC class I dependent immune reaction, peptides not only have to be able to bind to certain MHC class I molecules expressed by tumor cells, they subsequently also have to be recognized by T cells bearing specific T cell receptors (TCR).

The current classification of tumor associated antigens comprises the following major groups:

a) Cancer-testis antigens: The first TAAs ever identified that can be recognized by T cells belong to this class, which was originally called cancer-testis (CT) antigens because of the expression of its members in histologically different human tumors and, among normal tissues, only in spermatocytes/spermatogonia of testis and, occasionally, in placenta. Since the cells of testis do not express class I and II HLA molecules, these antigens cannot be recognized by T cells in normal tissues and can therefore be considered as immunologically tumor-specific. Well-known examples for CT antigens are the MAGE family members or NY-ESO-1.

b) Differentiation antigens: These TAAs are shared between tumors and the normal tissue from which the tumor arose; most are found in melanomas and normal melanocytes. Many of these melanocyte lineage-related proteins are involved in the biosynthesis of melanin and are therefore not tumor specific but nevertheless are widely used for cancer immunotherapy. Examples include, but are not limited to, tyrosinase and Melan-A/MART-1 for melanoma or PSA for prostate cancer.

c) Overexpressed TAAs: Genes encoding widely expressed TAAs have been detected in histologically different types of tumors as well as in many normal tissues, generally with lower expression levels. It is possible that many of the epitopes processed and

potentially presented by normal tissues are below the threshold level for T-cell recognition, while their overexpression in tumor cells can trigger an anticancer response by breaking previously established tolerance. Prominent examples for this class of TAAs are Her-2/neu, Survivin, Telomerase or WT1.

d) Tumor specific antigens: These unique TAAs arise from mutations of normal genes (such as β-catenin, CDK4, etc.). Some of these molecular changes are associated with neoplastic transformation and/or progression. Tumor specific antigens are generally able to induce strong immune responses without bearing the risk for autoimmune reactions against normal tissues. On the other hand, these TAAs are in most cases only relevant to the exact tumor on which they were identified and are usually not shared between many individual tumors. Tumor-specificity (or -association) of a peptide may also arise if the peptide originates from a tumor- (-associated) exon in case of proteins with tumor-specific (-associated) isoforms.

e) TAAs arising from abnormal post-translational modifications: Such TAAs may arise from proteins which are neither specific nor overexpressed in tumors but nevertheless become tumor associated by posttranslational processes primarily active in tumors. Examples for this class arise from altered glycosylation patterns leading to novel epitopes in tumors as for MUC1 or events like protein splicing during degradation which may or may not be tumor specific.

f) Oncoviral proteins: These TAAs are viral proteins that may play a critical role in the oncogenic process and, because they are foreign (not of human origin), they can evoke a T-cell response. Examples of such proteins are the human papilloma type 16 virus proteins, E6 and E7, which are expressed in cervical carcinoma.

For proteins to be recognized by cytotoxic T-lymphocytes as tumor-specific or -associated antigens, and to be used in a therapy, particular prerequisites must be fulfilled. The antigen should be expressed mainly by tumor cells and not, or in comparably small amounts, by normal healthy tissues. In a preferred embodiment, the peptide should be over-presented by tumor cells as compared to normal healthy tissues. It is furthermore desirable that the respective antigen is not only present in a type of tumor, but also in high concentrations (i.e. copy numbers of the respective

peptide per cell). Tumor-specific and tumor-associated antigens are often derived from proteins directly involved in transformation of a normal cell to a tumor cell due to their function, e.g. in cell cycle control or suppression of apoptosis. Additionally, downstream targets of the proteins directly causative for a transformation may be upregulated und thus may be indirectly tumor-associated. Such indirect tumor-associated antigens may also be targets of a vaccination approach (Singh-Jasuja et al., 2004). It is essential that epitopes are present in the amino acid sequence of the antigen, in order to ensure that such a peptide ("immunogenic peptide"), being derived from a tumor associated antigen, leads to an *in vitro* or *in vivo* T-cell-response.

Basically, any peptide able to bind an MHC molecule may function as a T-cell epitope. A prerequisite for the induction of an *in vitro* or *in vivo* T-cell-response is the presence of a T cell having a corresponding TCR and the absence of immunological tolerance for this particular epitope.

Therefore, TAAs are a starting point for the development of a T cell based therapy including but not limited to tumor vaccines. The methods for identifying and characterizing the TAAs are based on the use of T-cells that can be isolated from patients or healthy subjects, or they are based on the generation of differential transcription profiles or differential peptide expression patterns between tumors and normal tissues.

However, the identification of genes over-expressed in tumor tissues or human tumor cell lines, or selectively expressed in such tissues or cell lines, does not provide precise information as to the use of the antigens being transcribed from these genes in an immune therapy. This is because only an individual subpopulation of epitopes of these antigens are suitable for such an application since a T cell with a corresponding TCR has to be present and the immunological tolerance for this particular epitope needs to be absent or minimal. In a very preferred embodiment of the invention it is therefore important to select only those over- or selectively presented peptides against which a functional and/or a proliferating T cell can be found. Such a functional T cell is defined

as a T cell, which upon stimulation with a specific antigen can be clonally expanded and is able to execute effector functions ("effector T cell").

In case of TCRs and antibodies according to the invention the immunogenicity of the underlying peptides is secondary. For TCRs and antibodies according to the invention the presentation is the determining factor.

Both therapeutic and diagnostic uses against additional cancerous diseases are disclosed in the following more detailed description of the underlying proteins (polypeptides) of the peptides according to the invention.

Differential expression of COL18A1 was reported for bladder cancer, rhabdoid tumors and ovarian carcinoma and specific polymorphisms within the gene were shown to increase the risk for sporadic breast cancer (Fang et al., 2013; Gadd et al., 2010; Peters et al., 2005; Lourenco et al., 2006).

Changes in COPA gene expression and RNA editing were shown to be associated with hepatocellular carcinoma and an experimental study revealed anti-apoptotic effects of COPA in mesothelioma cells (Sudo et al., 2010; Qi et al., 2014; Wong et al., 2003).

The activity of CPB2 was shown to be significantly reduced in acute promyelocytic leukemia (Meijers et al., 2000).

CRP, an acute phase protein synthesized in the liver, was shown to be a prognostic marker in a variety of cancer types, amongst others renal cell carcinoma and multiple myeloma (Ljungberg, 2007; Fassas and Tricot, 2004).

CRYZ is a target gene of the tumor-suppressor p53 (Bansal et al., 2011). Its encoded protein zeta-crystallin was shown to directly interact with the mRNA of the anti-apoptotic molecule bcl-2 and to stabilize the over-expression of bcl-2 in T-cell acute lymphocytic leukemia (Lapucci et al., 2010).

Over-expression of CSRP2 is associated with de-differentiation of hepatocellular carcinoma (Midorikawa et al., 2002).

CYB5A encodes an enzyme which detoxifies carcinogenic molecules and is a prognostic factor for pancreatic cancer (Blanke et al., 2014; Giovannetti et al., 2014).

Increased expression levels of CYP27A1 are associated with endometrial carcinoma, breast cancer and colorectal cancer (Bergada et al., 2014; Nelson et al., 2013; Matusiak and Benya, 2007).

Over-expression of CYP2E1 was reported in colorectal cancer, specific polymorphisms are associated with bladder and lung cancer and in breast cancer cells (Ye et al., 2014; Patel et al., 2014; Deng et al., 2014; Leung et al., 2013).

CYP2J2 is an enzyme, which was shown to be over-expressed in a variety of human cancers, including esophageal, lung, breast, stomach, liver and colon cancer (Jiang et al., 2005; Narjoz et al., 2014).

CYP4F8 was shown to be highly expressed in prostate cancer (Vainio et al., 2011). CYP4F2 and CYP4F3 were both shown to be over-expressed in pancreatic ductal adenocarcinoma and CYP4F2 alone in ovarian cancer (Gandhi et al., 2013; Alexanian et al., 2012).

Expression of CYP4F11 was shown to be regulated by NF-κB and p53 (Kalsotra et al., 2004; Bell and Strobel, 2012; Goldstein et al., 2013).

Genetic variants of CYPAF12 are significantly associated with gemcitabine response in pancreatic cancer patients (Goldstein et al., 2013; Harris et al., 2014).

High levels of DAP3 correlate on the one hand with better responses to chemotherapy in gastric cancer and better clinical outcome in breast cancer, but on the other hand over-expression of DAP3 was reported in thyroid oncocytic tumors and invasive glioblastoma (Jia et al., 2014; Wazir et al., 2012; Jacques et al., 2009; Mariani et al., 2001).

PEX19 is essential for peroxisomal biogenesis, but was also shown to directly interact with p19ARF, ultimately leading to a retention of this factor in the cytoplasm and to an inactivation of p53 tumor-suppressive function (Sugihara et al., 2001).

DDX11, belonging to the DEAH family of DNA helicases, is highly expressed in advanced melanoma (Bhattacharya et al., 2012).

NME4 is a nucleoside diphosphate kinase, over-expressed in colon and gastric cancer, as well as in myelodysplastic syndrome, in the latter disease being associated with poor prognosis (Kracmarova et al., 2008; Seifert et al., 2005).

DENND5B acts as GDP-GTP exchange factor to activate Rab-GTPases (Yoshimura et al., 2010).

DIEXF was shown to mediate the non-proteasomal degradation of the tumor-suppressor p53 (Tao et al., 2013).

DOCK7 is a guanine nucleotide exchange factor, which was shown to be over-expressed in glioblastoma and to increase glioblastoma cell invasion in response to HGF by activating Rac-1 (Murray et al., 2014).

In hepatocellular carcinoma cell lines, DRG2 was shown to be down-regulated during chemotherapeutic drug induced apoptosis, and over-expression of DRG2 inhibits doxorubicin induced apoptosis in these cells (Chen et al., 2012a).

DROSHA, one of the two critical enzymes in microRNA biosynthesis, is over-expressed in a number of cancers including gastrointestinal tumors, breast cancer and cervical cancer and appears to enhance proliferation, colony formation and migration of tumor cells (Avery-Kiejda et al., 2014; Havens et al., 2014; Zhou et al., 2013b).

SNPs in the DUSP14 gene are associated with altered melanoma risk (Yang et al., 2014a; Liu et al., 2013b).

A whole exome sequencing study uncovered somatic mutations within the DYNC1H1 gene in patients with intra-ductal papillary mucinous neoplasm of the pancreas (Furukawa et al., 2011).

EEF2 protein was shown to be over-expressed in lung, esophageal, pancreatic, breast and prostate cancer, in glioblastoma multiforme and in non-Hodgkin's lymphoma and to play an oncogenic role in cancer cell growth (Oji et al., 2014; Zhu et al., 2014a).

Mutations within the gene of EFR3A were identified in colorectal adenoma samples (Bojjireddy et al., 2014; Zhou et al., 2013a).

EIF2B5 encodes one subunit of the translation initiation factor B. Single nucleotide polymorphisms in this gene were described to be associated with survival time in ovarian cancer (Goode et al., 2010).

EIF3A, the eukaryotic translation initiation factor 3, subunit A is over-expressed in cancers of breast, lung, cervix, esophagus, stomach and colon and was shown to be involved in cell cycle regulation (Dong and Zhang, 2006).

EIF4E is a potent oncogene elevated in up to 30% of human malignancies, including carcinomas of the breast, prostate, lung, head, and neck as well as in many leukemias and lymphomas (Carroll and Borden, 2013).

ELOVL2 was shown to be over-expressed in hepatocellular carcinoma (Jakobsson et al., 2006; Zekri et al., 2012).

EPRS encodes a multifunctional aminoacyl-tRNA synthetase, which was reported to be a tumor-associated antigen in colon cancer (Line et al., 2002).

EXOSC4 promotor activity is increased in hepatocellular carcinoma, due to DNA hypomethylation. EXOSC4 effectively and specifically inhibits cancer cell growth and cell invasive capacities (Drazkowska et al., 2013; Stefanska et al., 2014).

The hydrolytic enzyme FUCA2was found to be essential for H. pylori adhesion to human gastric cancer cells (Liu et al., 2009a).

GABRQ encodes the GABAA receptor theta subunit. GABA was shown to stimulate human hepatocellular carcinoma growth through the over-expressed GABAA receptor theta subunit (Li et al., 2012).

In squamous cell carcinoma over-expression of GALNT2 was reported to enhance the invasive potential of tumor cells by modifying O-glycosylation and EGFR activity (Lin et al., 2014; Hua et al., 2012a; Wu et al., 2011).

High levels of GGH have been associated with cellular resistance to anti-folates, in particular methotrexate and with poor prognosis in invasive breast cancer and pulmonary endocrine tumors (Schneider and Ryan, 2006; Shubbar et al., 2013; He et al., 2004).

GLUL is over-expressed in human breast carcinoma cells and astrocytomas (Zhuang et al., 2011; Collins et al., 1997; Christa et al., 1994; Cadoret et al., 2002).

GNPAT was reported to be implicated in growth inhibition and apoptosis induction in metastatic melanoma (Ofman et al., 2001; Qin et al., 2013).

Deletions in the chromosomal region of GOLGA4 have been reported in cervical carcinoma and in-frame mRNA fusion of GOLGA4 with PDGFRB in myeloproliferative neoplasms (Senchenko et al., 2003; Hidalgo-Curtis et al., 2010).

GPAM is expressed in human breast cancer, which is associated with changes in the cellular metabolism and better overall survival (Brockmoller et al., 2012).

High serum levels of GPT were reported to increase the risk of gastrointestinal cancer and are associated with carcinogenesis and recurrence in hepatitis C virus-induced hepatocellular carcinoma (Kunutsor et al., 2014; Tarao et al., 1997; Tarao et al., 1999).

GRB14 has been shown to be up-regulated in breast cancer, where high expression was significantly associated with better disease-free and overall survival (Huang et al., 2013; Balogh et al., 2012).

Single nucleotide polymorphisms in the GTF2H4 gene were reported to increase the risk to develop smoking-related lung cancer and papilloma virus-induced cervical cancer (Mydlikova et al., 2010; Buch et al., 2012; Wang et al., 2010).

Different studies suggest an important role of HSPA2 in disease progression of cervical cancer, renal cell carcinoma and bladder cancer. Polymorphisms within the gene are associated with the development of gastric cancer (Singh and Suri, 2014; Ferrer-Ferrer et al., 2013; Garg et al., 2010a; Garg et al., 2010b).

HSPA8 was shown to be over-expressed in esophageal squamous cell carcinoma. Furthermore, HSPA8 is over-expressed in multiple myeloma and colonic carcinoma and BCR-ABL1-induced expression of HSPA8 promotes cell survival in chronic myeloid leukemia (Dadkhah et al., 2013; Wang et al., 2013a; Chatterjee et al., 2013; Kubota et al., 2010; Jose-Eneriz et al., 2008).

MDN1 was described to be a candidate tumor suppressor gene, mutated in breast cancers of the luminal B type (Cornen et al., 2014).

MIA3, also known as transport and Golgi organization protein 1 (TANGO), was reported to be down-regulated in colon and hepatocellular carcinomas and to play a tumor-suppressive role in these entities (Arndt and Bosserhoff, 2007). In contrast, a study in oral squamous cell carcinoma indicates an association of MIA3 expression with tumor progression, metastasis formation and clinical stage, pointing towards an oncogenic action of MIA3 (Sasahira et al., 2014).

CPSF6 was identified as one gene within a “poised gene cassette” associated with significant differences in metastatic and invasive potential of several tumor types, like breast, colon, liver, lung, esophageal and thyroid cancer (Yu et al., 2008).

Low levels of MPDZ expression were reported to be associated with poor prognosis in breast cancer patients (Martin et al., 2004).

NAA35, also known as MAK10, encodes the N(alpha)-acetyltransferase 35, NatC auxiliary subunit. In patients with esophageal squamous cell carcinoma a highly cancer enriched chimeric GOLM1-MAK10 RNA was detected, which encodes a secreted fusion protein, potentially useful as molecular marker (Zhang et al., 2013b).

NAV2 was shown to be specifically expressed in a group of colon cancers and treatment of colon-cancer cells with antisense oligonucleotides for NAV2 induced apoptosis (Ishiguro et al., 2002).

NCSTN over-expression is indicative of worse overall survival in estrogen-receptor-negative breast cancer patients and high levels of Nicastrin and Notch4 were detected in endocrine therapy resistant breast cancer cells, where their activation ultimately drives invasive behavior (Sarajlic et al., 2014; Lombardo et al., 2014).

NKD1 protein is reduced, but NKD1 mRNA is elevated in non-small cell lung cancer, the former correlating with increased invasive potential and poor prognosis (Zhang et al., 2011). NKD1 mRNA was also found to be elevated in cells from human colon tumors (Yan et al., 2001; Zhang et al., 2011).

In esophageal cancer, NUDC was reported to be associated with nodal metastasis, whereas over-expression of NUDC in prostate cancer cells leads to a block in cell division (Hatakeyama et al., 2006; Lin et al., 2004).

A study investigating the role of the Notch signaling pathway in ovarian cancer reported a higher frequency of RFNG expression in adenoma compared to carcinoma (Gu et al., 2012; Hopfer et al., 2005).

RINT1 is described as an oncogene in glioblastoma multiforme and as a moderately penetrant cancer susceptibility gene seen in breast cancer as well as in Lynch syndrome-related cancers (Ngeow and Eng, 2014; Quayle et al., 2012).

High expression of RORC was found to be associated with longer metastasis-free survival in breast cancer. Attenuated RORC expression in somatotroph adenomas is associated with increased tumor size and a blunted clinical response to somatostatin treatment (Cadenas et al., 2014; Lekva et al., 2013).

RPL17 was reported to promote multidrug resistance by suppressing drug-induced apoptosis (Shi et al., 2004b).

Increased expression of RPS29 was reported in gastric and colorectal cancer (Takemasa et al., 2012; Sun et al., 2005).

SAMM50 encodes a component of the Sorting and Assembly Machinery (SAM) of the mitochondrial outer membrane, which functions in the assembly of beta-barrel proteins into the outer mitochondrial membrane. A growth promoting chimeric mRNA (SAMM50-

PARVB) was detected in breast and ovarian cancer cells and in a number of samples from breast, stomach, colon, kidney and uterus cancer (Plebani et al., 2012).

SERPINF2 encodes the major inhibitor of plasmin, which degrades fibrin and various other proteins. The plasma level of the plasmin-alpha 2-plasmin inhibitor complex was shown to be a predictor of survival in non-small cell lung carcinoma and low activity of alpha 2-antiplasmin has been observed in the blood of the patients with prostatic carcinoma (Zietek et al., 1996; Taguchi et al., 1996).

Over-expression of SF3B3 is significantly correlated with overall survival and endocrine resistance in estrogen receptor-positive breast cancer (Gokmen-Polar et al., 2014).

Protein levels of SHC1 are elevated in prostate, metastatic breast, ovarian and thyroid cancer and different isoforms and are thought to function as a primary adaptor protein for mediating the mitogenic signals of steroids at the non-genomic level (Alam et al., 2009; Rajendran et al., 2010).

AMACR is used as a biomarker in prostate cancer, since it is highly over-expressed in this entity (Wu et al., 2014). Furthermore, it is used as an immunohistochemical marker for the diagnosis of renal cell carcinoma (Ross et al., 2012).

Experimental data suggest that C1QTNF3 expression may play a role in osteosarcoma tumor growth, associated with activation of the ERK1/2 signaling pathway and that it is a novel anti-apoptotic adipokine that protects mesenchymal stem cells from hypoxia/serum deprivation-induced apoptosis through the PI3K/Akt signaling pathway (Hou et al., 2014; Akiyama et al., 2009).

GPC3 is expressed by most hepatocellular carcinomas. Two therapeutic approaches for HCC that target GPC3 are currently being tested in phase II clinical trials: a humanized GPC3 monoclonal antibody and a vaccine that consists of two GPC3-derived peptides. The peptides used in the latter study are distinct from the peptide presented in this

document. GPC3 expression has also been identified in all yolk sac tumors, some squamous cell carcinomas of the lung and clear cell carcinomas of the ovary (Filmus and Capurro, 2013; Kandil and Cooper, 2009).

MAGEB2 is classified as cancer testis antigen, since it is expressed in testis and placenta, and in a significant fraction of tumors of various histological types, amongst others multiple myeloma and head and neck squamous cell carcinoma (Pattani et al., 2012; van et al., 2011).

MAPKAPK5 encodes a tumor suppressor and member of the serine/threonine kinase family. MAPKAPK5 was shown to be under-expressed in colorectal cancer, leading to an increased activity of the myc oncoprotein and to decrease cancer formation by suppressing oncogenic ras activity in a murine model of hematopoietic cancer (Yoshizuka et al., 2012; Kress et al., 2011).

Over-expression of USP14 is associated with increased tumor cell proliferation and poor prognosis in epithelial ovarian, non-small cell lung and colorectal cancer (Wang et al., 2015; Wu et al., 2013a; Shinji et al., 2006).

C4A has been described as a biomarker for polycystic ovary syndrome and endometrial cancer and experimental data suggest that C4 can mediate cancer growth (Galazis et al., 2013; Rutkowski et al., 2010).

CAPZB was reported to be over-expressed in human papillomaviruses 18-positive oral squamous cell carcinomas and was identified as prostate cancer susceptibility locus (Lo et al., 2007; Nwosu et al., 2001).

Single nucleotide polymorphisms within the gene for CFHR5 are associated with event-free survival in follicular lymphoma (Charbonneau et al., 2012).

CLIP1 encodes the CAP-GLY domain containing linker protein 1, which links endocytic vesicles to microtubules. This gene is highly expressed in Reed-Sternberg cells of Hodgkin disease and breast cancer and appears to be implicated in the migration and invasion of breast cancer and pancreatic cancer cells (Sun et al., 2013; Suzuki and Takahashi, 2008; Li et al., 2014a; Sun et al., 2012).

CLU may inhibit tumor progression, whereas in advanced neoplasia, it may offer a significant survival advantage in the tumor by suppressing many therapeutic stressors and enhancing metastasis. CLU has been shown to play a critical role in prostate cancer pathogenesis, to regulate the aggressive behavior of human clear renal cell carcinoma cells through modulating ERK1/2 signaling and MMP-9 expression and to confer resistance to treatment in advanced stages of lung cancer (Trougakos, 2013; Panico et al., 2009; Takeuchi et al., 2014; Wang et al., 2014).

The fusion gene SEC16A-NOTCH1 was reported as first recurrent fusion gene in breast cancer (Edwards and Howarth, 2012).

Recurrent deletion of the SHQ1 gene has been observed in prostate and cervical cancer, implicating a tumor-suppressive role of SHQ1 (Krohn et al., 2013; Lando et al., 2013).

In clear cell renal cell carcinomas and bladder cancer high SLC16A1 expression is associated with poor prognostic factors and predicts tumor progression. In colorectal cancer single nucleotide polymorphisms in the SLC16A1 gene may affect clinical outcomes and can be used to predict the response to adjuvant chemotherapy (Kim et al., 2015; Fei et al., 2014a; Fei et al., 2014a).

Glioblastoma have been shown to release glutamate at high levels, which may stimulate tumor cell proliferation and facilitates tumor invasion, and to down-regulate SLC1A2, which correlated with higher tumor grade, implicating its potential role in glial tumor progression. Furthermore, in gastric cancer a fusion gene of SLC1A2 with CD44 has

been detected and may represent a class of gene fusions that establish a pro-oncogenic metabolic milieu favoring tumor growth and survival (Tao et al., 2011; de Groot et al., 2005).

High expression of SLC3A2 is associated with tumor growth, biological aggressiveness, and survival of patients with biliary tract cancer and significantly contributes to poor prognosis of non-small cell lung cancer patients through promoting cell proliferation via the PI3K/Akt pathway. Furthermore, over-expression of SLC3A2 together with integrin ß1, integrin ß3 and Fak is associated with the progression and liver metastases of colorectal cancer (Kaira et al., 2014; Fei et al., 2014b; Sun et al., 2014).

Evidences of SLC9A3R1 involvement in cancer development are present in hepatocellular carcinoma, schwannoma, glioblastoma, colorectal cancer and particularly in breast cancer (Saponaro et al., 2014).

NFYC has been reported to promote the expression of oncogenes in gastric cancer and prostate cancer cells (Zhang et al., 2014a; Gong et al., 2013).

THY1 is a candidate tumor suppressor gene in nasopharyngeal carcinoma bearing anti-invasive activity (Lung et al., 2010).

TIMM17A is over-expressed in 21T breast cancer cells and mRNA expression in breast cancer tissues was correlated with tumor progression (Xu et al., 2010).

TMEM209 is widely expressed in lung cancer (Fujitomo et al., 2012).

TNK2 also known as ACK1 tyrosine kinase is activated, amplified or mutated in a wide variety of human cancers. The de-regulated kinase is oncogenic and its activation correlates with progression to metastatic stage. ACK1 inhibitors have shown promise in pre-clinical studies (Mahajan and Mahajan, 2013).

TRIM55 encodes a RING zinc finger protein which associates transiently with microtubules, myosin and titin during muscle sarcomere assembly and is also involved in signaling from the sarcomere to the nucleus (Pizon et al., 2002).

RNA interference of Ufd1 protein can sensitize a hydroxycamptothecin-resistant colon cancer cell line SW1116/HCPT to hydroxyl-camptothecin (Chen et al., 2011a; Chen et al., 2011c).

In colorectal cancer the UGT1A1 gene is silenced through methylation and thus is regarded as the target point of research for irinotecan (CPT-11) drug resistance and control mechanisms for the reversal of drug resistance (Xie et al., 2014).

UGT1A10 is expressed in gastric and biliary tissue (Strassburg et al., 1997) and its over-expression significantly increased the cytotoxicity of the antitumor agent 5-dimethylaminopropylamino-8-hydroxytriazoloacridinone C-1305 (Pawlowska et al., 2013). Furthermore UGT1A10 catalyzes the glucuronidation of xenobiotics, mutagens, and reactive metabolites and thus acts as indirect antioxidant. Xenobiotic (XRE) and antioxidant (ARE) response elements were detected in the promoters of UGT1A8, UGT1A9, and UGT1A10 (Kalthoff et al., 2010).

UGT1A8 is primarily expressed in the gastrointestinal tract (Gregory et al., 2003) and mRNA expression is up-regulated upon treatment with chemo-preventive agent sulforaphane (SFN) (Wang et al., 2012).

UGT1A7 haplotype is associated with an increased risk of hepatocellular carcinoma in hepatitis B carriers (Kong et al., 2008).

UGT1A6 is over-expressed in breast cancer cells resistant to methotrexate (de Almagro et al., 2011) and induced by β-Naphthoflavone a putative chemo-preventive agent (Hanioka et al., 2012).

UGT1A9 is mainly expressed in liver and kidneys (Gregory et al., 2003). UGT1A9 germline polymorphisms are potential predictors for prostate cancer recurrence after prostatectomy (Laverdiere et al., 2014).

UGT1A4 promoter and coding region polymorphisms lead to a variability in the glucuronidation of anastrozole, an aromatase inhibitor for breast cancer patients (Edavana et al., 2013).

UPF1 is part of the nonsense-mediated mRNA decay (NMD) machinery and may have a functional role in prostate cancer progression and metastasis (Yang et al., 2013). Further the UPF1 RNA surveillance gene is commonly mutated in pancreatic adenosquamous carcinoma (Liu et al., 2014).

UQCRB is a subunit of mitochondrial complex III. Inhibition of UQCRB in tumor cells suppresses hypoxia-induced tumor angiogenesis (Jung et al., 2013). Two SNPs in the 3' untranslated region of UQCRB are candidates as prognostic markers for colorectal cancer (Lascorz et al., 2012).

Copy number alterations of USO1 correlated with differential gene expression in superficial spreading melanoma compared to nodular melanoma (Rose et al., 2011).

Significant reductions in both USP10 and SIRT6 protein expression was detected in human colon cancers (Lin et al., 2013).

UTP18 also alters translation to promote stress resistance and growth, and is frequently gained and over-expressed in cancer (Yang et al., 2014b).

VARS rs2074511 polymorphism was associated with survival in patients with triple negative type breast cancer and thus may be considered as a prognostic factor for survival in patients with early breast cancer (Chae et al., 2011).

VMP1, a stress-induced autophagy-associated protein, is also induced by the oncogene KRAS (Lo Re et al., 2012). VMP1 is over-expressed in poorly differentiated human pancreatic cancer as a response to chemotherapeutic drugs (Gilabert et al., 2013). A significant down-regulation of VMP1 was found in human HCC tissues and closely correlated with multiple tumor nodes, absence of capsular formation, vein invasion and poor prognosis of HCC (Guo et al., 2012).

WDR26 protects myocardial cells against oxidative stress (Feng et al., 2012).

ZC3H7A is part of the CCCH zinc finger protein family known as regulators of macrophage activation (Liang et al., 2008). ZC3H7A was found to have higher allele frequencies of functional mutations in the metastatic tumor of pancreatic ductal adenocarcinoma (Zhou et al., 2012).

FASN is a fatty acid synthase and involved in the enhanced lipid synthesis in different types of cancer, including breast, pancreatic, prostate, liver, ovarian, colon and endometrial cancer (Wu et al., 2014; Zhao et al., 2013).

FGG is up-regulated in hepatocellular carcinoma as well as in prostate, lung and breast cancers (Vejda et al., 2002; Zhu et al., 2009).

FMO5 is a monooxygenase that is the dominant liver-specific FMO, and it is up-regulated in estrogen receptor alpha-positive breast tumors (Bieche et al., 2004; Zhang and Cashman, 2006).

HADHA mRNA is reduced with the progression of de-differentiation in HCC (Tanaka et al., 2013) and in estrogen receptor alpha-negative breast tumors (Mamtani and Kulkarni, 2012).

Genetic variation in the HAL gene might play a role in the development of skin cancer (Welsh et al., 2008).

HLTF is a member of the SWI/SNF family of transcriptional regulators with helicase and E3 ubiquitin ligase activity and was found to be inactivated by hypermethylation in colon, gastric, uterine, bladder and lung tumors (Debauve et al., 2008; Castro et al., 2010; Garcia-Baquero et al., 2014).

HDAC10 is a histone deacetylase and transcriptional regulator. Expression of HDAC10 was significantly decreased in gastric cancer tissues as compared with adjacent tissues (Jin et al., 2014). HDAC10 is inversely related to lymph node metastasis in human patients with cervical squamous cell carcinoma (Song et al., 2013). HDAC10 is hypermethylated in malignant adrenocortical tumors (Fonseca et al., 2012). HDAC10 levels are increased in chronic lymphocytic leukemia (Wang et al., 2011). HDAC10-589C>T promoter polymorphism was significantly associated with HCC occurrence among chronic HBV patients as well as HCC acceleration among chronic HBV patients (Park et al., 2007). Reduced expression of class II histone deacetylase genes is associated with poor prognosis in lung cancer patients (Osada et al., 2004).

Low HIP1R expression is strongly associated with poor outcome in diffuse large B-cell lymphoma patients (Wong et al., 2014).

HM13 is a signal peptide peptidase and affected cell viability in colorectal adenoma (Sillars-Hardebol et al., 2012).

Serum HPR levels in patients with malignant lymphoma were significantly higher than in non-diseased control groups and HPR expression increased with disease progress (Epelbaum et al., 1998). HPR expression parallels increased malignant potential in breast cancers and HPR-positive breast cancers are more likely to recur after primary resection and are associated with shorter disease-free intervals (Shurbaji et al., 1991).

A variant (rs932335) in the HSD11B1 gene is associated with colorectal cancer and breast cancer (Feigelson et al., 2008; Wang et al., 2013b).

HSD17B6 expression in tissues from prostate cancer patients undergoing androgen deprivation therapy (ADT) was significantly higher than that in tissues of untreated individuals (Ishizaki et al., 2013).

HSPE1 is a mitochondrial chaperonin with functions in protein folding and cell signaling (NF-kappaB and WNT signaling). Increased Hsp10 levels have been found in tumor cells in large bowel cancer, exocervical cancer, prostate cancer, mantle cell lymphoma, and serous ovarian cancer. In bronchial carcinogenesis, decreased levels of Hsp10 have been reported (David et al., 2013).

Ovarian carcinoma xenografts transplanted into the flanks of nude mice and treated with paclitaxel showed a diminished IDI1 expression compared to untreated xenograft (Bani et al., 2004).

IGFBPL1 is a regulator of insulin-growth factors and is down-regulated in breast cancer cell lines by aberrant hypermethylation. Methylation in IGFBPL1 was clearly associated with worse overall survival and disease-free survival (Smith et al., 2007).

The androgen-sensitive microsome-associated protein IKBKAP modulated the expression of prostate epithelial and neuronal markers, attenuated proliferation through an androgen receptor-dependent mechanism, and co-regulated androgen receptor-mediated transcription in LNCaP prostate adenocarcinoma cells (Martinez et al., 2011).

INTS8 is part of a marker panel that discriminates gastric carcinomas from adjacent noncancerous tissues (Cheng et al., 2013).

A IRS2-derived peptide pIRS-21097-1105 was presented on HLA-A2(+) melanomas and breast, ovarian, and colorectal carcinomas (Zarling et al., 2014). IRS-2 1057 DD genotype and D allele were significantly associated with HCC risk (Rashad et al., 2014).

ITGA7 is the alpha chain of the laminin-1 receptor dimer integrin alpha-7/beta-1. ITGA7 is a tumor-suppressor gene that is critical for suppressing the growth of malignant tumors. Mutational analysis revealed *ITGA7* mutations in prostate cancer, hepatocellular carcinoma, soft tissue leiomyosarcoma, and glioblastoma multiforme. ITGA7 was down-regulated in non-metastatic prostate cancer and leiomyosarcoma (Tan et al., 2013).

ITIH4 was down-regulated in several tumor tissues including colon, stomach, ovary, lung, kidney, rectum and prostate (Hamm et al., 2008). Low serum ITIH4 levels are associated with shorter survival in HBV-associated HCC patients (Noh et al., 2014). Significantly increased ITIH4 serum concentrations were observed in breast cancer and ITIH4 serum levels were significantly decreased after surgery (van, I et al., 2010).

A missense mutation was identified in SHKBP1, which acts downstream of FLT3, a receptor tyrosine kinase mutated in about 30% of AML cases (Greif et al., 2011). SHKBP1 is one of several potential protein biomarker candidates for classifying well-differentiated small intestine neuroendocrine tumors (WD-SI-NETs) at different stage of disease (Darmanis et al., 2013).

KLB expression is elevated in HCC tissues compared to matched non-tumor tissue (Poh et al., 2012).

The LBP polymorphism rs2232596 is associated with a significantly increased risk of colorectal carcinoma in Han Chinese (Chen et al., 2011b). LBP is a candidate serum biomarker in ovarian carcinoma (Boylan et al., 2010). LBP was reduced significantly after treatment with chemotherapy in small-cell lung carcinoma patients (Staal-van den Brekel AJ et al., 1997).

LBR mRNA expression was directly associated with tumor grade and Nottingham Prognostic Index in breast cancer (Wazir et al., 2013). LBR is heavily expressed in papillary thyroid carcinoma cells, but an abnormal folding of the protein might explain its lack of immunohistochemical reactivity and be associated with an anomalous folding of the nuclear membrane (Recupero et al., 2010).

LEPR dysregulation has been reported in a variety of malignant cells including colon cancer, hepatocellular carcinoma, endometrial cancer, thyroid cancer, breast cancer and lung cancer (Ntikoudi et al., 2014; Surmacz, 2013; Uddin et al., 2011).

LIG1 single-nucleotide polymorphisms are associated with the risk of lung cancer, endometrial cancer and glioma (Doherty et al., 2011; Lee et al., 2008; Liu et al., 2009b).

LRPPRC expression in gastric cancer tissues is significantly higher than that in paired control tissue (Li et al., 2014b). LRPPRC levels serve as a prognosis marker of patients with prostate adenocarcinomas (PCA), and patients with high LRPPRC levels survive a shorter period after surgery than those with low levels of LRPPRC (Jiang et al., 2014). LRPPRC is abundantly expressed in various types of tumors, such as lung adenocarcinoma, esophageal squamous cell carcinoma, stomach, colon, mammary and endometrial adenocarcinoma, and lymphoma (Tian et al., 2012).

MANEA expression is regulated by androgens in prostate cancer cells (Romanuik et al., 2009).

OPLAH is expressed in lung, breast, kidney, colon and ovary normal and tumor tissues and OPLAH levels are significantly higher in normal specimens than tumors for individual patients (Srivenugopal and Ali-Osman, 1997).

ORM2 glycoforms provide valuable information for differentiation between primary and secondary liver cancer (Mackiewicz and Mackiewicz, 1995). ORM2 levels in plasma

were confirmed to be significantly elevated in patients suffering from colorectal carcinoma compared with the controls (Zhang et al., 2012). Fucosylated glycoform ORM2 levels were significantly higher in adenocarcinoma lung cancer cases compared to controls (Ahn et al., 2014). ORM2 is a putative biomarkers for early diagnosis of cholangiocarcinoma (Rucksaken et al., 2012).

Increased tetrahydrobiopterin levels result in an enhancement of PAH activity and PAH protein in human hepatoma cells (McGuire, 1991).

PARP14 is highly expressed in myeloma plasma cells and associated with disease progression and poor survival. PARP14 is critically involved in JNK2-dependent survival. PARP14 was found to promote the survival of myeloma cells by binding and inhibiting JNK1 (Barbarulo et al., 2013).

PC levels are elevated in liver tumors and lung cancer (Chang and Morris, 1973; Fan et al., 2009).

Increased PCNT levels and centrosomal abnormalities have been described in a variety of hematologic malignancies and solid tumors, including AML, CML, mantle cell lymphoma, breast cancer and prostate cancer (Delaval and Doxsey, 2010).

PIGN is a cancer chromosomal instability (CIN)-suppressor gene that is subject to frequent copy number loss in CIN(+) colorectal cancer (Burrell et al., 2013).

PIPOX expression varied according to subtype of breast cancer, with HER-2 type tumors showing elevated expression and triple negative breast cancer subtype showing decreased expression. Tumoral PIPOX negativity was associated with shorter disease-free survival (Yoon et al., 2014). PIPOX was reduced in prostate tumors and reduced the oncogenic potential of prostate cells by metabolizing sarcosine (Khan et al., 2013).

Increased PSMD4 levels were detected in colon cancer, myeloma and hepatocellular carcinoma (Arlt et al., 2009; Midorikawa et al., 2002; Shaughnessy, Jr. et al., 2011).

PLIN2 is significantly increased in patients with clear cell and papillary renal cell carcinoma compared with controls. The preoperative urinary concentrations of PLIN2 reflects the tumor size and stage (Morrissey et al., 2014). PLIN2 expression is significantly higher in lung adenocarcinoma specimens than in normal tissues and lung squamous cell carcinomas (Zhang et al., 2014b).

PLK4 frequently undergoes rearrangement or loss in human cancers, at a particularly high rate in hepatocellular carcinomas, but also in colorectal cancer, head and neck cancer (Swallow et al., 2005). PLK4 is over-expressed in breast cancer (Marina and Saavedra, 2014).

QARS is a member of the aminoacyl-tRNA synthetases (ARS) and charges tRNAs with glutamine. ARS expression and polymorphisms are associated with breast cancer and glioblastoma (He et al., 2014b; Kim et al., 2012).

The methylated PMF1 gene is a diagnostic and prognostic biomarker for patients with bladder cancer (Kandimalla et al., 2013).

Several human tumors and hematologic malignancies up-regulated PON2, including thyroid gland, prostate, pancreas, testis, endometrium/uterus, liver and kidney cancer, lymphoid tissues, urinary bladder tumors, ALL and CML, and such over-expression provided resistance to different chemotherapeutics (imatinib, doxorubicine, staurosporine, or actinomycin) (Witte et al., 2011).

PRKAR2A is a regulatory subunit of protein kinase A. PRKAR2A markedly increased survival of prostate cancer cells lines treated with Taxol and Taxotere (Zynda et al., 2014). PRKAR2A is over-expressed in lung adenocarcinoma (Bidkhori et al., 2013).

PRPF6 is a member of the tri-snRNP (small ribonucleoprotein) spliceosome complex that drives colon cancer proliferation by preferential splicing of genes associated with growth regulation (Adler et al., 2014). PRPF6 is over-expressed in lung adenocarcinoma (Bidkhori et al., 2013).

PSMC4 is significantly and coherently up-regulated in prostate carcinoma cells compared with the corresponding adjacent normal prostate tissue (Hellwinkel et al., 2011).

QPRT expression increases with malignancy in glioma and, in recurrent glioblastomas after radiochemotherapy, QPRT expression is associated with a poor prognosis (Sahm et al., 2013). QPRT is a potential marker for the immunohistochemical screening of follicular thyroid nodules (Hinsch et al., 2009).

RABGGTB is over-expressed in chemotherapy-refractory diffuse large B-cell lymphoma (Linderoth et al., 2008).

RAD21 is over-expressed in gastrointestinal tumors, colorectal carcinoma, advanced endometrial cancer, prostate cancer and breast cancer (Atienza et al., 2005; Deb et al., 2014; Porkka et al., 2004; Supernat et al., 2012; Xu et al., 2014).

RAD23B has a potential role in breast cancer progression (Linge et al., 2014). The single nucleotide polymorphism RAD23B rs1805329 was significantly associated with development and recurrence of HCC in Japanese patients with HCV (Tomoda et al., 2012).

RASAL2 is a RAS-GTPase-activating protein with tumor suppressor functions in estrogen receptor-positive breast cancer, ovarian cancer and lung cancer (Li and Li, 2014; Huang et al., 2014). In contrast, RASAL2 is oncogenic in triple-negative breast cancer and drives mesenchymal invasion and metastasis (Feng et al., 2014a).

Depletion of RNMT effectively and specifically inhibits cancer cell growth and cell invasive capacities in different types of cancer, inclusing liver cancer (Stefanska et al., 2014).

Over-expression of ROCK1 or mutations in the ROCK1 gene that lead to an elevated kinase activity have been reported for several cancers, including lung cancer, gastric carcinoma, CML and AML (Rath and Olson, 2012).

RPL10A is a c-Myc targeted gene and may contribute to hepatocyte transformation (Hunecke et al., 2012).

Inv(3) and t(3;3) breakpoints, which are associated with a particularly poor prognosis in myeloid leukemia or myelodysplasia, cluster in a region that is located centromeric and downstream of the RPN1 gene (Wieser, 2002).

RRBP1 is over-expressed in lung cancer and breast cancer (Telikicherla et al., 2012; Tsai et al., 2013).

SCFD1 expression is increased in erosive gastritis, which is linked to gastric carcinoma (Galamb et al., 2008).

ABCB1 encodes P-glycoprotein (P-gp) which is expressed in normal cells of various organs such as intestine, liver, kidney, brain, and placenta. P-gp overexpression and genetic polymorphisms have been detected in colorectal carcinoma, tumors derived from the adrenal gland, lung cancer and ALL (Zhang et al., 2013a; Fojo et al., 1987; Gervasini et al., 2006; Jamroziak et al., 2004).

ABCB10 encodes for an ABC transporter of the sub-family B (MDR/TAP). ABCB10 was shown to be involved in the cisplatin resistance of KCP-4 human epidermoid carcinoma cells (Oiso et al., 2014).

The expression of ABCB11 was shown to be up-regulated in the pancreatic ductal adenocarcinoma, one of the most drug-resistant cancers. Thus it may contribute to the generally poor treatment response of this cancer (Mohelnikova-Duchonova et al., 2013).

The up-regulated expression of ABCC2 in primary fallopian tube carcinomas is associated with poor prognosis (Halon et al., 2013).

ABCC6 was down-regulated in colorectal cancer of non-responders to palliative chemotherapy (Hlavata et al., 2012). In contrast, it was up-regulated in the gemcitabine-resistant human NSCLC A549 cells (Ikeda et al., 2011).

The expression of ACACA was shown to be up-regulated in numerous human cancers, such as breast, prostate and liver carcinoma and correlated with enhanced lipogenesis of cancer cells. The various ACACA inhibitors showed a therapeutical effect in treatment of cancer cell lines by suppression of cell proliferation and inducing of cell death through apoptosis (Zu et al., 2013).

ACLY is aberrantly expressed in various tumors, such as breast, liver, colon, lung and prostate cancers, and is correlated reversely with tumor stage and differentiation (Zu et al., 2012).

ACSL3 is over-expressed in lung cancer and based on preclinical investigation is a promising new therapeutic target in lung cancer (Pei et al., 2013). The up-regulated expression of ACSL3 can serve as a potential biomarker of estrogen receptor-specific breast cancer risk (Wang et al., 2013c).

ACSL4 is over-expressed in estrogen receptor-negative breast tumors and androgen receptor-negative breast and prostate tumors. The loss of steroid hormone sensitivity was associated with induction of ACSL4 expression (Monaco et al., 2010). The onset up-regulation of ACSL4 was shown to occur during the transformation from adenoma to adenocarcinoma (Cao et al., 2001).

The methylation of ACSS3 was found to be associated with at least one of the classical risk factors, namely age, stage or MYCN status in neuroblastoma (Decock et al., 2012).

The deletion of ADSSL1 was frequently observed in carcinogen-induced mouse primary lung adenocarcinomas, mouse and human lung adenocarcinomas cell lines and associated with a more extensive chromosome instability phenotype in the primary mouse lung tumors (Miller et al., 2009).

AGFG2 was identified to be one of 14 prognostic gene candidates in identifying cases of hormone receptor-negative or triple-negative breast cancers likely to remain free of metastatic relapse (Yau et al., 2010).

AGT is a very potent anti-angiogenic factor, which was shown to exert anti-tumoral effects in vitro and in vivo (Bouquet et al., 2006). In transgenic mice, the over-expression of human AGT was shown to decrease angiogenesis and thus delaying tumor progression of hepatocarcinoma (Vincent et al., 2009).

AKR1C4 encodes for a human aldo-keto reductase family 1 member C4 and catalyzes the reduction of retinaldehyde to retinol (Ruiz et al., 2011). Thus, the depletion of retinaldehyde down-regulates the biosynthesis of retinoic acid and is followed by blockage of retinoid signaling, which favors tumor progression (Tang and Gudas, 2011; Ruiz et al., 2012)

The expression of ALDH1L1 was shown to be down-regulated in HCC and gliomas. The down-regulation of ALDH1L1 in those cancers was associated with poorer prognosis and more aggressive phenotype (Rodriguez et al., 2008; Chen et al., 2012b)

The expression of ALG3 was shown to be enhanced in esophageal squamous cell carcinoma and cervical cancer (Shi et al., 2014; Choi et al., 2007). In esophageal

squamous cell carcinoma the increased expression of ALG3 correlated with lymph node metastasis (Shi et al., 2014).

ANKS1A was identified as a novel target of Src family kinases which are known to be implicated in the development of some colorectal cancers (Emaduddin et al., 2008).

APOA1 encodes for apolipoprotein A-I, the major protein component of high density lipoprotein (HDL) in plasma. In multiple animal tumor models, APOA1 showed a potent immune-modulatory role in the tumorigenesis and was shown to suppress tumor growth and metastasis by supporting innate and adaptive immune processes (Zamanian-Daryoush et al., 2013).

APOA2 was shown to be significantly decreased in pancreatic cancer patients (Honda et al., 2012). In contrast, the increased expression of APOA2 was associated with HCC (Liu et al., 2007).

In alpha-fetoprotein-negative HBV-related HCC, APOB was found to be one of the 14 differentially expressed proteins which could be associated with HCC progression (He et al., 2014a). In advanced breast cancer, APOB was found to be the one of six differentially expressed proteins which could predict the responsiveness to neoadjuvant chemotherapy and relapse-free survival of patients (Hyung et al., 2011).

By stage III colorectal cancer patients and in human melanoma cells, AQP9 was associated with increased chemoresistance (Dou et al., 2013; Gao et al., 2012).

ARG1 was shown to be a sensitive and specific marker in distinguishing of HCC from other metastatic tumors in liver (Sang et al., 2013). ARG1 may contribute to local immune suppression in NSCLC (Rotondo et al., 2009).

The phosphorylated and thus more active form of ARSB protein was found to be increased in peripheral leukocytes from patients with chronic myelogenous leukemia compared to healthy donors (Uehara et al., 1983).

In ovarian cancer cells, the down-regulation of ASNA1 was shown to increase the sensitivity to the chemotherapy drugs cisplatin, carboplatin, oxaliplatin and arsenite (Hemmingsson et al., 2009).

ASPH was shown to be over-expressed in various cancers and cancer cell lines (Yang et al., 2010). Immunization with ASPH-loaded dendritic cells generated cytotoxicity against cholangiocarcinoma cells in vitro and significantly suppressed intrahepatic tumor growth and metastasis (Noda et al., 2012).

ATP1A2 was found among 31 proteins which were significantly up-regulated in glioblastoma (Com et al., 2012). In contrast, ATP1A2 was shown to be down-regulated in bone marrow-infiltrating metastatic neuroblastomas (Morandi et al., 2012).

ATP1A3 was found among 31 proteins, which were significantly up-regulated in glioblastoma (Com et al., 2012).

ATP6V1C1 may promote breast cancer growth and bone metastasis through regulation of lysosomal V-ATPase activity. ATP6V1C1 knockdown significantly inhibited mouse 4T1 mammary tumor cell xenograft tumor growth, metastasis, and osteolytic lesions in vivo (Feng et al., 2013). ATP6V1C1 was shown to be over-expressed in oral squamous cell carcinoma and was associated with tumor cell mobility (Otero-Rey et al., 2008).

ATP7B is associated with cancer resistance to cisplatin, the widely used anti-cancer drug (Dmitriev, 2011).

AXIN2 encodes for Axin- (axis inhibition) related protein 2, which presumably plays an important role in the regulation of the stability of beta-catenin in the Wnt signaling

pathway (Salahshor and Woodgett, 2005). Furthermore, AXIN2 was shown to repress the expression of the oncogene c-MYC (Rennoll et al., 2014).

In HCC, the low expression of BAAT was associated with poorer survival compared to the patients with higher expression of BAAT (Furutani et al., 1996).

A strong decrease of transcripts of BHMT and BHMT2 was shown in HepG2 cells and in HCC samples compared to normal liver tissue (Pellanda et al., 2012).

C12orf44 was shown to be essential for autophagy and interact with ULK1 in an Atg13-dependent manner (Mercer et al., 2009). Autophagy has dual roles in cancer, acting as both a tumor suppressor by preventing the accumulation of damaged proteins and organelles and as a mechanism of cell survival that can promote the growth of established tumors (Yang et al., 2011b).

C17orf70 is a component of the Fanconi anemia core complex and is essential for the complex stability. The Fanconi anemia core complex plays a central role in the DNA damage response network. The Fanconi anemia core complex-mediated DNA damage response involves breast cancer susceptibility gene products, BRCA1 and BRCA2 (Ling et al., 2007).

C19orf80 encodes for hepatocellular carcinoma-associated gene TD26 and was shown to be one of 5 loci with highest methylation levels in HCC and lowest in control tissue (Ammerpohl et al., 2012).

CCT7 was found to be a part of a protein sub-network, which is significantly discriminative of late stage human colorectal cancer (Nibbe et al., 2009).

CDK6 has been shown to regulate the activity of tumor suppressor protein Rb. CDK6 can exert its tumor-promoting function by enhancing proliferation and stimulating angiogenesis (Kollmann et al., 2013). The pharmacological inhibition of CDK6 was

shown to inhibit the growth differentiation of abnormal leukemic cells (Placke et al., 2014).

CFH may play a role in cutaneous squamous cell carcinoma progression (Riihila et al., 2014). CFH may play a key role in the resistance of complement-mediated lysis in various cancer cells and was shown to be over-expressed in NSCLC, which was associated with poorer prognosis (Cui et al., 2011).

An inactivating mutation of CLPTM1 was found in prostate cancer cells (Rossi et al., 2005).

CMAS encodes for cytidine monophosphate N-acetylneuraminic acid synthetase, which catalyzes the activation of sialic acid and its transformation to a cytidine monophosphate diester. The activated sialic acid is used for N-glycosylation, a common post-translational modification during cellular differentiation. The increased expression of sialic acid sugars on the surface of cancer cells is one of well-known tumor characteristics (Bull et al., 2014).

TF (Transferrin) is one of the most widely used tumor-targeted ligands, because TF receptors (TFRs) are over-expressed on malignant cells and play a key role in cellular iron uptake through the interaction with TF (Biswas et al., 2013). The expression level of TFRs has been suggested to correlate with tumor stage or cancer progression (Tortorella and Karagiannis, 2014).

TH1L might play an important role in regulation of proliferation and invasion in human breast cancer, and could be a potential target for human breast cancer treatment (Zou et al., 2010).

THTPA hydrolysis might be responsible for the anti-proliferative effects of Ndrg-1. Ndrg-1 has been shown to reduce the invasion and metastasis of breast, colon, prostate and pancreatic cancer (Kovacevic et al., 2008).

SMYD3 promotes cancer invasion by epigenetic up-regulation of the metalloproteinase MMP-9 (Medjkane et al., 2012). Expression of SMYD3 is undetectable or very weak in many types of normal human tissue, whereas over-expression of SMYD3 has been linked with the development and progression of gastric, colorectal, hepatocellular, prostate and breast cancers (Hamamoto et al., 2006; Liu et al., 2014; Liu et al., 2013a).

A link between STAT2 and tumorigenesis was observed in transgenic mice lacking STAT2 (Yue et al., 2015) or expressing constitutively IFN-α in the brain (Wang et al., 2003).

TACC3 is over-expressed in many human cancers, including ovarian cancer, breast cancer, squamous cell carcinoma and lymphoma (Ma et al., 2003; Jacquemier et al., 2005; Lauffart et al., 2005).

SPBP is also shown to repress the transcriptional activity of estrogen receptor α (ERα). Over-expression of SPBP inhibited the proliferation of an ERα-dependent breast cancer cell line (Gburcik et al., 2005). In the cell nucleus, SPBP displays relatively low mobility and is enriched in chromatin dense regions, clearly indicating that it is a chromatin binding protein (Darvekar et al., 2012). TCF20 is important for enhanced induction of proteins involved in the cellular defensive program against oxidative stress (Darvekar et al., 2014).

C3 is a prominent element of the inflammatory tumor microenvironment (Rutkowski et al., 2010) and activation can give a tumor growth advantage (Markiewski et al., 2008). Enzymatic cleavage of C3 leads to the production of the anaphylatoxin C3a, an inflammatory mediator and chemoattractant, and C3b (Sahu et al., 1998).

CLN3 is an anti-apoptotic gene in NT2 neuronal precursor cells and a few types of cancers (Zhu et al., 2014b). It is involved in intracellular trafficking and regulation in neuronal and non-neuronal cells (Rakheja et al., 2008; Getty and Pearce, 2011) and it is

implicated in several important signaling pathways (Persaud-Sawin et al., 2002). CLN3 mRNA and protein are over-expressed in a number of cancer cell lines including breast, colon, malignant melanoma, prostate, ovarian, neuroblastoma, and glioblastoma multiforme, but not lung or pancreatic cancer cell lines (Rylova et al., 2002).

SLC13A5 is one of 7 CIMP-marker genes. CIMP (CpG island methylator phenotype) of clear cell renal cell carcinomas (ccRCCs) is characterized by accumulation of DNA methylation at CpG islands and poorer patient outcome (Tian et al., 2014; Arai et al., 2012).

SLC35B2 is involved in in coordinated transcriptional regulation during induction of sialyl sulfo-Lex glycan biosynthesis during acute inflammation (Huopaniemi et al., 2004) and in the sulfation of the 6-sulfolactosamine epitope in a human colorectal carcinoma cell line (Kamiyama et al., 2006). Colorectal carcinoma cell lines as well as human colorectal tissues express SLC35B2 (Kamiyama et al., 2011).

PLOD1 expression is associated with human breast cancer progression (Gilkes et al., 2013).

PRDX5 is up-regulated in many malignant tumors (Urig and Becker, 2006) and inhibition of PRDX5 could prevent the tumor initiation and progression, suggesting PRDX5 to be a promising target for cancer therapy. Its highly nucleophilic and accessible selenocysteine active site might be the prime target for drug design (Liu et al., 2012).

Increased expression of PSMD8 in the peripheral lung may be potentially informative as to what critical cell populations are involved in the development of invasive cancers (Zhou et al., 1996).

SNRPD1 is a core spliceosomal protein, which is up-regulated in malignant tumors..

Reduced expression of the SPTBN1 is associated with worsened prognosis in pancreatic cancer (Jiang et al., 2010).

SQSTM1 functions as a signaling hub for various signal transduction pathways, such as NF-κB signaling, apoptosis, and Nrf2 activation, whose dysregulation is associated with Paget disease of bone and tumorigenesis (Komatsu et al., 2012).

PCNA expression predicts survival in anorectal malignant melanoma (Ben-Izhak et al., 2002). A cancer-associated isoform of PCNA (caPCNA) was identified that contained an unusual pattern of methyl ester groups on numerous glutamic and aspartic acid residues within PCNA (Hoelz et al., 2006).

Depleting SRP54 in several tumor cell lines did not produce overt cellular phenotypes, such as growth arrest or death, even in cells selected for stable reduction of SRP components (Ren et al., 2004).

At the molecular level, STAT1 inhibits the proliferation of both mouse and human tumor cells treated with IFN-γ via its ability to increase the expression of cyclin-dependent kinase inhibitor p21Cip1, or to decrease c-myc expression (Ramana et al., 2000). The anti-tumor activity of STAT1 is further supported by its ability to inhibit angiogenesis and tumor metastasis in mouse models (Huang et al., 2002). Increased STAT1 mRNA levels were shown to be part of a molecular signature associated with better prediction of the metastatic outcome for patients with hormone receptor negative and triple-negative breast cancers (Yau et al., 2010).

Fine-needle aspirate samples from follicular neoplasms demonstrated that malignant nodules over-express STT3A as compared with benign disease (Patel et al., 2011).

A meta-analysis showed that the STXBP4/COX11 rs6504950 polymorphism is significantly correlated with breast cancer risk (Tang et al., 2012).

A peptide consisting or consisting essentially of the amino acid sequence as indicated herein can have one or two non-anchor amino acids (see below regarding the anchor motif) exchanged without that the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I or –II is substantially changed or is negatively affected, when compared to the non-modified peptide. In another embodiment, in a peptide consisting essentially of the amino acid sequence as indicated herein, one or two amino acids can be exchanged with their conservative exchange partners (see herein below) without that the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I or –II is substantially changed, or is negatively affected, when compared to the non-modified peptide.

The present invention further relates to a peptide according to the present invention, wherein said peptide is modified and/or includes non-peptide bonds as described herein below.

The present invention further relates to a peptide according to the present invention, wherein said peptide is part of a fusion protein, in particular fused to the N-terminal amino acids of the HLA-DR antigen-associated invariant chain (Ii), or fused to (or into the sequence of) an antibody, such as, for example, an antibody that is specific for dendritic cells, i.e. binds to dendritic cells.

The present invention further relates to a nucleic acid, encoding for a peptide according to the present invention. The present invention further relates to the nucleic acid according to the present invention that is DNA, cDNA, PNA, RNA or combinations thereof.

The present invention further relates to an expression vector capable of expressing, expressing, and/or presenting a nucleic acid according to the present invention.

The present invention further relates to a peptide according to the present invention, a nucleic acid according to the present invention or an expression vector according to the present invention for use in medicine.

The present invention further relates to antibodies as described further below, and methods of making them. Preferred are antibodies that are specific for the peptides of the present invention, and/or for the peptides of the present invention when bound to their MHC. Preferred antibodies can be monoclonal.

The present invention further relates to T-cell receptors (TCR), in particular soluble TCR (sTCRs) targeting the peptides according to the invention and/or the peptide –MHC complexes thereof, and methods of making them.

The present invention further relates to antibodies or other binding molecules targeting the peptides according to the invention and/or the peptide–MHC complexes thereof, and methods of making them.

The present invention further relates to a host cell comprising a nucleic acid according to the present invention or an expression vector as described before. The present invention further relates to the host cell according to the present invention that is an antigen presenting cell. The present invention further relates to the host cell according to the present invention, wherein the antigen presenting cell is a dendritic cell.

The present invention further relates to aptamers. Aptamers (see for example WO 2014/191359 and the literature cited therein) are short single-stranded nucleic acid or peptide molecules, which can fold into defined three-dimensional structures and recognize specific target structures. They have appeared to be suitable alternatives for developing targeted therapies. Aptamers have been shown to selectively bind to a variety of complex targets with high affinity and specificity.

Aptamers recognizing cell surface located molecules have been identified within the past decade and provide means for developing diagnostic and therapeutic approaches. Since aptamers have been shown to possess almost no toxicity and immunogenicity they are promising candidates for biomedical applications. Indeed aptamers, for example prostate-specific membrane-antigen recognizing aptamers, have been successfully employed for targeted therapies and shown to be functional in xenograft in vivo models. Furthermore, aptamers recognizing specific tumour cell lines have been identified.

DNA aptamers can be selected to reveal broad-spectrum recognition properties for various cancer cells, and particularly those derived from solid tumours, while non-tumourgenic and primary healthy cells are not recognized. If the identified aptamers recognise not only a specific tumour sub-type but rather interact with a series of tumours, this renders the aptamers applicable as so-called broad-spectrum diagnostics and therapeutics.

Further, investigation of cell-binding behaviour with flow cytometry showed that aptamers revealed very good apparent affinities in the nanomolar range.

Aptamers are useful for diagnostic and therapeutic purposes. Further, it could be shown that some of the aptamers are taken up by tumour cells and thus can function as molecular vehicles for the targeted delivery of anti-cancer agents such as siRNA into tumour cells.

Aptamers can be selected against complex targets such as cells and tissues and complexes of the peptides comprising, preferably consisting of, a sequence according to any of SEQ ID NO 1 to SEQ ID NO 300, according to the present invention with the MHC molecule, using the cell-SELEX (Systematic Evolution of Ligands by Exponential enrichment) technique.

As used herein, the term "scaffold" refers to a molecule that specifically binds to an (eg antigenic) determinant. In one embodiment, a scaffold is able to direct the entity to which it is attached (e.g. a (second) antigen binding moiety) to a target site, for example to a specific type of tumor cell or tumor stroma bearing the antigenic determinant (e.g. the complex of a peptide according to the application at hand). In another embodiment a scaffold is able to activate signaling through its target antigen, for example a T cell receptor complex antigen. Scaffolds include but are not limited to antibodies and fragments thereof, antigen binding domains of an antibody, comprising an antibody heavy chain variable region and an antibody light chain variable region, binding proteins comprising at least one ankyrin repeat motif and Single domain antigen binding (SDAB) molecules, apatmers, (soluble) TCRs and (modified) cells such as allogenic or autologous T cells.

Each scaffold can comprise a labelling which provides that the bound scaffold can be detected by determining the presence or absence of a signal provided by the label. For example, the scaffold can be labelled with a fluorescent dye or any other applicable cellular marker molecule. Such marker molecules are well known in the art. For example a fluorescence-labelling, for example provided by a fluorescence dye, can provide a visualisation of the bound aptamer by fluorescence or laser scanning microscopy or flow cytometry.

Each scaffold can be conjugated with a second active molecule such as for example IL-21, anti-CD3, anti-CD28. Polypeptide scaffolds are described, for example, in the background section of WO 2014/071978A1, and the references as cited therein.

The present invention further relates to a method of producing a peptide according to the present invention, said method comprising culturing the host cell according to the present invention, and isolating the peptide from the host cell and/or its culture medium.

The present invention further relates to an *in vitro* method for producing activated T-cells, the method comprising contacting *in vitro* T cells with antigen loaded human class

I or II MHC molecules expressed on the surface of a suitable antigen-presenting cell for a period of time sufficient to activate said T cells in an antigen specific manner, wherein said antigen is at least one peptide according to the present invention. The present invention further relates to a method, wherein the antigen is loaded onto class I or II MHC molecules expressed on the surface of a suitable antigen-presenting cell by contacting a sufficient amount of the antigen with an antigen-presenting cell.

The present invention further relates to the method according to the present invention, wherein the antigen-presenting cell comprises an expression vector capable of expressing said peptide containing SEQ ID NO: 1 to SEQ ID NO: 300, or a variant amino acid sequence thereof.

The present invention further relates to activated T cells, produced by the method according to the present invention, which selectively recognize a cell which aberrantly expresses a polypeptide comprising an amino acid sequence according to the present invention.

The present invention further relates to a method of killing target cells in a patient which target cells aberrantly express a polypeptide comprising any amino acid sequence according to the present invention, the method comprising administering to the patient an effective number of T cells as according to the present invention.

The present invention further relates to the use of any peptide described, a nucleic acid according to the present invention, an expression vector according to the present invention, a cell according to the present invention, or an activated T-cell according to the present invention as a medicament or in the manufacture of a medicament.

The present invention further relates to a use according to the present invention, wherein said medicament is a vaccine, a cell, a cell population, such as, for example, a cell line, sTCRs and monoclonal antibodies.

The present invention further relates to a use according to the present invention, wherein the medicament is active against cancer.

The present invention further relates to a use according to the present invention, wherein said cancer cells are cells of HCC.

The present invention further relates to particular marker proteins and biomarkers based on the peptides according to the present invention that can be used in the diagnosis and/or prognosis of HCC.

Furthermore, the present invention relates to the use of these novel targets for cancer treatment.

Further, the present invention relates to a method for producing a personalized anti-cancer vaccine for an individual patient using a database (herein designated also as “warehouse”) of pre-screened tumor associated peptides.

Stimulation of an immune response is dependent upon the presence of antigens recognized as foreign by the host immune system. The discovery of the existence of tumor associated antigens has raised the possibility of using a host's immune system to intervene in tumor growth. Various mechanisms of harnessing both the humoral and cellular arms of the immune system are currently being explored for cancer immunotherapy.

Specific elements of the cellular immune response are capable of specifically recognizing and destroying tumor cells. The isolation of T-cells from tumor-infiltrating cell populations or from peripheral blood suggests that such cells play an important role in natural immune defense against cancer. CD8-positive T-cells in particular, which recognize Class I molecules of the major histocompatibility complex (MHC)-bearing peptides of usually 8 to 10 amino acid residues derived from proteins or defect ribosomal products (DRIPS) located in the cytosol, play an important role in this

response. The MHC-molecules of the human are also designated as human leukocyte-antigens (HLA).

The term “peptide” is used herein to designate a series of amino acid residues, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of the adjacent amino acids. The peptides are preferably 9 amino acids in length, but can be as short as 8 amino acids in length, and as long as 10, 11, 12, or 13 and in case of MHC class II peptides (elongated variants of the peptides of the invention) they can be as long as 14, 15, 16, 17, 18, 19 or 20 amino acids in length.

Furthermore, the term “peptide” shall include salts of a series of amino acid residues, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of the adjacent amino acids. Preferably, the salts are pharmaceutical acceptable salts of the peptides, such as, for example, the chloride or acetate (trifluoroacetate) salts. It has to be noted that the salts of the peptides according to the present invention differ substantially from the peptides in their state(s) *in vivo*, as the peptides are not salts *in vivo*.

The term “peptide” shall also include “oligopeptide”. The term “oligopeptide” is used herein to designate a series of amino acid residues, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of the adjacent amino acids. The length of the oligopeptide is not critical to the invention, as long as the correct epitope or epitopes are maintained therein. The oligopeptides are typically less than about 30 amino acid residues in length, and greater than about 15 amino acids in length.

The term “the peptides of the present invention” shall also include the peptides consisting of or comprising a peptide as defined above according to SEQ ID NO: 1 to SEQ ID NO: 300.

The term “polypeptide” designates a series of amino acid residues, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of the adjacent amino acids. The length of the polypeptide is not critical to the invention as long as the correct epitopes are maintained. In contrast to the terms peptide or oligopeptide, the term polypeptide is meant to refer to molecules containing more than about 30 amino acid residues.

A peptide, oligopeptide, protein or polynucleotide coding for such a molecule is “immunogenic” (and thus is an “immunogen” within the present invention), if it is capable of inducing an immune response. In the case of the present invention, immunogenicity is more specifically defined as the ability to induce a T-cell response. Thus, an “immunogen” would be a molecule that is capable of inducing an immune response, and in the case of the present invention, a molecule capable of inducing a T-cell response. In another aspect, the immunogen can be the peptide, the complex of the peptide with MHC, oligopeptide, and/or protein that is used to raise specific antibodies or TCRs against it.

A class I T cell “epitope” requires a short peptide that is bound to a class I MHC receptor, forming a ternary complex (MHC class I alpha chain, beta-2-microglobulin, and peptide) that can be recognized by a T cell bearing a matching T-cell receptor binding to the MHC/peptide complex with appropriate affinity. Peptides binding to MHC class I molecules are typically 8-14 amino acids in length, and most typically 9 amino acids in length.

In humans there are three different genetic loci that encode MHC class I molecules (the MHC-molecules of the human are also designated human leukocyte antigens (HLA)): HLA-A, HLA-B, and HLA-C. HLA-A*01, HLA-A*02, and HLA-B*07 are examples of different MHC class I alleles that can be expressed from these loci.

Table 6: Expression frequencies F of HLA-A*02 and HLA-A*24 and the most frequent HLA-DR serotypes. Frequencies are deduced from haplotype frequencies Gf within the

American population adapted from Mori et al. (Mori M, et al. HLA gene and haplotype frequencies in the North American population: the National Marrow Donor Program Donor Registry. Transplantation. 1997 Oct 15;64(7):1017-27) employing the Hardy-Weinberg formula $F=1-(1-Gf)^2$. Combinations of A*02 or A*24 with certain HLA-DR alleles might be enriched or less frequent than expected from their single frequencies due to linkage disequilibrium. For details refer to Chanock et al. (S.J. Chanock, et al (2004) HLA-A, -B, -Cw, -DQA1 and DRB1 in an African American population from Bethesda, USA Human Immunology, 65: 1223-1235).

Allele	Population	Calculated phenotype from allele frequency
A*02	Caucasian (North America)	49.1%
A*02	African American (North America)	34.1%
A*02	Asian American (North America)	43.2%
A*02	Latin American (North American)	48.3%
DR1	Caucasian (North America)	19.4%
DR2	Caucasian (North America)	28.2%
DR3	Caucasian (North America)	20.6%
DR4	Caucasian (North America)	30.7%
DR5	Caucasian (North America)	23.3%
DR6	Caucasian (North America)	26.7%
DR7	Caucasian (North America)	24.8%
DR8	Caucasian (North America)	5.7%
DR9	Caucasian (North America)	2.1%
DR1	African (North) American	13.20%
DR2	African (North) American	29.80%
DR3	African (North) American	24.80%
DR4	African (North) American	11.10%
DR5	African (North) American	31.10%
DR6	African (North) American	33.70%
DR7	African (North) American	19.20%
DR8	African (North) American	12.10%
DR9	African (North) American	5.80%
DR1	Asian (North) American	6.80%
DR2	Asian (North) American	33.80%
DR3	Asian (North) American	9.20%
DR4	Asian (North) American	28.60%
DR5	Asian (North) American	30.00%

Allele	Population	Calculated phenotype from allele frequency
DR6	Asian (North) American	25.10%
DR7	Asian (North) American	13.40%
DR8	Asian (North) American	12.70%
DR9	Asian (North) American	18.60%
DR1	Latin (North) American	15.30%
DR2	Latin (North) American	21.20%
DR3	Latin (North) American	15.20%
DR4	Latin (North) American	36.80%
DR5	Latin (North) American	20.00%
DR6	Latin (North) American	31.10%
DR7	Latin (North) American	20.20%
DR8	Latin (North) American	18.60%
DR9	Latin (North) American	2.10%
A*24	Philippines	65%
A*24	Russia Nenets	61%
A*24:02	Japan	59%
A*24	Malaysia	58%
A*24:02	Philippines	54%
A*24	India	47%
A*24	South Korea	40%
A*24	Sri Lanka	37%
A*24	China	32%
A*24:02	India	29%
A*24	Australia West	22%
A*24	USA	22%
A*24	Russia Samara	20%
A*24	South America	20%
A*24	Europe	18%

The peptides of the invention, preferably when included into a vaccine of the invention as described herein bind to A*02 or A*24. A vaccine may also include pan-binding MHC class II peptides. Therefore, the vaccine of the invention can be used to treat cancer in patients that are either A*02 positive, A*24 positive or positive for A*02 and A*24, whereas no selection for MHC class II allotypes is necessary due to the pan-binding nature of these peptides.

Combining for example A*02 and A*24 peptides in one vaccine has the advantage that a higher percentage of any patient population can be treated compared with addressing either MHC class I allele alone. While in most populations less than 50% of patients could be addressed by either allele alone, the vaccine of the invention can treat at least 60% of patients in any relevant population. Specifically, the following percentages of patients will be positive for at least one of these alleles in various regions: USA 61%, Western Europe 62%, China 75%, South Korea 77%, Japan 86% (calculated from www.allelefrequencies.net).

As used herein, reference to a DNA sequence includes both single stranded and double stranded DNA. Thus, the specific sequence, unless the context indicates otherwise, refers to the single strand DNA of such sequence, the duplex of such sequence with its complement (double stranded DNA) and the complement of such sequence. The term "coding region" refers to that portion of a gene which either naturally or normally codes for the expression product of that gene in its natural genomic environment, i.e., the region coding *in vivo* for the native expression product of the gene.

The coding region can be derived from a non-mutated ("normal"), mutated or altered gene, or can even be derived from a DNA sequence, or gene, wholly synthesized in the laboratory using methods well known to those of skill in the art of DNA synthesis.

In a preferred embodiment, the term "nucleotide sequence" refers to a heteropolymer of deoxyribonucleotides.

The nucleotide sequence coding for a particular peptide, oligopeptide, or polypeptide may be naturally occurring or they may be synthetically constructed. Generally, DNA segments encoding the peptides, polypeptides, and proteins of this invention are assembled from cDNA fragments and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene that is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

As used herein the term “a nucleotide coding (or encoding) for a peptide” refers to a nucleotide sequence coding for the peptide including artificial (man-made) start and stop codons compatible for the biological system the sequence is to be expressed by, for example, a dendritic cell or another cell system useful for the production of TCRs.

The term “expression product” means the polypeptide or protein that is the natural translation product of the gene and any nucleic acid sequence coding equivalents resulting from genetic code degeneracy and thus coding for the same amino acid(s).

The term “fragment”, when referring to a coding sequence, means a portion of DNA comprising less than the complete coding region, whose expression product retains essentially the same biological function or activity as the expression product of the complete coding region.

The term “DNA segment” refers to a DNA polymer, in the form of a separate fragment or as a component of a larger DNA construct, which has been derived from DNA isolated at least once in substantially pure form, i.e., free of contaminating endogenous materials and in a quantity or concentration enabling identification, manipulation, and recovery of the segment and its component nucleotide sequences by standard biochemical methods, for example, by using a cloning vector. Such segments are provided in the form of an open reading frame uninterrupted by internal non-translated sequences, or introns, which are typically present in eukaryotic genes. Sequences of non-translated DNA may be present downstream from the open reading frame, where the same do not interfere with manipulation or expression of the coding regions.

The term “primer” means a short nucleic acid sequence that can be paired with one strand of DNA and provides a free 3'-OH end at which a DNA polymerase starts synthesis of a deoxyribonucleotide chain.

The term “promoter” means a region of DNA involved in binding of RNA polymerase to initiate transcription.

The term “isolated” means that the material is removed from its original environment (e.g., the natural environment, if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

The polynucleotides, and recombinant or immunogenic polypeptides, disclosed in accordance with the present invention may also be in “purified” form. The term “purified” does not require absolute purity; rather, it is intended as a relative definition, and can include preparations that are highly purified or preparations that are only partially purified, as those terms are understood by those of skill in the relevant art. For example, individual clones isolated from a cDNA library have been conventionally purified to electrophoretic homogeneity. Purification of starting material or natural material to at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. Furthermore, a claimed polypeptide which has a purity of preferably 99.999%, or at least 99.99% or 99.9%; and even desirably 99% by weight or greater is expressly contemplated.

The nucleic acids and polypeptide expression products disclosed according to the present invention, as well as expression vectors containing such nucleic acids and/or such polypeptides, may be in “enriched form”. As used herein, the term “enriched” means that the concentration of the material is at least about 2, 5, 10, 100, or 1000 times its natural concentration (for example), advantageously 0.01 %, by weight, preferably at least about 0.1% by weight. Enriched preparations of about 0.5%, 1%, 5%, 10%, and 20% by weight are also contemplated. The sequences, constructs, vectors,

clones, and other materials comprising the present invention can advantageously be in enriched or isolated form.

The term “active fragment” means a fragment, usually of a peptide, polypeptide or nucleic acid sequence, that generates an immune response (i.e., has immunogenic activity) when administered, alone or optionally with a suitable adjuvant or in a vector, to an animal, such as a mammal, for example, a rabbit or a mouse, and also including a human, such immune response taking the form of stimulating a T-cell response within the recipient animal, such as a human. Alternatively, the "active fragment" may also be used to induce a T-cell response *in vitro*.

As used herein, the terms “portion”, “segment“ and “fragment,“ when used in relation to polypeptides, refer to a continuous sequence of residues, such as amino acid residues, which sequence forms a subset of a larger sequence. For example, if a polypeptide were subjected to treatment with any of the common endopeptidases, such as trypsin or chymotrypsin, the oligopeptides resulting from such treatment would represent portions, segments or fragments of the starting polypeptide. When used in relation to polynucleotides, these terms refer to the products produced by treatment of said polynucleotides with any of the endonucleases.

In accordance with the present invention, the term “percent homology”, “percent identity” or “percent identical”, when referring to a sequence, means that a sequence is compared to a claimed or described sequence after alignment of the sequence to be compared (the “Compared Sequence”) with the described or claimed sequence (the “Reference Sequence”). The Percent Identity is then determined according to the following formula:

Percent Identity = 100 [1 -(C/R)]

wherein C is the number of differences between the Reference Sequence and the Compared Sequence over the length of alignment between the Reference Sequence and the Compared Sequence, wherein
(i) each base or amino acid in the Reference Sequence that does not have a corresponding aligned base or amino acid in the Compared Sequence and
(ii) each gap in the Reference Sequence and
(iii) each aligned base or amino acid in the Reference Sequence that is different from an aligned base or amino acid in the Compared Sequence, constitutes a difference and
(iiii) the alignment has to start at position 1 of the aligned sequences;
and R is the number of bases or amino acids in the Reference Sequence over the length of the alignment with the Compared Sequence with any gap created in the Reference Sequence also being counted as a base or amino acid.

If an alignment exists between the Compared Sequence and the Reference Sequence for which the Percent Identity as calculated above is about equal to or greater than a specified minimum Percent Identity then the Compared Sequence has the specified minimum Percent Identity to the Reference Sequence even though alignments may exist in which the herein above calculated Percent Identity is less than the specified Percent Identity.

The original (unmodified) peptides as disclosed herein can be modified by the substitution of one or more residues at different, possibly selective, sites within the peptide chain, if not otherwise stated. Preferably those substitutions are located at the end of the amino acid chain. Such substitutions may be of a conservative nature, for example, where one amino acid is replaced by an amino acid of similar structure and characteristics, such as where a hydrophobic amino acid is replaced by another hydrophobic amino acid. Even more conservative would be replacement of amino acids of the same or similar size and chemical nature, such as where leucine is replaced by isoleucine. In studies of sequence variations in families of naturally occurring homologous proteins, certain amino acid substitutions are more often tolerated than others, and these are often show correlation with similarities in size, charge, polarity,

and hydrophobicity between the original amino acid and its replacement, and such is the basis for defining ”conservative substitutions.”

Conservative substitutions are herein defined as exchanges within one of the following five groups: Group 1-small aliphatic, nonpolar or slightly polar residues (Ala, Ser, Thr, Pro, Gly); Group 2-polar, negatively charged residues and their amides (Asp, Asn, Glu, Gln); Group 3-polar, positively charged residues (His, Arg, Lys); Group 4-large, aliphatic, nonpolar residues (Met, Leu, Ile, Val, Cys); and Group 5-large, aromatic residues (Phe, Tyr, Trp).

Less conservative substitutions might involve the replacement of one amino acid by another that has similar characteristics but is somewhat different in size, such as replacement of an alanine by an isoleucine residue. Highly non-conservative replacements might involve substituting an acidic amino acid for one that is polar, or even for one that is basic in character. Such “radical” substitutions cannot, however, be dismissed as potentially ineffective since chemical effects are not totally predictable and radical substitutions might well give rise to serendipitous effects not otherwise predictable from simple chemical principles.

Of course, such substitutions may involve structures other than the common L-amino acids. Thus, D-amino acids might be substituted for the L-amino acids commonly found in the antigenic peptides of the invention and yet still be encompassed by the disclosure herein. In addition, amino acids possessing non-standard R groups (i.e., R groups other than those found in the common 20 amino acids of natural proteins) may also be used for substitution purposes to produce immunogens and immunogenic polypeptides according to the present invention.

If substitutions at more than one position are found to result in a peptide with substantially equivalent or greater antigenic activity as defined below, then combinations of those substitutions will be tested to determine if the combined

substitutions result in additive or synergistic effects on the antigenicity of the peptide. At most, no more than 4 positions within the peptide would simultaneously be substituted.

The peptides of the invention can be elongated by up to four amino acids, that is 1, 2, 3 or 4 amino acids can be added to either end in any combination between 4:0 and 0:4.

Combinations of the elongations according to the invention can be depicted from Table 7:

C-terminus	N-terminus
4	0
3	0 or 1
2	0 or 1 or 2
1	0 or 1 or 2 or 3
0	0 or 1 or 2 or 3 or 4
N-terminus	C-terminus
4	0
3	0 or 1
2	0 or 1 or 2
1	0 or 1 or 2 or 3
0	0 or 1 or 2 or 3 or 4

The amino acids for the elongation/extension can be the peptides of the original sequence of the protein or any other amino acid(s). The elongation can be used to enhance the stability or solubility of the peptides.

The term “T-cell response” means the specific proliferation and activation of effector functions induced by a peptide *in vitro* or *in vivo*. For MHC class I restricted CTLs, effector functions may be lysis of peptide-pulsed, peptide-precursor pulsed or naturally peptide-presenting target cells, secretion of cytokines, preferably Interferon-gamma, TNF-alpha, or IL-2 induced by peptide, secretion of effector molecules, preferably granzymes or perforins induced by peptide, or degranulation.

Preferably, when the T cells specific for a peptide according to the present invention are tested against the substituted peptides, the peptide concentration at which the substituted peptides achieve half the maximal increase in lysis relative to background is

no more than about 1 mM, preferably no more than about 1 μM, more preferably no more than about 1 nM, and still more preferably no more than about 100 pM, and most preferably no more than about 10 pM. It is also preferred that the substituted peptide be recognized by T cells from more than one individual, at least two, and more preferably three individuals.

Thus, the epitopes of the present invention may be identical to naturally occurring tumor-associated or tumor-specific epitopes or may include epitopes that differ by no more than four residues from the reference peptide, as long as they have substantially identical antigenic activity.

MHC class I molecules can be found on most cells having a nucleus which present peptides that result from proteolytic cleavage of mainly endogenous, cytosolic or nuclear proteins, DRIPS, and larger peptides. However, peptides derived from endosomal compartments or exogenous sources are also frequently found on MHC class I molecules. This non-classical way of class I presentation is referred to as cross-presentation in literature.

Since both types of response, CD8 and CD4 dependent, contribute jointly and synergistically to the anti-tumor effect, the identification and characterization of tumor-associated antigens recognized by either CD8-positive T cells (MHC class I molecule) or by CD4-positive T cells (MHC class II molecule) is important in the development of tumor vaccines. It is therefore an object of the present invention, to provide compositions of peptides that contain peptides binding to MHC complexes of either class.

Considering the severe side-effects and expense associated with treating cancer better prognosis and diagnostic methods are desperately needed. Therefore, there is a need to identify other factors representing biomarkers for cancer in general and HCC in particular. Furthermore, there is a need to identify factors that can be used in the treatment of cancer in general and HCC in particular.

The present invention provides peptides that are useful in treating cancers/tumors, preferably HCC that over- or exclusively present the peptides of the invention. These peptides were shown by mass spectrometry to be naturally presented by HLA molecules on primary human HCC samples.

The source gene/protein (also designated “full-length protein” or “underlying protein”) from which the peptides are derived were shown to be highly overexpressed in cancer compared with normal tissues – “normal tissues” in relation to this invention shall mean either healthy liver cells or other normal tissue cells, demonstrating a high degree of tumor association of the source genes (see example 2). Moreover, the peptides themselves are strongly over-presented on tumor tissue – “tumor tissue” in relation to this invention shall mean a sample from a patient suffering from HCC, but not on normal tissues (see Example 1).

HLA-bound peptides can be recognized by the immune system, specifically T lymphocytes. T cells can destroy the cells presenting the recognized HLA/peptide complex, e.g. HCC cells presenting the derived peptides.

The peptides of the present invention have been shown to be capable of stimulating T cell responses and / or are over-presented and thus can be used for the production of antibodies and / or TCRs, in particular sTCRs, according to the present invention (see Example 3). Furthermore, the peptides when complexed with the respective MHC can be used for the production of antibodies and/or TCRs, in particular sTCRs, according to the present invention, as well. Respective methods are well known to the person of skill, and can be found in the respective literature as well. Thus, the peptides of the present invention are useful for generating an immune response in a patient by which tumor cells can be destroyed. An immune response in a patient can be induced by direct administration of the described peptides or suitable precursor substances (e.g. elongated peptides, proteins, or nucleic acids encoding these peptides) to the patient, ideally in combination with an agent enhancing the immunogenicity (i.e. an adjuvant).

The immune response originating from such a therapeutic vaccination can be expected to be highly specific against tumor cells because the target peptides of the present invention are not presented on normal tissues in comparable copy numbers, preventing the risk of undesired autoimmune reactions against normal cells in the patient.

A “pharmaceutical composition” preferably is preferably a composition suitable for administration to a human being in a medical setting. Preferably, a pharmaceutical composition is sterile and produced according to GMP guidelines.

The pharmaceutical compositions comprise the peptides either in the free form or in the form of a pharmaceutically acceptable salt (see also above). As used herein, "a pharmaceutically acceptable salt" refers to a derivative of the disclosed peptides wherein the peptide is modified by making acid or base salts of the agent. For example, acid salts are prepared from the free base (typically wherein the neutral form of the drug has a neutral –NH2 group) involving reaction with a suitable acid. Suitable acids for preparing acid salts include both organic acids, e.g., acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, malic acid, malonic acid, succinic acid, maleic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methane sulfonic acid, ethane sulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like, as well as inorganic acids, e.g., hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid phosphoric acid and the like. Conversely, preparation of basic salts of acid moieties which may be present on a peptide are prepared using a pharmaceutically acceptable base such as sodium hydroxide, potassium hydroxide, ammonium hydroxide, calcium hydroxide, trimethylamine or the like.

In an especially preferred embodiment, the pharmaceutical compositions comprise the peptides as salts of acetic acid (acetates), trifluoro acetates or hydrochloric acid (chlorides).

Especially preferred is a composition and/or the use of said composition, e.g. in the form of a vaccine, comprising the peptides having a sequence according to the SEQ ID

NOs 1, 2, 7, 225, 228, 301, 303, and 312 or a scaffold reactive against the peptides having a sequence according to the SEQ ID NOs 1, 2, 7, 225, 228, 301, 303, and 312 and their complexes to MHC molecules.

In addition to being useful for treating cancer, the peptides of the present invention are also useful as diagnostics. Since the peptides were generated from HCC cells and since it was determined that these peptides are not or at lower levels present in normal tissues, these peptides can be used to diagnose the presence of a cancer.

The presence of claimed peptides on tissue biopsies in blood samples can assist a pathologist in diagnosis of cancer. Detection of certain peptides by means of antibodies, mass spectrometry or other methods known in the art can tell the pathologist that the tissue sample is malignant or inflamed or generally diseased, or can be used as a biomarker for HCC. Presence of groups of peptides can enable classification or sub-classification of diseased tissues.

The detection of peptides on diseased tissue specimen can enable the decision about the benefit of therapies involving the immune system, especially if T-lymphocytes are known or expected to be involved in the mechanism of action. Loss of MHC expression is a well described mechanism by which infected of malignant cells escape immuno-surveillance. Thus, presence of peptides shows that this mechanism is not exploited by the analyzed cells.

The peptides of the present invention might be used to analyze lymphocyte responses against those peptides such as T cell responses or antibody responses against the peptide or the peptide complexed to MHC molecules. These lymphocyte responses can be used as prognostic markers for decision on further therapy steps. These responses can also be used as surrogate markers in immunotherapy approaches aiming to induce lymphocyte responses by different means, e.g. vaccination of protein, nucleic acids, autologous materials, adoptive transfer of lymphocytes. In gene therapy settings, lymphocyte responses against peptides can be considered in the assessment of side

effects. Monitoring of lymphocyte responses might also be a valuable tool for follow-up examinations of transplantation therapies, e.g. for the detection of graft versus host and host versus graft diseases.

The peptides of the present invention can be used to generate and develop specific antibodies against MHC/peptide complexes. These can be used for therapy, targeting toxins or radioactive substances to the diseased tissue. Another use of these antibodies can be targeting radionuclides to the diseased tissue for imaging purposes such as PET. This use can help to detect small metastases or to determine the size and precise localization of diseased tissues.

Therefore, it is a further aspect of the invention to provide a method for producing a recombinant antibody specifically binding to a human major histocompatibility complex (MHC) class I or II being complexed with a HLA-restricted antigen, the method comprising: immunizing a genetically engineered non-human mammal comprising cells expressing said human major histocompatibility complex (MHC) class I or II with a soluble form of a MHC class I or II molecule being complexed with said HLA-restricted antigen; isolating mRNA molecules from antibody producing cells of said non-human mammal; producing a phage display library displaying protein molecules encoded by said mRNA molecules; and isolating at least one phage from said phage display library, said at least one phage displaying said antibody specifically binding to said human major histocompatibility complex (MHC) class I or II being complexed with said HLA-restricted antigen.

It is a further aspect of the invention to provide an antibody that specifically binds to a human major histocompatibility complex (MHC) class I or II being complexed with a HLA-restricted antigen, wherein the antibody preferably is a polyclonal antibody, monoclonal antibody, bi-specific antibody and/or a chimeric antibody.

Yet another aspect of the present invention then relates to a method of producing said antibody specifically binding to a human major histocompatibility complex (MHC) class I

or II being complexed with a HLA-restricted antigen, the method comprising: immunizing a genetically engineered non-human mammal comprising cells expressing said human major histocompatibility complex (MHC) class I or II with a soluble form of a MHC class I or II molecule being complexed with said HLA-restricted antigen; isolating mRNA molecules from antibody producing cells of said non-human mammal; producing a phage display library displaying protein molecules encoded by said mRNA molecules; and isolating at least one phage from said phage display library, said at least one phage displaying said antibody specifically bindable to said human major histocompatibility complex (MHC) class I or II being complexed with said HLA-restricted antigen. Respective methods for producing such antibodies and single chain class I major histocompatibility complexes, as well as other tools for the production of these antibodies are disclosed in WO 03/068201, WO 2004/084798, WO 01/72768, WO 03/070752, and Cohen CJ, et al. Recombinant antibodies with MHC-restricted, peptide-specific, T-cell receptor-like specificity: new tools to study antigen presentation and TCR-peptide-MHC interactions. J Mol Recognit. 2003 Sep-Oct;16(5):324-32.; Denkberg G, et al. Selective targeting of melanoma and APCs using a recombinant antibody with TCR-like specificity directed toward a melanoma differentiation antigen. J Immunol. 2003 Sep 1;171(5):2197-207; and Cohen CJ, et al. Direct phenotypic analysis of human MHC class I antigen presentation: visualization, quantitation, and in situ detection of human viral epitopes using peptide-specific, MHC-restricted human recombinant antibodies. J Immunol. 2003 Apr 15; 170(8):4349-61, which for the purposes of the present invention are all explicitly incorporated by reference in their entireties.

Preferably, the antibody is binding with a binding affinity of below 20 nanomolar, preferably of below 10 nanomolar, to the complex, which is regarded as “specific” in the context of the present invention.

It is a further aspect of the invention to provide a method for producing a soluble T-cell receptor (sTCR) recognizing a specific peptide-MHC complex. Such soluble T-cell receptors can be generated from specific T-cell clones, and their affinity can be increased by mutagenesis targeting the complementarity-determining regions. For the

purpose of T-cell receptor selection, phage display can be used (US 2010/0113300, Liddy N, et al. Monoclonal TCR-redirected tumor cell killing. Nat Med 2012 Jun;18(6):980-987). For the purpose of stabilization of T-cell receptors during phage display and in case of practical use as drug, alpha and beta chain can be linked e.g. by non-native disulfide bonds, other covalent bonds (single-chain T-cell receptor), or by dimerization domains (see Boulter JM, et al. Stable, soluble T-cell receptor molecules for crystallization and therapeutics. Protein Eng 2003 Sep;16(9):707-711.; Card KF, et al. A soluble single-chain T-cell receptor IL-2 fusion protein retains MHC-restricted peptide specificity and IL-2 bioactivity. Cancer Immunol Immunother 2004 Apr;53(4):345-357; and Willcox BE, et al. Production of soluble alphabeta T-cell receptor heterodimers suitable for biophysical analysis of ligand binding. Protein Sci 1999 Nov; 8 (11):2418-2423). The T-cell receptor can be linked to toxins, drugs, cytokines (see, for example, US 2013/0115191), domains recruiting effector cells such as an anti-CD3 domain, etc., in order to execute particular functions on target cells. Moreover, it could be expressed in T cells used for adoptive transfer. Further information can be found in WO 2004/033685A1 and WO 2004/074322A1. A combination of sTCRs is described in WO 2012/056407A1. Further methods for the production are disclosed in WO 2013/057586A1.

In addition, the peptides and/or the TCRs or antibodies or other binding molecules of the present invention can be used to verify a pathologist's diagnosis of a cancer based on a biopsied sample.

In order to select over-presented peptides, a presentation profile is calculated showing the median sample presentation as well as replicate variation. The profile juxtaposes samples of the tumor entity of interest to a baseline of normal tissue samples. Each of these profiles can then be consolidated into an over-presentation score by calculating the p-value of a Linear Mixed-Effects Model (J. Pinheiro, et al. The nlme Package: Linear and Nonlinear Mixed Effects Models. 2007) adjusting for multiple testing by False Discovery Rate (Y. Benjamini and Y. Hochberg. Controlling the False Discovery Rate: A

Practical and Powerful Approach to Multiple Testing. Journal of the Royal Statistical Society. Series B (Methodological), Vol.57 (No.1):289-300, 1995).

For the identification and relative quantitation of HLA ligands by mass spectrometry, HLA molecules from shock-frozen tissue samples were purified and HLA-associated peptides were isolated. The isolated peptides were separated and sequences were identified by online nano-electrospray-ionization (nanoESI) liquid chromatography-mass spectrometry (LC-MS) experiments. The resulting peptide sequences were verified by comparison of the fragmentation pattern of natural TUMAPs recorded from HCC samples (N = 16 A*02-positive samples including thirteen A*02:01-positive samples, N = 15 A*24-positive samples) with the fragmentation patterns of corresponding synthetic reference peptides of identical sequences. Since the peptides were directly identified as ligands of HLA molecules of primary tumors, these results provide direct evidence for the natural processing and presentation of the identified peptides on primary cancer tissue obtained from 31 HCC patients.

The discovery pipeline XPRESIDENT® v2.1 (see, for example, US 2013-0096016, which is hereby incorporated by reference in its entirety) allows the identification and selection of relevant over-presented peptide vaccine candidates based on direct relative quantitation of HLA-restricted peptide levels on cancer tissues in comparison to several different non-cancerous tissues and organs. This was achieved by the development of label-free differential quantitation using the acquired LC-MS data processed by a proprietary data analysis pipeline, combining algorithms for sequence identification, spectral clustering, ion counting, retention time alignment, charge state deconvolution and normalization.

Presentation levels including error estimates for each peptide and sample were established. Peptides exclusively presented on tumor tissue and peptides over-presented in tumor versus non-cancerous tissues and organs have been identified.

HLA-peptide complexes from HCC tissue samples were purified and HLA-associated peptides were isolated and analyzed by LC-MS (see examples). All TUMAPs contained in the present application were identified with this approach on primary HCC samples confirming their presentation on primary HCC.

TUMAPs identified on multiple HCC tumor and normal tissues were quantified using ion-counting of label-free LC-MS data. The method assumes that LC-MS signal areas of a peptide correlate with its abundance in the sample. All quantitative signals of a peptide in various LC-MS experiments were normalized based on central tendency, averaged per sample and merged into a bar plot, called presentation profile. The presentation profile consolidates different analysis methods like protein database search, spectral clustering, charge state deconvolution (decharging) and retention time alignment and normalization.

The present invention relates to a peptide comprising a sequence that is selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 300, or a variant thereof which is at least 90% homologous (preferably identical) to SEQ ID NO: 1 to SEQ ID NO: 300 or a variant thereof that induces T cells cross-reacting with said peptide, wherein said peptide is not the underlying full-length polypeptide.

The present invention further relates to a peptide comprising a sequence that is selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 300 or a variant thereof which is at least 90% homologous (preferably identical) to SEQ ID NO: 1 to SEQ ID NO: 300, wherein said peptide or variant has an overall length of between 8 and 100, preferably between 8 and 30, and most preferred between 8 and 14 amino acids.

The present invention further relates to the peptides according to the invention that have the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I or -II.

The present invention further relates to the peptides according to the invention wherein the peptide consists or consists essentially of an amino acid sequence according to SEQ ID NO: 1 to SEQ ID NO: 300.

The present invention further relates to the peptides according to the invention, wherein the peptide is (chemically) modified and/or includes non-peptide bonds.

The present invention further relates to the peptides according to the invention, wherein the peptide is part of a fusion protein, in particular comprising N-terminal amino acids of the HLA-DR antigen-associated invariant chain (Ii), or wherein the peptide is fused to (or into) an antibody, such as, for example, an antibody that is specific for dendritic cells.

The present invention further relates to a nucleic acid, encoding the peptides according to the invention, provided that the peptide is not the complete (full) human protein.

The present invention further relates to the nucleic acid according to the invention that is DNA, cDNA, PNA, RNA or combinations thereof.

The present invention further relates to an expression vector capable of expressing a nucleic acid according to the present invention.

The present invention further relates to a peptide according to the present invention, a nucleic acid according to the present invention or an expression vector according to the present invention for use in medicine, in particular in the treatment of HCC.

The present invention further relates to a host cell comprising a nucleic acid according to the invention or an expression vector according to the invention.

The present invention further relates to the host cell according to the present invention that is an antigen presenting cell, and preferably a dendritic cell.

The present invention further relates to the method according to the present invention, where-in the antigen is loaded onto class I or II MHC molecules expressed on the surface of a suitable antigen-presenting cell by contacting a sufficient amount of the antigen with an antigen-presenting cell.

The present invention further relates to the method according to the invention, wherein the antigen-presenting cell comprises an expression vector capable of expressing said peptide containing SEQ ID NO: 1 to SEQ ID NO: 300 or said variant amino acid sequence.

The present invention further relates to the use of any peptide described, a nucleic acid ac-cording to the present invention, an expression vector according to the present invention, a cell according to the present invention, or an activated cytotoxic T lymphocyte according to the present invention as a medicament or in the manufacture of a medicament. The present invention further relates to a use according to the present invention, wherein the medicament is active against cancer.

The present invention further relates to a use according to the invention, wherein the medicament is a vaccine. The present invention further relates to a use according to the invention, wherein the medicament is active against cancer.

The present invention further relates to a use according to the invention, wherein said cancer cells are HCC cells or other solid or haematological tumor cells such as pancreatic cancer, brain cancer, kidney cancer, colon or rectal cancer, or leukemia.

The present invention further relates to particular marker proteins and biomarkers based on the peptides according to the present invention, herein called “targets” that can be used in the diagnosis and/or prognosis of HCC. The present invention also relates to the use of these novel targets for cancer treatment.

The term “antibody” or ”antibodies“ is used herein in a broad sense and includes both polyclonal and monoclonal antibodies. In addition to intact or “full” immunoglobulin molecules, also included in the term ”antibodies“ are fragments (e.g. CDRs, Fv, Fab and Fc fragments) or polymers of those immunoglobulin molecules and humanized versions of immunoglobulin molecules, as long as they exhibit any of the desired properties (e.g., specific binding of a HCC marker polypeptide, delivery of a toxin to a HCC cell expressing a cancer marker gene at an increased level, and/or inhibiting the activity of a HCC marker polypeptide) according to the invention.

Whenever possible, the antibodies of the invention may be purchased from commercial sources. The antibodies of the invention may also be generated using well-known methods. The skilled artisan will understand that either full length HCC marker polypeptides or fragments thereof may be used to generate the antibodies of the invention. A polypeptide to be used for generating an antibody of the invention may be partially or fully purified from a natural source, or may be produced using recombinant DNA techniques.

For example, a cDNA encoding a peptide according to the present invention, such as a peptide according to SEQ ID NO: 1 to SEQ ID NO: 300 polypeptide, or a variant or fragment thereof, can be expressed in prokaryotic cells (e.g., bacteria) or eukaryotic cells (e.g., yeast, insect, or mammalian cells), after which the recombinant protein can be purified and used to generate a monoclonal or polyclonal antibody preparation that specifically bind the HCC marker polypeptide used to generate the antibody according to the invention.

One of skill in the art will realize that the generation of two or more different sets of monoclonal or polyclonal antibodies maximizes the likelihood of obtaining an antibody with the specificity and affinity required for its intended use (e.g., ELISA, immunohistochemistry, *in vivo* imaging, immunotoxin therapy). The antibodies are tested for their desired activity by known methods, in accordance with the purpose for which the antibodies are to be used (e.g., ELISA, immunohistochemistry,

immunotherapy, etc.; for further guidance on the generation and testing of antibodies, see, e.g., Harlow and Lane, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1988, new 2nd edition 2013). For example, the antibodies may be tested in ELISA assays or, Western blots, immunohistochemical staining of formalin-fixed cancers or frozen tissue sections. After their initial *in vitro* characterization, antibodies intended for therapeutic or *in vivo* diagnostic use are tested according to known clinical testing methods.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a substantially homogeneous population of antibodies, i.e.; the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. The monoclonal antibodies herein specifically include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired antagonistic activity (US 4,816,567, which is hereby incorporated in its entirety).

Monoclonal antibodies of the invention may be prepared using hybridoma methods. In a hybridoma method, a mouse or other appropriate host animal is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in US 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies).

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art. For instance, digestion can be performed using papain. Examples of papain digestion are described in WO 94/29348 and US 4,342,566. Papain digestion of antibodies typically produces two identical antigen binding fragments, called Fab fragments, each with a single antigen binding site, and a residual Fc fragment. Pepsin treatment yields a F(ab')2 fragment and a pFc' fragment.

The antibody fragments, whether attached to other sequences or not, can also include insertions, deletions, substitutions, or other selected modifications of particular regions or specific amino acids residues, provided the activity of the fragment is not significantly altered or impaired compared to the non-modified antibody or antibody fragment. These modifications can provide for some additional property, such as to remove/add amino acids capable of disulfide bonding, to increase its bio-longevity, to alter its secretory characteristics, etc. In any case, the antibody fragment must possess a bioactive property, such as binding activity, regulation of binding at the binding domain, etc. Functional or active regions of the antibody may be identified by mutagenesis of a specific region of the protein, followed by expression and testing of the expressed polypeptide. Such methods are readily apparent to a skilled practitioner in the art and can include site-specific mutagenesis of the nucleic acid encoding the antibody fragment.

The antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab' or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a

non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin.

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (US 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production can be employed. For example, it has been described that the homozygous deletion of the antibody heavy chain joining region gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will

result in the production of human antibodies upon antigen challenge. Human antibodies can also be produced in phage display libraries.

Antibodies of the invention are preferably administered to a subject in a pharmaceutically acceptable carrier. Typically, an appropriate amount of a pharmaceutically-acceptable salt is used in the formulation to render the formulation isotonic. Examples of the pharmaceutically-acceptable carrier include saline, Ringer's solution and dextrose solution. The pH of the solution is preferably from about 5 to about 8, and more preferably from about 7 to about 7.5. Further carriers include sustained release preparations such as semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, liposomes or microparticles. It will be apparent to those persons skilled in the art that certain carriers may be more preferable depending upon, for instance, the route of administration and concentration of antibody being administered.

The antibodies can be administered to the subject, patient, or cell by injection (e.g., intravenous, intraperitoneal, subcutaneous, intramuscular), or by other methods such as infusion that ensure its delivery to the bloodstream in an effective form. The antibodies may also be administered by intratumoral or peritumoral routes, to exert local as well as systemic therapeutic effects. Local or intravenous injection is preferred.

Effective dosages and schedules for administering the antibodies may be determined empirically, and making such determinations is within the skill in the art. Those skilled in the art will understand that the dosage of antibodies that must be administered will vary depending on, for example, the subject that will receive the antibody, the route of administration, the particular type of antibody used and other drugs being administered. A typical daily dosage of the antibody used alone might range from about 1 (µg/kg to up to 100 mg/kg of body weight or more per day, depending on the factors mentioned above. Following administration of an antibody, preferably for treating HCC, the efficacy of the therapeutic antibody can be assessed in various ways well known to the skilled practitioner. For instance, the size, number, and/or distribution of cancer in a subject

receiving treatment may be monitored using standard tumor imaging techniques. A therapeutically-administered antibody that arrests tumor growth, results in tumor shrinkage, and/or prevents the development of new tumors, compared to the disease course that would occurs in the absence of antibody administration, is an efficacious antibody for treatment of cancer.

Because the peptides as mentioned in the Tables above of the invention and thus their underlying polypeptides are highly expressed in HCC, and are expressed at rather to extremely low levels in normal cells, the inhibition of a protein selected from the group consisting of protein products of the following genes: Preferred for the inhibition and for antibodies and/or TCRs against are GLUL, GPAM, PLIN2, SLC16A1, SLC9A3R1, PCBD1, SEC16A, AKR1C4, ABCB11, HAL, CYP2E1, C4A, C4B, ALDH1L1, CRP, ACSL4, EEF2, HLTF, FBXO22, GALK1, TMCO1, TMEM33, ZNF318, IPO9, AMACR, C1QTNF3, CYP4F8, CYP4F3, CYP4F11, CYP4F12, CYP4F2, MOCOS, A1CF, COL18A1, HPR, LBP, C19orf80, CFHR5, ITIH4, TMEM110, LARP4, LMF2, SLC10A5, and SLC16A11; still preferred for the inhibition and for antibodies and/or TCRs against are ANKFY1, C12orf44, C16orf58, CPSF1, DCAF8, PEX19, DDX11, DDX12P, DECR2, NME4, DENND5B, DYM, EDC4, ERI3, FAM20A, FNDC3A,GPR107, GYG2, HEATR2, IFT81, KCTD3,SHKBP1, KIAA1324L, KLHL24, MARCH6, MBTPS2, MIR1279, CPSF6, NOC4L, NXF1, PANK2, PCNXL3, PIPSL, PSMD4, PSMD14, SLC35B1, TCP11L2, THNSL2, THOC2, TOMM5, TRAPPC6B, TRIM54, TRIM55, TRIM63, UGGT2, URB1, VPS54, WIZ, ZNF451, RFTN2, SCFD1, SERINC5, CCT7P2, CMAS, ANKS1A, C17orf70, CCT7, CDK5RAP2, CLPTM1, and most preferred for the inhibition and for antibodies and/or TCRs against are APOB, FASN, and/or COPA; and expression or of the activity of these markers may be preferably integrated into a therapeutic strategy, e.g. for treating or preventing HCC.

The principle of antisense therapy is based on the hypothesis that sequence-specific suppression of gene expression (via transcription or translation) may be achieved by intra-cellular hybridization between genomic DNA or mRNA and a complementary antisense species. The formation of such a hybrid nucleic acid duplex interferes with

transcription of the target tumor antigen-encoding genomic DNA, or processing/transport/translation and/or stability of the target tumor antigen mRNA.

Antisense nucleic acids can be delivered by a variety of approaches. For example, antisense oligonucleotides or anti-sense RNA can be directly administered (e.g., by intravenous injection) to a subject in a form that allows uptake into tumor cells. Alternatively, viral or plasmid vectors that encode antisense RNA (or RNA fragments) can be introduced into cells *in vivo*. Antisense effects can also be induced by sense sequences; however, the extent of phenotypic changes is highly variable. Phenotypic changes induced by effective antisense therapy are assessed according to changes in, e.g., target mRNA levels, target protein levels, and/or target protein activity levels.

In a specific example, inhibition of HCC target/marker function by antisense gene therapy may be accomplished by direct administration of antisense tumor marker RNA to a subject. The antisense tumor marker RNA may be produced and isolated by any standard technique, but is most readily produced by in vitro transcription using an antisense tumor marker cDNA under the control of a high efficiency promoter (e.g., the T7 promoter). Administration of anti-sense tumor marker RNA to cells can be carried out by any of the methods for direct nucleic acid administration described below.

An alternative strategy for inhibiting the function of a protein selected from the group consisting of the above-mentioned proteins, and most preferred of APOB, FASN, and/or COPA, involves use of a nucleic acid (e.g. siRNA, or a nucleic acid coding for an anti-protein antibody or a portion thereof, which can be transferred into cancer cells or other cells, leading to intracellular antibody expression and secretion), a protein or small molecule, or any other compound targeting the expression, translation, and/or biological function of this protein.

In the methods described above, which include the administration and uptake of exogenous DNA into the cells of a subject (i.e., gene transduction or transfection), the nucleic acids of the present invention can be in the form of naked DNA or the nucleic

acids can be in a vector for delivering the nucleic acids to the cells for inhibition of HCC marker protein expression. The vector can be a commercially available preparation, such as an adenovirus vector (Quantum Biotechnologies, Inc. (Laval, Quebec, Canada). Delivery of the nucleic acid or vector to cells can be via a variety of mechanisms. As one example, delivery can be via a liposome, using commercially available liposome preparations such as Lipofectin, Lipofectamine (GIBCO-25 BRL, Inc., Gaithersburg, Md.), Superfect (Qiagen, Inc. Hilden, Germany) and Transfectam (Promega Biotec, Inc., Madison, Wis., US), as well as other liposomes developed according to procedures standard in the art. In addition, the nucleic acid or vector of this invention can be delivered *in vivo* by electroporation, the technology for which is available from Genetronics, Inc. (San Diego, US) as well as by means of a Sonoporation machine (ImaRx Pharmaceutical Corp., Tucson, Arizona, US).

As one example, vector delivery can be via a viral system, such as a retroviral vector system that can package a recombinant retroviral genome. The recombinant retrovirus can then be used to infect and thereby deliver to the infected cells antisense nucleic acid that inhibits expression of a protein selected from the group consisting of the above-mentioned proteins. The exact method of introducing the altered nucleic acid into mammalian cells is, of course, not limited to the use of retroviral vectors. Other techniques are widely available for this procedure including the use of adenoviral vectors, adeno-associated viral (AAV) vectors, lentiviral vectors, pseudotyped retroviral vectors. Physical transduction techniques can also be used, such as liposome delivery and receptor-mediated and other endocytosis mechanisms. This invention can be used in conjunction with any of these or other commonly used gene transfer methods.

The antibodies may also be used for *in vivo* diagnostic assays. Generally, the antibody is labeled with a radionucleotide (such as ^{111}In, ^{99}Tc, ^{14}C, ^{131}I, ^{3}H, ^{32}P or ^{35}S) so that the tumor can be localized using immunoscintiography. In one embodiment, antibodies or fragments thereof bind to the extracellular domains of two or more targets of a protein selected from the group consisting of the above-mentioned proteins, and the affinity value (Kd) is less than 1 x 10μM.

Antibodies for diagnostic use may be labeled with probes suitable for detection by various imaging methods. Methods for detection of probes include, but are not limited to, fluorescence, light, confocal and electron microscopy; magnetic resonance imaging and spectroscopy; fluoroscopy, computed tomography and positron emission tomography. Suitable probes include, but are not limited to, fluorescein, rhodamine, eosin and other fluorophores, radioisotopes, gold, gadolinium and other lanthanides, paramagnetic iron, fluorine-18 and other positron-emitting radionuclides. Additionally, probes may be bi- or multi-functional and be detectable by more than one of the methods listed. These antibodies may be directly or indirectly labeled with said probes. Attachment of probes to the antibodies includes covalent attachment of the probe, incorporation of the probe into the antibody, and the covalent attachment of a chelating compound for binding of probe, amongst others well recognized in the art. For immunohistochemistry, the disease tissue sample may be fresh or frozen or may be embedded in paraffin and fixed with a preservative such as formalin. The fixed or embedded section contains the sample are contacted with a labeled primary antibody and secondary antibody, wherein the antibody is used to detect the expression of the proteins in situ.

As mentioned above, the present invention thus provides a peptide comprising a sequence that is selected from the group of consisting of SEQ ID NO: 1 to SEQ ID NO: 300 or a variant thereof which is 90% homologous to SEQ ID NO: 1 to SEQ ID NO: 300, or a variant thereof that will induce T cells cross-reacting with said peptide. The peptides of the invention have the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I or elongated versions of said peptides to class II.

In the present invention, the term “homologous” refers to the degree of identity (see Percent Identity above) between sequences of two amino acid sequences, i.e. peptide or polypeptide sequences. The aforementioned “homology” is determined by comparing two sequences aligned under optimal conditions over the sequences to be compared.

Such a sequence homology can be calculated by creating an alignment using, for example, the ClustalW algorithm. Commonly available sequence analysis software, more specifically, Vector NTI, GENETYX or other analysis tools are provided by public databases.

A person skilled in the art will be able to assess, whether T cells induced by a variant of a specific peptide will be able to cross-react with the peptide itself (Fong L, et al. Altered peptide ligand vaccination with Flt3 ligand expanded dendritic cells for tumor immunotherapy. Proc Natl Acad Sci USA. 2001 Jul 17;98(15):8809-14; Zaremba S, et al. Identification of an enhancer agonist cytotoxic T lymphocyte peptide from human carcinoembryonic antigen. Cancer Res. 1997 Oct 15;57(20):4570-7; Colombetti S, et al. Impact of orthologous melan-A peptide immunizations on the anti-self melan-A/HLA-A2 T cell cross-reactivity. J Immunol. 2006 Jun 1;176(11):6560-7; Appay V, et al. Decreased specific CD8+ T cell cross-reactivity of antigen recognition following vaccination with Melan-A peptide. Eur J Immunol. 2006 Jul;36(7):1805-14).

By a "variant" of the given amino acid sequence the inventors mean that the side chains of, for example, one or two of the amino acid residues are altered (for example by replacing them with the side chain of another naturally occurring amino acid residue or some other side chain) such that the peptide is still able to bind to an HLA molecule in substantially the same way as a peptide consisting of the given amino acid sequence in consisting of SEQ ID NO: 1 to SEQ ID NO: 300. For example, a peptide may be modified so that it at least maintains, if not improves, the ability to interact with and bind to the binding groove of a suitable MHC molecule, such as HLA-A*02 or -DR, and in that way it at least maintains, if not improves, the ability to bind to the TCR of activated T cells.

These T cells can subsequently cross-react with cells and kill cells that express a polypeptide that contains the natural amino acid sequence of the cognate peptide as defined in the aspects of the invention. As can be derived from the scientific literature (Godkin A, et al. Use of eluted peptide sequence data to identify the binding

characteristics of peptides to the insulin-dependent diabetes susceptibility allele HLA-DQ8 (DQ 3.2). Int Immunol. 1997 Jun;9(6):905-11) and databases (Rammensee H. et al. SYFPEITHI: database for MHC ligands and peptide motifs. Immunogenetics. 1999 Nov; 50(3-4):213-9), certain positions of HLA binding peptides are typically anchor residues forming a core sequence fitting to the binding motif of the HLA receptor, which is defined by polar, electrophysical, hydrophobic and spatial properties of the polypeptide chains constituting the binding groove. Thus, one skilled in the art would be able to modify the amino acid sequences set forth in SEQ ID NO: 1 to SEQ ID NO 300, by maintaining the known anchor residues, and would be able to determine whether such variants maintain the ability to bind MHC class I or II molecules. The variants of the present invention retain the ability to bind to the TCR of activated T cells, which can subsequently cross-react with and kill cells that express a polypeptide containing the natural amino acid sequence of the cognate peptide as defined in the aspects of the invention.

The amino acid residues that do not substantially contribute to interactions with the T-cell receptor can be modified by replacement with another amino acid whose incorporation does not substantially affect T-cell reactivity and does not eliminate binding to the relevant MHC. Thus, apart from the proviso given, the peptide of the invention may be any peptide (by which term the inventors include oligopeptide or polypeptide), which includes the amino acid sequences or a portion or variant thereof as given.

Those amino acid residues that do not substantially contribute to interactions with the TCR can be modified by replacement with another amino acid whose incorporation does not substantially affect T-cell reactivity and does not eliminate binding to the relevant MHC. Thus, apart from the proviso given, the peptide of the invention may be any peptide (by which term the inventors include oligopeptide or polypeptide), which includes the amino acid sequences or a portion or variant thereof as given.

Table 8: Variants and motif of the peptides according to SEQ ID NO: 1, 117, and 246

Position	1	2	3	4	5	6	7	8	9
SEQ ID NO. 1	V	M	A	P	F	T	M	T	I
Variants									V
									L
									A
		L							V
		L							L
		L							
		L							A
		A							V
		A							L
		A							
		A							A
		V							V
		V							L
		V							
		V							A
		T							V
		T							L
		T							
		T							A
		Q							V
		Q							L
		Q							
		Q							A
Position	1	2	3	4	5	6	7	8	9
SEQ ID NO 246	K	L	I	S	S	Y	Y	N	V
Variants		I							L
		I							I
		I							
		I							A
		M							L
		M							I
		M							
		M							A
		A							L
		A							I

		A							
		A							A
		V							L
		V							I
		V							
		V							A
		T							L
		T							I
		T							
		T							A
		Q							L
		Q							I
		Q							
		Q							A
Position	1	2	3	4	5	6	7	8	9
SEQ ID NO. 117	Y	A	F	P	K	S	I	T	V
Variants									L
									I
									A
		M							L
		M							I
		M							
		M							A
		L							L
		L							I
		L							
		L							A
		V							L
		V							I
		V							
		V							A
		T							L
		T							I
		T							
		T							A
		Q							L
		Q							I
		Q							
		Q							A

Longer peptides may also be suitable. It is also possible that MHC class I epitopes, although usually between 8 and 11 amino acids long, are generated by peptide processing from longer peptides or proteins that include the actual epitope. It is preferred that the residues that flank the actual epitope are residues that do not substantially affect proteolytic cleavage necessary to expose the actual epitope during processing.

Accordingly, the present invention provides peptides and variants of MHC class I epitopes, wherein the peptide or variant has an overall length of between 8 and 100, preferably between 8 and 30, and most preferred between 8 and 14, namely 8, 9, 10, 11, 12, 13, 14 amino acids, in case of the elongated class II binding peptides the length can also be 15, 16, 17, 18, 19, 20, 21 or 22 amino acids.

Of course, the peptide or variant according to the present invention will have the ability to bind to a molecule of the human major histocompatibility complex (MHC) class I or II. Binding of a peptide or a variant to a MHC complex may be tested by methods known in the art.

In a particularly preferred embodiment of the invention the peptide consists or consists essentially of an amino acid sequence according to SEQ ID NO: 1 to SEQ ID NO: 300.

“Consisting essentially of” shall mean that a peptide according to the present invention, in addition to the sequence according to any of SEQ ID NO: 1 to SEQ ID NO 300 or a variant thereof contains additional N- and/or C-terminally located stretches of amino acids that are not necessarily forming part of the peptide that functions as an epitope for MHC molecules epitope.

Nevertheless, these stretches can be important to provide an efficient introduction of the peptide according to the present invention into the cells. In one embodiment of the present invention, the peptide is part of a fusion protein which comprises, for example,

the 80 N-terminal amino acids of the HLA-DR antigen-associated invariant chain (p33, in the following “Ii”) as derived from the NCBI, GenBank Accession number X00497. In other fusions, the peptides of the present invention can be fused to an antibody as described herein, or a functional part thereof, in particular into a sequence of an antibody, so as to be specifically targeted by said antibody, or, for example, to or into an antibody that is specific for dendritic cells as described herein.

In addition, the peptide or variant may be modified further to improve stability and/or binding to MHC molecules in order to elicit a stronger immune response. Methods for such an optimization of a peptide sequence are well known in the art and include, for example, the introduction of reverse peptide bonds or non-peptide bonds.

In a reverse peptide bond amino acid residues are not joined by peptide (-CO-NH-) linkages but the peptide bond is reversed. Such retro-inverso peptidomimetics may be made using methods known in the art, for example such as those described in Meziere et al (1997) J. Immunol. 159, 3230-3237, incorporated herein by reference. This approach involves making pseudopeptides containing changes involving the backbone, and not the orientation of side chains. Meziere et al (1997) show that for MHC binding and T helper cell responses, these pseudopeptides are useful. Retro-inverse peptides, which contain NH-CO bonds instead of CO-NH peptide bonds, are much more resistant to proteolysis.

A non-peptide bond is, for example, -CH_2-NH, -CH_2S-, -CH_2CH_2-, -CH=CH-, -$COCH_2$-, -CH(OH)CH_2-, and -CH_2SO-. US 4,897,445 provides a method for the solid phase synthesis of non-peptide bonds (-CH_2-NH) in polypeptide chains which involves polypeptides synthesized by standard procedures and the non-peptide bond synthesized by reacting an amino aldehyde and an amino acid in the presence of $NaCNBH_3$.

Peptides comprising the sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, to enhance

the stability, bioavailability, and/or affinity of the peptides. For example, hydrophobic groups such as carbobenzoxyl, dansyl, or t-butyloxycarbonyl groups may be added to the peptides' amino termini. Likewise, an acetyl group or a 9-fluorenylmethoxy-carbonyl group may be placed at the peptides' amino termini. Additionally, the hydrophobic group, t-butyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini.

Further, the peptides of the invention may be synthesized to alter their steric configuration. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer. Still further, at least one of the amino acid residues of the peptides of the invention may be substituted by one of the well-known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or binding action of the peptides of the invention.

Similarly, a peptide or variant of the invention may be modified chemically by reacting specific amino acids either before or after synthesis of the peptide. Examples for such modifications are well known in the art and are summarized e.g. in R. Lundblad, Chemical Reagents for Protein Modification, 3rd ed. CRC Press, 2005, which is incorporated herein by reference. Chemical modification of amino acids includes but is not limited to, modification by acylation, amidination, pyridoxylation of lysine, reductive alkylation, trinitrobenzylation of amino groups with 2,4,6-trinitrobenzene sulphonic acid (TNBS), amide modification of carboxyl groups and sulphydryl modification by performic acid oxidation of cysteine to cysteic acid, formation of mercurial derivatives, formation of mixed disulphides with other thiol compounds, reaction with maleimide, carboxymethylation with iodoacetic acid or iodoacetamide and carbamoylation with cyanate at alkaline pH, although without limitation thereto. In this regard, the skilled person is referred to Chapter 15 of Current Protocols In Protein Science, Eds. Coligan et al. (John Wiley and Sons NY 1995-2000) for more extensive methodology relating to chemical modification of proteins.

Briefly, modification of e.g. arginyl residues in proteins is often based on the reaction of vicinal dicarbonyl compounds such as phenylglyoxal, 2,3-butanedione, and 1,2-cyclohexanedione to form an adduct. Another example is the reaction of methylglyoxal with arginine residues. Cysteine can be modified without concomitant modification of other nucleophilic sites such as lysine and histidine. As a result, a large number of reagents are available for the modification of cysteine. The websites of companies such as Sigma-Aldrich (http://www.sigma-aldrich.com) provide information on specific reagents.

Selective reduction of disulfide bonds in proteins is also common. Disulfide bonds can be formed and oxidized during the heat treatment of biopharmaceuticals. Woodward's Reagent K may be used to modify specific glutamic acid residues. N-(3-(dimethylamino)propyl)-N'-ethylcarbodiimide can be used to form intra-molecular crosslinks between a lysine residue and a glutamic acid residue. For example, diethylpyrocarbonate is a reagent for the modification of histidyl residues in proteins. Histidine can also be modified using 4-hydroxy-2-nonenal. The reaction of lysine residues and other α-amino groups is, for example, useful in binding of peptides to surfaces or the cross-linking of proteins/peptides. Lysine is the site of attachment of poly(ethylene)glycol and the major site of modification in the glycosylation of proteins. Methionine residues in proteins can be modified with e.g. iodoacetamide, bromoethylamine, and chloramine T.

Tetranitromethane and N-acetylimidazole can be used for the modification of tyrosyl residues. Cross-linking via the formation of dityrosine can be accomplished with hydrogen peroxide/copper ions.

Recent studies on the modification of tryptophan have used N-bromosuccinimide, 2-hydroxy-5-nitrobenzyl bromide or 3-bromo-3-methyl-2-(2-nitrophenylmercapto)-3H-indole (BPNS-skatole).

Successful modification of therapeutic proteins and peptides with PEG is often associated with an extension of circulatory half-life while cross-linking of proteins with glutaraldehyde, polyethylene glycol diacrylate and formaldehyde is used for the preparation of hydrogels. Chemical modification of allergens for immunotherapy is often achieved by carbamylation with potassium cyanate.

A peptide or variant, wherein the peptide is modified or includes non-peptide bonds is a preferred embodiment of the invention. Generally, peptides and variants (at least those containing peptide linkages between amino acid residues) may be synthesized by the Fmoc-polyamide mode of solid-phase peptide synthesis as disclosed by Lukas et al. (Solid-phase peptide synthesis under continuous-flow conditions. Proc Natl Acad Sci U S A. May 1981; 78(5): 2791–2795), and references as cited therein. Temporary N-amino group protection is afforded by the 9-fluorenylmethyloxycarbonyl (Fmoc) group. Repetitive cleavage of this highly base-labile protecting group is done using 20% piperidine in N, N-dimethylformamide. Side-chain functionalities may be protected as their butyl ethers (in the case of serine threonine and tyrosine), butyl esters (in the case of glutamic acid and aspartic acid), butyloxycarbonyl derivative (in the case of lysine and histidine), trityl derivative (in the case of cysteine) and 4-methoxy-2,3,6-trimethylbenzenesulphonyl derivative (in the case of arginine). Where glutamine or asparagine are C-terminal residues, use is made of the 4,4'-dimethoxybenzhydryl group for protection of the side chain amido functionalities. The solid-phase support is based on a polydimethyl-acrylamide polymer constituted from the three monomers dimethylacrylamide (backbone-monomer), bisacryloylethylene diamine (cross linker) and acryloylsarcosine methyl ester (functionalizing agent). The peptide-to-resin cleavable linked agent used is the acid-labile 4-hydroxymethyl-phenoxyacetic acid derivative. All amino acid derivatives are added as their preformed symmetrical anhydride derivatives with the exception of asparagine and glutamine, which are added using a reversed N, N-dicyclohexyl-carbodiimide/1hydroxybenzotriazole mediated coupling procedure. All coupling and deprotection reactions are monitored using ninhydrin, trinitrobenzene sulphonic acid or isotin test procedures. Upon completion of synthesis, peptides are cleaved from the resin support with concomitant removal of

side-chain protecting groups by treatment with 95% trifluoroacetic acid containing a 50 % scavenger mix. Scavengers commonly used include ethandithiol, phenol, anisole and water, the exact choice depending on the constituent amino acids of the peptide being synthesized. Also a combination of solid phase and solution phase methodologies for the synthesis of peptides is possible (see, for example, Bruckdorfer et al., 2004, and the references as cited therein).

Trifluoroacetic acid is removed by evaporation in vacuo, with subsequent trituration with diethyl ether affording the crude peptide. Any scavengers present are removed by a simple extraction procedure which on lyophilization of the aqueous phase affords the crude peptide free of scavengers. Reagents for peptide synthesis are generally available from e.g. Calbiochem-Novabiochem (Nottingham, UK).

Purification may be performed by any one, or a combination of, techniques such as re-crystallization, size exclusion chromatography, ion-exchange chromatography, hydrophobic interaction chromatography and (usually) reverse-phase high performance liquid chromatography using e.g. acetonitril/water gradient separation.

Analysis of peptides may be carried out using thin layer chromatography, electrophoresis, in particular capillary electrophoresis, solid phase extraction (CSPE), reverse-phase high performance liquid chromatography, amino-acid analysis after acid hydrolysis and by fast atom bombardment (FAB) mass spectrometric analysis, as well as MALDI and ESI-Q-TOF mass spectrometric analysis.

A further aspect of the invention provides a nucleic acid (for example a polynucleotide) encoding a peptide or peptide variant of the invention. The polynucleotide may be, for example, DNA, cDNA, PNA, RNA or combinations thereof, either single- and/or double-stranded, or native or stabilized forms of polynucleotides, such as, for example, polynucleotides with a phosphorothioate backbone and it may or may not contain introns so long as it codes for the peptide. Of course, only peptides that contain naturally occurring amino acid residues joined by naturally occurring peptide bonds are

encodable by a polynucleotide. A still further aspect of the invention provides an expression vector capable of expressing a polypeptide according to the invention.

A variety of methods have been developed to link polynucleotides, especially DNA, to vectors for example via complementary cohesive termini. For instance, complementary homopolymer tracts can be added to the DNA segment to be inserted to the vector DNA. The vector and DNA segment are then joined by hydrogen bonding between the complementary homopolymeric tails to form recombinant DNA molecules.

Synthetic linkers containing one or more restriction sites provide an alternative method of joining the DNA segment to vectors. Synthetic linkers containing a variety of restriction endonuclease sites are commercially available from a number of sources including International Biotechnologies Inc. New Haven, CN, USA.

A desirable method of modifying the DNA encoding the polypeptide of the invention employs the polymerase chain reaction as disclosed by Saiki RK, et al. (Diagnosis of sickle cell anemia and beta-thalassemia with enzymatically amplified DNA and nonradioactive allele-specific oligonucleotide probes. N Engl J Med. 1988 Sep 1;319(9):537-41). This method may be used for introducing the DNA into a suitable vector, for example by engineering in suitable restriction sites, or it may be used to modify the DNA in other useful ways as is known in the art. If viral vectors are used, pox- or adenovirus vectors are preferred.

The DNA (or in the case of retroviral vectors, RNA) may then be expressed in a suitable host to produce a polypeptide comprising the peptide or variant of the invention. Thus, the DNA encoding the peptide or variant of the invention may be used in accordance with known techniques, appropriately modified in view of the teachings contained herein, to construct an expression vector, which is then used to transform an appropriate host cell for the expression and production of the polypeptide of the invention. Such techniques include those disclosed, for example, in US 4,440,859,

4,530,901, 4,582,800, 4,677,063, 4,678,751, 4,704,362, 4,710,463, 4,757,006, 4,766,075, and 4,810,648.

The DNA (or in the case of retroviral vectors, RNA) encoding the polypeptide constituting the compound of the invention may be joined to a wide variety of other DNA sequences for introduction into an appropriate host. The companion DNA will depend upon the nature of the host, the manner of the introduction of the DNA into the host, and whether episomal maintenance or integration is desired.

Generally, the DNA is inserted into an expression vector, such as a plasmid, in proper orientation and correct reading frame for expression. If necessary, the DNA may be linked to the appropriate transcriptional and translational regulatory control nucleotide sequences recognized by the desired host, although such controls are generally available in the expression vector. The vector is then introduced into the host through standard techniques. Generally, not all of the hosts will be transformed by the vector. Therefore, it will be necessary to select for transformed host cells. One selection technique involves incorporating into the expression vector a DNA sequence, with any necessary control elements, that codes for a selectable trait in the transformed cell, such as antibiotic resistance.

Alternatively, the gene for such selectable trait can be on another vector, which is used to co-transform the desired host cell.

Host cells that have been transformed by the recombinant DNA of the invention are then cultured for a sufficient time and under appropriate conditions known to those skilled in the art in view of the teachings disclosed herein to permit the expression of the polypeptide, which can then be recovered.

Many expression systems are known, including bacteria (for example *E. coli* and *Bacillus subtilis*), yeasts (for example *Saccharomyces cerevisiae*), filamentous fungi (for example *Aspergillus spec.*), plant cells, animal cells and insect cells. Preferably, the

system can be mammalian cells such as CHO cells available from the ATCC Cell Biology Collection.

A typical mammalian cell vector plasmid for constitutive expression comprises the CMV or SV40 promoter with a suitable poly A tail and a resistance marker, such as neomycin. One example is pSVL available from Pharmacia, Piscataway, NJ, USA. An example of an inducible mammalian expression vector is pMSG, also available from Pharmacia. Useful yeast plasmid vectors are pRS403-406 and pRS413-416 and are generally available from Stratagene Cloning Systems, La Jolla, CA 92037, USA. Plasmids pRS403, pRS404, pRS405 and pRS406 are Yeast Integrating plasmids (YIps) and incorporate the yeast selectable markers HIS3, TRP1, LEU2 and URA3. Plasmids pRS413-416 are Yeast Centromere plasmids (Ycps). CMV promoter-based vectors (for example from Sigma-Aldrich) provide transient or stable expression, cytoplasmic expression or secretion, and N-terminal or C-terminal tagging in various combinations of FLAG, 3xFLAG, c-myc or MAT. These fusion proteins allow for detection, purification and analysis of recombinant protein. Dual-tagged fusions provide flexibility in detection.

The strong human cytomegalovirus (CMV) promoter regulatory region drives constitutive protein expression levels as high as 1 mg/L in COS cells. For less potent cell lines, protein levels are typically ~0.1 mg/L. The presence of the SV40 replication origin will result in high levels of DNA replication in SV40 replication permissive COS cells. CMV vectors, for example, can contain the pMB1 (derivative of pBR322) origin for replication in bacterial cells, the b-lactamase gene for ampicillin resistance selection in bacteria, hGH polyA, and the f1 origin. Vectors containing the pre-pro-trypsin leader (PPT) sequence can direct the secretion of FLAG fusion proteins into the culture medium for purification using ANTI-FLAG antibodies, resins, and plates. Other vectors and expression systems are well known in the art for use with a variety of host cells.

In another embodiment two or more peptides or peptide variants of the invention are encoded and thus expressed in a successive order (similar to “beads on a string” constructs). In doing so, the peptides or peptide variants may be linked or fused

together by stretches of linker amino acids, such as for example LLLLLL, or may be linked without any additional peptide(s) between them. These constructs can also be used for cancer therapy, and may induce immune responses both involving MHC I and MHC II.

The present invention also relates to a host cell transformed with a polynucleotide vector construct of the present invention. The host cell can be either prokaryotic or eukaryotic. Bacterial cells may be preferred prokaryotic host cells in some circumstances and typically are a strain of *E. coli* such as, for example, the *E. coli* strains DH5 available from Bethesda Research Laboratories Inc., Bethesda, MD, USA, and RR1 available from the American Type Culture Collection (ATCC) of Rockville, MD, USA (No ATCC 31343). Preferred eukaryotic host cells include yeast, insect and mammalian cells, preferably vertebrate cells such as those from a mouse, rat, monkey or human fibroblastic and colon cell lines. Yeast host cells include YPH499, YPH500 and YPH501, which are generally available from Stratagene Cloning Systems, La Jolla, CA 92037, USA. Preferred mammalian host cells include Chinese hamster ovary (CHO) cells available from the ATCC as CCL61, NIH Swiss mouse embryo cells NIH/3T3 available from the ATCC as CRL 1658, monkey kidney-derived COS-1 cells available from the ATCC as CRL 1650 and 293 cells which are human embryonic kidney cells. Preferred insect cells are Sf9 cells which can be transfected with baculovirus expression vectors. An overview regarding the choice of suitable host cells for expression can be found in, for example, the textbook of Paulina Balbás and Argelia Lorence “Methods in Molecular Biology Recombinant Gene Expression, Reviews and Protocols,” Part One, Second Edition, ISBN 978-1-58829-262-9, and other literature known to the person of skill.

Transformation of appropriate cell hosts with a DNA construct of the present invention is accomplished by well-known methods that typically depend on the type of vector used. With regard to transformation of prokaryotic host cells, see, for example, Cohen et al (1972) Proc. Natl. Acad. Sci. USA 69, 2110, and Sambrook et al (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY.

Transformation of yeast cells is described in Sherman et al (1986) Methods In Yeast Genetics, A Laboratory Manual, Cold Spring Harbor, NY. The method of Beggs (1978) Nature 275,104-109 is also useful. With regard to vertebrate cells, reagents useful in transfecting such cells, for example calcium phosphate and DEAE-dextran or liposome formulations, are available from Stratagene Cloning Systems, or Life Technologies Inc., Gaithersburg, MD 20877, USA. Electroporation is also useful for transforming and/or transfecting cells and is well known in the art for transforming yeast cell, bacterial cells, insect cells and vertebrate cells.

Successfully transformed cells, i.e. cells that contain a DNA construct of the present invention, can be identified by well-known techniques such as PCR. Alternatively, the presence of the protein in the supernatant can be detected using antibodies.

It will be appreciated that certain host cells of the invention are useful in the preparation of the peptides of the invention, for example bacterial, yeast and insect cells. However, other host cells may be useful in certain therapeutic methods. For example, antigen-presenting cells, such as dendritic cells, may usefully be used to express the peptides of the invention such that they may be loaded into appropriate MHC molecules. Thus, the current invention provides a host cell comprising a nucleic acid or an expression vector according to the invention.

In a preferred embodiment the host cell is an antigen presenting cell, in particular a dendritic cell or antigen presenting cell. APCs loaded with a recombinant fusion protein containing prostatic acid phosphatase (PAP) were approved by the U.S. Food and Drug Administration (FDA) on April 29, 2010, to treat asymptomatic or minimally symptomatic metastatic HRPC (Sipuleucel-T) (Small EJ, et al. Placebo-controlled phase III trial of immunologic therapy with sipuleucel-T (APC8015) in patients with metastatic, asymptomatic hormone refractory prostate cancer. J Clin Oncol. 2006 Jul 1;24(19):3089-94. Rini et al. Combination immunotherapy with prostatic acid phosphatase pulsed antigen-presenting cells (provenge) plus bevacizumab in patients

with serologic progression of prostate cancer after definitive local therapy. Cancer. 2006 Jul 1;107(1):67-74).

A further aspect of the invention provides a method of producing a peptide or its variant, the method comprising culturing a host cell and isolating the peptide from the host cell or its culture medium.

In another embodiment the peptide, the nucleic acid or the expression vector of the invention are used in medicine. For example, the peptide or its variant may be prepared for intravenous (i.v.) injection, sub-cutaneous (s.c.) injection, intradermal (i.d.) injection, intraperitoneal (i.p.) injection, intramuscular (i.m.) injection. Preferred methods of peptide injection include s.c., i.d., i.p., i.m., and i.v. Preferred methods of DNA injection include i.d., i.m., s.c., i.p. and i.v. Doses of e.g. between 50 µg and 1.5 mg, preferably 125 µg to 500 µg, of peptide or DNA may be given and will depend on the respective peptide or DNA. Dosages of this range were successfully used in previous trials (Walter et al Nature Medicine 18, 1254–1261 (2012)).

Another aspect of the present invention includes an *in vitro* method for producing activated T cells, the method comprising contacting *in vitro* T cells with antigen loaded human MHC molecules expressed on the surface of a suitable antigen-presenting cell for a period of time sufficient to activate the T cell in an antigen specific manner, wherein the antigen is a peptide according to the invention. Preferably a sufficient amount of the antigen is used with an antigen-presenting cell.

Preferably the mammalian cell lacks or has a reduced level or function of the TAP peptide transporter. Suitable cells that lack the TAP peptide transporter include T2, RMA-S and Drosophila cells. TAP is the transporter associated with antigen processing.

The human peptide loading deficient cell line T2 is available from the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland 20852, USA under Catalogue No CRL 1992; the Drosophila cell line Schneider line 2 is available from the

ATCC under Catalogue No CRL 19863; the mouse RMA-S cell line is described in Karre et al. (Ljunggren, H.-G., and K. Karre. 1985. J. Exp. Med. 162:1745).

Preferably, before transfection the host cell expresses substantially no MHC class I molecules. It is also preferred that the stimulator cell expresses a molecule important for providing a co-stimulatory signal for T-cells such as any of B7.1, B7.2, ICAM-1 and LFA 3. The nucleic acid sequences of numerous MHC class I molecules and of the co-stimulator molecules are publicly available from the GenBank and EMBL databases.

In case of a MHC class I epitope being used as an antigen, the T cells are CD8-positive T cells.

If an antigen-presenting cell is transfected to express such an epitope, preferably the cell comprises an expression vector capable of expressing a peptide containing SEQ ID NO: 1 to SEQ ID NO: 300, or a variant amino acid sequence thereof.

A number of other methods may be used for generating T cells in vitro. For example, autologous tumor-infiltrating lymphocytes can be used in the generation of CTL. Plebanski et al. (Induction of peptide-specific primary cytotoxic T lymphocyte responses from human peripheral blood. Eur J Immunol. 1995 Jun;25(6):1783-7) make use of autologous peripheral blood lymphocytes (PLBs) in the preparation of T cells. Furthermore, the production of autologous T cells by pulsing dendritic cells with peptide or polypeptide, or via infection with recombinant virus is possible. Also, B cells can be used in the production of autologous T cells. In addition, macrophages pulsed with peptide or polypeptide, or infected with recombinant virus, may be used in the preparation of autologous T cells. S. Walter et al. 2003 (Cutting edge: predetermined avidity of human CD8 T cells expanded on calibrated MHC/anti-CD28-coated microspheres. J Immunol. 2003 Nov 15;171(10):4974-8) describe the in vitro priming of T cells by using artificial antigen presenting cells (aAPCs), which is also a suitable way for generating T cells against the peptide of choice. In the present invention, aAPCs were generated by the coupling of preformed MHC:peptide complexes to the surface of

polystyrene particles (microbeads) by biotin:streptavidin biochemistry. This system permits the exact control of the MHC density on aAPCs, which allows to selectively elicit high- or low-avidity antigen-specific T cell responses with high efficiency from blood samples. Apart from MHC:peptide complexes, aAPCs should carry other proteins with co-stimulatory activity like anti-CD28 antibodies coupled to their surface. Furthermore such aAPC-based systems often require the addition of appropriate soluble factors, e. g. cytokines, like interleukin-12.

Allogeneic cells may also be used in the preparation of T cells and a method is described in detail in WO 97/26328, incorporated herein by reference. For example, in addition to *drosophila* cells and T2 cells, other cells may be used to present antigens such as CHO cells, baculovirus-infected insect cells, bacteria, yeast, vaccinia-infected target cells. In addition plant viruses may be used (see, for example, Porta et al. (1994) Development of cowpea mosaic virus as a high-yielding system for the presentation of foreign peptides. Virology. 1994 Aug 1;202(2):949-55) which describes the development of cowpea mosaic virus as a high-yielding system for the presentation of foreign peptides.

The activated T cells that are directed against the peptides of the invention are useful in therapy. Thus, a further aspect of the invention provides activated T cells obtainable by the foregoing methods of the invention.

Activated T cells, which are produced by the above method, will selectively recognize a cell that aberrantly expresses a polypeptide that comprises an amino acid sequence of SEQ ID NO: 1 to SEQ ID NO 300.

Preferably, the T cell recognizes the cell by interacting through its TCR with the HLA/peptide-complex (for example, binding). The T cells are useful in a method of killing target cells in a patient whose target cells aberrantly express a polypeptide comprising an amino acid sequence of the invention wherein the patient is administered an effective number of the activated T cells. The T cells that are administered to the

patient may be derived from the patient and activated as described above (i.e. they are autologous T cells). Alternatively, the T cells are not from the patient but are from another individual. Of course, it is preferred if the individual is a healthy individual. By “healthy individual” the inventors mean that the individual is generally in good health, preferably has a competent immune system and, more preferably, is not suffering from any disease that can be readily tested for, and detected.

In vivo, the target cells for the CD8-positive T cells according to the present invention can be cells of the tumor (which sometimes express MHC class II) and/or stromal cells surrounding the tumor (tumor cells) (which sometimes also express MHC class II; (Dengjel et al., 2006)).

The T cells of the present invention may be used as active ingredients of a therapeutic composition. Thus, the invention also provides a method of killing target cells in a patient whose target cells aberrantly express a polypeptide comprising an amino acid sequence of the invention, the method comprising administering to the patient an effective number of T cells as defined above.

By ”aberrantly expressed“ the inventors also mean that the polypeptide is over-expressed compared to normal levels of expression or that the gene is silent in the tissue from which the tumor is derived but in the tumor it is expressed. By ”over-expressed“ the inventors mean that the polypeptide is present at a level at least 1.2-fold of that present in normal tissue; preferably at least 2-fold, and more preferably at least 5-fold or 10-fold the level present in normal tissue.

T cells may be obtained by methods known in the art, e.g. those described above.

Protocols for this so-called adoptive transfer of T cells are well known in the art. Reviews can be found in: Gattinoni L, et al. Adoptive immunotherapy for cancer: building on success. Nat Rev Immunol. 2006 May;6(5):383-93. Review. and Morgan

RA, et al. Cancer regression in patients after transfer of genetically engineered lymphocytes. Science. 2006 Oct 6;314(5796):126-9).

Any molecule of the invention, i.e. the peptide, nucleic acid, antibody, expression vector, cell, activated T cell, T-cell receptor or the nucleic acid encoding it is useful for the treatment of disorders, characterized by cells escaping an immune response. Therefore any molecule of the present invention may be used as medicament or in the manufacture of a medicament. The molecule may be used by itself or combined with other molecule(s) of the invention or (a) known molecule(s).

Preferably, the medicament of the present invention is a vaccine. It may be administered directly into the patient, into the affected organ or systemically i.d., i.m., s.c., i.p. and i.v., or applied *ex vivo* to cells derived from the patient or a human cell line which are subsequently administered to the patient, or used *in vitro* to select a subpopulation of immune cells derived from the patient, which are then re-administered to the patient. If the nucleic acid is administered to cells in vitro, it may be useful for the cells to be transfected so as to co-express immune-stimulating cytokines, such as interleukin-2. The peptide may be substantially pure, or combined with an immune-stimulating adjuvant (see below) or used in combination with immune-stimulatory cytokines, or be administered with a suitable delivery system, for example liposomes. The peptide may also be conjugated to a suitable carrier such as keyhole limpet haemocyanin (KLH) or mannan (see for example WO 95/18145). The peptide may also be tagged, may be a fusion protein, or may be a hybrid molecule. The peptides whose sequence is given in the present invention are expected to stimulate CD4 or CD8 T cells. However, stimulation of CD8 T cells is more efficient in the presence of help provided by CD4 T-helper cells. Thus, for MHC Class I epitopes that stimulate CD8 T cells the fusion partner or sections of a hybrid molecule suitably provide epitopes which stimulate CD4-positive T cells. CD4- and CD8-stimulating epitopes are well known in the art and include those identified in the present invention.

In one aspect, the vaccine comprises at least one peptide having the amino acid sequence set forth SEQ ID No. 1 to SEQ ID No. 300, and at least one additional peptide, preferably two to 50, more preferably two to 25, even more preferably two to 20 and most preferably two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen or eighteen peptides. The peptide(s) may be derived from one or more specific TAAs and may bind to MHC class I molecules.

In another aspect, the vaccine comprises at least one peptide having the amino acid sequence set forth in SEQ ID NO: 1 to SEQ ID NO: 300, and at least one additional peptide, preferably two to 50, more preferably two to 25, even more preferably two to 20 and most preferably two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen or eighteen peptides. The peptide(s) may be derived from one or more specific TAAs and may bind to MHC class I molecules.

The polynucleotide may be substantially pure, or contained in a suitable vector or delivery system. The nucleic acid may be DNA, cDNA, PNA, RNA or a combination thereof. Methods for designing and introducing such a nucleic acid are well known in the art. An overview is provided by e.g. (Pascolo et al., Human peripheral blood mononuclear cells transfected with messenger RNA stimulate antigen-specific cytotoxic T-lymphocytes in vitro. Cell Mol Life Sci. 2005 Aug;62(15):1755-62). Polynucleotide vaccines are easy to prepare, but the mode of action of these vectors in inducing an immune response is not fully understood. Suitable vectors and delivery systems include viral DNA and/or RNA, such as systems based on adenovirus, vaccinia virus, retroviruses, herpes virus, adeno-associated virus or hybrids containing elements of more than one virus. Non-viral delivery systems include cationic lipids and cationic polymers and are well known in the art of DNA delivery. Physical delivery, such as via a “gene-gun” may also be used. The peptide or peptides encoded by the nucleic acid may be a fusion protein, for example with an epitope that stimulates T cells for the respective opposite CDR as noted above.

The medicament of the invention may also include one or more adjuvants. Adjuvants are substances that non-specifically enhance or potentiate the immune response (e.g., immune responses mediated by CD8-positive T cells and helper-T (TH) cells to an antigen, and would thus be considered useful in the medicament of the present invention. Suitable adjuvants include, but are not limited to, 1018 ISS, aluminum salts, AMPLIVAX®, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, flagellin or TLR5 ligands derived from flagellin, FLT3 ligand, GM-CSF, IC30, IC31, Imiquimod (ALDARA®), resiquimod, ImuFact IMP321, Interleukins as IL-2, IL-13, IL-21, Interferon-alpha or -beta, or pegylated derivatives thereof, IS Patch, ISS, ISCOMATRIX, ISCOMs, JuvImmune®, LipoVac, MALP2, MF59, monophosphoryl lipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, water-in-oil and oil-in-water emulsions, OK-432, OM-174, OM-197-MP-EC, ONTAK, OspA, PepTel® vector system, poly(lactid co-glycolid) [PLG]-based and dextran microparticles, talactoferrin SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, Aquila's QS21 stimulon, which is derived from saponin, mycobacterial extracts and synthetic bacterial cell wall mimics, and other proprietary adjuvants such as Ribi's Detox, Quil, or Superfos. Adjuvants such as Freund's or GM-CSF are preferred. Several immunological adjuvants (e.g., MF59) specific for dendritic cells and their preparation have been described previously (Allison and Krummel, 1995 The Yin and Yang of T cell costimulation. Science. 1995 Nov 10;270(5238):932-3). Also cytokines may be used. Several cytokines have been directly linked to influencing dendritic cell migration to lymphoid tissues (e.g., TNF-), accelerating the maturation of dendritic cells into efficient antigen-presenting cells for T-lymphocytes (e.g., GM-CSF, IL-1 and IL-4) (U.S. Pat. No. 5,849,589, specifically incorporated herein by reference in its entirety) and acting as immunoadjuvants (e.g., IL-12, IL-15, IL-23, IL-7, IFN-alpha. IFN-beta) (Gabrilovich, 1996 Production of vascular endothelial growth factor by human tumors inhibits the functional maturation of dendritic cells Nat Med. 1996 Oct;2(10):1096-103).

CpG immunostimulatory oligonucleotides have also been reported to enhance the effects of adjuvants in a vaccine setting. Without being bound by theory, CpG

oligonucleotides act by activating the innate (non-adaptive) immune system via Toll-like receptors (TLR), mainly TLR9. CpG triggered TLR9 activation enhances antigen-specific humoral and cellular responses to a wide variety of antigens, including peptide or protein antigens, live or killed viruses, dendritic cell vaccines, autologous cellular vaccines and polysaccharide conjugates in both prophylactic and therapeutic vaccines. More importantly it enhances dendritic cell maturation and differentiation, resulting in enhanced activation of TH1 cells and strong cytotoxic T-lymphocyte (CTL) generation, even in the absence of CD4 T cell help. The TH1 bias induced by TLR9 stimulation is maintained even in the presence of vaccine adjuvants such as alum or incomplete Freund's adjuvant (IFA) that normally promote a TH2 bias. CpG oligonucleotides show even greater adjuvant activity when formulated or co-administered with other adjuvants or in formulations such as microparticles, nanoparticles, lipid emulsions or similar formulations, which are especially necessary for inducing a strong response when the antigen is relatively weak. They also accelerate the immune response and enable the antigen doses to be reduced by approximately two orders of magnitude, with comparable antibody responses to the full-dose vaccine without CpG in some experiments (Krieg, 2006). US 6,406,705 B1 describes the combined use of CpG oligonucleotides, non-nucleic acid adjuvants and an antigen to induce an antigen-specific immune response. A CpG TLR9 antagonist is dSLIM (double Stem Loop Immunomodulator) by Mologen (Berlin, Germany) which is a preferred component of the pharmaceutical composition of the present invention. Other TLR binding molecules such as RNA binding TLR 7, TLR 8 and/or TLR 9 may also be used.

Other examples for useful adjuvants include, but are not limited to chemically modified CpGs (e.g. CpR, Idera), dsRNA analogues such as Poly(I:C) and derivates thereof (e.g. AmpliGen®, Hiltonol®, poly-(ICLC), poly(IC-R), poly(I:C12U), non-CpG bacterial DNA or RNA as well as immunoactive small molecules and antibodies such as cyclophosphamide, sunitinib, Bevacizumab®, celebrex, NCX-4016, sildenafil, tadalafil, vardenafil, sorafenib, temozolomide, temsirolimus, XL-999, CP-547632, pazopanib, VEGF Trap, ZD2171, AZD2171, anti-CTLA4, other antibodies targeting key structures of the immune system (e.g. anti-CD40, anti-TGFbeta, anti-TNFalpha receptor) and

SC58175, which may act therapeutically and/or as an adjuvant. The amounts and concentrations of adjuvants and additives useful in the context of the present invention can readily be determined by the skilled artisan without undue experimentation.

Preferred adjuvants are anti-CD40, imiquimod, resiquimod, GM-CSF, cyclophosphamide, sunitinib, bevacizumab, interferon-alpha, CpG oligonucleotides and derivates, poly-(I:C) and derivates, RNA, sildenafil, and particulate formulations with PLG or virosomes.

In a preferred embodiment, the pharmaceutical composition according to the invention the adjuvant is selected from the group consisting of colony-stimulating factors, such as Granulocyte Macrophage Colony Stimulating Factor (GM-CSF, sargramostim), cyclophosphamide, imiquimod, resiquimod, and interferon-alpha.

In a preferred embodiment, the pharmaceutical composition according to the invention the adjuvant is selected from the group consisting of colony-stimulating factors, such as Granulocyte Macrophage Colony Stimulating Factor (GM-CSF, sargramostim), cyclophosphamide, imiquimod and resiquimod. In a preferred embodiment of the pharmaceutical composition according to the invention, the adjuvant is cyclophosphamide, imiquimod or resiquimod. Even more preferred adjuvants are Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, poly-ICLC (Hiltonol®) and anti-CD40 mAB, or combinations thereof.

This composition is used for parenteral administration, such as subcutaneous, intradermal, intramuscular or oral administration. For this, the peptides and optionally other molecules are dissolved or suspended in a pharmaceutically acceptable, preferably aqueous carrier. In addition, the composition can contain excipients, such as buffers, binding agents, blasting agents, diluents, flavors, lubricants, etc. The peptides can also be administered together with immune stimulating substances, such as cytokines. An extensive listing of excipients that can be used in such a composition, can be, for example, taken from A. Kibbe, Handbook of Pharmaceutical Excipients, 3rd Ed.,

2000, American Pharmaceutical Association and pharmaceutical press. The composition can be used for a prevention, prophylaxis and/or therapy of adenomateous or cancerous diseases. Exemplary formulations can be found in, for example, EP2112253.

The present invention provides a medicament that useful in treating cancer, in particular HCC and other malignancies.

The present invention is further directed at a kit comprising:
(a) a container containing a pharmaceutical composition as described above, in solution or in lyophilized form;
(b) optionally a second container containing a diluent or reconstituting solution for the lyophilized formulation; and
(c) optionally, instructions for (i) use of the solution or (ii) reconstitution and/or use of the lyophilized formulation.

The kit may further comprise one or more of (iii) a buffer, (iv) a diluent, (v) a filter, (vi) a needle, or (v) a syringe. The container is preferably a bottle, a vial, a syringe or test tube; and it may be a multi-use container. The pharmaceutical composition is preferably lyophilized.

Kits of the present invention preferably comprise a lyophilized formulation of the present invention in a suitable container and instructions for its reconstitution and/or use. Suitable containers include, for example, bottles, vials (e.g. dual chamber vials), syringes (such as dual chamber syringes) and test tubes. The container may be formed from a variety of materials such as glass or plastic. Preferably the kit and/or container contain/s instructions on or associated with the container that indicates directions for reconstitution and/or use. For example, the label may indicate that the lyophilized formulation is to be reconstituted to peptide concentrations as described above. The label may further indicate that the formulation is useful or intended for subcutaneous administration.

The container holding the formulation may be a multi-use vial, which allows for repeat administrations (e.g., from 2-6 administrations) of the reconstituted formulation. The kit may further comprise a second container comprising a suitable diluent (e.g., sodium bicarbonate solution).

Upon mixing of the diluent and the lyophilized formulation, the final peptide concentration in the reconstituted formulation is preferably at least 0.15 mg/mL/peptide (=75 µg) and preferably not more than 3 mg/mL/peptide (=1500 µg). The kit may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

Kits of the present invention may have a single container that contains the formulation of the pharmaceutical compositions according to the present invention with or without other components (e.g., other compounds or pharmaceutical compositions of these other compounds) or may have distinct container for each component.

Preferably, kits of the invention include a formulation of the invention packaged for use in combination with the co-administration of a second compound (such as adjuvants (e.g. GM-CSF), a chemotherapeutic agent, a natural product, a hormone or antagonist, an anti-angiogenesis agent or inhibitor, an apoptosis-inducing agent or a chelator) or a pharmaceutical composition thereof. The components of the kit may be pre-complexed or each component may be in a separate distinct container prior to administration to a patient. The components of the kit may be provided in one or more liquid solutions, preferably, an aqueous solution, more preferably, a sterile aqueous solution. The components of the kit may also be provided as solids, which may be converted into liquids by addition of suitable solvents, which are preferably provided in another distinct container.

The container of a therapeutic kit may be a vial, test tube, flask, bottle, syringe, or any other means of enclosing a solid or liquid. Usually, when there is more than one component, the kit will contain a second vial or other container, which allows for separate dosing. The kit may also contain another container for a pharmaceutically acceptable liquid. Preferably, a therapeutic kit will contain an apparatus (e.g., one or more needles, syringes, eye droppers, pipette, etc.), which enables administration of the agents of the invention that are components of the present kit.

The present formulation is one that is suitable for administration of the peptides by any acceptable route such as oral (enteral), nasal, ophthal, subcutaneous, intradermal, intramuscular, intravenous or transdermal. Preferably, the administration is s.c., and most preferably i.d. administration may be by infusion pump.

Since the peptides of the invention were isolated from HCC, the medicament of the invention is preferably used to treat HCC.

The present invention further includes a method for producing a personalized pharmaceutical for an individual patient comprising manufacturing a pharmaceutical composition comprising at least one peptide selected from a warehouse of pre-screened TUMAPs, wherein the at least one peptide used in the pharmaceutical composition is selected for suitability in the individual patient. In one embodiment , the pharmaceutical composition is a vaccine. The method could also be adapted to produce T cell clones for down-stream applications, such as TCR isolations, or soluble antibodies and other treatment options.

A “personalized pharmaceutical” shall mean specifically tailored therapies for one individual patient that will only be used for therapy in such individual patient, including actively personalized cancer vaccines and adoptive cellular therapies using autologous patient tissue.

As used herein, the term “warehouse” shall refer to a group of peptides that have been pre-screened for immunogenicity and/or over-presentation in a particular tumor type. The term “warehouse” is not intended to imply that the particular peptides included in the vaccine have been pre-manufactured and stored in a physical facility, although that possibility is contemplated. It is expressly contemplated that the peptides may be manufactured *de novo* for each individualized vaccine produced, or may be pre-manufactured and stored. The warehouse (e.g. in the form of a database) is composed of tumor-associated peptides which were highly overexpressed in the tumor tissue of HCC patients with various HLA-A HLA-B and HLA-C alleles. It may contain MHC class I and MHC class II peptides or elongated MHC class I peptides. In addition to the tumor associated peptides collected from several HCC tissues, the warehouse may contain HLA-A*02 and HLA-A*24 marker peptides. These peptides allow comparison of the magnitude of T-cell immunity induced by TUMAPS in a quantitative manner and hence allow important conclusion to be drawn on the capacity of the vaccine to elicit anti-tumor responses. Secondly, they function as important positive control peptides derived from a “non-self” antigen in the case that any vaccine-induced T-cell responses to TUMAPs derived from “self” antigens in a patient are not observed. And third, it may allow conclusions to be drawn, regarding the status of immunocompetence of the patient.

TUMAPs for the warehouse are identified by using an integrated functional genomics approach combining gene expression analysis, mass spectrometry, and T-cell immunology (XPresident ®). The approach assures that only TUMAPs truly present on a high percentage of tumors but not or only minimally expressed on normal tissue, are chosen for further analysis. For initial peptide selection, HCC samples from patients and blood from healthy donors were analyzed in a stepwise approach:

1. HLA ligands from the malignant material were identified by mass spectrometry
2. Genome-wide messenger ribonucleic acid (mRNA) expression analysis was used to identify genes over-expressed in the malignant tissue (HCC) compared with a range of normal organs and tissues
3. Identified HLA ligands were compared to gene expression data. Peptides over-presented or selectively presented on tumor tissue, preferably encoded by selectively

expressed or over-expressed genes as detected in step 2 were considered suitable TUMAP candidates for a multi-peptide vaccine.
4. Literature research was performed in order to identify additional evidence supporting the relevance of the identified peptides as TUMAPs
5. The relevance of over-expression at the mRNA level was confirmed by redetection of selected TUMAPs from step 3 on tumor tissue and lack of (or infrequent) detection on healthy tissues.
6. In order to assess, whether an induction of *in vivo* T-cell responses by the selected peptides may be feasible, in vitro immunogenicity assays were performed using human T cells from healthy donors as well as from HCC patients.

It is important to realize that the immune response triggered by the vaccine according to the invention attacks the cancer in different cell-stages and different stages of development. Furthermore different cancer associated signaling pathways are attacked. This is an advantage over vaccines that address only one or few targets, which may cause the tumor to easily adapt to the attack (tumor escape). Furthermore, not all individual tumors express the same pattern of antigens. Therefore, a combination of several tumor-associated peptides ensures that every single tumor bears at least some of the targets. The composition was specifically designed in such a way that each HLA-A*02 and/or HLA-A*24-positive tumor is expected to express several of the antigens and cover several independent pathways necessary for tumor growth and maintenance. For each of the peptide subsets specific for the two HLA class I alleles (A*02 and A*24) this is independently ensured based on the underlying experimental analyses. Thus, the vaccine can easily be used “off-the–shelf” for a larger patient population. This means that a pre-selection of patients to be treated with the vaccine can be restricted to HLA typing, does not require any additional biomarker assessments for antigen expression, but it is still ensured that several targets are simultaneously attacked by the induced immune response, which is important for efficacy (Banchereau et al., 2001; Walter et al., 2012).

In an aspect, the peptides are pre-screened for immunogenicity before being included in the warehouse. By way of example, and not limitation, the immunogenicity of the peptides included in the warehouse is determined by a method comprising *in vitro* T-cell priming through repeated stimulations of CD8+ T cells from healthy donors with artificial antigen presenting cells loaded with peptide/MHC complexes and anti-CD28 antibody.

This method is preferred for rare cancers and patients with a rare expression profile. In contrast to multi-peptide cocktails with a fixed composition as currently developed the warehouse allows a significantly higher matching of the actual expression of antigens in the tumor with the vaccine. Selected single or combinations of several “off-the-shelf” peptides will be used for each patient in a multitarget approach. In theory an approach based on selection of e.g. 5 different antigenic peptides from a library of 50 would already lead to approximately 17 million possible drug product (DP) compositions.

In an aspect, the peptides are selected for inclusion in the vaccine based on their suitability for the individual patient based on the method according to the present invention as described herein, or as below.

The HLA phenotype, transcriptomic and peptidomic data is gathered from the patient’s tumor material, and blood samples to identify the most suitable peptides for each patient containing “warehouse” and patient-unique (i.e. mutated) TUMAPs. Those peptides will be chosen, which are selectively or over-expressed in the patients tumor and, where possible, show strong *in vitro* immunogenicity if tested with the patients’ individual PBMCs.

Preferably, the peptides included in the vaccine are identified by a method comprising: (a) identifying tumor-associated peptides (TUMAPs) presented by a tumor sample from the individual patient; (b) comparing the peptides identified in (a) with a warehouse (database) of peptides as described above; and (c) selecting at least one peptide from the warehouse (database) that correlates with a tumor-associated peptide identified in the patient. For example, the TUMAPs presented by the tumor sample are identified by:

(a1) comparing expression data from the tumor sample to expression data from a sample of normal tissue corresponding to the tissue type of the tumor sample to identify proteins that are over-expressed or aberrantly expressed in the tumor sample; and (a2) correlating the expression data with sequences of MHC ligands bound to MHC class I and/or class II molecules in the tumor sample to identify MHC ligands derived from proteins over-expressed or aberrantly expressed by the tumor. Preferably, the sequences of MHC ligands are identified by eluting bound peptides from MHC molecules isolated from the tumor sample, and sequencing the eluted ligands. Preferably, the tumor sample and the normal tissue are obtained from the same patient.

In addition to, or as an alternative to, selecting peptides using a warehousing (database) model, TUMAPs may be identified in the patient *de novo*, and then included in the vaccine. As one example, candidate TUMAPs may be identified in the patient by (a1) comparing expression data from the tumor sample to expression data from a sample of normal tissue corresponding to the tissue type of the tumor sample to identify proteins that are over-expressed or aberrantly expressed in the tumor sample; and (a2) correlating the expression data with sequences of MHC ligands bound to MHC class I and/or class II molecules in the tumor sample to identify MHC ligands derived from proteins over-expressed or aberrantly expressed by the tumor. As another example, proteins may be identified containing mutations that are unique to the tumor sample relative to normal corresponding tissue from the individual patient, and TUMAPs can be identified that specifically target the mutation. For example, the genome of the tumor and of corresponding normal tissue can be sequenced by whole genome sequencing: For discovery of non-synonymous mutations in the protein-coding regions of genes, genomic DNA and RNA are extracted from tumor tissues and normal non-mutated genomic germline DNA is extracted from peripheral blood mononuclear cells (PBMCs). The applied NGS approach is confined to the re-sequencing of protein coding regions (exome re-sequencing). For this purpose, exonic DNA from human samples is captured using vendor-supplied target enrichment kits, followed by sequencing with e.g. a HiSeq2000 (Illumina). Additionally, tumor mRNA is sequenced for direct quantification of gene expression and validation that mutated genes are expressed in the patients'

tumors. The resultant millions of sequence reads are processed through software algorithms. The output list contains mutations and gene expression. Tumor-specific somatic mutations are determined by comparison with the PBMC-derived germline variations and prioritized. The *de novo* identified peptides can then be tested for immunogenicity as described above for the warehouse, and candidate TUMAPs possessing suitable immunogenicity are selected for inclusion in the vaccine.

In one exemplary embodiment, the peptides included in the vaccine are identified by: (a) identifying tumor-associated peptides (TUMAPs) presented by a tumor sample from the individual patient by the method as described above; (b) comparing the peptides identified in a) with a warehouse of peptides that have been prescreened for immunogenicity and overpresentation in tumors as compared to corresponding normal tissue; (c) selecting at least one peptide from the warehouse that correlates with a tumor-associated peptide identified in the patient; and (d) optionally, selecting at least one peptide identified de novo in (a) confirming its immunogenicity.

In one exemplary embodiment, the peptides included in the vaccine are identified by: (a) identifying tumor-associated peptides (TUMAPs) presented by a tumor sample from the individual patient; and (b) selecting at least one peptide identified de novo in (a) and confirming its immunogenicity.

Once the peptides for a personalized peptide based vaccine are selected, the vaccine is produced. The vaccine preferably is a liquid formulation consisting of the individual peptides dissolved in 33% DMSO.

Each peptide to be included into a product is dissolved in DMSO. The concentration of the single peptide solutions has to be chosen depending on the number of peptides to be included into the product. The single peptide-DMSO solutions are mixed in equal parts to achieve a solution containing all peptides to be included in the product with a concentration of ~2.5 mg/ml per peptide. The mixed solution is then diluted 1:3 with water for injection to achieve a concentration of 0.826 mg/ml per peptide in 33% DMSO.

The diluted solution is filtered through a 0.22 µm sterile filter. The final bulk solution is obtained.

Final bulk solution is filled into vials and stored at -20°C until use. One vial contains 700 µL solution, containing 0.578 mg of each peptide. Of this, 500 µL (approx. 400 µg per peptide) will be applied for intradermal injection.

The present invention will now be described in the following examples which describe preferred embodiments thereof, nevertheless, without being limited thereto. For the purposes of the present invention, all references as cited herein are incorporated by reference in their entireties.

In the Figures,

Figure 1 shows the over-presentation of various peptides in normal tissues (dark gray) and HCC (light gray). Figure 1A) APOB, Peptide: ALVDTLKFV (A*02) (SEQ ID NO: 7), tissues from left to right; 1 adipose tissues, 3 adrenal glands, 2 arteries, 2 bone marrows, 7 brains, 3 breasts, 13 colons, 4 esophagi, 2 gallbladders, 3 GI tracts, 3 hearts, 16 kidneys, 4 leukocyte samples, 45 lungs, 1 lymph node, 1 ovary, 7 pancreas, 1 peripheral nerve, 1 pituitary gland, 3 pleuras, 1 prostate, 6 recti, 3 sceletal muscles, 1 serous membrane, 3 skins, 4 spleens, 7 stomachs, 1 testis, 2 thymi, 3 thyroid glands, 2 uteri, 2 veins, and 20 livers; Figure 1B) ALDH1L1, Peptide: KLQAGTVFV (A*02) (SEQ ID NO: 2), tissues from left to right: 1 adipose tissues, 3 adrenal glands, 2 arteries, 2 bone marrows, 7 brains, 3 breasts, 13 colons, 4 esophagi, 2 gallbladders, 3 GI tracts, 3 hearts, 16 kidneys, 4 leukocyte samples, 45 lungs, 1 lymph node, 1 ovary, 7 pancreas, 1 peripheral nerve, 1 pituitary gland, 3 pleuras, 1 prostate, 6 recti, 3 sceletal muscles, 1 serous membrane, 3 skins, 4 spleens, 7 stomachs, 1 testis, 2 thymi, 3 thyroid glands, 2 uteri, 2 veins, and 20 livers; Figure 1C) C8B, Peptide: AYLLQPSQF (A*24) (SEQ ID NO: 200), tissues from left to right: including 2 adrenal glands, 1 artery, 4 brains, 1 breast, 5 colons, 1 hearts, 13 kidneys, 9 lungs, 3 pancreas, 2 recti, 3 skins, 1 spleen, 12 stomachs, 1 thymus, 2 uteri, and 9 livers; Figure 1D) RAD23B Peptide: KIDEKNFVV

(SEQ ID NO: 63) 1 serous membrane, 1 adipose tissue, 3 adrenal glands, 2 arteries, 2 bone marrows, 7 brains, 3 breasts, 13 colons, 2 gallbladders, 3 GI tracts, 3 hearts, 12 kidneys, 4 leukocytes, 19 livers, 43 lungs, 1 lymph node, 1 ovary, 6 pancreases, 1 peripheral nerve, 1 pituitary gland, 3 pleuras, 1 prostate, 6 rectums, 3 skeletal muscles, 3 skins, 4 spleens, 5 stomachs, 1 testis, 2 thymi, 3 thyroid glands, 2 uteri, 2 veins, 4 esophagi; Figure 1E) RAD23B Peptide: KIDEKNFVV (SEQ ID NO: 63), shown are only samples on which the peptide was presented: 5 cell-lines, 1 normal tissue (1 adrenal gland), 16 cancer tissues (2 brain cancers, 4 liver cancers, 5 lung cancers, 1 rectum cancer, 1 urinary bladder cancer, 3 uterus cancers) (from left to right); Figure 1F) RFNG RLPPDTLLQQV (SEQ ID NO: 92), shown are only samples on which the peptide was presented: 1 serous membrane, 1 adipose tissue, 3 adrenal glands, 2 arteries, 2 bone marrows, 7 brains, 3 breasts, 13 colons, 2 gallbladders, 3 GI tracts, 3 hearts, 12 kidneys, 4 leukocytes, 19 livers, 43 lungs, 1 lymph node, 1 ovary, 6 pancreases, 1 peripheral nerve, 1 pituitary gland, 3 pleuras, 1 prostate, 6 rectums, 3 skeletal muscles, 3 skins, 4 spleens, 5 stomachs, 1 testis, 2 thymi, 3 thyroid glands, 2 uteri, 2 veins, 4 esophagi; Figure 1G) RFNG Peptide: RLPPDTLLQQV (SEQ ID NO: 92), shown are only samples on which the peptide was presented: 2 cell-lines, 2 normal tissues (2 adrenal glands), 17 cancer tissues (1 brain cancer, 1 breast cancer, 1 esophageal cancer, 5 liver cancers, 4 lung cancers, 1 ovarian cancer, 1 prostate cancer, 2 urinary bladder cancers, 1 uterus cancer) (from left to right); Figure 1H) FLVCR1 Peptide: SVWFGPKEV (SEQ ID NO: 104) 1 serous membrane, 1 adipose tissue, 3 adrenal glands, 2 arteries, 2 bone marrows, 7 brains, 3 breasts, 13 colons, 2 gallbladders, 3 GI tracts, 3 hearts, 12 kidneys, 4 leukocytes, 19 livers, 43 lungs, 1 lymph node, 1 ovary, 6 pancreases, 1 peripheral nerve, 1 pituitary gland, 3 pleuras, 1 prostate, 6 rectums, 3 skeletal muscles, 3 skins, 4 spleens, 5 stomachs, 1 testis, 2 thymi, 3 thyroid glands, 2 uteri, 2 veins, 4 esophagi; Figure 1I) FLVCR1 Peptide: SVWFGPKEV (SEQ ID NO: 104), shown are only samples on which the peptide was presented: 9 cell lines, 1 normal tissue (1 small intestine), 16 cancer tissues (1 brain cancer, 1 breast cancer, 5 liver cancers, 5 lung cancers, 1 skin cancer, 1 stomach cancer, 1 urinary bladder cancer, 1 uterus cancer) (from left to right); Figure 1J) IKBKAP Peptide: LLFPHPVNQV (SEQ ID NO: 156) 1 serous membrane, 1 adipose tissue, 3 adrenal glands, 2 arteries,

2 bone marrows, 7 brains, 3 breasts, 13 colons, 2 gallbladders, 3 GI tracts, 3 hearts, 12 kidneys, 4 leukocytes, 19 livers, 43 lungs, 1 lymph node, 1 ovary, 6 pancreases, 1 peripheral nerve, 1 pituitary gland, 3 pleuras, 1 prostate, 6 rectums, 3 skeletal muscles, 3 skins, 4 spleens, 5 stomachs, 1 testis, 2 thymi, 3 thyroid glands, 2 uteri, 2 veins, 4 esophagi; Figure 1K) IKBKAP Peptide: LLFPHPVNQV (SEQ ID NO: 156), shown are only samples on which the peptide was presented: 7 cell-lines, 2 primary cultures, 1 normal tissue (1 colon), 34 cancer tissues (1 bone marrow cancer, 1 breast cancer, 1 colon cancer, 2 esophageal cancers, 2 leukocytic leukemia cancers, 4 liver cancers, 11 lung cancers, 3 lymph node cancers, 5 ovarian cancers, 4 urinary bladder cancers) (from left to right); Figure 1L) NKD1 Peptide: FLDTPIAKV (SEQ ID NO: 47), 1 serous membrane, 1 adipose tissue, 3 adrenal glands, 2 arteries, 2 bone marrows, 7 brains, 3 breasts, 13 colons, 2 gallbladders, 3 GI tracts, 3 hearts, 12 kidneys, 4 leukocytes, 19 livers, 43 lungs, 1 lymph node, 1 ovary, 6 pancreases, 1 peripheral nerve, 1 pituitary gland, 3 pleuras, 1 prostate, 6 rectums, 3 skeletal muscles, 3 skins, 4 spleens, 5 stomachs, 1 testis, 2 thymi, 3 thyroid glands, 2 uteri, 2 veins, 4 esophagi; Figure 1M) NKD1 Peptide: FLDTPIAKV (SEQ ID NO: 47), shown are only samples on which the peptide was presented: 1 other disease (encephalocele), 2 normal tissues (1 lung, 1 spleen), 35 cancer tissues (5 brain cancers, 6 colon cancers, 1 esophageal cancer, 6 liver cancers, 9 lung cancers, 1 ovarian cancer, 1 prostate cancer, 4 rectum cancers, 2 stomach cancers) (from left to right).

Figure 2 shows exemplary expression profiles (relative expression compared to normal kidney) of source genes of the present invention that are highly over-expressed or exclusively expressed in HCC in a panel of normal tissues (dark gray) and 12 HCC samples (gray). Figure 2A) APOB, tissues from left to right: 1 adrenal gland, 1 artery, 1 bone marrow, 1 brain (whole), 1 breast, 1 colon, 1 esophagus, 1 heart, 3 kidneys, 1 leukocyte sample, 1 liver, 1 lung, 1lymph node, 1 ovary, 1 pancreas, 1 placenta, 1 prostate, 1 salivary gland, 1 skeletal muscle, 1 skin, 1 small intestine, 1 spleen, 1 stomach, 1 testis, 1 thymus, 1 thyroid gland, 1 urinary bladder, 1 uterine cervix, 1 uterus, 1 vein; Figure 2B) AMACR, tissues from left to right: 1 adrenal gland, 1 artery, 1 bone marrow, 1 brain (whole), 1 breast, 1 colon, 1 esophagus, 1 heart, 3 kidneys, 1

leukocyte sample, 1 liver, 1 lung, 1lymph node, 1 ovary, 1 pancreas, 1 placenta, 1 prostate, 1 salivary gland, 1 skeletal muscle, 1 skin, 1 small intestine, 1 spleen, 1 stomach, 1 testis, 1 thymus, 1 thyroid gland, 1 urinary bladder, 1 uterine cervix, 1 uterus, 1 vein; Figure 2C) ALDH1L1, tissues from left to right: 1 adrenal gland, 1 artery, 1 bone marrow, 1 brain (whole), 1 breast, 1 colon, 1 esophagus, 1 heart, 3 kidneys, 1 leukocyte sample, 1 liver, 1 lung, 1lymph node, 1 ovary, 1 pancreas, 1 placenta, 1 prostate, 1 salivary gland, 1 skeletal muscle, 1 skin, 1 small intestine, 1 spleen, 1 stomach, 1 testis, 1 thymus, 1 thyroid gland, 1 urinary bladder, 1 uterine cervix, 1 uterus, 1 vein; Figure 2D) FGG, tissues from left to right: 1 adrenal gland, 1 artery, 1 bone marrow, 1 brain (whole), 1 breast, 1 colon, 1 esophagus, 1 heart, 3 kidneys, 1 leukocyte sample, 1 liver, 1 lung, 1lymph node, 1 ovary, 1 pancreas, 1 placenta, 1 prostate, 1 salivary gland, 1 skeletal muscle, 1 skin, 1 small intestine, 1 spleen, 1 stomach, 1 testis, 1 thymus, 1 thyroid gland, 1 urinary bladder, 1 uterine cervix, 1 uterus, 1 vein; Figure 2E) C8B, tissues from left to right: 1 adrenal gland, 1 artery, 1 bone marrow, 1 brain (whole), 1 breast, 1 colon, 1 esophagus, 1 heart, 3 kidneys, 1 leukocyte sample, 1 liver, 1 lung, 1lymph node, 1 ovary, 1 pancreas, 1 placenta, 1 prostate, 1 salivary gland, 1 skeletal muscle, 1 skin, 1 small intestine, 1 spleen, 1 stomach, 1 testis, 1 thymus, 1 thyroid gland, 1 urinary bladder, 1 uterine cervix, 1 uterus, 1 vein; and Figure 2F) HSD17B6, tissues from left to right: including 1 adrenal gland, 1 artery, 1 bone marrow, 1 brain (whole), 1 breast, 1 colon, 1 esophagus, 1 heart, 3 kidneys, 1 leukocyte sample, 1 liver, 1 lung, 1lymph node, 1 ovary, 1 pancreas, 1 placenta, 1 prostate, 1 salivary gland, 1 skeletal muscle, 1 skin, 1 small intestine, 1 spleen, 1 stomach, 1 testis, 1 thymus, 1 thyroid gland, 1 urinary bladder, 1 uterine cervix, 1 uterus, and 1 vein.

Figure 3 shows exemplary flow cytometry results after peptide-specific multimer staining. Further explanations see example 4.

Figure 4 shows exemplary flow cytometry results after peptide-specific multimer staining. Further explanations see example 4.

EXAMPLES

EXAMPLE 1: Identification and quantitation of tumor associated peptides presented on the cell surface

Tissue samples

Patients' tumor tissues were obtained from Universitätsklinik für Allgemeine, Viszeral- und Transplantationschirurgie, Tübingen, Germany; Istituto Nazionale Tumori "Pascale". Molecular Biology and Viral Oncology Unit, Via Mariano, Naples, Italy; Bio-Options Inc., Brea, CA, USA; ProteoGenex Inc., Culver City, CA, USA; Asterand Europe, Royston Herts, United Kingdom. Written informed consents of all patients had been given before surgery. Tissues were shock-frozen immediately after surgery and stored until isolation of TUMAPs at -70°C or below.

Isolation of HLA peptides from tissue samples

HLA peptide pools from shock-frozen tissue samples were obtained by immune precipitation from solid tissues according to a slightly modified protocol (Falk, K., 1991; Seeger, F.H.T., 1999) using the HLA-A*02-specific antibody BB7.2, the HLA-A, -B, -C-specific antibody W6/32, CNBr-activated sepharose, acid treatment, and ultrafiltration.

Mass spectrometry analyses

The HLA peptide pools as obtained were separated according to their hydrophobicity by reversed-phase chromatography (nanoAcquity UPLC system, Waters) and the eluting peptides were analyzed in LTQ- velos and fusion hybrid mass spectrometers (ThermoElectron) equipped with an ESI source. Peptide pools were loaded directly onto the analytical fused-silica micro-capillary column (75 µm i.d. x 250 mm) packed with 1.7 µm C18 reversed-phase material (Waters) applying a flow rate of 400 nL per minute. Subsequently, the peptides were separated using a two-step 180 minute-binary gradient from 10% to 33% B at a flow rate of 300 nL per minute. The gradient was composed of Solvent A (0.1% formic acid in water) and solvent B (0.1% formic acid in acetonitrile). A gold coated glass capillary (PicoTip, New Objective) was used for introduction into the nanoESI source. The LTQ-Orbitrap mass spectrometers were operated in the data-

dependent mode using a TOP5 strategy. In brief, a scan cycle was initiated with a full scan of high mass accuracy in the orbitrap (R = 30 000), which was followed by MS/MS scans also in the orbitrap (R = 7500) on the 5 most abundant precursor ions with dynamic exclusion of previously selected ions. Tandem mass spectra were interpreted by SEQUEST and additional manual control. The identified peptide sequence was assured by comparison of the generated natural peptide fragmentation pattern with the fragmentation pattern of a synthetic sequence-identical reference peptide.

Label-free relative LC-MS quantitation was performed by ion counting i.e. by extraction and analysis of LC-MS features (Mueller et al. 2007a). The method assumes that the peptide's LC-MS signal area correlates with its abundance in the sample. Extracted features were further processed by charge state deconvolution and retention time alignment (Mueller et al. 2007b; Sturm et al. 2008). Finally, all LC-MS features were cross-referenced with the sequence identification results to combine quantitative data of different samples and tissues to peptide presentation profiles. The quantitative data were normalized in a two-tier fashion according to central tendency to account for variation within technical and biological replicates. Thus each identified peptide can be associated with quantitative data allowing relative quantification between samples and tissues. In addition, all quantitative data acquired for peptide candidates was inspected manually to assure data consistency and to verify the accuracy of the automated analysis. For each peptide a presentation profile was calculated showing the mean sample presentation as well as replicate variations. The profiles juxtapose HCC samples to a baseline of normal tissue samples.

Presentation profiles of exemplary over-presented peptides are shown in Figure 1. Presentation scores for exemplary peptides are shown in Table 8.

Table 8: Presentation scores. The table lists peptides that are very highly over-presented on tumors compared to a panel of normal tissues (+++), highly over-presented on tumors compared to a panel of normal tissues (++) or over-presented on tumors compared to a panel of normal tissues (+). S* = phosphoserine

SEQ ID No.	Sequence	PeptidePresentation
1	VMAPFTMTI	+++
2	KLQAGTVFV	+++
4	KLQDFSDQL	+++
5	ALVEQGFTV	+++
6	KLSPTVVGL	+++
7	ALVDTLKFV	+++
8	KLLEEATISV	+
9	ALANQKLYSV	+
10	SLLEEFDFHV	+++
11	SLSQELVGV	+
12	FLAELAYDL	+++
14	ALADLTGTVV	+++
15	LLYGHTVTV	+
16	SLLGGNIRL	++
17	RVAS*PTSGV	+
19	FLEETKATV	+++
20	KLSNVLQQV	+++
21	QLIEVSSPITL	+++
22	RIAGIRGIQGV	+++
23	RLYDPASGTISL	+
24	SLAEEKLQASV	+++
25	SLDGKAALTEL	+++
26	SLLHTIYEV	+++
27	TLPDFRLPEI	+++
28	TLQDHLNSL	+++
29	YIQDEINTI	+++
30	YLGEGPRMV	++
31	YQMDIQQEL	++
32	ALNAVRLLV	+++
33	LLHGHIVEL	+
34	SLAEGTATV	+++
38	ALADVVHEA	+
39	ALDPKANFST	+++
40	ALLAEGITWV	+
42	ALLGGNVRMML	+++
44	ALQDAIRQL	+
47	FLDTPIAKV	+
49	FLYPEKDEPT	+++
51	GLAEELVRA	+

52	GLFNAELLEA	+
53	GLIHLEGDTV	+++
54	GLLDPNVKSIFV	+++
55	GLYGRTIEL	+
56	GVLPGLVGV	+
57	HLTEAIQYV	++
58	ILADLNLSV	+
59	ILADTFIGV	++
60	ILSPLSVAL	+
61	KIADFELPTI	+++
62	KIAGTNAEV	++
66	KLHEEIDRV	++
67	KLKETIQKL	+++
70	KLLDLETERILL	++
71	KLLDNWDSV	+++
72	KLSEAVTSV	+
75	KQMEPLHAV	+
76	LLADIGGDPFAA	+++
77	LLHEENFSV	+
79	LLLSTGYEA	+++
81	NLASFIEQVAV	++
82	NVFDGLVRV	+
83	QLHDFVMSL	+++
84	QLTPVLVSV	++
85	RILPKVLEV	+
86	RLAAFYSQV	+++
88	RLIDRIKTV	+++
89	RLIEEIKNV	+++
91	RLPDIPLRQV	+
93	RLYTMDGITV	+++
94	RMSDVVKGV	+++
96	SLLEEPNVIRV	++
97	SLLPQLIEV	++
98	SLLSPEHLQYL	++
99	SLSAFLPSL	+++
101	SLWEGGVRGV	+++
103	SMGDHLWVA	+++
107	TLGQFYQEV	+++
108	TLLKKISEA	+++
109	TLYALSHAV	+
111	TVMDIDTSGTFNV	+

113	VLMDKLVEL	++
114	VLSQVYSKV	+++
116	WVIPAISAV	+++
117	YAFPKSITV	+++
119	YLDKNLTVSV	+
120	YLGEEYVKA	+++
121	YLITGNLEKL	+
122	YLSQAADGAKVL	+++
123	YLWDLDHGFAGV	++
124	LLIDVVTYL	+++
126	TLLDSPIKV	++
127	VLIGSNHSL	+
128	GLAFSLNGV	+
129	SQADVIPAV	+
130	ALDAGAVYTL	++
131	ALDSGAFQSV	++
132	ALHEEVVGV	+
133	ALLEMDARL	+
134	ALLETNPYLL	++
135	ALLGKIEKV	+
137	ALPTVLVGV	++
139	ALSSKPAEV	+
142	AVIGGLIYV	++
144	FIQLITGV	+
146	FLWTEQAHTV	+
147	GLAPGGLAVV	+
148	GLFAPLVFL	+++
151	HLAKVTAEV	+
154	KLTDHLKYV	+
161	RLLDEQFAV	+
162	RLMSALTQV	++
163	RLTESVLYL	++
164	RMLIKLLEV	+
167	SLAESSFDV	++
168	SLAVLVPIV	+
169	SLFEWFHPL	+
170	SLHNGVIQL	+
171	SLIPAVLTV	+
172	SLLNFLQHL	+
173	SLTSEIHFL	+
174	TLAELGAVQV	+

176	TLGQIWDV	+
177	VLDEPYEKV	+
179	YIHNILYEV	++
180	YLGPHIASVTL	++
181	YLLEKFVAV	+
184	VVLDGGQIVTV	+
185	ALFPALRPGGFQA	++
186	VLLAQIIQV	+
187	SYPTFFPRF	+
188	RYSAGWDAKF	+
189	AFSPDSHYLLF	+++
190	RYNEKCFKL	+++
191	KYPDIISRI	++
192	SYITKPEKW	+
193	IYPGAFVDL	+++
194	QYASRFVQL	+++
195	RYAPPPSFSEF	+++
196	AYLKWISQI	+++
197	RWPKKSAEF	+
198	LYWSHPRKF	+
200	AYLLQPSQF	+++
201	AYVNTFHNI	+++
202	AYGTYRSNF	+++
203	YYGILQEKI	+++
204	KYRLTYAYF	++
205	VYGLQRNLL	+
206	KWPETPLLL	+++
208	SYNPAENAVLL	++
210	AYPAIRYLL	++
211	IYIPSYFDF	++
212	VYGDVISNI	+++
213	YYNKVSTVF	+
214	IYVTSIEQI	+++
217	DYIPYVFKL	+++
218	VYQGAIRQI	+
219	GVMAGDIYSV	+
220	SLLEKELESV	++
221	ALCEENMRGV	+
224	ALASVIKEL	+
225	KMDPVAYRV	+
226	AVLGPLGLQEV	+

227	ALLKVNQEL	+
228	YLITSVELL	++
229	KMFESFIESV	++
230	VLTEFTREV	+
231	RLFNDPVAMV	++
233	ALLGKLDAI	+
234	YLEPYLKEV	+
236	ALADKELLPSV	++
237	ALRGEIETV	+++
238	AMPPPPPQGV	++
239	FLLGFIPAKA	+
240	FLWERPTLLV	+++
241	FVLPLLGLHEA	++
242	GLFAPVHKV	+
243	GLLDNPELRV	+++
244	KIAELLENV	+
245	KLGAVFNQV	+
248	KLNDLIQRL	+
249	LLLGERVAL	+++
250	NLAEVVERV	++
251	RLFADILNDV	++
252	RTIEYLEEV	+
253	RVPPPPQSV	+
255	SLFGQDVKAV	+++
256	SLFQGVEFHYV	+
257	SLLEKAGPEL	+++
258	SLMGPVVHEV	+
260	TLMDMRLSQV	++
261	VLFQEALWHV	++
263	VLYPSLKEI	+
264	VMQDPEFLQSV	++
265	WLIEDGKVVTV	++
266	SLLESNKDLLL	+
267	ALNENINQV	+
268	KLYQEVEIASV	+
269	YLMEGSYNKV	+
270	SVLDQKILL	++
271	LLLDKLILL	+
272	QQLDSKFLEQV	+
273	AILETAPKEV	++
274	ALAEALKEV	+

275	ALIEGAGILL	++
276	ALLEADVNIKL	+
277	ALLEENSTPQL	+
278	ALTSVVVTL	+
279	ALWTGMHTI	+
281	GLLAGDRLVEV	+
282	GQFPSYLETV	++
283	ILSGIGVSQV	+
284	KLDAFVEGV	+
286	KVLDKVFRA	+
288	LLDDSLVSI	+
289	LLLEEGGLVQV	++
290	NLIDLDDLYV	++
292	RIPAYFVTV	+
293	FLASESLIKQI	++
295	SLFSSPPEI	++
297	TLFYSLREV	+
298	TMAKESSIIGV	++
299	ALLRVTPFI	+
301	VLADFGARV	+++
302	KIQEILTQV	+++
303	GVYDGEEHSV	+
304	SLIDQFFGV	+++
305	GVLENIFGV	+
308	ALLRTVVSV	+
309	GLIEIISNA	+
310	SLWGGDVVL	+
311	FLIPIYHQV	+
312	RLGIKPESV	+++
313	LTAPPEALLMV	+
314	YLAPFLRNV	+
315	KVLDGSPIEV	+
316	LLREKVEFL	+
317	KLPEKWESV	++
318	KLNEINEKI	+
319	KLFNEFIQL	+
320	GLADNTVIAKV	+
322	ILYDIPDIRL	+
324	RLFETKITQV	++
326	ALSDGVHKI	++
327	GLNEEIARV	++

328	RLEEDDGDVAM	+
329	SLIEDLILL	+++
330	SMSADVPLV	++
332	AMLAVLHTV	+
334	SILTIEDGIFEV	+
335	SLLPVDIRQYL	++
336	YLPTFFLTV	+
337	TLLAAEFLKQV	+
338	KLFDSDPITVTV	+++
340	KVFDEVIEV	+
342	AMSSKFFLV	+
343	LLLPDYYLV	+
345	SYNPLWLRI (A*24)	+++
346	LYQILQGIVF (A*24)	+++
347	ALNPADITV	+

EXAMPLE 2

Expression profiling of genes encoding the peptides of the invention

Over-presentation or specific presentation of a peptide on tumor cells compared to normal cells is sufficient for its usefulness in immunotherapy, and some peptides are tumor-specific despite their source protein occurring also in normal tissues. Still, mRNA expression profiling adds an additional level of safety in selection of peptide targets for immunotherapies. Especially for therapeutic options with high safety risks, such as affinity-matured TCRs, the ideal target peptide will be derived from a protein that is unique to the tumor and not found on normal tissues.

RNA sources and preparation

Surgically removed tissue specimens were provided as indicated above (see Example 1) after written informed consent had been obtained from each patient. Tumor tissue specimens were snap-frozen immediately after surgery and later homogenized with mortar and pestle under liquid nitrogen. Total RNA was prepared from these samples using TRI Reagent (Ambion, Darmstadt, Germany) followed by a cleanup with RNeasy (QIAGEN, Hilden, Germany); both methods were performed according to the manufacturer's protocol.

Total RNA from healthy human tissues was obtained commercially (Ambion, Huntingdon, UK; Clontech, Heidelberg, Germany; Stratagene, Amsterdam, Netherlands; BioChain, Hayward, CA, USA). The RNA from several individuals (between 2 and 123 individuals) was mixed such that RNA from each individual was equally weighted.

Quality and quantity of all RNA samples were assessed on an Agilent 2100 Bioanalyzer (Agilent, Waldbronn, Germany) using the RNA 6000 Pico LabChip Kit (Agilent).

Microarray experiments

Gene expression analysis of all tumor and normal tissue RNA samples was performed by Affymetrix Human Genome (HG) U133A or HG-U133 Plus 2.0 oligonucleotide microarrays (Affymetrix, Santa Clara, CA, USA). All steps were carried out according to the Affymetrix manual. Briefly, double-stranded cDNA was synthesized from 5–8 µg of total RNA, using SuperScript RTII (Invitrogen) and the oligo-dT-T7 primer (MWG Biotech, Ebersberg, Germany) as described in the manual. *In vitro* transcription was performed with the BioArray High Yield RNA Transcript Labelling Kit (ENZO Diagnostics, Inc., Farmingdale, NY, USA) for the U133A arrays or with the GeneChip IVT Labelling Kit (Affymetrix) for the U133 Plus 2.0 arrays, followed by cRNA fragmentation, hybridization, and staining with streptavidin-phycoerythrin and biotinylated anti-streptavidin antibody (Molecular Probes, Leiden, Netherlands). Images were scanned with the Agilent 2500A GeneArray Scanner (U133A) or the Affymetrix Gene-Chip Scanner 3000 (U133 Plus 2.0), and data were analyzed with the GCOS software (Affymetrix), using default settings for all parameters. For normalization, 100 housekeeping genes provided by Affymetrix were used. Relative expression values were calculated from the signal log ratios given by the software and the normal kidney sample was arbitrarily set to 1.0. Exemplary expression profiles of source genes of the present invention that are highly over-expressed or exclusively expressed in HCC are shown in Figure 2. Expression scores for further exemplary genes are shown in Table 9.

Table 9: Expression scores. The table lists peptides from genes that are very highly overexpressed in tumors compared to a panel of normal tissues (+++),highly overexpressed in tumors compared to a panel of normal tissues (++) or overexpressed in tumors compared to a panel of normal tissues (+).

SEQ ID No	Sequence	Gene Expression
1	VMAPFTMTI	+++
2	KLQAGTVFV	++
3	ILDDNMQKL	+
4	KLQDFSDQL	+++
5	ALVEQGFTV	+++
7	ALVDTLKFV	+++
10	SLLEEFDFHV	+
13	GLIDTETAMKAV	+++
19	FLEETKATV	+++
20	KLSNVLQQV	+++
21	QLIEVSSPITL	+++
25	SLDGKAALTEL	+++
27	TLPDFRLPEI	+++
28	TLQDHLNSL	+++
29	YIQDEINTI	+++
31	YQMDIQQEL	+++
38	ALADVVHEA	+
39	ALDPKANFST	+
41	ALLELDEPLVL	+++
42	ALLGGNVRMML	+
44	ALQDAIRQL	+
45	ALQDQLVLV	++
46	AMAEMKVVL	++
48	FLLEQPEIQV	+
49	FLYPEKDEPT	+++
50	FTIPKLYQL	+++
52	GLFNAELLEA	+++
53	GLIHLEGDTV	+++
55	GLYGRTIEL	+++
60	ILSPLSVAL	+
61	KIADFELPTI	+++
62	KIAGTNAEV	+
66	KLHEEIDRV	+++

67	KLKETIQKL	+++
68	KLLAATVLLL	+++
73	KLTLVIISV	+++
74	KLYDLELIV	+++
76	LLADIGGDPFAA	+
81	NLASFIEQVAV	+
82	NVFDGLVRV	+++
83	QLHDFVMSL	+++
84	QLTPVLVSV	++
85	RILPKVLEV	++
87	RLFEENDVNL	+++
90	RLLDVLAPLV	+
93	RLYTMDGITV	+++
94	RMSDVVKGV	+
95	SICNGVPMV	++
97	SLLPQLIEV	+++
100	SLVGDIGNVNM	+++
103	SMGDHLWVA	+
105	SVYDGKLLI	+
106	TLAAIIHGA	++
107	TLGQFYQEV	+++
109	TLYALSHAV	+++
110	TVGGSEILFEV	+++
113	VLMDKLVEL	+++
114	VLSQVYSKV	+++
116	WVIPAISAV	++
117	YAFPKSITV	+
119	YLDKNLTVSV	++
120	YLGEEYVKA	+++
124	LLIDVVTYL	+++
126	TLLDSPIKV	+++
129	SQADVIPAV	++
130	ALDAGAVYTL	++
132	ALHEEVVGV	++
141	AMGEKSFSV	+
142	AVIGGLIYV	+++
145	FLIAEYFEHV	++
146	FLWTEQAHTV	++
148	GLFAPLVFL	+
149	GLLSGLDIMEV	+++
154	KLTDHLKYV	+++

157	QLLPNLRAV	+
158	RIISGLVKV	++
160	RLLAKIICL	+++
163	RLTESVLYL	++
165	RVIEHVEQV	++
168	SLAVLVPIV	+++
172	SLLNFLQHL	+
173	SLTSEIHFL	+
175	TLFEHLPHI	++
177	VLDEPYEKV	++
182	YLLHFPMAL	+++
183	YLYNNEEQVGL	+++
187	SYPTFFPRF	+
188	RYSAGWDAKF	+++
192	SYITKPEKW	+
193	IYPGAFVDL	+
200	AYLLQPSQF	+++
204	KYRLTYAYF	+++
206	KWPETPLLL	+
215	IYTGNISSF	+++
217	DYIPYVFKL	+++
218	VYQGAIRQI	+++
228	YLITSVELL	+
233	ALLGKLDAI	+
249	LLLGERVAL	+
255	SLFGQDVKAV	+
259	TLITDGMRSV	+
263	VLYPSLKEI	+
273	AILETAPKEV	+
275	ALIEGAGILL	+
286	KVLDKVFRA	+
296	SLLSGRISTL	+
298	TMAKESSIIGV	+
301	VLADFGARV	++
302	KIQEILTQV	+
315	KVLDGSPIEV	++
318	KLNEINEKI	+++
320	GLADNTVIAKV	+
324	RLFETKITQV	++
327	GLNEEIARV	+
336	YLPTFFLTV	+

341	YLAIGIHEL	++
345	SYNPLWLRI (A*24)	++

EXAMPLE 3: UV-ligand exchange/Peptide binding to HLA-A*02 and HLA-A*24

Candidate peptides for T cell based therapies according to the present invention were further tested for their MHC binding capacity (affinity). The individual peptide-MHC complexes were produced by UV-ligand exchange, where a UV-sensitive peptide is cleaved upon UV-irradiation, and exchanged with the peptide of interest as analyzed. Only peptide candidates that can effectively bind and stabilize the peptide-receptive MHC molecules prevent dissociation of the MHC complexes. To determine the yield of the exchange reaction, an ELISA was performed based on the detection of the light chain (β2m) of stabilized MHC complexes. The assay was performed as generally described in Rodenko et al. (Rodenko B, Toebes M, Hadrup SR, van Esch WJ, Molenaar AM, Schumacher TN, Ovaa H. Generation of peptide-MHC class I complexes through UV-mediated ligand exchange. Nat Protoc. 2006;1(3):1120-32.).

96 well MAXISorp plates (NUNC) were coated over night with 2ug/ml streptavidin in PBS at room temperature, washed 4x and blocked for1h at 37°C in 2% BSA containing blocking buffer. Refolded HLA-A*0201/MLA-001 monomers served as standards, covering the range of 15-500 ng/ml. Peptide-MHC monomers of the UV-exchange reaction were diluted 100 fold in blocking buffer. Samples were incubated for 1h at 37°C, washed four times, incubated with 2ug/ml HRP conjugated anti-β2m for 1h at 37°C, washed again and detected with TMB solution that is stopped with NH_2SO_4. Absorption was measured at 450nm. Candidate peptides that show a high exchange yield (preferably higher than 50%, most preferred higher than 75%) are generally preferred for a generation and production of antibodies or fragments thereof, and/or T cell receptors or fragments thereof, as they show sufficient avidity to the MHC molecules and prevent dissociation of the MHC complexes.

Table 10A: MHC class I binding scores

<20 % = +; 20 % - 49 % = ++; 50 % - 75 %= +++; >= 75 % = ++++

Seq ID	Peptide code	Peptide exchange
12	GPC3-001	++++
5	APOB-001	++++
7	APOB-002	++++
1	APOB-003	++++
13	HSD11B1-001	++++
227	SAMM-001	++++
4	APOB-004	++++
232	MAPKAPK5-001	++++
10	USO-001	++++
304	USP14-001	++++
219	ADF-012	++++
223	IDI1-001	++++
224	IFT81-001	++++
14	NCST-001	++++
228	ACSL4-001	++++
230	IPO9-001	++++
15	SLC35B2-001	++++
16	ACSL3-001	++++
303	MAGEB2-001	+++
226	THT-001	+++
8	DYM-001	+++
6	AXIN2-001	+++
225	QAR-001	+++
2	ALDH1L1-001	+++
221	EEF2-001	+++
220	DRG2-001	+++
301	C1QTNF3-001	+++
11	ZNF318-001	+++

Table 10B: MHC class I binding scores

Binding of HLA-class I restricted peptides to HLA-A*02 or HLA-A*24 depending from peptide sequence was classified by peptide exchange yield: ≥10% = +; ≥20% = ++; ≥50 = +++; ≥ 75% = ++++. S* = phosphoserine.

SEQ ID No	Sequence	Peptide exchange
1	VMAPFTMTI	"++++"
2	KLQAGTVFV	"+++"

SEQ ID No	Sequence	Peptide exchange
3	ILDDNMQKL	"+++"
4	KLQDFSDQL	"++++"
5	ALVEQGFTV	"++++"
6	KLSPTVVGL	"+++"
7	ALVDTLKFV	"++++"
8	KLLEEATISV	"+++"
9	ALANQKLYSV	"+++"
10	SLLEEFDFHV	"++++"
11	SLSQELVGV	"+++"
12	FLAELAYDL	"++++"
13	GLIDTETAMKAV	"++++"
14	ALADLTGTVV	"++++"
15	LLYGHTVTV	"++++"
16	SLLGGNIRL	"++++"
17	RVAS*PTSGV	"+++"
18	ALYGKTEVV	"+++"
19	FLEETKATV	"+++"
20	KLSNVLQQV	"++++"
21	QLIEVSSPITL	"++++"
22	RIAGIRGIQGV	"++++"
23	RLYDPASGTISL	"+++"
24	SLAEEKLQASV	"+++"
25	SLDGKAALTEL	"+++"
26	SLLHTIYEV	"+++"
27	TLPDFRLPEI	"++++"
28	TLQDHLNSL	"+++"
29	YIQDEINTI	"+++"
30	YLGEGPRMV	"+++"
31	YQMDIQQEL	"+++"
32	ALNAVRLLV	"++++"
33	LLHGHIVEL	"+++"
34	SLAEGTATV	"+++"
35	SLQESILAQV	"+++"
36	ILNVDGLIGV	"+++"
37	LLLPLLPPLSP	"+++"
38	ALADVVHEA	"+++"
39	ALDPKANFST	"+++"
40	ALLAEGITWV	"+++"
41	ALLELDEPLVL	"++++"

SEQ ID No	Sequence	Peptide exchange
42	ALLGGNVRMML	"+++"
43	ALLGVWTSV	"++"
44	ALQDAIRQL	"++++"
45	ALQDQLVLV	"++++"
46	AMAEMKVVL	"+++"
47	FLDTPIAKV	"++"
48	FLLEQPEIQV	"+++"
49	FLYPEKDEPT	"++"
50	FTIPKLYQL	"++"
51	GLAEELVRA	"++"
52	GLFNAELLEA	"+++"
53	GLIHLEGDTV	"+++"
54	GLLDPNVKSIFV	"+++"
55	GLYGRTIEL	"+++"
56	GVLPGLVGV	"+++"
57	HLTEAIQYV	"+++"
58	ILADLNLSV	"++++"
59	ILADTFIGV	"+++"
60	ILSPLSVAL	"++++"
61	KIADFELPTI	"++++"
62	KIAGTNAEV	"++"
63	KIDEKNFVV	"+++"
64	KILEETLYV	"+++"
65	KLFSGDELLEV	"+++"
66	KLHEEIDRV	"+++"
67	KLKETIQKL	"+++"
68	KLLAATVLLL	"++"
69	KLLDEVTYLEA	"++++"
70	KLLDLETERILL	"++++"
71	KLLDNWDSV	"++++"
72	KLSEAVTSV	"+++"
74	KLYDLELIV	"+++"
75	KQMEPLHAV	"++"
76	LLADIGGDPFAA	"+++"
77	LLHEENFSV	"+++"
78	LLIDDEYKV	"+++"
80	LLYEGKLTL	"++++"
81	NLASFIEQVAV	"+++"
82	NVFDGLVRV	"+++"

SEQ ID No	Sequence	Peptide exchange
83	QLHDFVMSL	"++++"
84	QLTPVLVSV	"+++"
85	RILPKVLEV	"+++"
86	RLAAFYSQV	"+++"
87	RLFEENDVNL	"+++"
88	RLIDRIKTV	"++"
89	RLIEEIKNV	"++"
90	RLLDVLAPLV	"+++"
91	RLPDIPLRQV	"+++"
92	RLPPDTLLQQV	"+++"
93	RLYTMDGITV	"++"
94	RMSDVVKGV	"+++"
95	SICNGVPMV	"+++"
96	SLLEEPNVIRV	"++++"
97	SLLPQLIEV	"++++"
98	SLLSPEHLQYL	"+++"
99	SLSAFLPSL	"++++"
100	SLVGDIGNVNM	"++"
101	SLWEGGVRGV	"+++"
102	SLWSVARGV	"+++"
103	SMGDHLWVA	"+++"
104	SVWFGPKEV	"+++"
105	SVYDGKLLI	"++++"
106	TLAAIIHGA	"+++"
107	TLGQFYQEV	"++++"
108	TLLKKISEA	"+++"
109	TLYALSHAV	"+++"
110	TVGGSEILFEV	"++++"
111	TVMDIDTSGTFNV	"+++"
112	VLGEVKVGV	"++++"
113	VLMDKLVEL	"++++"
114	VLSQVYSKV	"+++"
115	VVLDDKDYFL	"+++"
116	WVIPAISAV	"++++"
117	YAFPKSITV	"+++"
118	YLDDEKNWGL	"+++"
119	YLDKNLTVSV	"+++"
120	YLGEEYVKA	"++"
121	YLITGNLEKL	"+++"

SEQ ID No	Sequence	Peptide exchange
122	YLSQAADGAKVL	"++"
123	YLWDLDHGFAGV	"+++"
124	LLIDVVTYL	"++++"
125	ALYGRLEVV	"++++"
126	TLLDSPIKV	"+++"
127	VLIGSNHSL	"++++"
128	GLAFSLNGV	"++++"
129	SQADVIPAV	"+++"
130	ALDAGAVYTL	"++++"
131	ALDSGAFQSV	"+++"
132	ALHEEVVGV	"+++"
133	ALLEMDARL	"+++"
134	ALLETNPYLL	"++++"
135	ALLGKIEKV	"+++"
136	ALLNQHYQV	"+++"
137	ALPTVLVGV	"++++"
138	ALSQVTLLL	"++++"
139	ALSSKPAEV	"+++"
140	ALTSISAGV	"++++"
141	AMGEKSFSV	"++++"
142	AVIGGLIYV	"++++"
145	FLIAEYFEHV	"++"
146	FLWTEQAHTV	"++"
147	GLAPGGLAVV	"+++"
148	GLFAPLVFL	"++++"
149	GLLSGLDIMEV	"++++"
150	GLSNLGIKSI	"++++"
151	HLAKVTAEV	"+++"
152	KLDNNLDSV	"+++"
154	KLTDHLKYV	"+++"
156	LLFPHPVNQV	"++++"
157	QLLPNLRAV	"+++"
158	RIISGLVKV	"++"
159	RLFPDGIVTV	"+++"
160	RLLAKIICL	"++"
161	RLLDEQFAV	"+++"
162	RLMSALTQV-	"++"
163	RLTESVLYL	"+++"
164	RMLIKLLEV	"+++"

SEQ ID No	Sequence	Peptide exchange
165	RVIEHVEQV	"++++"
166	SILDIVTKV	"+++"
167	SLAESSFDV	"+++"
168	SLAVLVPIV	"+++"
169	SLFEWFHPL	"+++"
170	SLHNGVIQL	"+++"
171	SLIPAVLTV	"+++"
172	SLLNFLQHL	"+++"
173	SLTSEIHFL	"+++"
174	TLAELGAVQV	"+++"
175	TLFEHLPHI	"+++"
176	TLGQIWDV	"++++"
177	VLDEPYEKV	"+++"
178	YIFTTPKSV	"+++"
179	YIHNILYEV	"++++"
180	YLGPHIASVTL	"+++"
181	YLLEKFVAV	"+++"
182	YLLHFPMAL	"+++"
183	YLYNNEEQVGL	"++"
184	VVLDGGQIVTV	"+++"
185	ALFPALRPGGFQA	"+++"
186	VLLAQIIQV	"+++"
187	SYPTFFPRF	"++++"
188	RYSAGWDAKF	"++++"
189	AFSPDSHYLLF	"+++"
190	RYNEKCFKL	"++++"
191	KYPDIISRI	"++++"
192	SYITKPEKW	"++++"
193	IYPGAFVDL	"++++"
195	RYAPPPSFSEF	"++++"
196	AYLKWISQI	"++++"
197	RWPKKSAEF	"++++"
198	LYWSHPRKF	"++++"
199	KFVTVQATF	"++++"
200	AYLLQPSQF	"++++"
201	AYVNTFHNI	"++++"
202	AYGTYRSNF	"++++"
203	YYGILQEKI	"++++"
205	VYGLQRNLL	"++++"

SEQ ID No	Sequence	Peptide exchange
206	KWPETPLLL	"++++"
207	IYLERFPIF	"++++"
208	SYNPAENAVLL	"++++"
209	VFHPRQELI	"+++"
210	AYPAIRYLL	"++++"
211	IYIPSYFDF	"++++"
212	VYGDVISNI	"++++"
213	YYNKVSTVF	"++++"
214	IYVTSIEQI	"++++"
215	IYTGNISSF	"++++"
216	IYADVGEEF	"++++"
217	DYIPYVFKL	"++++"
218	VYQGAIRQI	"++++"
219	GVMAGDIYSV	"++++"
220	SLLEKELESV	"+++"
221	ALCEENMRGV	"+++"
222	LTDITKGV	"++"
223	FLFNTENKLLL	"++++"
224	ALASVIKEL	"+++"
225	KMDPVAYRV	"+++"
226	AVLGPLGLQEV	"+++"
227	ALLKVNQEL	"++++"
228	YLITSVELL	"++++"
229	KMFESFIESV	"+++"
230	VLTEFTREV	"++++"
231	RLFNDPVAMV	"++++"
232	KLAEIVKQV	"++++"
233	ALLGKLDAI	"++++"
234	YLEPYLKEV	"++++"
235	KLFEEIREI	"++++"
236	ALADKELLPSV	"+++"
237	ALRGEIETV	"+++"
238	AMPPPPPQGV	"++"
239	FLLGFIPAKA	"+++"
240	FLWERPTLLV	"+++"
241	FVLPLLGLHEA	"++"
242	GLFAPVHKV	"+++"
243	GLLDNPELRV	"+++"
244	KIAELLENV	"++++"
245	KLGAVFNQV	"++++"

SEQ ID No	Sequence	Peptide exchange
246	KLISSYYNV	"+++"
247	KLLDTMVDTFL	"++++"
248	KLNDLIQRL	"+++"
249	LLLGERVAL	"++++"
250	NLAEVVERV	"++++"
251	RLFADILNDV	"++++"
252	RTIEYLEEV	"+++"
253	RVPPPPQSV	"++"
254	RVQEAIAEV	"+++"
255	SLFGQDVKAV	"+++"
256	SLFQGVEFHYV	"+++"
257	SLLEKAGPEL	"+++"
258	SLMGPVVHEV	"+++"
259	TLITDGMRSV-	"++"
260	TLMDMRLSQV	"+++"
261	VLFQEALWHV	"+++"
262	VLPNFLPYNV	"+++"
263	VLYPSLKEI	"+++"
264	VMQDPEFLQSV	"++++"
265	WLIEDGKVVTV	"++++"
266	SLLESNKDLLL	"+++"
267	ALNENINQV	"+++"
268	KLYQEVEIASV	"++++"
269	YLMEGSYNKV	"+++"
270	SVLDQKILL	"+++"
271	LLLDKLILL	"++++"
272	QQLDSKFLEQV	"+++"
273	AILETAPKEV	"+++"
274	ALAEALKEV	"++++"
275	ALIEGAGILL	"+++"
276	ALLEADVNIKL	"++++"
277	ALLEENSTPQL	"+++"
278	ALTSVVVTL	"++++"
279	ALWTGMHTI	"+++"
280	ATLNIIHSV	"+++"
281	GLLAGDRLVEV	"+++"
282	GQFPSYLETV	"+++"
283	ILSGIGVSQV	"+++"
284	KLDAFVEGV	"+++"

SEQ ID No	Sequence	Peptide exchange
285	KLLDLSDSTSV	"+++"
286	KVLDKVFRA	"++++"
287	LIGEFLEKV	"++++"
288	LLDDSLVSI	"+++"
290	NLIDLDDLYV	"++++"
291	QLIDYERQL	"+++"
292	RIPAYFVTV	"++"
293	FLASESLIKQI	"++"
294	RLIDLHTNV	"++++"
295	SLFSSPPEI	"+++"
296	SLLSGRISTL	"+++"
297	TLFYSLREV	"+++"
298	TMAKESSIIGV	"++"
299	ALLRVTPFI	"+++"
300	TLAQQPTAV	"++"
302	KIQEILTQV	"++++"

EXAMPLE 4

***In vitro* immunogenicity for MHC class I presented peptides**

In order to obtain information regarding the immunogenicity of the TUMAPs of the present invention, the inventors performed investigations using an *in vitro* T-cell priming assay based on repeated stimulations of CD8+ T cells with artificial antigen presenting cells (aAPCs) loaded with peptide/MHC complexes and anti-CD28 antibody. This way the inventors could show immunogenicity for 22 HLA-A*0201 restricted TUMAPs of the invention so far, demonstrating that these peptides are T-cell epitopes against which CD8+ precursor T cells exist in humans (Table 11).

***In vitro* priming of CD8+ T cells**

In order to perform *in vitro* stimulations by artificial antigen presenting cells loaded with peptide-MHC complex (pMHC) and anti-CD28 antibody, the inventors first isolated CD8+ T cells from fresh HLA-A*02 leukapheresis products via positive selection using CD8 microbeads (Miltenyi Biotec, Bergisch-Gladbach, Germany) of healthy donors obtained from the University clinics Mannheim, Germany, after informed consent.

PBMCs and isolated CD8+ lymphocytes were incubated in T-cell medium (TCM) until use consisting of RPMI-Glutamax (Invitrogen, Karlsruhe, Germany) supplemented with 10% heat inactivated human AB serum (PAN-Biotech, Aidenbach, Germany), 100 U/ml Penicillin/100 µg/ml Streptomycin (Cambrex, Cologne, Germany), 1 mM sodium pyruvate (CC Pro, Oberdorla, Germany), 20 µg/ml Gentamycin (Cambrex). 2.5 ng/ml IL-7 (PromoCell, Heidelberg, Germany) and 10 U/ml IL-2 (Novartis Pharma, Nürnberg, Germany) were also added to the TCM at this step.

Generation of pMHC/anti-CD28 coated beads, T-cell stimulations and readout was performed in a highly defined *in vitro* system using four different pMHC molecules per stimulation condition and 8 different pMHC molecules per readout condition.

The purified co-stimulatory mouse IgG2a anti human CD28 Ab 9.3 (Jung et al., 1987) was chemically biotinylated using Sulfo-N-hydroxysuccinimidobiotin as recommended by the manufacturer (Perbio, Bonn, Germany). Beads used were 5.6 µm diameter streptavidin coated polystyrene particles (Bangs Laboratories, Illinois, USA).

pMHC used for positive and negative control stimulations were A*0201/MLA-001 (peptide ELAGIGILTV from modified Melan-A/MART-1) and A*0201/DDX5-001 (YLLPAIVHI from DDX5), respectively.

800.000 beads / 200 µl were coated in 96-well plates in the presence of 4 x 12.5 ng different biotin-pMHC, washed and 600 ng biotin anti-CD28 were added subsequently in a volume of 200 µl. Stimulations were initiated in 96-well plates by co-incubating $1x10^6$ CD8+ T cells with $2x10^5$ washed coated beads in 200 µl TCM supplemented with 5 ng/ml IL-12 (PromoCell) for 3 days at 37°C. Half of the medium was then exchanged by fresh TCM supplemented with 80 U/ml IL-2 and incubating was continued for 4 days at 37°C. This stimulation cycle was performed for a total of three times. For the pMHC multimer readout using 8 different pMHC molecules per condition, a two-dimensional combinatorial coding approach was used as previously described (Andersen et al., 2012) with minor modifications encompassing coupling to 5 different fluorochromes.

Finally, multimeric analyses were performed by staining the cells with Live/dead near IR dye (Invitrogen, Karlsruhe, Germany), CD8-FITC antibody clone SK1 (BD, Heidelberg, Germany) and fluorescent pMHC multimers. For analysis, a BD LSRII SORP cytometer equipped with appropriate lasers and filters was used. Peptide specific cells were calculated as percentage of total CD8+ cells. Evaluation of multimeric analysis was done using the FlowJo software (Tree Star, Oregon, USA). *In vitro* priming of specific multimer+ CD8+ lymphocytes was detected by by comparing to negative control stimulations. Immunogenicity for a given antigen was detected if at least one evaluable *in vitro* stimulated well of one healthy donor was found to contain a specific CD8+ T-cell line after *in vitro* stimulation (i.e. this well contained at least 1% of specific multimer+ among CD8+ T-cells and the percentage of specific multimer+ cells was at least 10x the median of the negative control stimulations).

***In vitro* immunogenicity for HCC peptides**

For tested HLA class I peptides, *in vitro* immunogenicity could be demonstrated by generation of peptide specific T-cell lines. Exemplary flow cytometry results after TUMAP-specific multimer staining for three peptides of the invention are shown in Figure 3 and Figure 4 together with corresponding negative controls. Results for 22 peptides from the invention are summarized in Table 11A.

Table 11A: in vitro immunogenicity of HLA class I peptides of the invention

Exemplary results of *in vitro* immunogenicity experiments conducted by the applicant for the peptides of the invention. <20 % = +; 20 % - 49 % = ++; 50 % - 69 %= +++; >= 70 % = ++++

Seq ID	Peptide ID	wells	donors
225	QAR-001	+++	++++
1	APOB-003	++	++++
2	ALDH1L1-001	++	++++
301	C1QTNF3-001	++	++++
15	SLC35B2-001	++	++++
16	ACSL3-001	++	++++
12	GPC3-001	+	++++
7	APOB-002	+	++++

Seq ID	Peptide ID	wells	donors
303	MAGEB2-001	+	++
227	SAMM-001	+	+++
4	APOB-004	+	++++
226	THT-001	+	++++
6	AXIN2-001	+	++
232	MAPKAPK5-001	+	+++
10	USO-001	+	++
304	USP14-001	+	++++
219	ADF-012	+	++++
224	IFT81-001	+	+++
11	ZNF318-001	+	++
14	NCST-001	+	++
228	ACSL4-001	+	++
230	IPO9-001	+	++++

Table 11B: in vitro immunogenicity of additional HLA class I peptides of the invention

Exemplary results of *in vitro* immunogenicity experiments conducted by the applicant for HLA-A*24 restricted peptides of the invention. Results of *in vitro* immunogenicity experiments are indicated. Percentage of positive wells and donors (among evaluable) are summarized as indicated 1-20 % = +; 20 % - 49 % = ++; 50 % - 69 %= +++; >= 70 %= ++++

SEQ ID No	Sequence	Wells positive [%]	Donors positive [%]
187	SYPTFFPRF	"+"	"++++"
189	AFSPDSHYLLF	"+"	"++"
190	RYNEKCFKL	"+"	"++"
191	KYPDIISRI	"+"	"++++"
192	SYITKPEKW	"+"	"+++"
193	IYPGAFVDL	"+"	"+++"
194	QYASRFVQL	"+"	"+++"
196	AYLKWISQI	"+"	"+++"
197	RWPKKSAEF	"+"	"++"
198	LYWSHPRKF	"+"	"++"
199	KFVTVQATF	"+"	"++"
201	AYVNTFHNI	"++"	"++++"
202	AYGTYRSNF	"+"	"++++"

203	YYGILQEKI	"+"	"+++"
205	VYGLQRNLL	"+"	"+++"
207	IYLERFPIF	"++"	"++++"
208	SYNPAENAVLL	"+"	"+++"
209	VFHPRQELI	"++"	"++++"
210	AYPAIRYLL	"+"	"++++"
211	IYIPSYFDF	"++"	"++++"
212	VYGDVISNI	"+"	"++++"
215	IYTGNISSF	"+"	"++"
216	IYADVGEEF	"+"	"++"
217	DYIPYVFKL	"+++"	"++++"
218	VYQGAIRQI	"+"	"+++"

Exemplary results of peptide-specific *in vitro* CD8+ T cell responses of a healthy HLA-A*02+ donor (Figure 3)

CD8+ T cells were primed using artificial APCs coated with anti-CD28 mAb and HLA-A*02 in complex with IMA-APOB-002 (Seq ID No 7) peptide (A, right panel) or IMA-APOB-003 (B, right panel, Seq ID No 1), or IMA-ALDH1L1-001 (C, right panel, Seq ID No 2), respectively. After three cycles of stimulation, the detection of peptide-reactive cells was performed by 2D multimer staining with A*02/ APOB-002 (A) or A*02/ APOB-003 (B), or A*02/ALDH1L1-001. Left panels (A, B, C) show control staining of cells stimulated with irrelevant A*02/peptide complexes. Viable singlet cells were gated for CD8+ lymphocytes. Boolean gates helped excluding false-positive events detected with multimers specific for different peptides. Frequencies of specific multimer+ cells among CD8+ lymphocytes are indicated.

Exemplary results of peptide-specific *in vitro* CD8+ T cell responses of a healthy HLA-A*24+ donor (Figure 4)

CD8+ T cells were primed using artificial APCs coated with anti-CD28 mAb and HLA-A*24 in complex with IMA-KLHL24-001 (Seq ID No 190) peptide (A, right panel) or IMA-APOB-006 (B, right panel, Seq ID No 218), respectively. After three cycles of stimulation, the detection of peptide-reactive cells was performed by 2D multimer staining with A*24/ KLHL24-001 (A) or A*24/ APOB-006 (B). Left panels (A and B) show control staining of cells stimulated with irrelevant A*24/peptide complexes. Viable singlet

cells were gated for CD8+ lymphocytes. Boolean gates helped excluding false-positive events detected with multimers specific for different peptides. Frequencies of specific multimer+ cells among CD8+ lymphocytes are indicated.

Example 5: Syntheses of peptides

All peptides were synthesized using standard and well-established solid phase peptide synthesis using the Fmoc-strategy. Identity and purity of each individual peptide have been determined by mass spectrometry and analytical RP-HPLC. The peptides were obtained as white to off-white lyophilizates (trifluoro acetate salt) in purities of >50%. All TUMAPs are preferably administered as trifluoro-acetate salts or acetate salts, other salt-forms are also possible.

Reference List

Adler, A. S. et al., Genes Dev. **28** (2014)

Ahn, Y. H. et al., J Proteomics. **106** (2014)

Akiyama, H. et al., Oncol Rep. **21** (2009)

Alam, S. M. et al., Endocr.Relat Cancer **16** (2009)

Aleman, G. et al., Am J Physiol Endocrinol.Metab **289** (2005)

Alexanian, A. et al., Cancer Genomics Proteomics. **9** (2012)

Altenhofer, S. et al., J Biol.Chem. **285** (2010)

Alvarez, C. et al., J Biol.Chem. **276** (2001)

Ammerpohl, O. et al., Int.J Cancer **130** (2012)

Andersen, R. S. et al., Nat.Protoc. **7** (2012)

Arai, E. et al., Carcinogenesis **33** (2012)

Araki, T. et al., J Biol.Chem. **286** (2011)

Arlt, A. et al., Oncogene **28** (2009)

Arndt, S. et al., Oncol Rep. **18** (2007)

Arner, E. S. et al., Eur.J Biochem. **267** (2000)

Atienza, J. M. et al., Mol Cancer Ther **4** (2005)

Avery-Kiejda, K. A. et al., BMC.Cancer **14** (2014)

Bachmann, S. B. et al., Mol Cancer **13** (2014)

Balogh, K. et al., Oncogene **31** (2012)

Bani, M. R. et al., Mol Cancer Ther **3** (2004)

Bansal, N. et al., PLoS.One. **6** (2011)

Barbarulo, A. et al., Oncogene **32** (2013)

Bell, J. C. et al., Drug Metab Dispos. **40** (2012)

Ben-Izhak, O. et al., Histopathology **41** (2002)

Bergada, L. et al., Lab Invest **94** (2014)

Bergeron, M. J. et al., Mol Aspects Med. **34** (2013)

Bhattacharya, C. et al., Mol Cancer **11** (2012)

Bhogaraju, S. et al., Science **341** (2013)

Bidkhori, G. et al., PLoS.One. **8** (2013)

Bieche, I. et al., Breast Cancer Res **6** (2004)

Biswas, S. et al., Biochim.Biophys.Acta **1832** (2013)

Blanke, K. L. et al., Cancer Causes Control **25** (2014)

Bodine, S. C. et al., Science **294** (2001)

Boehringer, J. et al., Biochem.J **448** (2012)

Bojjireddy, N. et al., J Cell Sci. (2014)

Booth, D. G. et al., EMBO J **30** (2011)

Bouquet, C. et al., Mol Ther **14** (2006)

Boylan, K. L. et al., Proteome.Sci. **8** (2010)

Braumuller, H. et al., Nature (2013)

Brockmoller, S. F. et al., J Proteome.Res **11** (2012)

Buch, S. C. et al., Mol Carcinog. **51 Suppl 1** (2012)

Bull, C. et al., Cancer Res **74** (2014)

Burrell, R. A. et al., Nature **494** (2013)

Butterfield, L. H. et al., Clin Cancer Res **12** (2006)

Butterfield, L. H. et al., Clin.Cancer Res. **9** (2003)

Byrne, A. et al., Exp.Cell Res **316** (2010)

Cadenas, C. et al., Cell Cycle **13** (2014)

Cadoret, A. et al., Oncogene **21** (2002)

Cao, H. et al., Biochemistry **41** (2002)

Cao, Y. et al., Cancer Research **61** (2001)

Cao-Ehlker, X. et al., J Biol.Chem. **288** (2013)

Carroll, M. et al., J Interferon Cytokine Res **33** (2013)

Carrouel, F. et al., J Dent.Res **87** (2008)

Castro, M. et al., J Transl.Med. **8** (2010)

Chae, Y. S. et al., Med.Oncol **28** (2011)

Chang, L. O. et al., Cancer Res **33** (1973)

Chang, Y. S. et al., Cancer Chemother.Pharmacol. **59** (2007)

Chapiro, J. et al., Radiol.Med. **119** (2014)

Charbonneau, B. et al., Am J Hematol. **87** (2012)

Chatterjee, M. et al., Haematologica **98** (2013)

Chen, J. et al., Biochem.Biophys.Res Commun. **420** (2012a)

Chen, M. et al., Proc.Natl.Acad.Sci.U.S.A **108** (2011a)

Chen, R. et al., World J Gastroenterol. **17** (2011b)

Chen, X. et al., J Dig.Dis. **12** (2011c)

Chen, X. Q. et al., Med.Oncol **29** (2012b)

Cheng, L. et al., Genomics **102** (2013)

Choi, Y. W. et al., Int.J Gynecol.Cancer **17** (2007)

Christa, L. et al., Gastroenterology **106** (1994)

Clark, A. G. et al., Cytoskeleton (Hoboken.) **69** (2012)

Claro da, Silva T. et al., Mol.Aspects Med. **34** (2013)

Cohen, L. et al., Nature **395** (1998)

Collins, C. L. et al., Surgery **122** (1997)

Com, E. et al., J Proteomics. **75** (2012)

Copps, K. D. et al., Diabetologia **55** (2012)

Cornen, S. et al., PLoS.ONE. **9** (2014)

Cornez, I. et al., Biochem.Pharmacol. **75** (2008)

Cowling, V. H., Oncogene **29** (2010)

Cui, T. et al., Int.J Oncol **39** (2011)

da Silva, M. G. et al., Exp.Clin Cardiol. **17** (2012)

Dadkhah, E. et al., Arch.Iran Med. **16** (2013)

Darmanis, S. et al., PLoS.One. **8** (2013)

Darvekar, S. et al., Biochem.J **442** (2012)

Darvekar, S. R. et al., PLoS.One. **9** (2014)

Datta, K. et al., J Biol.Chem. **284** (2009)

David, S. et al., Front Biosci.(Elite.Ed) **5** (2013)

de Almagro, M. C. et al., Biochem.Pharmacol. **81** (2011)

de Groot, J. F. et al., Cancer Res **65** (2005)

Deb, S. et al., Br.J Cancer **110** (2014)

Debauve, G. et al., Cell Mol Life Sci. **65** (2008)

Decker, T. et al., J Clin Invest **109** (2002)

Decock, A. et al., Genome Biol. **13** (2012)

Del Campo, E. M. et al., Mol Phylogenet.Evol. **66** (2013)

Delaval, B. et al., J Cell Biol. **188** (2010)

Deng, X. D. et al., Asian Pac.J Cancer Prev. **15** (2014)

Di, Gregorio E. et al., J Med.Genet. **50** (2013)

Diggle, C. P. et al., PLoS.Genet. **10** (2014)

Dimitrov, A. et al., Hum.Mol Genet. **18** (2009)

Dmitriev, O. Y., Biochem.Cell Biol. **89** (2011)

Doherty, J. A. et al., Cancer Epidemiol.Biomarkers Prev. **20** (2011)

Dong, Z. et al., Crit Rev.Oncol Hematol. **59** (2006)

Dou, R. et al., Cancer Lett. **336** (2013)

Drazkowska, K. et al., Nucleic Acids Res **41** (2013)

Edavana, V. K. et al., Drug Metab Dispos. **41** (2013)

Edwards, P. A. et al., Breast Cancer Res **14** (2012)

Elvenes, J. et al., PLoS.One. **6** (2011)

Emaduddin, M. et al., Cell Commun.Signal. **6** (2008)

Enguita-German, M. et al., World J Hepatol. **6** (2014)

Epelbaum, R. et al., Pathol.Oncol Res **4** (1998)

Fan, T. W. et al., Mol Cancer **8** (2009)

Fang, Z. Q. et al., Genet.Mol Res **12** (2013)

Fassas, A. B. et al., Leuk.Lymphoma **45** (2004)

Feferman, L. et al., Prostate Cancer Prostatic.Dis. **16** (2013)

Fei, F. et al., J Cancer Res Clin Oncol (2014a)

Fei, F. et al., Ann Surg.Oncol **21** (2014b)

Feigelson, H. S. et al., Breast Cancer Res **10** (2008)

Feng, L. et al., Cell Biochem.Funct. **29** (2011)

Feng, M. et al., J Clin Invest **124** (2014a)

Feng, S. et al., Int.J Biol.Sci. **9** (2013)

Feng, Y. et al., J Biol.Chem. **289** (2014b)

Feng, Y. et al., Free Radic.Res **46** (2012)

Fernandes, C. F. et al., Biochem.Biophys.Res Commun. **361** (2007)

Ferre, S. et al., J Am Soc Nephrol. **25** (2014)

Ferrer-Ferrer, M. et al., Arch.Med.Res **44** (2013)

Filmus, J. et al., FEBS J **280** (2013)

Fiorito, V. et al., Biochim.Biophys.Acta **1839** (2014)

Fojo, A. T. et al., Proc.Natl.Acad.Sci.U.S.A **84** (1987)

Fonseca, A. L. et al., Genes Chromosomes.Cancer **51** (2012)

Fossdal, G. et al., ScientificWorldJournal. **2012** (2012)

Fournier, T. et al., Biochim.Biophys.Acta **1482** (2000)

Fu, W. et al., J Cell Sci. **123** (2010)

Fujitomo, T. et al., Cancer Res **72** (2012)

Furukawa, T. et al., Sci.Rep. **1** (2011)

Furutani, M. et al., Hepatology **24** (1996)

Gadd, S. et al., Lab Invest **90** (2010)

Gailani, D., Trends Cardiovasc.Med. **10** (2000)

Galamb, O. et al., Helicobacter. **13** (2008)

Galazis, N. et al., Gynecol.Endocrinol. **29** (2013)

Gandhi, A. V. et al., Ann Surg.Oncol **20 Suppl 3** (2013)

Gao, L. et al., Mol Oncol **6** (2012)

Garcia-Baquero, R. et al., Tumour.Biol. **35** (2014)

Gardner-Stephen, D. A. et al., Drug Metab Dispos. **35** (2007)

Garg, M. et al., Cancer **116** (2010a)

Garg, M. et al., Eur.J Cancer **46** (2010b)

Gburcik, V. et al., Mol Cell Biol. **25** (2005)

Gergely, F. et al., Proc.Natl.Acad.Sci.U.S.A **97** (2000)

Gervasini, G. et al., Cancer **107** (2006)

Getty, A. L. et al., Cell Mol Life Sci. **68** (2011)

Gilabert, M. et al., J Cell Physiol **228** (2013)

Gilkes, D. M. et al., Mol Cancer Res **11** (2013)

Giovannetti, E. et al., J Natl.Cancer Inst. **106** (2014)

Gokmen-Polar, Y. et al., Mod.Pathol. (2014)

Goldstein, I. et al., Carcinogenesis **34** (2013)

Gong, Y. et al., Genet.Mol Res **12** (2013)

Goode, E. L. et al., Clin Cancer Res **16** (2010)

Gordon, E. M. et al., Am.J Pediatr.Hematol.Oncol **15** (1993)

Gotzmann, J. et al., Crit Rev.Eukaryot.Gene Expr. **9** (1999)

Gray, L. R. et al., Cell Mol Life Sci. **71** (2014)

Gregory, P. A. et al., J Biol.Chem. **278** (2003)

Greif, P. A. et al., Leukemia **25** (2011)

Gu, W. et al., PLoS.One. **7** (2012)

Guo, L. et al., Cancer Sci. **103** (2012)

Halon, A. et al., Arch.Gynecol.Obstet. **287** (2013)

Hamamoto, R. et al., Cancer Sci. **97** (2006)

Hamilton, S. R. et al., Glycobiology **15** (2005)

Hamm, A. et al., BMC.Cancer **8** (2008)

Hanioka, N. et al., Basic Clin Pharmacol.Toxicol. **110** (2012)

Harris, M. et al., Pharmacogenet.Genomics **24** (2014)

Hatakeyama, H. et al., Proteomics. **6** (2006)

Havens, M. A. et al., PLoS.Genet. **10** (2014)

He, P. et al., Hum.Pathol. **35** (2004)

He, X. et al., Neoplasma **61** (2014a)

He, Y. et al., Mol Carcinog. (2014b)

Hellwinkel, O. J. et al., Prostate Cancer Prostatic.Dis. **14** (2011)

Hemmingsson, O. et al., Oncol Rep. **22** (2009)

Hidalgo-Curtis, C. et al., Br.J Haematol. **148** (2010)

Hider, J. L. et al., BMC.Evol.Biol. **13** (2013)

Hinsch, N. et al., BMC.Cancer **9** (2009)

Hirota, Y. et al., Nucleic Acids Res **28** (2000)

Hlavata, I. et al., Mutagenesis **27** (2012)

Hoelz, D. J. et al., Proteomics. **6** (2006)

Holden, H. M. et al., Cell Mol Life Sci. **61** (2004)

Honda, K. et al., PLoS.One. **7** (2012)

Hong, Y. et al., J Biol.Chem. **274** (1999)

Hood, F. E. et al., Bioarchitecture. **1** (2011)

Hood, F. E. et al., J Cell Biol. **202** (2013)

Hopfer, O. et al., Br.J Cancer **93** (2005)

Horani, A. et al., Am J Hum.Genet. **91** (2012)

Hou, M. et al., Int.J Mol Med. **33** (2014)

Hu, D. G. et al., Drug Metab Rev. **46** (2014)

Hua, D. et al., Int.J Mol Med. **30** (2012a)

Hua, T. et al., J Biol.Chem. **287** (2012b)

Huang, O. et al., Jpn.J Clin Oncol **43** (2013)

Huang, S. et al., Oncogene **21** (2002)

Huang, Y. et al., Oncotarget. **5** (2014)

Hughes, H. et al., J Cell Sci. **123** (2010)

Hunecke, D. et al., J Pathol. **228** (2012)

Huopaniemi, L. et al., Glycobiology **14** (2004)

Hyung, S. W. et al., Mol Cell Proteomics. **10** (2011)

Iannitti, T. et al., Mar.Drugs **8** (2010)

Ichida, K. et al., Biochem.Biophys.Res Commun. **282** (2001)

Ignatova, I. D. et al., Am J Physiol Endocrinol.Metab **296** (2009)

Ikeda, R. et al., Int.J Oncol **38** (2011)

Inuzuka, M. et al., J Biol.Chem. **280** (2005)

Ishiguro, H. et al., Oncogene **21** (2002)

Ishizaki, F. et al., Sci.Rep. **3** (2013)

Ivashchenko, A. T. et al., Biomed.Res Int. **2013** (2013)

Jacquemier, J. et al., Cancer Res **65** (2005)

Jacques, C. et al., Br.J Cancer **101** (2009)

Jaffe, E. K. et al., Arch.Biochem.Biophys. **530** (2013)

Jakobsson, A. et al., Prog.Lipid Res **45** (2006)

Jamroziak, K. et al., Eur.J Haematol. **72** (2004)

Jeung, H. C. et al., Oncologist. **12** (2007)

Jia, Y. et al., Br.J Cancer **110** (2014)

Jiang, J. G. et al., Cancer Res **65** (2005)

Jiang, X. et al., Histol.Histopathol. **25** (2010)

Jiang, X. et al., Mol Carcinog. (2014)

Jin, Z. et al., Int.J Clin Exp.Pathol. **7** (2014)

Jockusch, H. et al., Proteomics. **14** (2014)

Johnson, M. A. et al., Ann N.Y.Acad.Sci. **1012** (2004)

Jose-Eneriz, E. S. et al., Br.J Haematol. **142** (2008)

Jung, G. et al., Proc Natl Acad Sci U S A **84** (1987)

Jung, H. J. et al., J Mol Med.(Berl) **91** (2013)

Kaira, K. et al., Hepatobiliary.Pancreat.Dis.Int. **13** (2014)

Kalsotra, A. et al., Toxicol.Appl.Pharmacol. **199** (2004)

Kalthoff, S. et al., J Biol.Chem. **285** (2010)

Kamiyama, S. et al., Glycobiology **21** (2011)

Kamiyama, S. et al., J Biol.Chem. **281** (2006)

Kandil, D. H. et al., Adv.Anat.Pathol. **16** (2009)

Kandimalla, R. et al., Nat Rev.Urol. **10** (2013)

Karvonen, U. et al., J Mol Biol. **382** (2008)

Kelleher, D. J. et al., Glycobiology **16** (2006)

Khan, A. P. et al., Neoplasia. **15** (2013)

Kim, Y. et al., Hum.Pathol. **46** (2015)

Kim, Y. W. et al., PLoS.One. **7** (2012)

Klein, C. J. et al., Neurology **82** (2014)

Kobayashi, T. et al., Biochem.J **400** (2006)

Kollmann, K. et al., Cancer Cell **24** (2013)

Komatsu, M. et al., Pharmacol.Res **66** (2012)

Kong, S. Y. et al., Cancer Sci. **99** (2008)

Kovacevic, Z. et al., Biochim.Biophys.Acta **1783** (2008)

Kracmarova, A. et al., Leuk.Lymphoma **49** (2008)

Kraemer, N. et al., Cell Mol Life Sci. **68** (2011)

Kress, T. R. et al., Mol Cell **41** (2011)

Krohn, A. et al., J Pathol. **231** (2013)

Krupenko, S. A. et al., Cell Growth Differ. **13** (2002)

Kubota, H. et al., Cell Stress.Chaperones. **15** (2010)

Kummel, D. et al., EMBO Rep. **6** (2005)

Kunutsor, S. K. et al., Int.J Cancer (2014)

Kuriyama, H. et al., Gene **253** (2000)

Laezza, F. et al., Mol Cell Neurosci. **34** (2007)

Lahiri, S. et al., PLoS.Biol. **12** (2014)

Lando, M. et al., J Pathol. **230** (2013)

Lapucci, A. et al., FASEB J **24** (2010)

Lascorz, J. et al., BMC.Med.Genet. **13** (2012)

Lauffart, B. et al., BMC.Womens Health **5** (2005)

Laverdiere, I. et al., Endocr.Relat Cancer (2014)

Leasure, C. D. et al., Plant Physiol **150** (2009)

Lee, C. H. et al., Hum.Reprod. **24** (2009)

Lee, K. W. et al., J Biol.Chem. **288** (2013)

Lee, S. J. et al., Toxicol.Lett. (2014)

Lee, W. C. et al., J Immunother. **28** (2005)

Lee, Y. C. et al., Int.J Cancer **122** (2008)

Lekva, T. et al., PLoS.One. **8** (2013)

LeRoy, P. J. et al., Cancer Res **67** (2007)

Leung, T. et al., Breast Cancer Res **15** (2013)

Levenson, V. V. et al., Somat.Cell Mol Genet. **25** (1999)

Levi, S. et al., Front Pharmacol. **5** (2014)

Li, D. et al., Protein Cell **5** (2014a)

Li, N. et al., Biochem.Biophys.Res Commun. **455** (2014)

Li, X. et al., Med.Oncol **31** (2014b)

Li, Y. et al., Mol Cell Biol. **29** (2009)

Li, Y. H. et al., World J Gastroenterol. **18** (2012)

Liang, J. et al., PLoS.One. **3** (2008)

Lillig, C. H. et al., Antioxid.Redox.Signal. **9** (2007)

Lin, C. H. et al., J Cell Biol. **189** (2010)

Lin, M. C. et al., Oral Oncol **50** (2014)

Lin, S. H. et al., Oncogene **23** (2004)

Lin, Z. et al., Cell Rep. **5** (2013)

Linderoth, J. et al., Br.J Haematol. **141** (2008)

Line, A. et al., Cancer Immunol Immunother. **51** (2002)

Ling, C. et al., EMBO J **26** (2007)

Linge, A. et al., J Proteome.Res **13** (2014)

Lioutas, A. et al., EMBO Rep. **14** (2013)

Liu, C. et al., Nat Med. **20** (2014)

Liu, C. et al., J Natl.Cancer Inst. **105** (2013a)

Liu, H. et al., Carcinogenesis **34** (2013b)

Liu, T. W. et al., Proc.Natl.Acad.Sci.U.S.A **106** (2009a)

Liu, W. et al., J Biol.Chem. **279** (2004)

Liu, Y. et al., Curr.Drug Targets. **13** (2012)

Liu, Y. et al., Cancer Epidemiol.Biomarkers Prev. **18** (2009b)

Liu, Y. et al., Oncol Rep. **18** (2007)

Ljungberg, B., Curr.Opin.Urol. **17** (2007)

Llovet, J. M. et al., N.Engl.J Med. **359** (2008)

Lo Re, A. E. et al., J Biol.Chem. **287** (2012)

Lo, W. Y. et al., J Proteome.Res **6** (2007)

Lombardo, Y. et al., Breast Cancer Res **16** (2014)

Lourenco, G. J. et al., Breast Cancer Res Treat. **100** (2006)

Lovelace, L. L. et al., J Biol.Chem. **286** (2011)

Lung, H. L. et al., Int J Cancer **127** (2010)

Lutcke, H., Eur.J Biochem. **228** (1995)

Ma, X. J. et al., Proc.Natl.Acad.Sci.U.S.A **100** (2003)

Mackiewicz, A. et al., Glycoconj.J **12** (1995)

Mahajan, K. et al., Cancer Lett. **338** (2013)

Mamtani, M. et al., BMC.Res Notes **5** (2012)

Mariani, L. et al., Clin Cancer Res **7** (2001)

Marina, M. et al., Front Biosci.(Landmark.Ed) **19** (2014)

Markiewski, M. M. et al., Nat Immunol **9** (2008)

Martin, T. A. et al., Eur.J Cancer **40** (2004)

Martinez, H. D. et al., Genes Cancer **2** (2011)

Mathison, J. et al., Pathobiology **59** (1991)

Matsubara, J. et al., Cancer Epidemiol.Biomarkers Prev. **20** (2011)

Matusiak, D. et al., J Histochem.Cytochem. **55** (2007)

McGuire, T. A., Md Med.J **40** (1991)

Medjkane, S. et al., Cell Cycle **11** (2012)

Meijers, J. C. et al., Br.J Haematol. **108** (2000)

Mercer, C. A. et al., Autophagy. **5** (2009)

Mercurio, F. A. et al., Biochemistry **51** (2012)

Midorikawa, Y. et al., Jpn.J Cancer Res. **93** (2002)

Miled, C. et al., Cancer Res **65** (2005)

Milkereit, P. et al., J Biol.Chem. **278** (2003)

Miller, J. C. et al., Mol Carcinog. **48** (2009)

Mohelnikova-Duchonova, B. et al., Pancreas **42** (2013)

Monaco, M. E. et al., Transl.Oncol **3** (2010)

Morandi, F. et al., PLoS.One. **7** (2012)

Morrissey, J. J. et al., Urology **83** (2014)

Mu, J. et al., J Biol.Chem. **272** (1997)

Murray, D. W. et al., Br.J Cancer **110** (2014)

Murray, J. I. et al., Mol Biol.Cell **15** (2004)

Murrin, L. C. et al., J Neuroimmune.Pharmacol. **2** (2007)

Murthy, K. G. et al., Genes Dev. **9** (1995)

Mydlikova, Z. et al., Neoplasma **57** (2010)

Narita, T. et al., Mol Cell Biol. **23** (2003)

Narjoz, C. et al., PLoS.One. **9** (2014)

Nelson, E. R. et al., Science **342** (2013)

Ngeow, J. et al., Cancer Discov. **4** (2014)

Nibbe, R. K. et al., Mol.Cell Proteomics. **8** (2009)

Nielsen, M. J. et al., Blood **108** (2006)

Noda, T. et al., Hepatology **55** (2012)

Noh, C. K. et al., Clin Biochem. **47** (2014)

Ntikoudi, E. et al., Cancer Treat.Rev. **40** (2014)

Nwosu, V. et al., Hum.Mol Genet. **10** (2001)

Obholz, K. L. et al., Dev.Biol. **298** (2006)

Oeffner, F. et al., Am J Hum.Genet. **84** (2009)

Ofman, R. et al., Biochem.Biophys.Res Commun. **281** (2001)

Ohshima, K. et al., Mol Biol.Evol. **27** (2010)

Oiso, S. et al., Oncol Rep. **31** (2014)

Oji, Y. et al., Int.J Oncol **44** (2014)

Osada, H. et al., Int.J Cancer **112** (2004)

Otero-Rey, E. M. et al., Oral Oncol **44** (2008)

Palmer, D. H. et al., Hepatology **49** (2009)

Panico, F. et al., Adv.Cancer Res **105** (2009)

Park, B. L. et al., Biochem.Biophys.Res Commun. **363** (2007)

Patel, M. R. et al., Laryngoscope **121** (2011)

Patel, S. A. et al., Br.J Cancer (2014)

Pattani, K. M. et al., PLoS.ONE. **7** (2012)

Pavelec, D. M. et al., Genetics **183** (2009)

Pawlowska, M. et al., Drug Metab Dispos. **41** (2013)

Pehlivan, D. et al., Eur.J Hum.Genet. **22** (2014)

Pei, Z. et al., PLoS.One. **8** (2013)

Pellanda, H. et al., Int.J Biochem.Cell Biol. **44** (2012)

Peng, R. et al., J Cell Biol. **157** (2002)

Perera, S. et al., J Muscle Res Cell Motil. **33** (2012)

Persaud-Sawin, D. A. et al., Hum.Mol Genet. **11** (2002)

Peters, D. G. et al., Cancer Epidemiol.Biomarkers Prev. **14** (2005)

Pizon, V. et al., J Cell Sci. **115** (2002)

Placke, T. et al., Blood **124** (2014)

Plebani, R. et al., Neoplasia. **14** (2012)

Poh, W. et al., Mol Cancer **11** (2012)

Porkka, K. P. et al., Genes Chromosomes.Cancer **39** (2004)

Pylypenko, O. et al., Mol Cell **11** (2003)

Qi, L. et al., Cancer Res **74** (2014)

Qin, Y. et al., Pigment Cell Melanoma Res **26** (2013)

Quayle, S. N. et al., Neuro Oncol **14** (2012)

Quek, H. H. et al., DNA Cell Biol. **16** (1997)

Quidville, V. et al., Cancer Res **73** (2013)

Rajadhyaksha, A. M. et al., Am.J Hum.Genet. **87** (2010)

Rajasekaran, A. K. et al., Nucleic Acids Res **23** (1995)

Rajendran, M. et al., Cancer Metastasis Rev. **29** (2010)

Rakheja, D. et al., Mol Genet.Metab **93** (2008)

Ramana, C. V. et al., EMBO J **19** (2000)

Rashad, N. M. et al., Cytokine **68** (2014)

Rath, N. et al., EMBO Rep. **13** (2012)

Recupero, D. et al., Rom.J Morphol.Embryol. **51** (2010)

Reinisch, W. et al., J Immunother. **25** (2002)

Rekdal, C. et al., J Biol.Chem. **275** (2000)

Ren, Y. G. et al., Mol Biol.Cell **15** (2004)

Rennoll, S. A. et al., Biochem.Biophys.Res Commun. **443** (2014)

Rifas, L. et al., Arthritis Rheum. **60** (2009)

Riihila, P. M. et al., J Invest Dermatol. **134** (2014)

Rodriguez, F. J. et al., J Neuropathol.Exp.Neurol. **67** (2008)

Rogov, V. et al., Mol Cell **53** (2014)

Romanuik, T. L. et al., BMC.Genomics **10** (2009)

Roodman, G. D., Ann N.Y.Acad.Sci. **1192** (2010)

Rosado, I. V. et al., RNA. **10** (2004)

Rose, A. E. et al., Cancer Res **71** (2011)

Ross, H. et al., Arch.Pathol.Lab Med. **136** (2012)

Rossi, M. R. et al., Cancer Genet.Cytogenet. **161** (2005)

Rotondo, R. et al., Int.J Cancer **125** (2009)

Rucksaken, R. et al., Cancer Biomark. **12** (2012)

Ruiz, F. X. et al., Biochem.J **440** (2011)

Ruiz, F. X. et al., Front Pharmacol. **3** (2012)

Rutkowski, M. J. et al., Mol Cancer Res **8** (2010)

Rylova, S. N. et al., Cancer Res **62** (2002)

Sahm, F. et al., Cancer Res **73** (2013)

Sahu, A. et al., Immunol Res **17** (1998)

Saito, T. et al., J Biol.Chem. **278** (2003)

Salahshor, S. et al., J Clin Pathol. **58** (2005)

Sang, W. et al., Zhonghua Bing.Li Xue.Za Zhi. **42** (2013)

Sangro, B. et al., J Clin Oncol **22** (2004)

Sanz, L. et al., Mol Cell Biol. **15** (1995)

Saponaro, C. et al., Cancer Biomark. **14** (2014)

Sarajlic, A. et al., Breast Cancer Res Treat. **143** (2014)

Sasahira, T. et al., Eur.J Cancer **50** (2014)

Schneider, E. et al., Clin Chim.Acta **374** (2006)

Schofield, A. V. et al., Crit Rev.Biochem.Mol Biol. **48** (2013)

Schulz, E. G. et al., Immunity. **30** (2009)

Seifert, M. et al., J Pathol. **205** (2005)

Senchenko, V. et al., Oncogene **22** (2003)

Shaughnessy, J. D., Jr. et al., Blood **118** (2011)

Shen, F. et al., J Cell Biochem. **112** (2011)

Shi, M. et al., World J Gastroenterol. **10** (2004a)

Shi, Y. et al., Exp.Cell Res **296** (2004b)

Shi, Z. Z. et al., Clin Transl.Oncol **16** (2014)

Shinji, S. et al., Oncol Rep. **15** (2006)

Shodeinde, A. et al., J Mol Biochem. **2** (2013)

Shubbar, E. et al., BMC.Cancer **13** (2013)

Shurbaji, M. S. et al., Am J Clin Pathol. **96** (1991)

Sillars-Hardebol, A. H. et al., Gut **61** (2012)

Singh, S. et al., Tumour.Biol. (2014)

Smith, P. et al., Clin Cancer Res **13** (2007)

Song, C. et al., J Biol.Chem. **288** (2013)

Srivenugopal, K. S. et al., Cancer Lett. **117** (1997)

Staal-van den Brekel AJ et al., Br.J Cancer **76** (1997)

Steen, H. C. et al., J Interferon Cytokine Res. **32** (2012)

Stefanska, B. et al., Clin Cancer Res **20** (2014)

Strassburg, C. P. et al., J Biol.Chem. **273** (1998)

Strassburg, C. P. et al., Mol Pharmacol. **52** (1997)

Sudo, H. et al., Genomics **95** (2010)

Sugihara, T. et al., J Biol.Chem. **276** (2001)

Sun, C. et al., Pathol.Res Pract. **210** (2014)

Sun, X. et al., J Pathol. **226** (2012)

Sun, X. et al., Protein Cell **4** (2013)

Sun, X. J. et al., Zhonghua Yi.Xue.Yi.Chuan Xue.Za Zhi. **22** (2005)

Supernat, A. et al., Oncol Lett. **4** (2012)

Surmacz, E., J Mammary.Gland.Biol.Neoplasia. **18** (2013)

Suzuki, K. et al., Biochem.Biophys.Res Commun. **368** (2008)

Swallow, C. J. et al., Oncogene **24** (2005)

Tabuchi, K. et al., J Neurosci. **22** (2002)

Taguchi, O. et al., Clin Chim.Acta **244** (1996)

Takayama, T. et al., Cancer **68** (1991)

Takayama, T. et al., Lancet **356** (2000)

Takeda, Y. et al., Glycobiology **24** (2014)

Takemasa, I. et al., Int.J Oncol **40** (2012)

Takeuchi, A. et al., Mol Cell Endocrinol. **384** (2014)

Tan, L. Z. et al., Am J Pathol. **183** (2013)

Tan, M. K. et al., Mol Cell Biol. **31** (2011)

Tanahashi, N. et al., Biochem.Biophys.Res Commun. **243** (1998)

Tanaka, M. et al., Mol Med.Rep. **7** (2013)

Tang, L. et al., Arch.Med.Res **43** (2012)

Tang, X. H. et al., Annu.Rev.Pathol. **6** (2011)

Tao, J. et al., Sci.Transl.Med. **3** (2011)

Tao, R. H. et al., Biochem.Biophys.Res Commun. **341** (2006)

Tao, T. et al., Cell Res **23** (2013)

Tarao, K. et al., Cancer **86** (1999)

Tarao, K. et al., Cancer **79** (1997)

Tasker, P. N. et al., Osteoporos.Int. **17** (2006)

Telikicherla, D. et al., Clin Proteomics. **9** (2012)

Tian, T. et al., Eur.J Cancer **48** (2012)

Tian, Y. et al., BMC.Cancer **14** (2014)

Tomiyama, K. et al., Proc.Natl.Acad.Sci.U.S.A **107** (2010)

Tomoda, T. et al., J Gastroenterol.Hepatol. **27** (2012)

Tong, J. et al., PLoS.One. **8** (2013)

Tortorella, S. et al., J Membr.Biol. **247** (2014)

Tran, E. et al., Science **344** (2014)

Trougakos, I. P., Gerontology **59** (2013)

Tsai, H. Y. et al., Oncogene **32** (2013)

Uddin, S. et al., Int.J Clin Exp.Pathol. **4** (2011)

Uehara, Y. et al., Cancer Res **43** (1983)

Urig, S. et al., Semin.Cancer Biol. **16** (2006)

Vainio, P. et al., Am.J Pathol. **178** (2011)

van der Spek, P. J. et al., Genomics **31** (1996)

van Zuylen, W. J. et al., PLoS.Pathog. **8** (2012)

van, den Broek, I et al., Proteomics.Clin Appl. **4** (2010)

van, Duin M. et al., Haematologica **96** (2011)

Vejda, S. et al., Mol Cell Proteomics. **1** (2002)

Vincent, F. et al., Cancer Res **69** (2009)

Wang, B. S. et al., Cell Stress.Chaperones. **18** (2013a)

Wang, D. et al., J Biol.Chem. **277** (2002)

Wang, J. et al., Eur.J Cancer Prev. **22** (2013b)

Wang, J. et al., J Clin Invest **112** (2003)

Wang, J. et al., Cancer Prev.Res (Phila) **6** (2013c)

Wang, J. C. et al., Oncology **81** (2011)

Wang, M. et al., Chin J Physiol **55** (2012)

Wang, S. K. et al., PLoS.Genet. **9** (2013d)

Wang, S. S. et al., PLoS.One. **5** (2010)

Wang, X. et al., Urol.Int. **92** (2014)

Wang, Y. et al., J Biol.Chem. **274** (1999)

Wang, Y. et al., Med.Oncol **32** (2015)

Wazir, U. et al., Cell Mol Biol.Lett. **18** (2013)

Wazir, U. et al., Anticancer Res **32** (2012)

Weiss, J. et al., Int.J Antimicrob.Agents **41** (2013)

Welsh, M. M. et al., Carcinogenesis **29** (2008)

Wieser, R., Leuk.Lymphoma **43** (2002)

Wilhelm, S. M. et al., Cancer Res. **64** (2004)

Williams, A. L. et al., Nature **506** (2014)

Witte, I. et al., Cell Death.Dis. **2** (2011)

Wong, K. K. et al., Leukemia **28** (2014)

Wong, N. et al., J Hepatol. **38** (2003)

Wu, L. et al., Ann Hematol. **91** (2012)

Wu, N. et al., Int.J Mol Sci. **14** (2013a)

Wu, W. et al., Sci.China Life Sci. **56** (2013b)

Wu, X. et al., Am.J Clin Exp.Urol. **2** (2014)

Wu, Y. M. et al., Cancer Res **71** (2011)

Xiao, J. et al., J Biol.Chem. **276** (2001)

Xie, F. W. et al., Neoplasma **61** (2014)

Xu, H. et al., Cell Rep. **9** (2014)

Xu, X. et al., Proteomics. **10** (2010)

Yan, D. et al., Proc.Natl.Acad.Sci.U.S.A **98** (2001)

Yang, C. et al., Virchows Arch. **463** (2013)

Yang, C. Y. et al., J Immunol **192** (2014a)

Yang, H. et al., Oncol Rep. **24** (2010)

Yang, H. W. et al., Oncogene **0** (2014b)

Yang, R. et al., Mol Cell Biol. **31** (2011a)

Yang, Z. J. et al., Mol Cancer Ther **10** (2011b)

Yau, C. et al., Breast Cancer Res **12** (2010)

Ye, X. H. et al., Mol Genet.Genomics (2014)

Yoon, J. K. et al., J Transl.Med. **12** (2014)

Yoshimura, S. et al., J Cell Biol. **191** (2010)

Yoshizuka, N. et al., Mol Cancer Res **10** (2012)

Yosten, G. L. et al., Am J Physiol Regul.Integr.Comp Physiol **303** (2012)

Yu, J. H. et al., RNA. **11** (2005)

Yu, K. et al., PLoS.Genet. **4** (2008)

Yue, C. et al., Int.J Cancer **136** (2015)

Zamanian-Daryoush, M. et al., J Biol.Chem. **288** (2013)

Zarling, A. L. et al., Cancer Res **74** (2014)

Zekri, A. R. et al., Asian Pac.J Cancer Prev. **13** (2012)

Zelcer, N. et al., Mol Cell Biol. **34** (2014)

Zhang, D. et al., Pak.J Med.Sci. **29** (2013a)

Zhang, H. et al., Oncotarget. **4** (2013b)

Zhang, H. T. et al., Biochim.Biophys.Acta **1839** (2014a)

Zhang, J. et al., Drug Metab Dispos. **34** (2006)

Zhang, S. et al., BMC.Cancer **11** (2011)

Zhang, X. et al., PLoS.One. **7** (2012)

Zhang, X. D. et al., Int.J Clin Exp.Med. **7** (2014b)

Zhao, Y. et al., Cell Death.Dis. **4** (2013)

Zhou, B. et al., Cancer Biol.Ther **13** (2012)

Zhou, D. et al., PLoS.One. **8** (2013a)

Zhou, J. et al., Oncol Rep. **30** (2013b)

Zhou, J. et al., Lung Cancer **14** (1996)

Zhu, H. et al., Cell Stress.Chaperones. (2014a)

Zhu, W. L. et al., Anticancer Res **29** (2009)

Zhu, X. et al., Biomed.Pharmacother. **68** (2014b)

Zhuang, Z. et al., J Neurosurg. **115** (2011)

Zietek, Z. et al., Pol.Tyg.Lek. **51** (1996)

Zou, W. et al., Cancer Sci. **101** (2010)

Zu, X. et al., Molecules. **18** (2013)

Zu, X. Y. et al., Recent Pat Anticancer Drug Discov. **7** (2012)

Zynda, E. R. et al., Cell Cycle **13** (2014)

CLAIMS

1. A peptide comprising the amino acid sequence of SEQ ID No. 53, and a pharmaceutical acceptable salt thereof, wherein said peptide has an overall length of from 10 to 30 amino acids, wherein said peptide has the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I, and wherein said peptide, when bound to MHC, is capable of being recognized by CD8 T cells.

2. The peptide or variant thereof according to claim 1, wherein said peptide has an overall length of from 10 to 16 amino acids, and most preferred wherein the peptide consists of an amino acid sequence according to SEQ ID No. 53.

3. The peptide according to Claim 1 or 2, wherein said peptide includes non-peptide bonds, and/or wherein said peptide is part of a fusion protein comprising N-terminal amino acids of the HLA-DR antigen-associated invariant chain (Ii).

4. An antibody, soluble or membrane-bound, that specifically recognizes the peptide according to any of claims 1 or 2, preferably the peptide according to any of claims 1 or 2 that is bound to an MHC molecule.

5. A T-cell receptor (TCR), soluble or membrane-bound, that is reactive with an HLA ligand, wherein said ligand has at least 88% identity to, and preferably consists of, the amino acid sequence selected from the group consisting of SEQ ID No. 53, wherein optionally said TCR is provided as a soluble molecule and further optionally carries a further effector function such as an immune stimulating domain or toxin.

6. A nucleic acid, encoding a peptide according to any one of claims 1 to 3, the antibody according to claim 4, the TCR according to claim 5, or an expression vector expressing said nucleic acid.

7. A host cell comprising the peptide according to any one of claims 1 to 3, or the nucleic acid or the expression vector according to claim 6, wherein said host cell preferably is an antigen presenting cell such as a dendritic cell, or a T cell or NK cell.

8. A method for producing the peptide according to any one of claims 1 to 3, the antibody according to claim 4, or the TCR according to claim 5, the method comprising culturing a host cell according to claim 7 that presents the peptide according to any one of claims 1 to 3, or expresses the nucleic acid or the expression vector according to claim 6, and isolating said peptide, said antibody or said TCR from the host cell and/or its culture medium.

9. An *in vitro* method for producing activated T lymphocytes, the method comprising contacting *in vitro* T cells with antigen loaded human class I MHC molecules expressed on the surface of a suitable antigen-presenting cell or an artificial construct mimicking an antigen-presenting cell for a period of time sufficient to activate said T cells in an antigen specific manner, wherein said antigen is a peptide according to claim 1 or 2.

10. An activated T cell, produced by the method according to claim 9, that selectively recognizes a cell which presents a polypeptide comprising an amino acid sequence given in claim 1 or 2.

11. A pharmaceutical composition comprising at least one active ingredient selected from the group consisting of the peptide according to any one of claims 1 to 3, the antibody according to claim 4, the TCR according to claim 5, the nucleic acid or the expression vector according to claim 6, the host cell comprising the expression vector according to claim 7, the activated T cell according to claim 10, and a pharmaceutically acceptable carrier, and optionally, pharmaceutically acceptable excipients and/or stabilizers.

12. The peptide according to any one of claims 1 to 3, the antibody according to claim 4, the TCR according to claim 5, the nucleic acid or the expression vector according to

claim 6, the host cell comprising the expression vector according to claim 7, the activated T cell according to claim 10, or the pharmaceutical composition according to claim 11 for use in medicine.

13. Use of the peptide according to any one of claims 1 to 3, the antibody according to claim 4, the TCR according to claim 5, the nucleic acid or the expression vector according to claim 6, the host cell comprising the expression vector according to claim 7, the activated T cell according to claim 10, or the pharmaceutical composition according to claim 11 in the manufacture of a medicament for the treatment of cancer.

14. The use according to claim 13, wherein said cancer is HHC, brain cancer, kidney cancer, pancreatic cancer, colon or rectal cancer or leukemia and other tumors that show an overexpression of CFHR5.

15. A kit comprising:
(a) a container comprising a pharmaceutical composition according to claim 11, in solution or in lyophilized form;
(b) optionally, a second container containing a diluent or reconstituting solution for the lyophilized formulation;
(c) optionally, at least one more peptide selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 52, and SEQ ID No. 54 to SEQ ID No. 346, and
(d) optionally, instructions for (i) use of the solution or (ii) reconstitution and/or use of the lyophilized formulation, and, optionally,
further comprising one or more of (iii) a buffer, (iv) a diluent, (v) a filter, (vi) a needle, or (v) a syringe.