Novel immunotherapy against several tumors of the blood, such as acute myeloid leukemia (AML)

The present invention relates to peptides, 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 cytotoxic T cell (CTL) peptide epitopes, alone or in combination with other tumor-associated peptides that serve as active pharmaceutical ingredients of vaccine compositions that stimulate anti-tumor immune responses. The present invention relates to several novel peptide sequences and their variants derived from HLA class I and HLA class II molecules of human tumor cells that can be used in vaccine compositions for eliciting anti-tumor immune responses.

Background of the invention

Acute myeloid leukemia (AML), also known as acute myelogenous leukemia or acute nonlymphocytic leukemia (ANLL), is a cancer of the myeloid line of blood cells, characterized by the rapid growth of abnormal white blood cells that accumulate in the bone marrow and interfere with the production of normal blood cells. AML is the most common acute leukemia affecting adults, and its incidence increases with age. Although AML is a relatively rare disease, accounting for approximately 1.2% of cancer deaths in the United States, its incidence is expected to increase as the population ages.

The symptoms of AML are caused by replacement of normal bone marrow with leukemic cells, which causes a drop in red blood cells, platelets, and normal white blood cells. These symptoms include fatigue, shortness of breath, easy bruising and bleeding, and increased risk of infection. Several risk factors and chromosomal abnormalities have been identified, but the specific cause is not clear. As an acute leukemia, AML progresses rapidly and is typically fatal within weeks or months if left untreated.

AML has several subtypes; treatment and prognosis varies among subtypes. Five-year survival varies from 15–70%, and relapse rate varies from 33–78%, depending on the

subtype. AML is treated initially with chemotherapy aimed at inducing a remission; patients may go on to receive additional chemotherapy or a hematopoietic stem cell transplant.

US 2005/0261190 A1 discloses polypeptide fragments of Fas associated Factor 1, which bind to Hsc70/Hsp70, ubiquinated protein or valosin containing protein. Some of the fragemtns include SEQ ID NO: 5 as disclosed herein.

Similarly, KR100692416 discloses a fragment of FAF-1 (Fas-associated Factor 1) as having inhibitory effects on angiogenesis and cell proliferation. Therefore, it is proosed as an anticancer agent, e.g. a tumor metastasis inhibitory agent. The fraction having inhibitory effect on tumor metastasis is composed of 290-345 amino acids of FAF1.

Hassan et al. (The human leukocyte antigen-presented ligandome of B lymphocytes. Mol Cell Proteomics. 2013 Jul;12(7):1829-43) disclose the identification and relative quantification of 14,500 peptide ligands constituting the HLA ligandome of B cells as a starting point for solving a wealth of specific immunological questions.

Kowalewski et al. (Mapping The HLA Ligandome Of Chronic Lymphocytic Leukemia – Towards Peptide Based Immunotherapy Blood 2013; 122(21):4123) describe a method to analyse the HLA class I peptidomes of 25 CLL patients and 35 healthy controls.

Despite the above, there remains a need for new efficacious and safe treatment option for cancers such as blood cancer, in particular acute myeloid leukemia (AML) and other cancers of the blood of different phenotypes which improve the well-being of the patients by not using excessive chemotherapeutic agents or other agents that may lead to severe side effects.

The present invention employs peptides that stimulate the immune system of the patient and act as anti-tumor-agents in a non-invasive fashion.

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 of SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605 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: 325 or SEQ ID NO: 448 to SEQ ID NO: 605, wherein said variant 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 SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605 or a variant 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: 325 or SEQ ID NO: 448 to SEQ ID NO: 605, wherein said peptide or variant thereof has an overall length for SEQ ID NO: 1 to SEQ ID NO: 325 of between 8 and 100, preferably between 8 and 30, and most preferred of between 8 and 14 amino acids, and for SEQ ID NO: SEQ ID NO: 448 to SEQ ID NO: 605 of between 12 and 100, preferably between 12 and 30, and most preferred of between 12 to 18 amino acids.

The following tables show the peptides according to the present invention, their respective SEQ ID NO, and the prospective source protein(s) for these peptides. All peptides in Table 1 bind to HLA A HLA B or HLA C alleles, peptides in Table 2 were identified as derived from AML-related antigens, and the peptides in Table 3 bind to HLA-DR (MHC class II) alleles. The class II peptides in Table 3 are further useful in the diagnosis and/or treatment of AML, Chronic lymphatic leukemia (CLL) and other hematological malignancies, which involve an over-expression or over-presentation of the respective underlying polypeptide.

Thus, the present invention relates in particular to a peptide of the present invention comprising a sequence according to SEQ ID NO: 448 to SEQ ID NO: 605 or a variant thereof, which is at least 80%, preferably at least 90%, homologous (preferably at least 80% or at least 90% identical) to SEQ ID NO: 448 to SEQ ID NO: 605, wherein said peptide or variant thereof has an overall length of between 12 and 100, preferably between 12 and 30, and most preferred of between 12 to 18 amino acids. The present invention relates in particular to a peptide of the present invention consisting of the sequence according to SEQ ID NO: 448 to SEQ ID NO: 605.

Table 1: Peptides according to the present invention, underlying polypeptides in bold

SEQ ID	Protein/Peptides	Number of positive AMLs [rep. frequency]	HLA
	FAF1 Fas (TNFRSF6) associated factor 1	**8 [53.3%]**	
1	AEQFRLEQI	1	B*44
2	FTAEFSSRY	2	A*03
3	HHDESVLTNVF	3	B*38:01
4	REQDEAYRL	1	B*44:25
5	RPVMPSRQI	1	B*07
6	VQREYNLNF	1	B*15
	PLXND1 plexin D1	**7 [46.7%]**	
7	GQLPITIQV	1	B*13:02
8	RAYADEVAV	1	B*51:01
9	REDKPPLAV	1	B*49:01
10	RVKDLDTEKY	2	B*15
11	SEQEMNAHL	1	B*44:25
12	YVLPLVHSL	1	A*02
13	LPLRFWVNI	1	B*51:01
	GMNN geminin, DNA replication inhibitor	**6 [40.0%]**	
14	EVAEHVQYM	3	A*26:01
15	YMAELIERL	3	A*02
	CPQ carboxypeptidase Q	**6 [40.0%]**	
16	ALASLIRSV	5	A*02
17	TVAEITGSKY	1	A*26:01
	ATP5L ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G	**5 [33.3%]**	
18	EIIGKRGIIGY	4	A*26, A*03:01
19	NLVEKTPAL	1	A*02
	ITGA5 integrin, alpha 5	**5 [33.3%]**	
20	IEDKAQILL	3	B*49:01/ B*40
21	SIYDDSYLGY	1	A*26:01
22	TTNHPINPK		A*11
	SKP1 S-phase kinase-associated protein 1	**5 [33.3%]**	
23	NAAILKKV	2	B*51:01
24	NYLDIKGLL	1	A*24
25	YLDIKGLLDV	2	A*02
	CHD1L chromodomain helicase DNA binding protein 1-like	**5 [33.3%]**	
26	EEVGDFIQRY	1	B*44:03
27	EVGDFIQRY	4	A*26:01, A*03
28	MKDLSLGGVL	1	n.a.
	TGFBRAP1 transforming growth factor, beta receptor associated protein 1	**5 [33.3%]**	
29	DEFITVHSM	1	B*18:01

30	EFITVHSML	2	A*23:01
31	GQLDVRELI	1	B*13:02
32	TQYIIHNY	1	B*15
	NGLY1 N-glycanase 1	**5 [33.3%]**	
33	EVVDVTWRY	4	A*26, A*03:01
34	KEALLRDTI	1	B*49:01
	APLP2 amyloid beta (A4) precursor-like protein 2	**5 [33.3%]**	
35	HGYENPTYK	4	A*03
36	SLLYKVPYV	1	A*02
	KIF2C kinesin family member 2C	**5 [33.3%]**	
37	AEIPLRMV	1	B*49:01
38	EVVYRFTAR	1	A*66
39	FPGLAIKI	2	B*51:01
40	IYNGKLFDL	1	A*24
41	IYNGKLFDLL	1	A*24
42	KEIDVISI	1	B*49:01
43	LEEQASRQI	1	B*49:01
44	TRMSTVSEL	1	B*39:01
	ELP3 elongator acetyltransferase complex subunit 3	**5 [33.3%]**	
45	SEETFRFEL	1	B*40
46	KLYPTLVIR	4	A*03
	DGKZ diacylglycerol kinase, zeta	**5 [33.3%]**	
47	ALRNQATMVQK	2 3	A*03:01
48	LLDHAPPEI	3	A*02
	MTCH2 mitochondrial carrier 2	**5 [33.3%]**	
49	GVLGTVVHGK	4	A*03:01
50	VQFIGRESKY	1	B*15
	SLC31A2 solute carrier family 31 (copper transporter), member 2	**4 [26.7%]**	
51	GQSLIHVI	1	B*52:15
52	VHSPAGMAL	1	B*38:01
53	VLYEGIKVGK	4	A*03
	ERLIN1 ER lipid raft associated 1	**4 [26.7%]**	
54	AVIEAEKIAQV	2	A*02
55	DRIEVVNML	1	B*39:01
56	IEAEKIAQV	1	B*49:01
	SERPINB2 serpin peptidase inhibitor, clade B (ovalbumin), member 2	**4 [26.7%]**	
57	IEDLKAQIL	1	B*49:01
58	YLLESVNKL	3	A*02
	ABHD2 abhydrolase domain containing 2	**4 [26.7%]**	
59	HRIYVPLML	1	B*39:01
60	KEYIPPLIW	1	B*4403
61	MDKLVVEY	2	B*15
	GAA glucosidase, alpha; acid	**4 [26.7%]**	
62	ALLGHILLH	1	A*03:01
63	ALLPHLYTL	2	A*02
64	HVAGETVAR	1	A*66
65	KVWPGSTAF	1	A*32

	OPRL1 opiate receptor like 1	**4 [26.7%]**	
66	ETAVAILRF	4	A*26, A*03:01
	WDR45B WD repeat domain 45B	**4 [26.7%]**	
67	RVYNTDPLKEK	4	A*03
	TUFM Tu translation elongation factor, mitochondrial	**4 [26.7%]**	
68	IGVEHVVVY	4	C*12:03
69	RQIGVEHVV	1	B*15
	MFAP1 microfibrillar-associated protein 1	**4 [26.7%]**	
70	DVFERPSAKK	1	A*66
71	EEFQFIKKA	2	B*40:02, B*50
72	THLVDQDTTSF	1	B*38
	ZNF543 zinc finger protein 543	**4 [26.7%]**	
73	ESADLIQHY	4	A*26, A*03:01
	STK4 serine/threonine kinase 4	**4 [26.7%]**	
74	EIIKEISIM	3	A*26
75	SVSDIIRLR	1	A*66
	ZKSCAN8 zinc finger with KRAB and SCAN domains 8	**4 [26.7%]**	
76	AVSLIREEW	2	A*32
77	GEKSESISV	1	B*49:01
78	FLTILPEEL	1	A*02:01
	FNDC3B fibronectin type III domain containing 3B	**4 [26.7%]**	
79	ILWETVPSM	1	A*02:01
80	LPVRTLSI	1	B*51:01
81	RESEYKQVY	1	B*44:03
82	SESLPVRTL	1	B*40
	TMEM164 transmembrane protein 164	**4 [26.7%]**	
83	RLLESVVVL	1	A*02:01
84	RPEEGKESL	1	B*07
85	THGKLVILF	2	B*38
	THOC7 THO complex 7 homolog	**4 [26.7%]**	
86	KELEHLSHI	1	B*49:01
87	REMENYEKI	2	B*49:01 B*44:25
88	VLLSTIHEL	2	A*02
	KLF2 Kruppel-like factor 2	**4 [26.7%]**	
89	KTYTKSSHLK	4	A*03
	TMEM126B transmembrane protein 126B	**4 [26.7%]**	
90	EIIEKNFDY	3	A*26
91	GTEEAPKVFK	1	A*11
92	KLMAIPLVF	1	B*15
	UFD1L ubiquitin fusion degradation 1 like	**4 [26.7%]**	
93	DIKRGIPN	1	Fragment of Seq 94
94	DIKRGIPNY	1	A*26
95	FLDITNPKA	2	A*02
	MUL1 mitochondrial E3 ubiquitin protein ligase 1	**4 [26.7%]**	

96	ALYSVYRQK	2	A*03
97	KVLALVFGF	1	B*15
98	SFTDVIGHY	1	A*29
	VCPIP1 valosin containing protein (p97)/p47 complex interacting protein 1	**4 [26.7%]**	
99	ASAAASGGLLK	3	A*03:01
100	ALLGVTGAPK	1	A*03
	FAM46A family with sequence similarity 46, member A	**4 [26.7%]**	
101	DEIKTLQRY	1	B*18:01
102	EAYVQKMV	1	B*51:01
103	VLHQDSGLGY	1	B*15
104	YLQNHFVGL	1	A*02
	KIF20B kinesin family member 20B	**4 [26.7%]**	
105	AEIEDIRVL	1	B*44:25
106	GQSRLIFTY	1	B*15
107	READFKETL	2	B*49:01, B*40
	CSF3R colony stimulating factor 3 receptor (granulocyte)	**4 [26.7%]**	
108	DTMGPSQHVY	1	A*26
109	ESRGPALTR	1	A*66
110	FQLPGLGTPPIT	1	C*12:03
111	RIQGYVVSW	1	A*32
	NOC4L nucleolar complex associated 4 homolog	**4 [26.7%]**	
112	LLDPSVFHV	3	A*02
113	RFFHLADLF	1	A*23:01
	EMILIN2 elastin microfibril interfacer 2	**4 [26.7%]**	
114	DSISGNLQR	1	A*66
115	ETEQTIQKL	1	n.a.
116	FLYPFLSHL	1	A*02
117	TLDQKIERV	3	A*02:01
	SHANK3 SH3 and multiple ankyrin repeat domains 3	**4 [26.7%]**	
118	DADSRAATV	1	B*51:01
119	DHEGFGFVL	1	B*38:01
120	GEAVKVLSI	1	B*49:01
121	NATDLLKVL	2	C*12:03
	UCK2 uridine-cytidine kinase 2	**4 [26.7%]**	
122	KEITEGKTV	1	B*40:02
123	YRQKQVVIL	2	C*07
124	VAINLIVQH	1	A*03:01
	PHPT1 phosphohistidine phosphatase 1	**4 [26.7%]**	
125	SQDKKIHVY	1	B*15
126	YHADIYDKV	3	B*38, B*39:01
	KIF15 kinesin family member 15	**4 [26.7%]**	
127	DAIKVFVRI	1	B*51:01
128	LEKAFSEI	1	B*49:01
129	MEKSDKNQ	1	n.a.
130	GQTGSGKTF	1	B*15
	SLC12A6 solute carrier family 12	**4 [26.7%]**	

	(potassium/chloride transporter), member 6		
131	DTSPDLSSR	1	A*66
132	KLNEVIVNK	3	A*03
	DOLK dolichol kinase	**4 [26.7%]**	
133	FAQIISVALI	1	A*02
134	IIFDRPLLY	3	A*03:01, A*29
	EEF2K eukaryotic elongation factor-2 kinase	**3 [20.0%]**	
135	DAVNQNTKLL	1	A*02
136	HHILADVSL	1	B*38:01
137	YPSEKRGEL	1	B*07
	PIK3R2 phosphoinositide-3-kinase, regulatory subunit 2 (beta)	**3 [20.0%]**	
138	SVVDLINHY	3	A*26
	TMEM194A transmembrane protein 194A	**3 [20.0%]**	
139	EIIEKDTKY	2	A*26
140	ENEEKLKEL	1	n.a.
	CCS copper chaperone for superoxide dismutase	**3 [20.0%]**	
141	ILGGPGTVQGV	3	A*02
	ZNF264 zinc finger protein 264	**3 [20.0%]**	
142	ESAALIHHY	2	A*26
143	YQRETPQV	1	B*52:15
	LYRM1 LYR motif containing 1	**3 [20.0%]**	
144	ARIEIGLHY	1	B*27:05
145	IPYPRPIHL	2	B*07, B*51:01
	NBN nibrin	**3 [20.0%]**	
146	DVSGKTALNQ	1	n.a.
147	TEFRSLVI	1	B*49:01
148	TLKSGDGITF	1	B*15
	TIPRL TIP41, TOR signaling pathway regulator-like	**3 [20.0%]**	
149	HEADKTYML	1	B*40
150	KFFEEVLLF	1	A*23:01
151	RVMPSSFFL	1	A*02:01
	RPS6KA4 ribosomal protein S6 kinase, 90kDa, polypeptide 4	**3 [20.0%]**	
152	YELDLREPAL	2	B*40
153	GAYGKVFLV	1	A*02:01
	RCBTB2 regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing protein 2	**3 [20.0%]**	
154	DHDLLKNF	2	B*38
155	EELQLIRQA	1	B*44
	PAK4 p21 protein (Cdc42/Rac)-activated kinase 4	**3 [20.0%]**	
156	AAELLKHPF	2	A*32
157	GRVKLSDFGF	1	B*27:01
	ERCC1 excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence)	**3 [20.0%]**	
158	KSNSIIVSPR	3	A*03
	DMD dystrophin	**3 [20.0%]**	
159	ETLERLQEL	1	A*02:01

160	KDDELSRQ	1	n.a.
161	LQQTNSEKI	1	B*13:02
	UNG uracil-DNA glycosylase	**3 [20.0%]**	
162	GEFGKPYFI	1	B*49:01
163	KDVKVVIL	1	B*40:02
164	RPVPPPPSL	1	B*07
	CPA3 carboxypeptidase A3	**3 [20.0%]**	
165	KEDIPGRHSY	1	B*44:02
166	KETKAVTNF	1	B*44:03
167	YEILIHDL	3	B*44:02, B*44:03, B*18:01
	AZU1 azurocidin 1	**3 [20.0%]**	
168	FPRFVNVTV	1	B*51:01
169	QVAGWGSQR	1	A*66
170	WIDGVLNNPGPG	1	n.a.
	ATP2B4 ATPase, Ca++ transporting, plasma membrane 4	**3 [20.0%]**	
171	SFMTHPEF	1	A*29
172	HYTIVFNTF	1	A*23:01
173	GTNDGPALKK	1	A*11
174	IEDPVRPEV	1	B*49:01
	MARK3 MAP/microtubule affinity-regulating kinase 3	**3 [20.0%]**	
175	NTASGGMTR	1	A*66
176	EVIETEKTLY	1	A*26:01
177	MKILNHPNI	1	B*15
	HLA-DMA major histocompatibility complex, class II, DM alpha	**3 [20.0%]**	
178	HEIDRYTAI	1	B*49:01
179	VFTLKPLEF	1	A*24
180	YWVPRNAL	1	C*05
	NDUFS1 NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa	**3 [20.0%]**	
181	EVSPNLVRY	2	A*26
182	LSEIAGMTLP	1	n.a.
	S100A11 S100 calcium binding protein A11	**3 [20.0%]**	
183	FLSFMNTEL	1	A*02:01
184	KAVPSQKRT	1	n.a.
185	LKAVPSQKRT	1	n.a.
186	SLIAVFQKY	1	B*15
	HAL histidine ammonia-lyase	**3 [20.0%]**	
187	IIKEKTVVY	1	B*15
188	LLEQKVWEV	1	A*02
189	SEIAESHRF	2	B*44:25
190	YLAIGIHEL	1	A*02
	PRIM1 primase, DNA, polypeptide 1 (49kDa)	**3 [20.0%]**	
191	IHDELQQSF	3	B*38
	RENBP renin binding protein	**3 [20.0%]**	
192	AHVIDKFLL	2	B*38
193	KAGGEFLLRY	1	A*32

	CCNG1 cyclin G1	**3 [20.0%]**	
194	FEVKDLLSL	1	B*49:01
195	FSKAKPSVL	2	A*02, B*51
	ZNF131 zinc finger protein 131	**3 [20.0%]**	
196	EAIKALEV	1	A*02:01
197	EVASAKQSVKY	1	A*26
198	IEFTYTAKL	1	B*49:01
199	LLADITSKY	1	B*15
	HRSP12 heat-responsive protein 12	**3 [20.0%]**	
200	VLVDRTIYI	3	A*02
	EIF6 eukaryotic translation initiation factor 6	**3 [20.0%]**	
201	IPVVHASI	1	B*51:01
202	TVADQVLVGSY	1	A*26:01
203	VALVHPDL	1	n.a.
	TMPRSS3 transmembrane protease, serine 3	**3 [20.0%]**	
204	LPDDKVTAL	3	C*03, C*12:41
	UBE2G2 ubiquitin-conjugating enzyme E2G 2	**3 [20.0%]**	
205	KIAKQIVQK	1	A*03
206	VEKILLSVV	2	B*49:01
	NOP14 NOP14 nucleolar protein	**3 [20.0%]**	
207	APAGARGGPA	1	B*07
208	EHLRKLEAE	1	n.a.
209	RFIPELINF	1	A*23:01
	TFCP2 transcription factor CP2	**3 [20.0%]**	
210	TEKIAQLF	1	B*18:01
211	KLHDETLTY	1	A*03
212	LHDETLTYL	1	B*38:01
	TARBP1 TAR (HIV-1) RNA binding protein 1	**3 [20.0%]**	
213	GPQEGNGPSLF	1	B*35:01
214	YLLQRAVEV	2	A*02
	TTLL12 tubulin tyrosine ligase-like family, member 12	**3 [20.0%]**	
215	FAALHGPAL	2	A*02
216	RMANLMGIEF	1	B*15
	HLX H2.0-like homeobox	**3 [20.0%]**	
217	DTFPGPYAVL	2	A*26
218	DTMPQTYKR	1	A*66
	CBX2 chromobox homolog 2	**3 [20.0%]**	
219	IEHVFVTDV	2	B*49:01
220	KESPTSVGF	1	B*40
	ZNF638 zinc finger protein 638	**3 [20.0%]**	
221	EAITAIMKY	1	A*26
222	KEKPAENTL	1	B*44:03
223	NEFQSQQNI	1	B*49:01
224	NVIDYGHASKY	1	A*32
	C3AR1 complement component 3a receptor 1	**3 [20.0%]**	
225	FAKSQSKTF	2	A*03, A*32
226	LPFSLAHL	1	B*51:01

	TAF9 TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor	**3 [20.0%]**	
227	APNYRLKSL	1	B*07
228	ILKDMGITEY	2	A*66, A*32
	FSCN1 fascin homolog 1, actin-bundling protein	**3 [20.0%]**	
229	AHDDGRWSL	1	B*38
230	KYLTAEAFGF	2	A*23:01
	ZNF805 zinc finger protein 805	**3 [20.0%]**	
231	ESAALIHHY	2	A*26
232	YQRETPQV	1	B*52:15
	CLEC12A C-type lectin domain family 12, member A	**3 [20.0%]**	
233	EELQRNISL	1	B*44:25
234	RPAALFLTL	1	B*07
235	SEELQRNISL	1	B*40
	SLX4IP SLX4 interacting protein	**3 [20.0%]**	
236	ETIDSRVQEY	3	A*26
	RLTPR RGD motif, leucine rich repeats, tropomodulin domain and proline-rich containing	**3 [20.0%]**	
237	EVSEQILHM	3	A*26
	RNF19B ring finger protein 19B	**3 [20.0%]**	
238	GTLSGGILSSGK	1	A*03
239	GVPIMLAY	2	n.a.
	DDX46 DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	**3 [20.0%]**	
240	EEVKEEVKKF	2	B*44:25, B*44:03
241	KTIAFLLPMF	1	A*32
	LRRC8D leucine rich repeat containing 8 family, member D	**3 [20.0%]**	
242	EVTTNIPKM	3	A*26
	C16orf62 chromosome 16 open reading frame 62	**3 [20.0%]**	
243	IHGDTVQNQL	2	B*38:01
244	RTMVKTLEY	1	A*03:01
	GOLGA7 golgin A7	**3 [20.0%]**	
245	ETVRTLNNLY	3	A*26
	RHOT1 ras homolog family member T1	**3 [20.0%]**	
246	HSIDKVTSR	2	A*66
247	VSNPKSFEY	1	A*32
	BBS1 Bardet-Biedl syndrome 1	**3 [20.0%]**	
248	GLGPTFKL	1	A*02:01
249	NKGISDIIKV	1	n.a.
250	TSTTRPVL	1	A*32
	CEP76 centrosomal protein 76kDa	**3 [20.0%]**	
251	VLGGKAFLEHL	1	A*02
252	YEFERTTSI	2	B*49:01
	GANC glucosidase, alpha; neutral C	**3 [20.0%]**	
253	YLDFTNPKV	3	A*02
	ATP8B4 ATPase, class I, type 8B, member 4	**3 [20.0%]**	
254	IPAVARTTTL	1	B*07
255	KQQLELDSI	1	B*15
256	KTTDTVSSF	1	A*32

	PPIL4 peptidylprolyl isomerase (cyclophilin)-like 4	**3 [20.0%]**	
257	DYLDGVHTVF	2	A*23:01
258	YLDGVHTVF	1	B* 15:01
	HPT1 choline phosphotransferase 1	**3 [20.0%]**	
259	TYVSGMLRF	1	A*23:01
260	DAIDGKQAR	2	A*66
	CHTF18 CTF18, chromosome transmission fidelity factor 18 homolog	**3 [20.0%]**	
261	DPMAPGVQGSLL	1	A*26:01
262	GLDPSQRPK	2	A*03
	DGCR8 DGCR8 microprocessor complex subunit	**3 [20.0%]**	
263	IEDSRVYEL	3	B*49:01, B*40
	ANKS1A ankyrin repeat and sterile alpha motif domain containing 1A	**3 [20.0%]**	
264	YVHSFLSSGY	3	A*26, A*03:01
	TOP1MT topoisomerase (DNA) I, mitochondrial	**3 [20.0%]**	
265	HEYTTKEVF	1	B*18:01
266	KLQEQLAQL	1	A*02:01
267	SIAAKILSY	1	A*03:01
	PHACTR3 phosphatase and actin regulator 3	**3 [20.0%]**	
268	KELLAVKL	1	B*49:01
269	KLKQTTSALEK	2	A*03
	CCDC115 coiled-coil domain containing 115	**3 [20.0%]**	
270	EVGPREAGLR	2	A*66
271	SEAQEGLQKF	1	B*44:25
	SORCS2 sortilin-related VPS10 domain containing receptor 2	**3 [20.0%]**	
272	DEAVLFVQV	3	B*18:01, B*40
	ACCS 1-aminocyclopropane-1-carboxylate synthase homolog	**3 [20.0%]**	
273	EVAKFLSFY	2	A*26
274	KLDQKLPEL	1	A*02:01
275	SVFEKSVGY	1	A*26:01
	ACBD6 acyl-CoA binding domain containing 6	**3 [20.0%]**	
276	NEGQTALHY	1	B*44:03
277	VEFPHSPEI	2	B*49:01
	ORAI3 ORAI calcium release-activated calcium modulator 3	**3 [20.0%]**	
278	RLQGELQAV	3	A*02
	SIKE1 suppressor of IKBKE 1	**3 [20.0%]**	
279	KELRELLSI	1	B*49:01
280	SLVDQSAAL	1	A*02:01
281	LELIMSKY	1	B*18:01
	C9orf156 chromosome 9 open reading frame 156	**3 [20.0%]**	
282	DIKPYIAEY	3	A*26
	EDEM2 ER degradation enhancer, mannosidase alpha-like 2	**3 [20.0%]**	
283	KLMAMFLEY	1	A*03:01

284	YTVEKREGY	2	A*26
	NUP85 nucleoporin 85kDa	**3 [20.0%]**	
285	FEFDIHQVI	2	B*49:01
286	SENPSKHDSF	1	B*44:25
	PANK2 pantothenate kinase 2	**3 [20.0%]**	
287	NFLRINTI	1	C*02
288	YSGPTSVSR	1	A*66
289	DIYGGDYERF	1	A*26:01
	SPATC1L spermatogenesis and centriole associated 1-like	**3 [20.0%]**	
290	SARLEKLGY	1	B*15
291	YVFPGVTRL	1	A*02
292	YYLNEIQSF	1	A*23:01
	IKZF4 IKAROS family zinc finger 4	**3 [20.0%]**	
293	YHSQDRYEF	3	B*39:01
	DHX33 DEAH (Asp-Glu-Ala-His) box polypeptide 33	**3 [20.0%]**	
294	FPPGRQVVM	2	C*12:03
295	ILDEAHERTI	1	A*02
	METTL7A methyltransferase like 7A	**3 [20.0%]**	
296	VIYNEQMASK	3	A*03
	QTRTD1 queuine tRNA-ribosyltransferase domain containing 1	**3 [20.0%]**	
297	EATSIKRVR	2	A*66
298	LPEDKPRLI	1	B*51:01
	TMBIM4 transmembrane BAX inhibitor motif containing 4	**3 [20.0%]**	
299	KYPLNLYLL	2	A*23:01, A*24
300	VHESPALILLF	1	B*38
	RAVER2 ribonucleoprotein, PTB-binding 2	**3 [20.0%]**	
301	EVTGHSKGY	2	A*26
302	RDSEELLQI	1	B*40
303	SPASKTTL	1	B*07
	SDAD1 SDA1 domain containing 1	**3 [20.0%]**	
304	DAKTVNVI	1	B*51:01
305	DSNATAAKM	1	n.a.
306	RTLNPQMLQK	1	A*03
307	RTLNPQMLQKK	1	A*03
	UCKL1 uridine-cytidine kinase 1-like 1	**3 [20.0%]**	
308	LMAEMGVHSV	1	A*02
309	RLLPPVGTGR	1	A*03
310	VRIGTILIQTNQ	1	n.a.
	STMN3 stathmin-like 3	**3 [20.0%]**	
311	KELSVLSLI	1	B*49:01
312	TQPHPNTVY	2	B*15
	CHIC2 cysteine-rich hydrophobic domain 2	**3 [20.0%]**	
313	ALEEQLLKY	3	A*26:01, A*03:01
	ODF2L outer dense fiber of sperm tails 2-like	**3 [20.0%]**	
314	DHFTGAIEKL	2	B*38
315	KILDLETEL	1	A*02:01

	PRR12 proline rich 12	**3 [20.0%]**	
316	AEDIPSLKL	2	B*40, B*44:25
317	DIPSLKLAL	1	A*26
318	GLDPNKPPEL	1	A*02
	FARSA phenylalanyl-tRNA synthetase, alpha subunit	**3 [20.0%]**	
319	FLRDPAEAL	1	A*02
320	GYGSQGYKY	1	A*29
321	KLLAEVTLK	1	A*03:01
322	SAADGPRVF	1	A*32
	CTDP1 CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	**3 [20.0%]**	
323	KLYELHVFTF	1	B*15
324	YELHVFTF	1	B*18:01
325	YLNKEIEEA	1	A*02

The table shows HLA class I ligandome-derived tumor associated antigens (LiTAAs) with representation frequencies ≥20% in AML patients (n=15) and representing HLA ligands (LiTAPs) annotated with respective HLA restriction. Abbreviations: rep., representation; n.a., not assigned

Table 2: Additional peptides according to the present invention related to underlying antigens described as related with AML

SEQ ID NO	Proteins, Peptides	Number of positive healthy donors (PBMC/BMNC) [rep. frequency %]	Number of positive AMLs [rep. frequency %]	HLA
	NPM1 nucleophosmin	**17[56.7] / 1[20.0]**	**9[60.0]**	
326	DENEHQLSL	1/0	3	B*18, B*40, B*44, B*44:25
327	EITPPVVLR	5/1	0	A*68,A*28, A*32
328	GFEITPPVVLR	4/1	0	A*68, A*28
329	HQLSLRTV	2/0	0	B*13, B*52
330	MSVQPTVSL	0/0	1	C*03
331	SIRDTPAKN	0/0	1	n.a.
332	SIRDTPAKNAQK	1/0	1	A*11
333	SPIKVTLATL	3/0	0	B*07
334	TPPVVLRL	6/0	2	B*51
335	VEAKFINY	0/0	1	B*18:01
336	YEGSPIKV	0/0	1	B*49:01
337	YEGSPIKVTL	3/0	3	B*40:01
	FLT3, fms-related	**0[0.0] / 0 0.0]**	**1[6.7]**	

SEQ ID NO	Proteins, Peptides	Number of positive healthy donors (PBMC/BMNC) [rep. frequency %]	Number of positive AMLs [rep. frequency %]	HLA
	tyrosine kinase 3			
338	SELKMMTQL	0/0	1	B*40
	PRAM1 PML-RARA regulated adaptor molecule 1	**4[13.3] / 1[20.0]**	**3[20.0]**	
339	EKDPQPQQL	1/0	0	n.a.
340	GYVPRTAL	1/0	0	A*24
341	KEKDPQPQQL	0/0	1	B*44:25
342	LPKKPSKLEL	1/0	1	B*07
343	RPSAASIDL	0/1	1	B*07
344	SRHPLSPGF	0/0	1	B*27:05
	BCL2 B-cell CLL/lymphoma 2	**1 [3.3] / 1[20.0]**	**2 [13.3]**	
345	TPRSPQPEL	0/1	1	B*07
346	GRIVAFFEF	0/0	1	B*27:05
347	HTPHPAASR	1/0	0	A*33
	BRAP BRCA1 associated protein	**1[3.3] / 1[20.0]**	**4 [26.7]**	
348	NPDELKTTV	1/0	0	n.a.
349	PSKQLPDQI	0/1	0	n.a.
350	VYVERAEVL	3/0	1	A*24
	NUDCD1 NudC domain containing 1	**6[20.0] / 0[0.0]**	**4 [26.7]**	
351	DPFIIIHSI	5/0	2	B*51
352	**EHSIATLLL**	**1/0**	**2**	**B*38, B*39**
	CYP1B1 cytochrome P450, family 1, subfamily B, polypeptide 1	**6[20.0] / 1[20.0]**	**1 [6.7]**	
353	FLDPRPLTV	6/1	1	A*02
354	SAFADRPAF	1/0	0	n.a.
	HMMR hyaluronan-mediated motility receptor (RHAMM)	**1[3.3] / 0[0.0]**	**2 [13.3]**	
355	DTTLPASAR	0/0	1	A*66
356	KLLEYIEEI	0/0	1	A*02
357	LEKQLIEL	1/0	0	n.a.
	TERT telomerase reverse transcriptase	**2[6.6] / 0[0.0]**	**0[0.0]**	
358	LMSVYVVEL	2/0		A*02
	MCL1 myeloid cell leukemia sequence 1	**15[50] / 0[0.0]**	**5[33.3]**	
359	ESITDVLVR	3/0	2	A*66
360	ETAFQGMLR	0/0	1	A*66
361	EVPDVTATPARL	1/0	0	n.a.
362	GRIVTLISF	3/0	1	B*27

SEQ ID NO	Proteins, Peptides	Number of positive healthy donors (PBMC/BMNC) [rep. frequency %]	Number of positive AMLs [rep. frequency %]	HLA
363	HVFSDGVTNW	2/0	0	A*25
364	REIGGGEAGAVI	1/0	0	B*49
365	RGWDGFVEF	0/0	1	A*32
366	RPAVLPLL	1/0	0	B*07
367	VEFFHVEDL	3/0	2	B*40, B*52, B*60
368	VQRNHETAF	3/0	2	B*15, B*62
	DNAJC2 DnaJ (Hsp40) homolog, subfamily C, member 2	**1[3.3] / 0[0.0]**	**0[0.0]**	
369	AELEAARL	1/0	0	B*44
	NUSAP1 nucleolar and spindle associated protein 1	**2[6.6] / 2[40.0]**	**5[33.3]**	
370	ATQTPVSNK	0/1	1	A*11
371	ESIDQYIER	1/1	2	A*33, A*66, A*68
372	FEEHNSMNEL	1/0	1	B*40
373	SVASTPISQR	0/1	1	A*68
374	VASTPISQR	0/1	0	A*68
	PRTN3 proteinase 3	**2[6.6] / 4[80.0]**	**2[13.3]**	
375	AEIVGGHEA	2/2	1	B*50, B*49
376	RPPSPALASV	0/1	0	B*07
377	SVAQVFLNNY	0/1	0	A*03
378	TQEPTQQHF	0/1	1	B*15
	RGS5 regulator of G-protein signaling 5	**1[3.3] / 0[0.0]**	**2[13.3]**	
379	KDITmKNLV	1/0	0	n.a.
380	mAEKAKQIY	0/0	2	n.a.
	SSX2IP synovial sarcoma, X breakpoint 2 interacting protein	**8[26.7] / 0[0.0]**	**0 [0.0]**	
381	KLDNQVSKV	6/0	0	A*02
382	SENVKLFSA	1/0	0	n.a.
383	VQKLQNII	1/0	0	B*13
	WT1 Wilms tumor 1	**10[33.3] / 0[0.0]**	**3[20.0]**	
384	AFTVHFSGQF	0/0	2	A*23
385	GVFRGIQDV	0/0	1	A*02:01
386	QRNMTKLQL	1/0	0	n.a.
387	RmFPNAPYL	9/0	1	A*02:01, E
	MAGED1 melanoma antigen family D, 1	**15[50.0] / 3[60.0]**	**6[40.0]**	

SEQ ID NO	Proteins, Peptides	Number of positive healthy donors (PBMC/BMNC) [rep. frequency %]	Number of positive AMLs [rep. frequency %]	HLA
388	EAAAEAKAR	1/0	1	A*66
389	IIKEYTDVY	1/0	0	B*15:01
390	KEIDKNDHL	1/0	0	B*40:01
391	KVSKASGVSK	2/0	1	A*03
392	MPATETKKV	1/0	0	B*07
393	NADPQAVTm	5/0	0	A*02
394	RSDmLKDII	0/0	1	n.a.
395	SESGAGLTRF	0/0	1	B*44:25
396	SMMQTLLTV	1/0	0	A*02
397	TEVSKTPEA	4/2	3	B*49:01
398	VEVPETPKA	2/1	1	B*50
399	DVYPEIIER	6/1	2	A*66, A*68
	AURKA aurora kinase A	**0[0.0] / 0[0.0]**	**1[6.7]**	
400	REVEIQSHL	0/0	1	B*49:01
	CCNA1 cyclin A1	**0[0.0] / 0[0.0]**	**2[13.3]**	
401	EPPAVLLL	0/0	1	B*51:01
402	LEADPFLKY	0/0	1	B*18:01
	MUC1 mucin 1, cell surface associated	**1[3.3] / 0[0.0]**	**0 [0.0]**	
403	TTQGQDVTLA	1/0	0	n.a.
	MPO myeloperoxidase	**0[0.0] / 3[60.0]**	**6[40.0]**	
404	AEYEDGFSIP	0/1	0	B*50
405	AQISLPRI	0/1	0	B*13
406	DFTPEPAAR	0/0	2	A*66
407	DNTGITTVSK	0/1	0	A*68
408	EEAKQLVDKAY	0/0	1	B*44
409	ERRESIKQ	0/0	1	n.a.
410	ETVGQLGTVLR	0/1	1	A*66, A*68
411	FEQVMRIGL	0/0	1	B*40
412	FSMQQRQAL	0/0	1	C*03
413	GVPFFSSLR	0/1	1	A*66, A*68
414	IVRFPTDQL	0/1	1	A*02
415	KQPVAATRTAV	0/0	1	B*15
416	LGASNRAFV	0/1	0	n.a.
417	NPRWDGERL	0/0	1	B*07
418	NVFTNAFRY	0/0	1	A*29
419	QPMEPNPRVPL	0/0	1	B*07
420	QPVAATRTAV	0/1	0	B*07
421	RLFEQVMRI	0/0	2	A*02
422	SEEPLARNL	0/0	1	B*40
423	TIRNQINAL	0/0	1	A*02
424	VLGPTAMRK	0/1	0	A*03
	RUNX1 runt-related	**2[6.6] / 0[0.0]**	**4[26.7]**	

SEQ ID NO	Proteins, Peptides	Number of positive healthy donors (PBMC/BMNC) [rep. frequency %]	Number of positive AMLs [rep. frequency %]	HLA
	transcription factor 1			
425	AELRNATAA	1/0	0	n.a.
426	DVPDGTLVTVm	1/0	3	A*26
427	LPIAFKVV	1/0	1	B*51
428	SAMGSATRY	0/0	1	A*32
	NUP214 nucleoporin 214kDa	**2[6.6] / 0[0.0]**	**3[20.0]**	
429	AEKQGHQW	1/0	0	B*44
430	GEQKPTGTF	0/0	1	B*44:25
431	GQFSKPFSF	1/0	0	B*15:01
432	IAFFDVRTF	0/0	1	C*12:03
433	LSAGKTSFSF	0/0	1	C*03
434	VSNKYGLVF	1/0	0	B*58
	CCNB1 Cyclin B1	**2[6.6] / 0[0.0]**	**3[20.0]**	
435	GEVDVEQHTL	2/0	2	B*40:01
436	VDVEQHTL	0/0	1	B*40:01
	HOXA9 Homeobox A9	**0[0.0] / 0[0.0]**	**1[6.6]**	
437	DAADELSVGRY	0/0	1	A*26:01
	MSLN mesothelin	**0[0.0] / 0[0.0]**	**1[6.6]**	
438	LSEADVRA	0/0	1	n.a.
	BIRC5 survivin	**2[6.6] / 0[0.0]**	**3[20.0]**	
439	ELTLGEFLK	2/0	2	A*68
440	ELTLGEFLKL	1/0	2	A*02
441	LTLGEFLK	1/0	1	n.a.
442	LTLGEFLKL	1/0	1	A*02
443	TLGEFLKL	1/0	2	A*02
	KLF2 kruppel like factor 2	**5[16.7] / 0[0.0]**	**4[26.7]**	
444	KTYTKSSHLK	5/0	4	A*03
	PRAME preferentially expressed antigen in melanoma	**1[3.3] / 0[0.0]**	**0[0.0]**	
445	SQLTTLSFY	1/0	0	B*15
	PASD1 pas domain containing 1	**0[0.0] / 0[0.0]**	**2[13.3]**	
446	KMQEKKKLQ	0/0	1	n.a.
447	LLGHLPAEI	0/0	1	B*51

The table shows presented HLA ligands derived from established AML-associated antigens annotated with sample of origin, representation frequencies in different tissue (15 AML samples, 30 PBMC samples, 5 BMNC samples) and corresponding HLA restriction. Abbreviations: rep., representation; n.a., not assigned.

The peptides in the following Table 3 are further useful in the diagnosis and/or treatment of hematological malignancies, AML and/or chronic lymphatic leukemia (CLL) cells, but preferably AML.

Table 3: MHC class II peptides according to the present invention

SEQ ID NO	Protein/Peptides	Number of positive AMLs [rep. frequency]
	A1BG alpha-1-B glycoprotein	**6 [50%]**
448	APVELILSDETLPAPE	3
449	ETPDFQLFKNGVAQEPV	1
450	LAPLEGARFALVRED	2
451	SPDRIFFHLNAVALGD	1
452	SPDRIFFHLNAVALGDG	2
	CORO1A coronin, actin binding protein, 1A	**5 [41.7%]**
453	EEMRKLQATVQELQKR	1
454	EEPLSLQELDTSSG	4
455	EMRKLQATVQELQKR	1
456	HLEEPLSLQELDTSSG	1
457	LEEPLSLQELDTSSG	2
	RPS5 ribosomal protein S5	**5 [41.7%]**
458	AGTVRRQAVDVSPLR	5
459	IGRAGTVRRQAVDVSPLR	1
460	RAGTVRRQAVDVSPLR	4
461	TVRRQAVDVSPLR	1
	C19orf10 chromosome 19 open reading frame 10	**5 [41.7%]**
462	GVVHSFSHNVGPGDK	2
463	GVVHSFSHNVGPGDKY	1
464	GVVHSFSHNVGPGDKYT	1
465	KTEEFEVTKTAVAHRP	1
466	KTEEFEVTKTAVAHRPG	3
467	VRPGGVVHSFSHNVGPGDK	1
468	VRPGGVVHSFSHNVGPGDKYT	1
	PLIN3 perilipin 3	**4 [33.3%]**
469	AEKGVRTLTAAAVSGAQ	1
470	AQPILSKLEPQIASASE	1
471	EKGVRTLTAAAVSGAQ	3
472	EKGVRTLTAAAVSGAQP	1
473	GVRTLTAAAVSGAQ	1
474	KGVRTLTAAAVSGAQ	1
	CLSTN1 calsyntenin 1	**4 [33.3%]**
475	DVNEYAPVFKEKSYK	1
476	HRSFVDLSGHNLA	1
477	HRSFVDLSGHNLANPH	1
478	HRSFVDLSGHNLANPHP	3
	HSP90B1 heat shock protein 90kDa beta (Grp94), member 1	**4 [33.3%]**
479	ALPEFDGKRFQNVAKEG	1
480	DSNEFSVIADPRG	1

SEQ ID NO	Protein/Peptides	Number of positive AMLs [rep. frequency]
481	DSNEFSVIADPRGN	1
482	DSNEFSVIADPRGNT	1
483	DSNEFSVIADPRGNTL	1
484	DSNEFSVIADPRGNTLG	1
485	PEFDGKRFQNVAK	1
486	SDSNEFSVIADPRGNTLG	1
487	SQKKTFEINPRHPLIR	1
488	ALPEFDGKRFQNVAKEG	1
489	PEFDGKRFQNVAK	2
490	PEFDGKRFQNVAKE	1
	B4GALT1 UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	**4 [33.3%]**
491	LNSLTYQVLDVQRYP	1
492	LPQLVGVSTPLQG	2
493	LPQLVGVSTPLQGG	1
494	LPQLVGVSTPLQGGS	3
495	RLPQLVGVSTPLQGGS	1
496	SDVDLIPMNDHNAYR	1
	SPN sialophorin	**4 [33.3%]**
497	GRRKSRQGSLAMEELK	1
498	RKSRQGSLAMEELK	3
499	SGPSLKGEEEPLVASEDGAVD	1
500	SGSGPSLKGEEEPLVASEDGAVD	1
	METAP1 methionyl aminopeptidase 1	**4 [33.3%]**
501	IKPGVTTEEIDHAVH	4
502	KPGVTTEEIDHAVH	3
	HSPG2 heparan sulfate proteoglycan 2	**4 [33.3%]**
503	DGVLRIQNLDQS	4
504	GAYFHDDGFLAFPG	1
505	TPYSFLPLPTIKDAYR	1
506	YPTPDISWSKLDGSLPP	1
507	YPTPDISWSKLDGSLPPD	1
	QSOX1 quiescin Q6 sulfhydryl oxidase 1	**3 [25.0%]**
508	ASHFEQMAAASMHR	3
	MANBA mannosidase, beta A, lysosomal	**3 [25.0%]**
509	GGQVIVAIPKLQTQQ	1
510	GQVIVAIPKLQTQ	1
511	GQVIVAIPKLQTQQ	1
512	IESTFDVVSSKPVG	2
	CREG1 cellular repressor of E1A-stimulated genes 1	**3 [25.0%]**
513	DWGALATISTLEAVRG	1
514	GRPFADVLSLSDGPPG	1
515	WGALATISTLEAVR	2
516	WGALATISTLEAVRG	2
	LDHA lactate dehydrogenase A	**3 [25.0%]**
517	ADELALVDVIEDK	1
518	GVSLKTLHPDLGTDK	2
519	IVSGKDYNVTANSKL	1

SEQ ID NO	Protein/Peptides	Number of positive AMLs [rep. frequency]
	CP ceruloplasmin (ferroxidase)	**3 [25.0%]**
520	DDNIKTYSDHPEK	1
521	DKVYVHLKNLASRPY	1
522	GDKVYVHLKNLASRPY	1
523	LDDNIKTYSDHPEK	1
524	TGDKVYVHLKNLASRPY	1
525	VYVHLKNLASRPY	1
	COL1A1 collagen, type I, alpha 1	**3 [25.0%]**
526	KTSRLPIIDVAPLDVGAPD	1
527	KTSRLPIIDVAPLDVGAPDQE	1
528	LPIIDVAPLDVGAPD	1
529	RLPIIDVAPLDVGAPD	3
530	RLPIIDVAPLDVGAPDQE	2
531	SRLPIIDVAPLDVGAPD	1
532	SRLPIIDVAPLDVGAPDQE	1
533	TSRLPIIDVAPLDVGAPD	1
534	TSRLPIIDVAPLDVGAPDQE	1
	CRP C-reactive protein, pentraxin-related	**3 [25.0%]**
535	DTSYVSLKAPLT	2
536	DTSYVSLKAPLTKP	1
537	DTSYVSLKAPLTKPL	1
538	ESDTSYVSLKAPLT	2
539	ESDTSYVSLKAPLTKPL	1
540	SDTSYVSLKAPLT	3
541	SDTSYVSLKAPLTKP	2
542	SDTSYVSLKAPLTKPL	2
	APRT adenine phosphoribosyltransferase	**3 [25.0%]**
543	DPASFRAAIGLLARH	3
	MBL2 mannose-binding lectin 2	**3 [25.0%]**
544	TEGQFVDLTGNRLTYT	3
	IFI30 interferon, gamma-inducible protein 30	**3 [25.0%]**
545	ALDFFGNGPPVNYK	1
546	ALDFFGNGPPVNYKTG	1
547	DFFGNGPPVNYKTG	2
548	LDFFGNGPPVNYK	1
549	LDFFGNGPPVNYKTG	1
550	QALDFFGNGPPVNYKTG	1
	LBP lipopolysaccharide binding protein	**3 [25.0%]**
551	AISDYVFNTASLVYH	1
552	AISDYVFNTASLVYHEE	2
553	ISDYVFNTASLVYH	1
554	ISDYVFNTASLVYHEE	3
555	YVFNTASLVYHEE	1
	RAB5A RAB5A, member RAS oncogene family	**3 [25.0%]**
556	IVIALSGNKADLA	1
557	SPNIVIALSGNKADL	1
558	SPNIVIALSGNKADLA	3
	ICAM3 intercellular adhesion molecule 3	**3 [25.0%]**

SEQ ID NO	Protein/Peptides	Number of positive AMLs [rep. frequency]
559	TPPRLVAPRFLEVE	1
560	TPPRLVAPRFLEVET	1
561	TPPRLVAPRFLEVETS	3
	MAN1A1 mannosidase, alpha, class 1A, member 1	**3 [25.0%]**
562	EIQRDILLEKKKVAQDQ	1
563	FGAIFFLPDSSK	1
564	IQRDILLEKKKVAQ	1
565	IQRDILLEKKKVAQD	1
566	IQRDILLEKKKVAQDQ	1
567	LSGVLFHSSPALQPA	1
568	RDILLEKKKVAQDQ	1
569	SSKLLSGVLFHSSPA	1
570	SSPALQPAADHKPGPG	1
	RBMX RNA binding motif protein, X-linked	**3 [25.0%]**
571	APPTRGPPPSYGGS	1
572	GNSRSAPPTRGPPPSYGGSSRY	1
573	RDYGHSSSRDDYPS	1
574	SPRDDGYSTKDSY	1
	PBX2 pre-B-cell leukemia homeobox 2	**3 [25.0%]**
575	GGSAAAAAAAAASGG	1
576	DNMLLAEGVSGPEK	2
	YARS tyrosyl-tRNA synthetase	**3 [25.0%]**
577	ADSLYVEKIDVGEAEPR	3
	TPM4 tropomyosin 4	**3 [25.0%]**
578	RIQLVEEELDRAQER	2
579	RRIQLVEEELDRAQER	1
	RPL36A ribosomal protein L36a	**3 [25.0%]**
580	HQPHKVTQYKKGKDSLY	2
581	RKKAKTTKKIVL	1
	GANAB glucosidase, alpha; neutral AB	**3 [25.0%]**
582	DVFRQYASLTGTQALPP	1
583	GTAQGELFLDDGHT	1
584	VFRQYASLTGTQALPP	1
	HSP90B2P heat shock protein 90kDa beta (Grp94), member 2, pseudogene	**3 [25.0%]**
585	PEFDGKRFQNVAK	1
586	PEFDGKRFQNVAKE	2
587	ALPEFDGKRFQNVAKEG	1
	LAIR1 leukocyte-associated immunoglobulin-like receptor 1	**3 [25.0%]**
588	ASPSESEARFRIDSVSEGNAGPY	1
589	EARFRIDSVSEGNAGP	1
590	ESEARFRIDSVSEGNAGP	1
591	ESEARFRIDSVSEGNAGPY	1
592	FRIDSVSEGNAGP	1
593	FRIDSVSEGNAGPY	1
594	SEARFRIDSVSEGNAGPY	3
595	SPSESEARFRIDSVSEGNAGPY	1

SEQ ID NO	Protein/Peptides	Number of positive AMLs [rep. frequency]
	GALNT7 UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	**3 [25.0%]**
596	GNQLFRINEANQL	1
597	GNQLFRINEANQLMQ	2
598	SPAMAGGLFAIERE	1
	ARRDC1 arrestin domain containing 1	**3 [25.0%]**
599	FIGNIAVNHAPVSPR	1
600	FIGNIAVNHAPVSPRPG	1
601	IGNIAVNHAPVSPRP	3
602	IGNIAVNHAPVSPRPG	1
	ERGIC1 endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1	**3 [25.0%]**
603	FEGQFSINKVPGNFH	3
604	FEGQFSINKVPGNFHVS	2
605	RFEGQFSINKVPGNFH	2

The table shows HLA class II ligandome-derived tumor-associated antigens (LiTAAs) with representation frequencies >20% in AML patients (n=12) and representing HLA ligands (LiTAPs). Abbreviations: rep., representation.

The peptides in the following Table 4 are both useful in the diagnosis and/or treatment of AML and/or CLL, and preferably AML.

Table 4: Peptides according to the present invention that can be used both for the treatment of AML and CLL

SEQ ID NO:	Sequence
448	APVELILSDETLPAPE
520	DDNIKTYSDHPEK
471	EKGVRTLTAAAVSGAQ
472	EKGVRTLTAAAVSGAQP
439	ELTLGEFLK
353	FLDPRPLTV
522	GDKVYVHLKNLASRPY
318	GLDPNKPPEL
178	HEIDRYTAI
68	IGVEHVVVY
201	IPVVHASI
474	KGVRTLTAAAVSGAQ
381	KLDNQVSKV
323	KLYELHVFTF
46	KLYPTLVIR

241	KTIAFLLPMF
450	LAPLEGARFALVRED
357	LEKQLIEL
491	LNSLTYQVLDVQRYP
492	LPQLVGVSTPLQG
493	LPQLVGVSTPLQGG
494	LPQLVGVSTPLQGGS
441	LTLGEFLK
442	LTLGEFLKL
498	RKSRQGSLAMEELK
495	RLPQLVGVSTPLQGGS
354	SAFADRPAF
45	SEETFRFEL
382	SENVKLFSA
445	SQLTTLSFY
443	TLGEFLKL
202	TVADQVLVGSY
179	VFTLKPLEF
296	VIYNEQMASK
383	VQKLQNII
525	VYVHLKNLASRPY
325	YLNKEIEEA
180	YWVPRNAL

Thus, particularly preferred is at least one peptide according to the present invention selected from the group consisting of SEQ ID NO: 448, 520, 471, 472, 439, 353, 522, 318, 178, 68, 201, 474, 381, 323, 46, 241, 450, 357, 491, 492, 493, 494, 441, 442, 498, 495, 354, 45, 382, 445, 443, 202, 179, 296, 383, 525, 325, and 180, and the use thereof in the treatment of AML and/or CLL as described herein.

The present invention furthermore relates to the peptides according to the present invention for use in the treatment of proliferative diseases other than AML, such as, for example, CLL. Nevertheless, as shown in the following table 5, many of the peptides according to the present invention can also be used in other indications.

Table 5: Peptides according to the present invention and their specific uses in other proliferative diseases, optionally in other organs.

Seq. ID	**Sequence**	**Proliferative disease and location thereof**
1	AEQFRLEQI	colon or rectum, lung, small cell carcinoma
2	FTAEFSSRY	colon or rectum, lung, small cell carcinoma

3	HHDESVLTNVF	colon or rectum, lung, small cell carcinoma
4	REQDEAYRL	colon or rectum, lung, small cell carcinoma
5	RPVMPSRQI	colon or rectum, lung, small cell carcinoma
6	VQREYNLNF	colon or rectum, lung, small cell carcinoma
7	GQLPITIQV	kidney, clear cell renal cell carcinoma, bone, non-ossifying fibroma
8	RAYADEVAV	kidney, clear cell renal cell carcinoma, bone, non-ossifying fibroma
9	REDKPPLAV	kidney, clear cell renal cell carcinoma, bone, non-ossifying fibroma
10	RVKDLDTEKY	kidney, clear cell renal cell carcinoma, bone, non-ossifying fibroma
11	SEQEMNAHL	kidney, clear cell renal cell carcinoma, bone, non-ossifying fibroma
12	YVLPLVHSL	kidney, clear cell renal cell carcinoma, bone, non-ossifying fibroma
13	LPLRFWVNI	liver, hepatocellular carcinoma, cancer, pancreas, adenocarcinoma
14	EVAEHVQYM	colon or rectum, prostate, benign nodular hyperplasia
15	YMAELIERL	colon or rectum, prostate, benign nodular hyperplasia
16	ALASLIRSV	thyroid gland, nodular hyperplasia
17	TVAEITGSKY	thyroid gland, nodular hyperplasia
18	EIIGKRGIIGY	colon or rectum, kidney, carcinoma
19	NLVEKTPAL	colon or rectum, kidney, carcinoma
20	IEDKAQILL	malignant fibrous histiocytoma
21	SIYDDSYLGY	malignant fibrous histiocytoma
22	TTNHPINPK	malignant fibrous histiocytoma
23	NAAILKKV	brain, glioblastoma, thyroid gland, nodular hyperplasia
24	NYLDIKGLL	brain, glioblastoma, thyroid gland, nodular hyperplasia
25	YLDIKGLLDV	brain, glioblastoma, thyroid gland, nodular hyperplasia
26	EEVGDFIQRY	lung, non-small cell lung carcinoma,
27	EVGDFIQRY	lung, non-small cell lung carcinoma,
28	MKDLSLGGVL	lung, non-small cell lung carcinoma,
29	DEFITVHSM	stomach, skin, basal cell carcinoma
30	EFITVHSML	stomach, skin, basal cell carcinoma
31	GQLDVRELI	stomach, skin, basal cell carcinoma
32	TQYIIHNY	stomach, skin, basal cell carcinoma
33	EVVDVTWRY	colon or rectum, lymph node, non-Hodgkin's lymphoma
34	KEALLRDTI	colon or rectum, lymph node, non-Hodgkin's lymphoma
35	HGYENPTYK	lung, non-small cell lung carcinoma, kidney, carcinoma
36	SLLYKVPYV	lung, non-small cell lung carcinoma, kidney, carcinoma

37	AEIPLRMV	stomach, metastatic, adenocarcinoma
38	EVVYRFTAR	stomach, metastatic, adenocarcinoma
39	FPGLAIKI	stomach, metastatic, adenocarcinoma
40	IYNGKLFDL	stomach, metastatic, adenocarcinoma
41	IYNGKLFDLL	stomach, metastatic, adenocarcinoma
42	KEIDVISI	stomach, metastatic, adenocarcinoma
43	LEEQASRQI	stomach, metastatic, adenocarcinoma
44	TRMSTVSEL	stomach, metastatic, adenocarcinoma
45	SEETFRFEL	stomach, adenocarcinoma, endometrium, adenocarcinoma
46	KLYPTLVIR	stomach, adenocarcinoma, endometrium, adenocarcinoma
47	ALRNQATMVQK	stomach, adenocarcinoma, non-Hodgkin's lymphoma, mycosis fungoides
48	LLDHAPPEI	stomach, adenocarcinoma, non-Hodgkin's lymphoma, mycosis fungoides
49	GVLGTVVHGK	colon or rectum, liver, focal nodular hyperplasia
50	VQFIGRESKY	colon or rectum, liver, focal nodular hyperplasia
51	GQSLIHVI	parathyroid gland, adenoma
52	VHSPAGMAL	parathyroid gland, adenoma
53	VLYEGIKVGK	parathyroid gland, adenoma
54	AVIEAEKIAQV	ovary, granulosa cell tumor,
55	DRIEVVNML	ovary, granulosa cell tumor,
56	IEAEKIAQV	ovary, granulosa cell tumor,
57	IEDLKAQIL	uterine cervix, squamous cell carcinoma,
58	YLLESVNKL	uterine cervix, squamous cell carcinoma,
59	HRIYVPLML	stomach, diffuse subtype adenocarcinoma, pancreas, adenocarcinoma
60	KEYIPPLIW	stomach, adenocarcinoma, pancreas, adenocarcinoma
61	MDKLVVEY	stomach, adenocarcinoma, pancreas, adenocarcinoma
62	ALLGHILLH	kidney, renal cell carcinoma, non-clear cell type,
63	ALLPHLYTL	kidney, renal cell carcinoma, non-clear cell type,
64	HVAGETVAR	kidney, renal cell carcinoma, non-clear cell type,
65	KVWPGSTAF	kidney, renal cell carcinoma, non-clear cell type,
66	ETAVAILRF	metastatic infiltrating lobular carcinoma of breast
67	RVYNTDPLKEK	endometrium, adenocarcinoma,
68	IGVEHVVVY	brain, cancer, kidney, oncocytoma
69	RQIGVEHVV	brain, cancer, kidney, oncocytoma
70	DVFERPSAKK	kidney, clear cell renal cell carcinoma, synovial sarcoma
71	EEFQFIKKA	kidney, clear cell renal cell carcinoma,

		synovial sarcoma
72	THLVDQDTTSF	kidney, clear cell renal cell carcinoma, synovial sarcoma
73	ESADLIQHY	pancreas, adenocarcinoma, kidney, renal cell carcinoma
74	EIIKEISIM	pancreas, adenocarcinoma, lymph node, Hodgkin's disease
75	SVSDIIRLR	pancreas, adenocarcinoma, lymph node, Hodgkin's disease
76	AVSLIREEW	stomach, adenocarcinoma, white blood cells, chronic lymphocytic leukemia
77	GEKSESISV	stomach, adenocarcinoma, white blood cells, chronic lymphocytic leukemia
78	FLTILPEEL	pancreas, adenocarcinoma, lung, adenocarcinoma
79	ILWETVPSM	colon or rectum, metastatic renal cell carcinoma
80	LPVRTLSI	colon or rectum, metastatic renal cell carcinoma
81	RESEYKQVY	colon or rectum, metastatic renal cell carcinoma
82	SESLPVRTL	colon or rectum, metastatic renal cell carcinoma
83	RLLESVVVL	lung, non-small cell lung carcinoma, spleen, chronic myeloid leukemia
84	RPEEGKESL	lung, non-small cell lung carcinoma, spleen, chronic myeloid leukemia
85	THGKLVILF	lung, non-small cell lung carcinoma, spleen, chronic myeloid leukemia
86	KELEHLSHI	stomach, adenocarcinoma,
87	REMENYEKI	stomach, adenocarcinoma,
88	VLLSTIHEL	stomach, adenocarcinoma,
89	KTYTKSSHLK	stomach, adenocarcinoma, brain, meningioma,
90	EIIEKNFDY	stomach, adenocarcinoma,
91	GTEEAPKVFK	stomach, adenocarcinoma,
92	KLMAIPLVF	stomach, adenocarcinoma,
93	DIKRGIPN	stomach, adenocarcinoma, lung, small cell carcinoma
94	DIKRGIPNY	stomach, adenocarcinoma, lung, small cell carcinoma
95	FLDITNPKA	stomach, differentiated subtype adenocarcinoma, lung, small cell carcinoma
96	ALYSVYRQK	kidney, angiomyolipoma
97	KVLALVFGF	kidney, angiomyolipoma
98	SFTDVIGHY	kidney, angiomyolipoma
99	ASAAASGGLLK	colon or rectum, spleen, extramedullary hematopoiesis
100	ALLGVTGAPK	colon or rectum, spleen, extramedullary hematopoiesis
101	DEIKTLQRY	stomach, adenocarcinoma, liver, carcinoid

		tumor, metastatic
102	EAYVQKMV	stomach, adenocarcinoma, liver, carcinoid tumor, metastatic
103	VLHQDSGLGY	stomach, adenocarcinoma, liver, carcinoid tumor, metastatic
104	YLQNHFVGL	stomach, adenocarcinoma, liver, carcinoid tumor, metastatic
105	AEIEDIRVL	stomach, metastatic, duodenum, adenocarcinoma
106	GQSRLIFTY	stomach, metastatic, duodenum, adenocarcinoma
107	READFKETL	stomach, metastatic, duodenum, adenocarcinoma
108	DTMGPSQHVY	lung, non-small cell lung carcinoma, spleen, extramedullary hematopoiesis
109	ESRGPALTR	lung, non-small cell lung carcinoma, spleen, extramedullary hematopoiesis
110	FQLPGLGTPPIT	lung, non-small cell lung carcinoma, spleen, extramedullary hematopoiesis
111	RIQGYVVSW	lung, non-small cell lung carcinoma, spleen, extramedullary hematopoiesis
112	LLDPSVFHV	stomach, adenocarcinoma, testis, seminoma
113	RFFHLADLF	stomach, adenocarcinoma, testis, seminoma
114	DSISGNLQR	stomach, metastatic, bone, non-ossifying fibroma
115	ETEQTIQKL	stomach, metastatic, bone, non-ossifying fibroma
116	FLYPFLSHL	stomach, metastatic, bone, non-ossifying fibroma
117	TLDQKIERV	stomach, metastatic, bone, non-ossifying fibroma
118	DADSRAATV	liver, hepatocellular carcinoma, kidney, renal cell carcinoma
119	DHEGFGFVL	liver, hepatocellular carcinoma, kidney, renal cell carcinoma
120	GEAVKVLSI	liver, hepatocellular carcinoma, kidney, renal cell carcinoma
121	NATDLLKVL	liver, hepatocellular carcinoma, kidney, renal cell carcinoma
122	KEITEGKTV	stomach, metastatic, rectum, adenocarcinoma
123	YRQKQVVIL	stomach, metastatic, rectum, adenocarcinoma
124	VAINLIVQH	stomach, metastatic, rectum, adenocarcinoma
127	DAIKVFVRI	stomach, adenocarcinoma, kidney, Wilm's tumor
128	LEKAFSEI	stomach, adenocarcinoma, kidney, Wilm's tumor
129	MEKSDKNQ	stomach, adenocarcinoma, kidney, Wilm's tumor
130	GQTGSGKTF	stomach, adenocarcinoma, rectum, adenocarcinoma
131	DTSPDLSSR	lung, non-small cell lung carcinoma, testis,

		seminoma
132	KLNEVIVNK	lung, non-small cell lung carcinoma, testis, seminoma
133	FAQIISVALI	stomach, adenocarcinoma, parathyroid gland, adenoma
134	IIFDRPLLY	stomach, adenocarcinoma, parathyroid gland, adenoma
135	DAVNQNTKLL	ovary, adenocarcinoma, clear cell type,
136	HHILADVSL	ovary, adenocarcinoma, clear cell type,
137	YPSEKRGEL	ovary, adenocarcinoma, clear cell type,
138	SVVDLINHY	brain, glioblastoma, bone, non-ossifying fibroma
139	EIIEKDTKY	stomach, metastatic, lung, large cell carcinoma
140	ENEEKLKEL	stomach, metastatic, lung, large cell carcinoma
141	ILGGPGTVQGV	liver, hepatocellular carcinoma, cancer, vulva, squamous cell carcinoma
142	ESAALIHHY	liver, hepatocellular carcinoma, fibromatosis
143	YQRETPQV	liver, hepatocellular carcinoma, fibromatosis
144	ARIEIGLHY	liver, focal nodular hyperplasia
145	IPYPRPIHL	liver, focal nodular hyperplasia
146	DVSGKTALNQ	kidney, clear cell renal cell carcinoma, stomach, gastrointestinal stromal tumor (GIST)
147	TEFRSLVI	kidney, clear cell renal cell carcinoma, stomach, gastrointestinal stromal tumor (GIST)
148	TLKSGDGITF	kidney, clear cell renal cell carcinoma, stomach, gastrointestinal stromal tumor (GIST)
149	HEADKTYML	stomach, adenocarcinoma,
150	KFFEEVLLF	stomach, adenocarcinoma,
151	RVMPSSFFL	stomach, adenocarcinoma,
152	YELDLREPAL	lung, non-small cell lung carcinoma, lung, adenocarcinoma
153	GAYGKVFLV	liver, hepatocellular carcinoma, kidney, angiomyolipoma
154	DHDLLKNF	kidney, clear cell renal cell carcinoma, kidney, polycystic kidney disease
155	EELQLIRQA	kidney, clear cell renal cell carcinoma, kidney, polycystic kidney disease
156	AAELLKHPF	prostate, adenocarcinoma
157	GRVKLSDFGF	prostate, adenocarcinoma
158	KSNSIIVSPR	brain, glioblastoma, brain, meningioma
159	ETLERLQEL	liver, hepatocellular carcinoma, cancer, parotid gland, pleomorphic adenoma
160	KDDELSRQ	liver, hepatocellular carcinoma, cancer, parotid gland, pleomorphic adenoma
161	LQQTNSEKI	kidney, clear cell renal cell carcinoma, parotid gland, pleomorphic adenoma

162	GEFGKPYFI	colon or rectum, testis, seminoma
163	KDVKVVIL	colon or rectum, testis, seminoma
164	RPVPPPPSL	colon or rectum, testis, seminoma
165	KEDIPGRHSY	stomach, adenocarcinoma, spleen, chronic myeloid leukemia
166	KETKAVTNF	stomach, adenocarcinoma, spleen, chronic myeloid leukemia
167	YEILIHDL	stomach, adenocarcinoma, spleen, chronic myeloid leukemia
168	FPRFVNVTV	spleen, chronic myeloid leukemia
169	QVAGWGSQR	spleen, chronic myeloid leukemia
170	WIDGVLNNPGPG	spleen, chronic myeloid leukemia
171	SFMTHPEF	stomach, adenocarcinoma, myometrium, leiomyoma
172	HYTIVFNTF	colon or rectum, myometrium, leiomyoma
173	GTNDGPALKK	colon or rectum, liver, hepatocellular carcinoma
174	IEDPVRPEV	colon or rectum, liver, hepatocellular carcinoma
175	NTASGGMTR	brain, glioblastoma, skin, squamous cell carcinoma
176	EVIETEKTLY	colon or rectum, breast, mucinous carcinoma
177	MKILNHPNI	colon or rectum, lung, squamous cell carcinoma
178	HEIDRYTAI	kidney, clear cell renal cell carcinoma, non-Hodgkin's lymphoma
179	VFTLKPLEF	kidney, clear cell renal cell carcinoma, non-Hodgkin's lymphoma
180	YWVPRNAL	kidney, clear cell renal cell carcinoma, non-Hodgkin's lymphoma
181	EVSPNLVRY	stomach, metastatic, pancreas, adenocarcinoma
182	LSEIAGMTLP	stomach, metastatic, pancreas, adenocarcinoma
183	FLSFMNTEL	lung, non-small cell lung carcinoma, stomach, adenocarcinoma
184	KAVPSQKRT	lung, non-small cell lung carcinoma, stomach, adenocarcinoma
185	LKAVPSQKRT	lung, non-small cell lung carcinoma, stomach, adenocarcinoma
186	SLIAVFQKY	lung, non-small cell lung carcinoma, stomach, adenocarcinoma
187	IIKEKTVVY	liver, hepatocellular carcinoma, cancer, liver, hepatocellular carcinoma
188	LLEQKVWEV	liver, hepatocellular carcinoma, cancer, liver, hepatocellular carcinoma
189	SEIAESHRF	liver, hepatocellular carcinoma, cancer, liver, hepatocellular carcinoma
190	YLAIGIHEL	liver, hepatocellular carcinoma, cancer, liver, hepatocellular carcinoma
191	IHDELQQSF	colon or rectum, spleen, chronic myeloid

		leukemia
192	AHVIDKFLL	kidney, renal cell carcinoma,
193	KAGGEFLLRY	kidney, renal cell carcinoma,
194	FEVKDLLSL	kidney, clear cell renal cell carcinoma, brain, meningioma
195	FSKAKPSVL	liver, hepatocellular carcinoma, breast, infiltrating lobular carcinoma
196	EAIKALEV	stomach, metastatic, lung, neuroendocrine carcinoma
197	EVASAKQSVKY	stomach, metastatic, lung, neuroendocrine carcinoma
198	IEFTYTAKL	stomach, metastatic, lung, neuroendocrine carcinoma
199	LLADITSKY	stomach, metastatic, lung, neuroendocrine carcinoma
200	VLVDRTIYI	liver, hepatocellular carcinoma, liver, focal nodular hyperplasia
201	IPVVHASI	stomach, adenocarcinoma, colon, adenocarcinoma
202	TVADQVLVGSY	stomach, adenocarcinoma, colon, adenocarcinoma
203	VALVHPDL	stomach, adenocarcinoma, colon, adenocarcinoma
204	LPDDKVTAL	stomach, metastatic, stomach, adenocarcinoma
205	KIAKQIVQK	lung, non-small cell lung carcinoma, lung, neuroendocrine carcinoma
206	VEKILLSVV	lung, non-small cell lung carcinoma, lung, neuroendocrine carcinoma
207	APAGARGGPA	colon or rectum, rectum, adenocarcinoma
208	EHLRKLEAE	colon or rectum, rectum, adenocarcinoma
209	RFIPELINF	colon or rectum, rectum, adenocarcinoma
210	TEKIAQLF	stomach, adenocarcinoma, ovary, adenocarcinoma
211	KLHDETLTY	stomach, adenocarcinoma, ovary, adenocarcinoma
212	LHDETLTYL	stomach, adenocarcinoma, ovary, adenocarcinoma
213	GPQEGNGPSLF	colon or rectum, synovial sarcoma
214	YLLQRAVEV	colon or rectum, synovial sarcoma
215	FAALHGPAL	squamous cell carcinoma,
216	RMANLMGIEF	squamous cell carcinoma,
217	DTFPGPYAVL	liposarcoma
218	DTMPQTYKR	liposarcoma
219	IEHVFVTDV	colon or rectum, lymph node, infiltrating ductal carcinoma of breast
220	KESPTSVGF	colon or rectum, lymph node, infiltrating ductal carcinoma of breast
221	EAITAIMKY	kidney, clear cell renal cell carcinoma, spleen, non-Hodgkin's lymphoma
222	KEKPAENTL	kidney, clear cell renal cell carcinoma, spleen,

		non-Hodgkin's lymphoma
223	NEFQSQQNI	kidney, clear cell renal cell carcinoma, spleen, non-Hodgkin's lymphoma
224	NVIDYGHASKY	kidney, clear cell renal cell carcinoma, spleen, non-Hodgkin's lymphoma
225	FAKSQSKTF	atypical lipoma
226	LPFSLAHL	atypical lipoma
227	APNYRLKSL	stomach, adenocarcinoma, metastatic renal cell carcinoma
228	ILKDMGITEY	stomach, adenocarcinoma, metastatic renal cell carcinoma
229	AHDDGRWSL	stomach, metastatic, lung, squamous cell carcinoma
230	KYLTAEAFGF	stomach, metastatic, lung, squamous cell carcinoma
231	ESAALIHHY	liver, hepatocellular carcinoma, fibromatosis
232	YQRETPQV	liver, hepatocellular carcinoma, fibromatosis
233	EELQRNISL	kidney, clear cell renal cell carcinoma, ovary, adenocarcinoma
234	RPAALFLTL	kidney, clear cell renal cell carcinoma, ovary, adenocarcinoma
235	SEELQRNISL	kidney, clear cell renal cell carcinoma, ovary, adenocarcinoma
236	ETIDSRVQEY	colon or rectum, ovary, teratoma
237	EVSEQILHM	stomach, metastatic, lymph node, non-Hodgkin's lymphoma
238	GTLSGGILSSGK	stomach, differentiated subtype adenocarcinoma, uterine, cervix, squamous cell carcinoma
239	GVPIMLAY	brain, glioblastoma, uterine cervix, squamous cell carcinoma
240	EEVKEEVKKF	lung, non-small cell lung carcinoma, thymus, thymoma
241	KTIAFLLPMF	lung, non-small cell lung carcinoma, thymus, thymoma
242	EVTTNIPKM	liver, hepatocellular carcinoma, cancer, adenoid cystic carcinoma
243	IHGDTVQNQL	colon or rectum, adrenal gland, adrenal cortical carcinoma
244	RTMVKTLEY	colon or rectum, adrenal gland, adrenal cortical carcinoma
245	ETVRTLNNLY	brain, glioblastoma, omentum, leiomyosarcoma, metastatic
246	HSIDKVTSR	colon or rectum, parathyroid gland, adenoma
247	VSNPKSFEY	colon or rectum, parathyroid gland, adenoma
248	GLGPTFKL	lung, non-small cell lung carcinoma, stomach, adenocarcinoma
249	NKGISDIIKV	lung, non-small cell lung carcinoma, stomach, adenocarcinoma
250	TSTTRPVL	lung, non-small cell lung carcinoma, stomach, adenocarcinoma

251	VLGGKAFLEHL	stomach, endometrium, adenocarcinoma
252	YEFERTTSI	stomach, endometrium, adenocarcinoma
253	YLDFTNPKV	liver, hepatocellular carcinoma, uterine cervix, squamous cell carcinoma
254	IPAVARTTTL	pancreas, adenocarcinoma, myometrium, leiomyoma
255	KQQLELDSI	pancreas, adenocarcinoma, myometrium, leiomyoma
256	KTTDTVSSF	pancreas, adenocarcinoma, myometrium, leiomyoma
257	DYLDGVHTVF	colon or rectum, fibromatosis
258	YLDGVHTVF	colon or rectum, fibromatosis
259	TYVSGMLRF	brain, glioblastoma, breast, carcinoma
260	DAIDGKQAR	brain, glioblastoma, liver, focal nodular hyperplasia
261	DPMAPGVQGSLL	lung, non-small cell lung carcinoma, uterine cervix, squamous cell carcinoma
262	GLDPSQRPK	lung, non-small cell lung carcinoma, uterine cervix, squamous cell carcinoma
263	IEDSRVYEL	stomach, metastatic, non-Hodgkin's lymphoma
264	YVHSFLSSGY	small Intestine, gastrointestinal stromal tumor
265	HEYTTKEVF	liver, hepatocellular carcinoma, cancer, colon, adenocarcinoma
266	KLQEQLAQL	liver, hepatocellular carcinoma, cancer, colon, adenocarcinoma
267	SIAAKILSY	liver, hepatocellular carcinoma, cancer, colon, adenocarcinoma
268	KELLAVKL	pancreas, adenocarcinoma, lung, adenocarcinoma
269	KLKQTTSALEK	pancreas, adenocarcinoma, lung, adenocarcinoma
270	EVGPREAGLR	kidney, clear cell renal cell carcinoma, kidney, transitional cell carcinoma
271	SEAQEGLQKF	kidney, clear cell renal cell carcinoma, kidney, transitional cell carcinoma
272	DEAVLFVQV	pancreas, adenocarcinoma, ovary, mucinous cystadenocarcinoma
273	EVAKFLSFY	kidney, clear cell renal cell carcinoma, kidney, angiomyolipoma
274	KLDQKLPEL	kidney, clear cell renal cell carcinoma, kidney, angiomyolipoma
275	SVFEKSVGY	kidney, clear cell renal cell carcinoma, kidney, angiomyolipoma
276	NEGQTALHY	colon or rectum, endometrium, Mullerian mixed tumor
277	VEFPHSPEI	colon or rectum, endometrium, Mullerian mixed tumor
278	RLQGELQAV	kidney, clear cell renal cell carcinoma, kidney, renal cell carcinoma
279	KELRELLSI	colon or rectum, fibromatosis

280	SLVDQSAAL	colon or rectum, fibromatosis
281	LELIMSKY	colon or rectum, ovary, thecoma-fibroma
282	DIKPYIAEY	pancreas, adenocarcinoma, thymus, thymoma
283	KLMAMFLEY	lung, adenocarcinoma,
284	YTVEKREGY	lung, adenocarcinoma,
285	FEFDIHQVI	stomach, metastatic, breast, carcinoma
286	SENPSKHDSF	stomach, metastatic, breast, carcinoma
287	NFLRINTI	colon or rectum, stomach, adenocarcinoma
288	YSGPTSVSR	colon or rectum, stomach, adenocarcinoma
289	DIYGGDYERF	colon or rectum, adrenal gland, adrenal cortical carcinoma
290	SARLEKLGY	stomach, metastatic, prostate, benign nodular hyperplasia
291	YVFPGVTRL	stomach, metastatic, prostate, benign nodular hyperplasia
292	YYLNEIQSF	stomach, metastatic, prostate, benign nodular hyperplasia
293	YHSQDRYEF	stomach, metastatic, non-Hodgkin's lymphoma
294	FPPGRQVVM	brain, cancer, lymph node, malignant melanoma
295	ILDEAHERTI	brain, cancer, lymph node, malignant melanoma
296	VIYNEQMASK	liver, hepatocellular carcinoma, cancer, liver, focal nodular hyperplasia
297	EATSIKRVR	colon or rectum, adenocarcinoma
298	LPEDKPRLI	colon or rectum, adenocarcinoma
299	KYPLNLYLL	kidney, clear cell renal cell carcinoma, lipoma
300	VHESPALILLF	kidney, clear cell renal cell carcinoma, lipoma
301	EVTGHSKGY	stomach, adenocarcinoma, rectum, adenocarcinoma
302	RDSEELLQI	stomach, adenocarcinoma, rectum, adenocarcinoma
303	SPASKTTL	stomach, adenocarcinoma, rectum, adenocarcinoma
304	DAKTVNVI	colon or rectum, testis, seminoma
305	DSNATAAKM	colon or rectum, testis, seminoma
306	RTLNPQMLQK	colon or rectum, testis, seminoma
307	RTLNPQMLQKK	colon or rectum, testis, seminoma
308	LMAEMGVHSV	stomach, metastatic, breast, carcinoma
309	RLLPPVGTGR	stomach, metastatic, breast, carcinoma
310	VRIGTILIQTNQ	stomach, metastatic, breast, carcinoma
311	KELSVLSLI	stomach, metastatic, lung, neuroendocrine carcinoma
312	TQPHPNTVY	stomach, metastatic, lung, neuroendocrine carcinoma
313	ALEEQLLKY	stomach, adenocarcinoma, malignant fibrous histiocytoma
314	DHFTGAIEKL	stomach, metastatic, breast, carcinoma
315	KILDLETEL	stomach, metastatic, breast, carcinoma

316	AEDIPSLKL	breast, carcinoma
317	DIPSLKLAL	breast, carcinoma
318	GLDPNKPPEL	breast, carcinoma
319	FLRDPAEAL	breast, carcinoma
320	GYGSQGYKY	breast, carcinoma
321	KLLAEVTLK	breast, carcinoma
322	SAADGPRVF	breast, carcinoma
323	KLYELHVFTF	colon, adenoma
324	YELHVFTF	colon, adenoma
325	YLNKEIEEA	colon, adenoma
326	DENEHQLSL	stomach, adenocarcinoma, colon, non-Hodgkin's lymphoma
327	EITPPVVLR	stomach, adenocarcinoma, colon, non-Hodgkin's lymphoma
328	GFEITPPVVLR	stomach, adenocarcinoma, colon, non-Hodgkin's lymphoma
329	HQLSLRTV	stomach, adenocarcinoma, colon, non-Hodgkin's lymphoma
330	MSVQPTVSL	stomach, adenocarcinoma, lymph node, non-Hodgkin's lymphoma
331	SIRDTPAKN	stomach, adenocarcinoma, lymph node, non-Hodgkin's lymphoma
332	SIRDTPAKNAQK	stomach, adenocarcinoma, lymph node, non-Hodgkin's lymphoma
333	SPIKVTLATL	stomach, adenocarcinoma, lymph node, non-Hodgkin's lymphoma
334	TPPVVLRL	stomach, adenocarcinoma, colon, non-Hodgkin's lymphoma
335	VEAKFINY	stomach, adenocarcinoma, colon, non-Hodgkin's lymphoma
336	YEGSPIKV	stomach, adenocarcinoma, colon, non-Hodgkin's lymphoma
337	YEGSPIKVTL	stomach, adenocarcinoma, colon, non-Hodgkin's lymphoma
338	SELKMMTQL	lymph node, non-Hodgkin's lymphoma
339	EKDPQPQQL	lung, non-small cell lung carcinoma, schwannoma
340	GYVPRTAL	lung, non-small cell lung carcinoma, schwannoma
341	KEKDPQPQQL	lung, non-small cell lung carcinoma, schwannoma
342	LPKKPSKLEL	lung, non-small cell lung carcinoma, schwannoma
343	RPSAASIDL	lung, non-small cell lung carcinoma, schwannoma
344	SRHPLSPGF	lung, non-small cell lung carcinoma, schwannoma
345	TPRSPQPEL	lung, non-small cell lung carcinoma, schwannoma
346	GRIVAFFEF	kidney, clear cell renal cell carcinoma, thyroid gland, nodular hyperplasia

347	HTPHPAASR	kidney, clear cell renal cell carcinoma, thyroid gland, nodular hyperplasia
348	NPDELKTTV	lung, non-small cell lung carcinoma, testis, seminoma
349	PSKQLPDQI	lung, non-small cell lung carcinoma, testis, seminoma
350	VYVERAEVL	lung, non-small cell lung carcinoma, testis, seminoma
351	DPFIIIHSI	colon or rectum, uterine cervix, squamous cell carcinoma
352	EHSIATLLL	colon or rectum, uterine cervix, squamous cell carcinoma
353	FLDPRPLTV	pancreas, adenocarcinoma, myometrium, leiomyoma
354	SAFADRPAF	pancreas, adenocarcinoma, myometrium, leiomyoma
355	DTTLPASAR	stomach, adenocarcinoma, rectum, adenocarcinoma
356	KLLEYIEEI	stomach, adenocarcinoma, rectum, adenocarcinoma
357	LEKQLIEL	stomach, adenocarcinoma, rectum, adenocarcinoma
358	LMSVYVVEL	liver, hepatocellular carcinoma, cancer
359	ESITDVLVR	pancreas, adenocarcinoma, stomach, adenocarcinoma
360	ETAFQGMLR	pancreas, adenocarcinoma, stomach, adenocarcinoma,
361	EVPDVTATPARL	pancreas, adenocarcinoma, stomach, adenocarcinoma,
362	GRIVTLISF	pancreas, adenocarcinoma, stomach, adenocarcinoma,
363	HVFSDGVTNW	pancreas, adenocarcinoma, stomach, adenocarcinoma,
364	REIGGGEAGAVI	pancreas, adenocarcinoma, stomach, adenocarcinoma,
365	RGWDGFVEF	pancreas, adenocarcinoma, stomach, adenocarcinoma,
366	RPAVLPLL	pancreas, adenocarcinoma, stomach, adenocarcinoma,
367	VEFFHVEDL	pancreas, adenocarcinoma, stomach, adenocarcinoma,
368	VQRNHETAF	pancreas, adenocarcinoma, stomach, adenocarcinoma,
369	AELEAARL	lung, non-small cell lung carcinoma, testis, seminoma
370	ATQTPVSNK	colon or rectum, rectum, adenocarcinoma
371	ESIDQYIER	colon or rectum, rectum, adenocarcinoma
372	FEEHNSMNEL	colon or rectum, rectum, adenocarcinoma
373	SVASTPISQR	colon or rectum, rectum, adenocarcinoma
374	VASTPISQR	colon or rectum, rectum, adenocarcinoma
375	AEIVGGHEA	spleen, extramedullary hematopoiesis

376	RPPSPALASV	spleen, extramedullary hematopoiesis
377	SVAQVFLNNY	spleen, extramedullary hematopoiesis
378	TQEPTQQHF	spleen, extramedullary hematopoiesis
379	KDITMKNLV	kidney, clear cell renal cell carcinoma, colon, non-Hodgkin's lymphoma
380	MAEKAKQIY	kidney, clear cell renal cell carcinoma, colon, non-Hodgkin's lymphoma
381	KLDNQVSKV	colon or rectum, prostate, benign nodular hyperplasia
382	SENVKLFSA	colon or rectum, prostate, benign nodular hyperplasia
383	VQKLQNII	colon or rectum, prostate, benign nodular hyperplasia
384	AFTVHFSGQF	omentum, adenocarcinoma
385	GVFRGIQDV	omentum, adenocarcinoma
386	QRNMTKLQL	omentum, adenocarcinoma
387	RMFPNAPYL	omentum, adenocarcinoma
388	EAAAEAKAR	lymph node, carcinoma of breast
389	IIKEYTDVY	lymph node, carcinoma of breast
390	KEIDKNDHL	lymph node, carcinoma of breast
391	KVSKASGVSK	lymph node, carcinoma of breast
392	MPATETKKV	lymph node, carcinoma of breast
393	NADPQAVTM	lymph node, carcinoma of breast
394	RSDMLKDII	lymph node, carcinoma of breast
395	SESGAGLTRF	lymph node, carcinoma of breast
396	SMMQTLLTV	lymph node, carcinoma of breast
397	TEVSKTPEA	lymph node, carcinoma of breast
398	VEVPETPKA	lymph node, carcinoma of breast
399	DVYPEIIER	brain, glioblastoma, lymph node, carcinoma of breast
400	REVEIQSHL	stomach, adenocarcinoma, stomach, adenocarcinoma
401	EPPAVLLL	lung, non-small cell lung carcinoma, omentum, adenocarcinoma
402	LEADPFLKY	lung, non-small cell lung carcinoma, omentum, adenocarcinoma
403	TTQGQDVTLA	stomach, adenocarcinoma, lung, adenocarcinoma
404	AEYEDGFSIP	pancreas, adenocarcinoma, bone, osteosarcoma
405	AQISLPRI	spleen, chronic myeloid leukemia
406	DFTPEPAAR	spleen, chronic myeloid leukemia
407	DNTGITTVSK	spleen, chronic myeloid leukemia
408	EEAKQLVDKAY	spleen, chronic myeloid leukemia
409	ERRESIKQ	spleen, chronic myeloid leukemia
410	ETVGQLGTVLR	spleen, chronic myeloid leukemia
411	FEQVMRIGL	spleen, chronic myeloid leukemia
412	FSMQQRQAL	spleen, chronic myeloid leukemia
413	GVPFFSSLR	spleen, chronic myeloid leukemia
414	IVRFPTDQL	spleen, chronic myeloid leukemia

415	KQPVAATRTAV	spleen, chronic myeloid leukemia
416	LGASNRAFV	spleen, chronic myeloid leukemia
417	NPRWDGERL	spleen, chronic myeloid leukemia
418	NVFTNAFRY	spleen, chronic myeloid leukemia
419	QPMEPNPRVPL	spleen, chronic myeloid leukemia
420	QPVAATRTAV	spleen, chronic myeloid leukemia
421	RLFEQVMRI	spleen, chronic myeloid leukemia
422	SEEPLARNL	spleen, chronic myeloid leukemia
423	TIRNQINAL	spleen, chronic myeloid leukemia
424	VLGPTAMRK	spleen, chronic myeloid leukemia
425	AELRNATAA	pancreas, adenocarcinoma, breast, carcinoma
426	DVPDGTLVTVM	pancreas, adenocarcinoma, breast, carcinoma
427	LPIAFKVV	pancreas, adenocarcinoma, breast, carcinoma
428	SAMGSATRY	pancreas, adenocarcinoma, breast, carcinoma
429	AEKQGHQW	stomach, metastatic, ovary, granulosa cell tumor
430	GEQKPTGTF	stomach, metastatic, ovary, granulosa cell tumor
431	GQFSKPFSF	stomach, metastatic, ovary, granulosa cell tumor
432	IAFFDVRTF	stomach, metastatic, ovary, granulosa cell tumor
433	LSAGKTSFSF	stomach, metastatic, ovary, granulosa cell tumor
434	VSNKYGLVF	stomach, metastatic, ovary, granulosa cell tumor
435	GEVDVEQHTL	colon or rectum, colon, adenocarcinoma
436	VDVEQHTL	colon or rectum, colon, adenocarcinoma
437	DAADELSVGRY	kidney, clear cell renal cell carcinoma, colon, adenoma
438	LSEADVRA	stomach, adenocarcinoma, lung, adenocarcinoma
439	ELTLGEFLK	stomach, metastatic, ovary, Mullerian mixed tumor
440	ELTLGEFLKL	stomach, metastatic, ovary, Mullerian mixed tumor
441	LTLGEFLK	stomach, metastatic, ovary, Mullerian mixed tumor
442	LTLGEFLKL	stomach, metastatic, ovary, Mullerian mixed tumor
443	TLGEFLKL	stomach, metastatic, ovary, Mullerian mixed tumor
444	KTYTKSSHLK	stomach, adenocarcinoma, brain, meningioma
445	SQLTTLSFY	lung, non-small cell lung carcinoma, omentum, adenocarcinoma
446	KMQEKKKLQ	liver, hepatocellular carcinoma, lung, large cell carcinoma
447	LLGHLPAEI	liver, hepatocellular carcinoma, lung, large cell carcinoma
448	APVELILSDETLPAPE	liver, hepatocellular carcinoma, cancer

449	ETPDFQLFKNGVAQEPV	liver, hepatocellular carcinoma, cancer
450	LAPLEGARFALVRED	liver, hepatocellular carcinoma, cancer
451	SPDRIFFHLNAVALGD	liver, hepatocellular carcinoma, cancer
452	SPDRIFFHLNAVALGDG	liver, hepatocellular carcinoma, cancer
453	EEMRKLQATVQELQKR	lymph node, non-Hodgkin's lymphoma
454	EEPLSLQELDTSSG	lymph node, non-Hodgkin's lymphoma
455	EMRKLQATVQELQKR	lymph node, non-Hodgkin's lymphoma
456	HLEEPLSLQELDTSSG	lymph node, non-Hodgkin's lymphoma
457	LEEPLSLQELDTSSG	lymph node, non-Hodgkin's lymphoma
462	GVVHSFSHNVGPGDK	liver, hepatocellular carcinoma, cancer, lung, adenocarcinoma
463	GVVHSFSHNVGPGDKY	liver, hepatocellular carcinoma, cancer, lung, adenocarcinoma
464	GVVHSFSHNVGPGDKYT	liver, hepatocellular carcinoma, cancer, lung, adenocarcinoma
465	KTEEFEVTKTAVAHRP	liver, hepatocellular carcinoma, cancer, lung, adenocarcinoma
466	KTEEFEVTKTAVAHRPG	liver, hepatocellular carcinoma, cancer, lung, adenocarcinoma
467	VRPGGVVHSFSHNVGPGDK	liver, hepatocellular carcinoma, cancer, lung, adenocarcinoma
468	VRPGGVVHSFSHNVGPGDKYT	liver, hepatocellular carcinoma, cancer, lung, adenocarcinoma
469	AEKGVRTLTAAAVSGAQ	pancreas, adenocarcinoma, bone, giant cell tumor of bone
470	AQPILSKLEPQIASASE	pancreas, adenocarcinoma, bone, giant cell tumor of bone
471	EKGVRTLTAAAVSGAQ	pancreas, adenocarcinoma, bone, giant cell tumor of bone
472	EKGVRTLTAAAVSGAQP	pancreas, adenocarcinoma, bone, giant cell tumor of bone
473	GVRTLTAAAVSGAQ	pancreas, adenocarcinoma, bone, giant cell tumor of bone
474	KGVRTLTAAAVSGAQ	pancreas, adenocarcinoma, bone, giant cell tumor of bone
475	DVNEYAPVFKEKSYK	brain, glioblastoma, parotid gland, pleomorphic adenoma
476	HRSFVDLSGHNLA	brain, glioblastoma, parotid gland, pleomorphic adenoma
477	HRSFVDLSGHNLANPH	brain, glioblastoma, parotid gland, pleomorphic adenoma
478	HRSFVDLSGHNLANPHP	brain, glioblastoma, parotid gland, pleomorphic adenoma
479	ALPEFDGKRFQNVAKEG	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
480	DSNEFSVIADPRG	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
481	DSNEFSVIADPRGN	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
482	DSNEFSVIADPRGNT	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia

483	DSNEFSVIADPRGNTL	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
484	DSNEFSVIADPRGNTLG	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
485	PEFDGKRFQNVAK	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
486	SDSNEFSVIADPRGNTLG	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
487	SQKKTFEINPRHPLIR	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
488	ALPEFDGKRFQNVAKEG	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
489	PEFDGKRFQNVAK	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
490	PEFDGKRFQNVAKE	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
491	LNSLTYQVLDVQRYP	kidney, clear cell renal cell carcinoma, endometrium, adenocarcinoma
492	LPQLVGVSTPLQG	kidney, clear cell renal cell carcinoma, endometrium, adenocarcinoma
493	LPQLVGVSTPLQGG	kidney, clear cell renal cell carcinoma, endometrium, adenocarcinoma
494	LPQLVGVSTPLQGGS	kidney, clear cell renal cell carcinoma, endometrium, adenocarcinoma
495	RLPQLVGVSTPLQGGS	kidney, clear cell renal cell carcinoma, endometrium, adenocarcinoma
496	SDVDLIPMNDHNAYR	kidney, clear cell renal cell carcinoma, endometrium, adenocarcinoma
497	GRRKSRQGSLAMEELK	rectum, adenocarcinoma
498	RKSRQGSLAMEELK	rectum, adenocarcinoma
499	SGPSLKGEEEPLVASEDGAVD	rectum, adenocarcinoma
500	SGSGPSLKGEEEPLVASEDGAVD	rectum, adenocarcinoma
501	IKPGVTTEEIDHAVH	endometrium, adenocarcinoma
502	KPGVTTEEIDHAVH	endometrium, adenocarcinoma
503	DGVLRIQNLDQS	pancreas, adenocarcinoma, myometrium, leiomyoma
504	GAYFHDDGFLAFPG	pancreas, adenocarcinoma, myometrium, leiomyoma
505	TPYSFLPLPTIKDAYR	pancreas, adenocarcinoma, myometrium, leiomyoma
506	YPTPDISWSKLDGSLPP	pancreas, adenocarcinoma, myometrium, leiomyoma
507	YPTPDISWSKLDGSLPPD	pancreas, adenocarcinoma, myometrium, leiomyoma
508	ASHFEQMAAASMHR	metastatic renal cell carcinoma
509	GGQVIVAIPKLQTQQ	parathyroid gland, adenoma
510	GQVIVAIPKLQTQ	parathyroid gland, adenoma
511	GQVIVAIPKLQTQQ	parathyroid gland, adenoma
512	IESTFDVVSSKPVG	parathyroid gland, adenoma
513	DWGALATISTLEAVRG	lung, non-small cell lung carcinoma, liver, hepatocellular carcinoma

514	GRPFADVLSLSDGPPG	lung, non-small cell lung carcinoma, liver, hepatocellular carcinoma
515	WGALATISTLEAVR	lung, non-small cell lung carcinoma, liver, hepatocellular carcinoma
516	WGALATISTLEAVRG	lung, non-small cell lung carcinoma, liver, hepatocellular carcinoma
517	ADELALVDVIEDK	kidney, clear cell renal cell carcinoma, kidney, renal cell carcinoma
518	GVSLKTLHPDLGTDK	kidney, clear cell renal cell carcinoma, kidney, renal cell carcinoma
519	IVSGKDYNVTANSKL	kidney, clear cell renal cell carcinoma, kidney, renal cell carcinoma
520	DDNIKTYSDHPEK	kidney, clear cell renal cell carcinoma, liver, hepatocellular carcinoma
521	DKVYVHLKNLASRPY	kidney, clear cell renal cell carcinoma, liver, hepatocellular carcinoma
522	GDKVYVHLKNLASRPY	kidney, clear cell renal cell carcinoma, liver, hepatocellular carcinoma
523	LDDNIKTYSDHPEK	kidney, clear cell renal cell carcinoma, liver, hepatocellular carcinoma
524	TGDKVYVHLKNLASRPY	kidney, clear cell renal cell carcinoma, liver, hepatocellular carcinoma
525	VYVHLKNLASRPY	kidney, clear cell renal cell carcinoma, liver, hepatocellular carcinoma
526	KTSRLPIIDVAPLDVGAPD	pancreas, adenocarcinoma, chondrosarcoma
527	KTSRLPIIDVAPLDVGAPDQE	pancreas, adenocarcinoma, chondrosarcoma
528	LPIIDVAPLDVGAPD	pancreas, adenocarcinoma, chondrosarcoma
529	RLPIIDVAPLDVGAPD	pancreas, adenocarcinoma, chondrosarcoma
530	RLPIIDVAPLDVGAPDQE	pancreas, adenocarcinoma, chondrosarcoma
531	SRLPIIDVAPLDVGAPD	pancreas, adenocarcinoma, chondrosarcoma
532	SRLPIIDVAPLDVGAPDQE	pancreas, adenocarcinoma, chondrosarcoma
533	TSRLPIIDVAPLDVGAPD	pancreas, adenocarcinoma, chondrosarcoma
534	TSRLPIIDVAPLDVGAPDQE	pancreas, adenocarcinoma, chondrosarcoma
535	DTSYVSLKAPLT	liver, hepatocellular carcinoma, cancer
536	DTSYVSLKAPLTKP	liver, hepatocellular carcinoma, cancer
537	DTSYVSLKAPLTKPL	liver, hepatocellular carcinoma, cancer
538	ESDTSYVSLKAPLT	liver, hepatocellular carcinoma, cancer
539	ESDTSYVSLKAPLTKPL	liver, hepatocellular carcinoma, cancer
540	SDTSYVSLKAPLT	liver, hepatocellular carcinoma, cancer
541	SDTSYVSLKAPLTKP	liver, hepatocellular carcinoma, cancer
542	SDTSYVSLKAPLTKPL	liver, hepatocellular carcinoma, cancer
543	DPASFRAAIGLLARH	kidney, clear cell renal cell carcinoma, colon, adenocarcinoma
544	TEGQFVDLTGNRLTYT	liver, hepatocellular carcinoma, cancer, liver, focal nodular hyperplasia
545	ALDFFGNGPPVNYK	lung, non-small cell lung carcinoma,
546	ALDFFGNGPPVNYKTG	lung, non-small cell lung carcinoma, bone, non-ossifying fibroma
547	DFFGNGPPVNYKTG	lung, non-small cell lung carcinoma, bone, non-ossifying fibroma

548	LDFFGNGPPVNYK	lung, non-small cell lung carcinoma, bone, non-ossifying fibroma
549	LDFFGNGPPVNYKTG	lung, non-small cell lung carcinoma, bone, non-ossifying fibroma
550	QALDFFGNGPPVNYKTG	lung, non-small cell lung carcinoma, bone, non-ossifying fibroma
551	AISDYVFNTASLVYH	liver, hepatocellular carcinoma, cancer
552	AISDYVFNTASLVYHEE	liver, hepatocellular carcinoma, cancer
553	ISDYVFNTASLVYH	liver, hepatocellular carcinoma, cancer
554	ISDYVFNTASLVYHEE	liver, hepatocellular carcinoma, cancer
555	YVFNTASLVYHEE	liver, hepatocellular carcinoma, cancer
556	IVIALSGNKADLA	brain, glioblastoma, endometrium, adenocarcinoma
557	SPNIVIALSGNKADL	brain, glioblastoma, endometrium, adenocarcinoma
558	SPNIVIALSGNKADLA	brain, glioblastoma, endometrium, adenocarcinoma
559	TPPRLVAPRFLEVE	stomach, metastatic, non-Hodgkin's lymphoma
560	TPPRLVAPRFLEVET	stomach, metastatic, non-Hodgkin's lymphoma
561	TPPRLVAPRFLEVETS	stomach, metastatic, non-Hodgkin's lymphoma
562	EIQRDILLEKKKVAQDQ	stomach, metastatic, liver, hepatic adenoma
563	FGAIFFLPDSSK	stomach, metastatic, liver, hepatic adenoma
564	IQRDILLEKKKVAQ	stomach, metastatic, liver, hepatic adenoma
565	IQRDILLEKKKVAQD	stomach, metastatic, liver, hepatic adenoma
566	IQRDILLEKKKVAQDQ	stomach, metastatic, liver, hepatic adenoma
567	LSGVLFHSSPALQPA	stomach, metastatic, liver, hepatic adenoma
568	RDILLEKKKVAQDQ	stomach, metastatic, liver, hepatic adenoma
569	SSKLLSGVLFHSSPA	stomach, metastatic, liver, hepatic adenoma
570	SSPALQPAADHKPGPG	stomach, metastatic, liver, hepatic adenoma
571	APPTRGPPPSYGGS	colon or rectum, thymus, thymoma,
572	GNSRSAPPTRGPPPSYGGSSRY	colon or rectum, thymus, thymoma,
573	RDYGHSSSRDDYPS	colon or rectum, thymus, thymoma,
574	SPRDDGYSTKDSY	colon or rectum, thymus, thymoma,
575	GGSAAAAAAAAASGG	liver, hepatocellular carcinoma, myometrium, leiomyoma
576	DNMLLAEGVSGPEK	liver, hepatocellular carcinoma, adrenal gland, adrenal cortical adenoma
577	ADSLYVEKIDVGEAEPR	esophagus, adenocarcinoma
578	RIQLVEEELDRAQER	pancreas, adenocarcinoma, intramuscular lipoma
579	RRIQLVEEELDRAQER	pancreas, adenocarcinoma, intramuscular lipoma
580	HQPHKVTQYKKGKDSLY	liposarcoma
581	RKKAKTTKKIVL	liposarcoma
582	DVFRQYASLTGTQALPP	liver, hepatocellular carcinoma, cancer, small intestine, gastrointestinal stromal tumor
583	GTAQGELFLDDGHT	liver, hepatocellular carcinoma, cancer, small

		intestine, gastrointestinal stromal tumor
584	VFRQYASLTGTQALPP	liver, hepatocellular carcinoma, cancer, small intestine, gastrointestinal stromal tumor
585	PEFDGKRFQNVAK	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
586	PEFDGKRFQNVAKE	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
587	ALPEFDGKRFQNVAKEG	liver, hepatocellular carcinoma, cancer, thyroid gland, nodular hyperplasia
588	ASPSESEARFRIDSVSEGNAGPY	pancreas, adenocarcinoma, lipoma
589	EARFRIDSVSEGNAGP	pancreas, adenocarcinoma, lipoma
590	ESEARFRIDSVSEGNAGP	pancreas, adenocarcinoma, lipoma
591	ESEARFRIDSVSEGNAGPY	pancreas, adenocarcinoma, lipoma
592	FRIDSVSEGNAGP	pancreas, adenocarcinoma, lipoma
593	FRIDSVSEGNAGPY	pancreas, adenocarcinoma, lipoma
594	SEARFRIDSVSEGNAGPY	pancreas, adenocarcinoma, lipoma
595	SPSESEARFRIDSVSEGNAGPY	pancreas, adenocarcinoma, lipoma
596	GNQLFRINEANQL	stomach, adenocarcinoma, prostate, adenocarcinoma
597	GNQLFRINEANQLMQ	stomach, adenocarcinoma, prostate, adenocarcinoma
598	SPAMAGGLFAIERE	stomach, adenocarcinoma, prostate, adenocarcinoma
599	FIGNIAVNHAPVSPR	stomach, adenocarcinoma, metastatic carcinoma of breast
600	FIGNIAVNHAPVSPRPG	stomach, adenocarcinoma, metastatic carcinoma of breast
601	IGNIAVNHAPVSPRP	stomach, adenocarcinoma, metastatic carcinoma of breast
602	IGNIAVNHAPVSPRPG	stomach, adenocarcinoma, metastatic carcinoma of breast
603	FEGQFSINKVPGNFH	kidney, clear cell renal cell carcinoma, prostate, adenocarcinoma
604	FEGQFSINKVPGNFHVS	kidney, clear cell renal cell carcinoma, prostate, adenocarcinoma
605	RFEGQFSINKVPGNFH	kidney, clear cell renal cell carcinoma, prostate, adenocarcinoma

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

atypical lipoma;

brain cancer and a proliferative disease selected from kidney oncocytoma and lymph node malignant melanoma; glioblastoma, and a proliferative disease selected from bone non-ossifying fibroma, meningioma, breast carcinoma, endometrial adenocarcinoma, omentum

leiomyosarcoma, parotid gland pleomorphic adenoma, skin squamous cell carcinoma, thyroid gland nodular hyperplasia, and uterine cervix squamous cell carcinoma;

breast lobular carcinoma;

breast intraductal carcinoma;

colon or rectal cancer, and a proliferative disease selected from adenocarcinoma, adrenal cortical carcinoma, breast mucinous carcinoma, adenocarcinoma, endometrium Mullerian mixed tumor, fibromatosis, kidney carcinoma, liver focal nodular hyperplasia, liver hepatocellular carcinoma, lung small cell carcinoma, lung squamous cell carcinoma, carcinoma of breast, lymph node non-Hodgkin's lymphoma, metastatic renal cell carcinoma, myometrium leiomyoma, ovary teratoma, ovary thecoma-fibroma, parathyroid gland adenoma, prostate benign nodular hyperplasia, rectum adenocarcinoma, spleen chronic myeloid leukemia, spleen extramedullary hematopoiesis, stomach adenocarcinoma, synovial sarcoma, testis seminoma, thymus thymoma, and uterine cervix squamous cell carcinoma;

colon adenoma;

endometrium adenocarcinoma;

esophagus, adenocarcinoma;

kidney angiomyolipoma;

kidney clear cell renal cell carcinoma and a proliferative disease selected from bone non-ossifying fibroma, brain meningioma, colon adenocarcinoma, colon adenoma, colon non-Hodgkin's lymphoma;

kidney clear cell renal cell carcinoma and a proliferative disease selected from endometrium adenocarcinoma, kidney angiomyolipoma, kidney polycystic kidney disease, kidney transitional cell carcinoma, lipoma non-Hodgkin's lymphoma, ovary adenocarcinoma, parotid gland pleomorphic adenoma, prostate adenocarcinoma, spleen non-Hodgkin's lymphoma, stomach gastrointestinal stromal tumor (GIST), synovial sarcoma, and thyroid gland nodular hyperplasia;

kidney, renal cell carcinoma; e.g. of the non-clear cell type;

liposarcoma;

liver focal nodular hyperplasia;

liver, hepatocellular carcinoma and a proliferative disease selected from adrenal gland adrenal cortical adenoma, breast carcinoma, adenoid cystic carcinoma, colon adenocarcinoma, liver focal nodular hyperplasia, liver hepatocellular carcinoma, lung adenocarcinoma, pancreas adenocarcinoma, parotid gland pleomorphic adenoma, small intestine gastrointestinal stromal tumor, thyroid gland nodular hyperplasia, fibromatosis, kidney angiomyolipoma, kidney renal

cell carcinoma, liver focal nodular hyperplasia, lung large cell carcinoma, myometrium leiomyoma, and uterine cervix squamous cell carcinoma; lung adenocarcinoma;
lung non-small cell lung carcinoma and a proliferative disease selected from bone non-ossifying fibroma, kidney carcinoma, liver hepatocellular carcinoma, lung adenocarcinoma, lung neuroendocrine carcinoma, omentum, adenocarcinoma, schwannoma, spleen chronic myeloid leukemia, spleen extramedullary hematopoiesis, stomach adenocarcinoma, testis seminoma, thymus thymoma, and uterine cervix squamous cell carcinoma;
lymph node infiltrating carcinoma of breast;
lymph node non-Hodgkin's lymphoma;
malignant fibrous histiocytoma;
metastatic infiltrating carcinoma of breast;
metastatic renal cell carcinoma;
omentum adenocarcinoma;
ovary adenocarcinoma clear cell type;
ovary granulosa cell tumor;
pancreas adenocarcinoma and a proliferative disease selected from bone giant cell tumor of bone, bone osteosarcoma, breast carcinoma, chondrosarcoma, intramuscular lipoma, lipoma, lung adenocarcinoma, lymph node Hodgkin's disease, myometrium, leiomyoma, ovary mucinous cystadenocarcinoma, stomach adenocarcinoma, and thymus thymoma;
parathyroid gland adenoma;
prostate adenocarcinoma;
rectum adenocarcinoma;
small intestine gastrointestinal stromal tumor;
spleen chronic myeloid leukemia;
spleen extramedullary hematopoiesis;
squamous cell carcinoma;
stomach adenocarcinoma and a proliferative disease selected from, brain meningioma, liver carcinoid tumor metastatic, prostate adenocarcinoma, and spleen chronic myeloid leukemia;
stomach differentiated subtype adenocarcinoma and a proliferative disease selected from colon adenocarcinoma, colon non-Hodgkin's lymphoma, endometrium adenocarcinoma, kidney Wilm's tumor, lung adenocarcinoma, lung small cell carcinoma, lymph node non-Hodgkin's lymphoma, malignant fibrous histiocytoma, metastatic infiltrating lobular carcinoma of breast, parathyroid gland adenoma, rectum adenocarcinoma, stomach adenocarcinoma, testis seminoma, and uterine cervix squamous cell carcinoma;

stomach adenocarcinoma, and a proliferative disease selected from lung adenocarcinoma, metastatic renal cell carcinoma, myometrium leiomyoma, non-Hodgkin's lymphoma, mycosis fungoides, ovary adenocarcinoma, pancreas adenocarcinoma, and white blood cells chronic lymphocytic leukemia;
stomach endometrium, adenocarcinoma;
metastatic stomach cancer, and a proliferative disease selected from adenocarcinoma, bone non-ossifying fibroma, breast carcinoma, duodenum adenocarcinoma, liver hepatic adenoma, lung large cell carcinoma, lung neuroendocrine carcinoma, lung squamous cell carcinoma, lymph node non-Hodgkin's lymphoma, ovary granulosa cell tumor, ovary Mullerian mixed tumor, pancreas adenocarcinoma, prostate benign nodular hyperplasia, rectum adenocarcinoma, and basal cell carcinoma;
thyroid gland nodular hyperplasia;
and uterine cervix squamous cell carcinoma.

ACBD6 encodes a modular protein that carries an acyl-CoA binding domain at its N terminus and two ankyrin motifs at its C terminus. ACBD6 expression is restricted to tissues and progenitor cells with functions in blood and vessel development. ACBD6 was detected in bone marrow, spleen, placenta, cord blood, circulating CD34+ progenitors, and embryonic-like stem cells derived from placenta (Soupene et al., 2008).

BRAP encodes the BRCA1 associated protein, which was identified by its ability to bind to the nuclear localization signal of BRCA1 and other proteins. It is a cytoplasmic protein which may regulate nuclear targeting by retaining proteins with a nuclear localization signal in the cytoplasm (RefSeq, 2002). BRAP has been described as leukemia-associated antigen (Greiner et al., 2003).

CDCA7L encodes the protein cell division cycle associated 7-like, which interacts with the oncogene c-Myc and potentiates its transforming activity (Huang et al., 2005). CDCA7L is strongly up-regulated in hepatocellular carcinoma and ectopic over-expression of CDCA7L promotes hepatocellular carcinoma cell proliferation and colony formation (Tian et al., 2013).

CHTF18 encodes a protein which together with CHTF8 and DCC1 is a component of an alternative replication factor C complex that loads PCNA onto DNA during S phase of the cell cycle (RefSeq, 2002). CHTF18 together with the other genes of the replication factor C

complex can induce synthetic lethal genetic interactions that decrease somatic cell proliferation in Caenorhabditis elegans. Due to this fact CHTF18 was identified as a candidate cancer drug target (McLellan et al., 2009). The co-occurrence of somatic mutations in ESCO1 and CHTF18 was statistically significant in non-endometrioid endometrial tumors (Price et al., 2014).

KIF15 encodes kinesin family member 15, a protein involved in the assembly and the stabilization of the mitotic spindle (Vanneste et al., 2009). In breast cancer, KIF15 was shown to be over-expressed and to be immunogenic, as anti-KIF15 antibodies could be isolated from breast cancer patients (Scanlan et al., 2001). Furthermore, KIF15 appears to be implicated in lung adenocarcinoma (Bidkhori et al., 2013).

NOP14 encodes a protein that plays a role in pre-18s rRNA processing and small ribosomal subunit assembly (RefSeq, 2002). Mutations within the NOP14 gene and abnormal expression has been detected in pancreatic cancer. In pancreatic cancer cells, NOP14 over-expression promotes migration, proliferation and colony formation (Zhou et al., 2012b; Zhou et al., 2012a). Down-regulation of NOP14 expression in whole blood samples of ovarian cancer patients correlated with poor prognosis (Isaksson et al., 2014).

NUDCD1 encodes NudC domain containing 1 known as well as ovarian cancer-associated antigen 66 (OVA66) (RefSeq, 2002). In human cancer cells, NUDCD1 influences tumorigenesis by regulating the type I insulin-like growth factor receptor (IGF-1R) signaling pathway (Rao et al., 2014a). NUDCD1 induces oncogenic transformation of NIH3T3, the mouse embryonic fibroblast cell line (Rao et al., 2014b).

PRIM1 encodes a protein which is the small 49 kDa primase subunit. Primase and DNA polymerase alpha are the two key enzymatic components for DNA replication in eukaryotic cells (RefSeq, 2002). PRIM1 was found to be amplified in 41% of 22 pediatric osteosarcoma samples. PRIM1 is co-amplified with the core 12q13 amplicon genes CDK4, SAS, and OS9, and was physically mapped very close to them (Yotov et al., 1999). The up-regulation of SIX1 expression in cervical cancer results in the up-regulation of multiple genes related to the initiation of DNA replication including PRIM1 (Liu et al., 2014).

QTRTD1 encodes a subunit of tRNA-guanine transglycosylase which plays a critical role in tRNA modification by synthesizing the 7-deazaguanosine queuosine. The encoded protein may play a role in the queuosine 5'-monophosphate salvage pathway (RefSeq, 2002).

SDAD1 encodes a poorly characterized protein, which might be involved in rRNA processing. Single nucleotide polymorphisms within the SDAD1 gene were shown to be associated with seasonal allergic rhinitis (Babbio et al., 2004; Zhang et al., 2005).

TARBP1 encodes the TAR (HIV-1) RNA binding protein 1 a double stranded RNA binding protein, which might disengage RNA polymerase II from HIV-1 TAR during transcriptional elongation (RefSeq, 2002). TARBP1 expression was shown to be significantly up-regulated in basal cell carcinoma and squamous cell carcinoma of the skin (Sand et al., 2012).

VCPIP1 (also known as VCIP135) and p47 are shown to function in Golgi and ER assembly (Uchiyama et al., 2002). VCPIP1 is down-regulated in breast cancer (Kuznetsova et al., 2007). VCPIP1 is one of the de-ubiquitinating enzymes, being part of the ovarian tumor family (OTU) (Enesa and Evans, 2014).

ZNF131 encodes the zinc finger protein 131, a poorly characterized transcriptional regulator, which might act as repressor of estrogen receptor alpha (Oh and Chung, 2012).

The present invention furthermore relates to the 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 -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: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605.

A peptide consisting essentially of the amino acid sequence as indicated 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, compared to the non-modified peptide. I

In another peptide consisting essentially of the amino acid sequence, one or two amino acids are exchanged with their conservative exchange partners (see herein below as well) 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, compared to the non-modified peptide.

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 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 medicine.

The present invention further relates to antibodies according to the present invention, and methods of making them.

The present invention further relates to T-cell receptors (TCR), in particular soluble TCR (sTCRs), according to the present invention, 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 a method of producing a peptide according to the present invention, the method comprising culturing the host cell according to the present invention, and isolating the peptide from the host cell or its culture medium.

The present invention further relates to an *in vitro* method for producing activated cytotoxic T lymphocytes (CTL), the method comprising contacting in vitro CTL 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 CTL in an antigen specific manner, wherein said antigen is any peptide according to the present invention.

The present invention further relates to the 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 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: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605, or said variant amino acid sequence.

The present invention further relates to activated cytotoxic T lymphocytes (CTL), 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 cytotoxic T lymphocytes (CTL) 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 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 said medicament is a vaccine.

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 hematological malignancies, AML or chronic lymphatic leukemia (CLL) cells.

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 hematological malignancies, AML or chronic lymphatic leukemia (CLL) cells, preferably AML.

Further, 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 warehouse (database) of prescreened 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 cytotoxic T-cells (CTL) from tumor-infiltrating cell populations or from peripheral blood suggests that such cells play an important role in natural immune defences 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).

There are two classes of MHC-molecules: MHC class I molecules that can be found on most cells having a nucleus. 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 present peptides that result from proteolytic cleavage of predominantly endogenous proteins, 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 the course of endocytosis, and are subsequently processed. Complexes of peptide and MHC class I molecules are recognized by CD8-positive cytotoxic T-lymphocytes 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 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 surprisingly 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)..

It was shown in mammalian animal models, e.g., mice, that even in the absence of CTL effector cells (i.e., 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).

Additionally, it was shown that CD4-positive T cells recognizing peptides from tumor-associated antigens presented by HLA class II molecules can counteract tumor progression via the induction of antibody (Ab) responses.

In contrast to tumor-associated peptides binding to HLA class I molecules, only a small number of class II ligands of tumor associated antigens (TAA) have been described to date.

Since the constitutive expression of HLA class II molecules is usually limited to cells of the immune system, 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; (Dengjel et al., 2006).

The antigens that are recognized by the tumor specific cytotoxic T lymphocytes, that is, their epitopes, 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, 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+ CTLs (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.

The present invention also relates to two new and very useful MHC class II peptides (according to SEQ ID NO: 448 to SEQ ID NO: 605). These peptides are particularly useful in the diagnosis and/or treatment of AML and other cancers over-expressing and/or over – presenting the antigens the peptides are derived from respectively.

The present invention also relates to so-called length variants of the inventive MHC class II peptides according to SEQ ID NO: 448 to SEQ ID NO: 605.

The length variants are generally N- and/or C-terminally extended (between 1 and 5, preferably 1 to 10 amino acids) or N- and/or C-terminally shortened (between 1 and 5 amino acids) peptides, which still can bind to MHC, and elicit a cellular immune response as described herein. As is known in the state of the art, peptides binding to class II proteins are not constrained in size and can vary from 11 to 30 amino acids in length. The peptide binding groove in the MHC class II molecules is open at both ends, which enables binding of peptides with relatively longer length. Though the "core" nine residues long segment contributes the most to the recognition of the peptide, the flanking regions are also important for the specificity of the peptide to the class II allele (see, for example, Meydan C, et al., Prediction of peptides binding to MHC class I and II alleles by temporal motif mining. BMC Bioinformatics. 2013; 14 Suppl 2: S13). Using the many software tools as available (e.g. as described above), the person of skill in the art will be able to identify the binding motif, and thus identify the possibilities for extensions and/or deletions of the MHC class II peptides according to Table 3, in order to create length variants.

For a peptide to trigger (elicit) a cellular immune response, it 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 being expressed by tumor cells, they also have to be recognized by T cells bearing specific T cell receptors (TCR).

The antigens that are recognized by the tumor specific cytotoxic T lymphocytes, that is, their epitopes, 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, up-regulated in cells of the respective tumor.

The current classification of tumor associated antigens comprises the following major groups:
a) Cancer-testis antigens: The first tumor associated antigens (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.

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 or in another 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 a 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. The Tübingen

approach: identification, selection, and validation of tumor-associated HLA peptides for cancer therapy. Cancer Immunol Immunother. 2004 Mar;53(3):187-95). In both cases it is essential that epitopes are present in the amino acid sequence of the antigen, since such a peptide ("immunogenic peptide") that is derived from a tumor associated antigen should lead to an *in vitro* or *in vivo* T-cell-response.

Basically, any peptide able to bind a 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 with a corresponding TCR and the absence of immunological tolerance for this particular epitope.

Therefore, TAAs are a starting point for the development of a tumor vaccine. The methods for identifying and characterizing the TAAs are based on the use of CTL 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 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.

T-helper cells 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 T_{H1} 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.

Uses against additional cancers are disclosed in the following more detailed description of the peptides according to the invention.

Detailed description of the invention

As used herein and except as noted otherwise all terms are defined as given below.

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, 13 or 14, and in case of MHC class II peptides they can be as long as 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.

The term “peptide” shall 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 include the peptides consisting of or comprising a peptide as defined above according to SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605.

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*A02 and the most frequent HLA-DR serotypes. Frequencies are deduced from haplotype frequencies G_f 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 $F=1-(1-G_f)^2$. Combinations of A*02 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)..

	Expression frequencies of HLA*02 and HLA-DR serotypes within North American subpopulations			
HLA Allele	Caucasian American	African American	Asian American	Latin American
A*02	49.1%	34.1%	43.2%	48.3%
DR1	19.4%	13.2%	6.8%	15.3%
DR2	28.2%	29.8%	33.8%	21.2%
DR3	20.6%	24.8%	9.2%	15.2%
DR4	30.7%	11.1%	28.6%	36.8%
DR5	23.3%	31.1%	30.0%	20.0%
DR6	26.7%	33.7%	25.1%	31.1%
DR7	24.8%	19.2%	13.4%	20.2%
DR8	5.7%	12.1%	12.7%	18.6%
DR9	2.1%	5.8%	18.6%	2.1%

Therefore, for therapeutic and diagnostic purposes a peptide that binds with appropriate affinity to several different HLA class II receptors is highly desirable. A peptide binding to several different HLA class II molecules is called a promiscuous binder.

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 from a non-mutated ("normal"), mutated or altered gene, or can even be 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.

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 going to be expressed by.

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 that generates an immune response (i.e., has immunogenic activity) when administered, alone or optionally with a suitable adjuvant, 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 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, these 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 the following 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 can be the peptides of the original sequence of the protein or any other amino acid. 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 CTLs 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 CTLs 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 4 residues from the reference peptide, as long as they have substantially identical antigenic activity.

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 now 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 explored for cancer immunotherapy.

Specific elements of the cellular immune response are capable of specifically recognizing and destroying tumor cells. The isolation of cytotoxic T-cells (CTL) from tumor-infiltrating cell

populations or from peripheral blood suggests that such cells play an important role in natural immune defences 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 12 residues derived from proteins or defect ribosomal products (DRIPS) located in the cytosols, play an important role in this response. The MHC-molecules of the human are also designated as human leukocyte-antigens (HLA).

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 CTLs (MHC class I molecule) or by CD4-positive CTLs (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 lung cancer in particular. Furthermore, there is a need to identify factors that can be used in the treatment of cancer in general and AML in particular.

The present invention provides peptides that are useful in treating cancers / tumors, preferably lung cancers, even more preferably AML and other cancers (see table 5) 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 AML 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 tumor tissue compared with normal tissues (see example 1, and Figure 2 for AML) demonstrating a high

degree of tumor association of the source genes. Moreover, the peptides themselves are strongly over-presented on tumor tissue but not on normal tissues (see example 1 and Figure 3).

HLA-bound peptides can be recognized by the immune system, specifically T lymphocytes/T cells. T cells can destroy the cells presenting the recognized HLA/peptide complex, e.g. lung cancer 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 1 and Figure 4). 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.

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 $-NH_2$ 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).

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 *lung cancer 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 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 is malignant or inflamed or generally diseased. 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 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 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, they can be used to verify a pathologist's diagnosis of a cancer based on a biopsied sample.

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 AML 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 tumor tissue obtained from AML 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.

In the context of the present invention, HLA-peptide complexes from 50 shock-frozen AML tumor 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 AML tumor samples confirming their presentation on primary AML.

TUMAPs identified on multiple AML 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 therefore relates to a peptide comprising a sequence that is selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605 or a variant thereof which is at least 90% homologous (preferably identical) to SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605 or a variant thereof that induces T cells cross-reacting with said peptide, wherein said peptide is not a 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: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605 or a variant thereof which is at least 90% homologous (preferably identical) to SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605, 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: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605.

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 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 invention.

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

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 invention that is an antigen presenting cell.

The present invention further relates to the host cell according to the invention, wherein the antigen presenting cell is a dendritic cell.

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

The present invention further relates to an *in vitro* method for producing activated cytotoxic T lymphocytes (CTL), the method comprising contacting *in vitro* CTL 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 CTL in an antigen specific manner, wherein said antigen is any peptide according to the invention.

The present invention further relates to the method as described, wherein said 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: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605 or said variant amino acid sequence.

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

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 invention, the method comprising administering to the patient an effective number of cytotoxic T lymphocytes (CTL) according to the invention.

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

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 AML cells or other non-solid tumor cells.

The present invention further relates to particular marker proteins and biomarkers that can be used in the prognosis of lung cancer.

Further, the present invention relates to the use of the novel targets as described in accordance with the present invention 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 or polymers of those immunoglobulin molecules and humanized versions of immunoglobulin molecules, so long as they exhibit any of the desired properties (e.g., specific binding of an lung cancer marker

polypeptide, delivery of a toxin to an lung cancer cell expressing a lung cancer marker gene at an increased level, and/or inhibiting the activity of a lung cancer 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 lung cancer 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: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605 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 lung cancer 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, Western blots, immunohistochemical staining of formalin-fixed lung 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 (U.S. Pat. No. 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 U.S. Pat. No. 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 U.S. Pat. No. 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 (U.S. Pat. No. 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 for treating lung cancer, 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 lung 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 lung cancer.

Because the peptides as mentioned in Tables 2 and 5 (specifically the ones associated with AML) of the invention and thus their underlying polypeptides are highly expressed in AML, and are expressed at rather to extremely low levels in normal cells, inhibition of ABCA13 and/or MMP12 expression or polypeptide activity may be preferably integrated into a therapeutic strategy for treating or preventing AML.

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 lung tumor marker function by antisense gene therapy may be accomplished by direct administration of antisense lung 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 ABCA13 and MMP12 function using gene therapy involves intracellular expression of an anti-ABCA13, -MMP12 antibody or a portion of an anti-ABCA13, -MMP12 antibody. For example, the gene (or gene fragment) encoding a monoclonal antibody that specifically binds to an ABCA13, MMP12 polypeptide and inhibits its biological activity is placed under the transcriptional control of a specific (e.g., tissue- or tumor-specific) gene regulatory sequence, within a nucleic acid expression vector. The vector is then administered to the subject such that it is taken up by lung cancer cells or other cells, which then secrete the anti-ABCA13, -MMP12 antibody and thereby block biological activity of the ABCA13, MMP12 polypeptide. Preferably, the ABCA13, MMP12 polypeptides are present at the extracellular surface of AML cancer cells.

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 AML tumor 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 ABCA13 and/or MMP12. 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 ABCA13 and MMP12 targets 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 ABCA13 and/or MMP12 proteins express *in situ*.

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: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605 or a variant thereof which is 90% homologous to SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605 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 and / or 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 U S A. 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: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605. 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 CTL.

These CTL 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: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605, 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 CTL, which can subsequently cross-react with and kill cells that express a polypeptide containing the natural amino acid sequence of the peptide according to the present invention.

Those 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.

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 also 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 class II binding peptides the length can also be 15, 16, 17, 18, 19, 20, 21 or 23 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. 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: 325, SEQ ID NO: 326: to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605.

"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: 325, SEQ ID NO: 326: to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605 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 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.

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 $-CH_2SO-$. United States Patent 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, amidation, 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 performing 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 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/hydroxybenzotriazole 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 T, et al. From production of peptides in milligram amounts for research to multi-tons quantities for drugs of the future. Curr Pharm Biotechnol. 2004 Feb;5(1):29-43. Review, 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 (UK) Ltd, Nottingham NG7 2QJ, 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 in US Patent Nos. 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 preprotrypsin 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.

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 then 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 1985 (Ljunggren, H.-G., and K. Karre. 1985. J. Exp. Med. 162:1745).

Preferably, the host cell before transfection 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 CTLs.

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: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605, or a variant amino acid sequence thereof as described herein.

A number of other methods may be used for generating CTL *in vitro*. For example, autologous tumor-infiltrating lymphocytes can be used in the generation of CTL. Plebanski et al (1995) (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 CTL. Furthermore, the production of autologous CTL 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 CTL. In addition, macrophages pulsed with peptide or polypeptide, or infected with recombinant virus, may be used in the preparation of autologous CTL. 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: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605.

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 CTL, 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 WO 95/18145 and Longenecker, 1993). 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 CTLs is more efficient in the presence of help provided by CD4 T-helper cells. Thus, for MHC Class I epitopes that stimulate CD8 CTL 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: 605 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: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605, 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., 2005 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 CTLs and helper-T (T_H) 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. Review). 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 T_{H1} cells and strong cytotoxic T-lymphocyte (CTL) generation, even in the absence of CD4 T cell help. The T_{H1} 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 T_{H2} 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 Pat. No. 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 derivatives 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 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, EP2113253.

Nevertheless depending on the number and the physico-chemical characteristics of the peptides of the invention further research is needed to provide formulations for specific combinations of peptides, especially combinations with more than 20 peptides that are stable for more than 12 to 18 months.

The present invention provides a medicament that useful in treating cancer, in particular AML, Chronic lymphatic leukemia (CLL) and other hematological 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 (=75µg) and preferably not more than 3 mg/mL/peptide (=1500µg). 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, a 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 tumor tissue related to AML, the medicament of the invention is preferably used to treat AML. In a preferred embodiment, the peptides of the invention derived from ABCA13 and MMP12 were isolated from AML, the medicament of the invention is preferably used to treat AML overexpressing these polypeptides.

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 (database) of pre-screened TUMAPs, wherein

the at least one peptide used in the pharmaceutical composition is selected for suitability in the individual patient. Preferably, 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.

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 over-presentation in a particular tumor type, e.g. in the form of a database or an actual storage unit. 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 or actual storage unit) is composed of tumor-associated peptides which were highly overexpressed in the tumor tissue of several HLA-A, HLA-B and HLA-C positive AML patients analyzed (see tables 1 to 3). It contains MHC class I and MHC class II peptides. In addition to the tumor associated peptides collected from several GBM tissues, the warehouse may contain an HLA-A*02 and an HLA-A*24 marker peptide. 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, it functions as an important positive control peptide 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 thirdly, it may allow conclusions to be drawn, regarding the status of immunocompetence of the patient population.

HLA class I and II TUMAPs for the warehouse (e.g. in the form of a database or actual storage unit) are identified by using an integrated functional genomics approach combining gene expression analysis, mass spectrometry, and T-cell immunology. 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 peptide selection, AML 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 by microarrays was used to identify genes over-expressed in the malignant tissue (AML) compared with a range of normal organs and tissues
3. Identified HLA ligands were compared to gene expression data. Peptides 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. 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 AML patients.

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 a method according to the present invention as herein and as follows.

The HLA phenotype, transcriptomic and peptidomic data will be gathered from the patient's tumor material and blood samples to identify the most suitable peptides for each patient containing warehouse (database) 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, showed 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 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 germ line 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 may then be tested for immunogenicity as described above for the warehouse (database), 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 methods described above; (b) comparing the peptides identified in a) with a warehouse (database) 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 (database) 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 are selected, the vaccine is manufactured.

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 ~2.5mg/ml per peptide. The mixed solution is then diluted 1:3 with water for injection to achieve a concentration of 0.826mg/ml per peptide in 33% DMSO. The diluted solution is filtered through a 0.22µm sterile filter. The final bulk solution is obtained.

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

The present invention will now be described in the following examples with reference to the accompanying figures that 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.

Brief description of the drawings

Figure 1 shows the HLA surface expression of primary AML samples and healthy donor HSCs. Quantification was performed *ex vivo* using QIFIKIT (Dako). (a) HLA class I (W6/32 mAb) expression of $CD34^+$ AML blasts compared to autologous $CD15^+$ normal monocytes. (b) HLA-DR (L243 mAb) expression of $CD34^+$ AML blasts compared to autologous $CD15^+$ normal monocytes. (c) HLA class I (W6/32 mAb) expression of $CD34^+$ AML blasts (n=5) and $CD34^+CD38^-$ hematopoietic stem cells (n=5) derived from healthy donors. (d) HLA-DR (L243 mAb) expression of $CD34^+$ AML blasts (n=5) and $CD34^+CD38^-$ hematopoietic stem cells (n = 5) derived from healthy donors. * $P<0.05$, *** $P< 0.001$, unpaired *t* test. Abbreviations: UPN, uniform patient number

Figure 2 shows the number of HLA ligand and source protein identifications from primary AML samples. Unique IDs (peptide sequences and corresponding source proteins) identified by LC-MS/MS for HLA class I (W6/32 mAb, n=15) and HLA class II (Tü39 mAb, n=12) in primary AML samples. Only samples fulfilling the threshold of ≥500 (HLA class I) and ≥100 (HLA class II) unique ligand identifications per sample were included in this study. Abbreviations: ID, identification; UPN, uniform patient number

Figure 3 shows the identification of peptide vaccine targets based on the characterization of the HLA class I ligandomes/ source proteomes of AML (n=15), PBMC (n=30) and BMNC (n=5) (a) Overlaps of the HLA class I ligand source proteins of AML, PBMC and BMNC. (b) Comparative profiling of HLA class I ligand source proteins based on the frequency of HLA restricted representation in AML, PBMC and BMNC. Absolute numbers of patients/donors positive for HLA restricted presentation of the respective source protein (x-axis) are indicated on the y-axis. Dashed lines indicate 100% representation for each respective cohort. The box on the left-hand side highlights the subset of source proteins showing AML-exclusive representation with frequencies >20% (LiTAAs: ligandome-derived tumor-associated antigens). (c) Representation analysis of published AML-associated antigens in HLA class I ligandomes. Bars indicate relative representation of respective antigens by HLA class I ligands in AML, PBMC and BMNC. (d) Subset-specific analysis of FLT3-ITD mutated (n=8) versus FLT3-WT (n=7) AML HLA class I ligandomes. Overlap analysis of AML-exclusive source proteins (as defined in (b)) for FLT3-ITD and FLT3-WT AML. (e) Comparative profiling of AML-exclusive HLA class I ligand source proteins based on the frequency of HLA restricted representation in FLT3-ITD and FLT3-WT AML. The box in the middle highlights the subset of shared source proteins, which includes 91.3% of the here defined LiTAAs.

Figure 4 shows the functional characterization of HLA class I AML-LiTAPs. (a) IFN-γ ELISPOT assay of AML patient PBMC after stimulation with 2 different A*03 restricted AML LiTAP (ligandome-derived tumor-associated peptide) pools ($P^I_1$and P^I_2). PHA served as positive control, stimulation with HIV GAG_{18-26} A*03 peptide as negative control. For P^I_1 and P^I_2 a significant IFN-γ production was observed. (b) Intracellular staining for IFN-γ and TNF-α of P^I_1 andP^I_2 stimulated AML patient PBMC (same as in (a)). PMA/Ionomycin served as positive control, HIV GAG_{18-26} A*03 peptide as negative control. (c) Cross-checking IFN-γ

ELISPOT assay of healthy donor PBMC after stimulation with A*03 restricted AML LiTAP pools $P^{I}_{1}$and P^{I}_{2}, revealed no significant IFN-γ production.

Figure 5 shows the identification of additional/synergistic peptide vaccine targets based on the characterization of the AML HLA class II ligandome. (a) Overlap analysis of the HLA class II ligand source proteomes of AML (n=12), PBMC (n=13) and BMNC (n=2). (b) Comparative profiling of HLA class II ligand source proteins based on the frequency of HLA restricted representation in AML, PBMC and BMNC. Absolute numbers of patients/donors positive for HLA restricted presentation of the respective source protein (x-axis) are indicated on the y-axis. Dashed lines indicate 100% representation for each respective cohort. The box on the left-hand side highlights the subset of source proteins showing AML-exclusive representation with frequencies >20%. (c) Overlap analysis of HLA class I and HLA class II AML-exclusive source proteins. (d) Of the 43 shared AML-exclusive source proteins a subset of 3 was identified to contain complete HLA class I ligands embedded in HLA class II peptides. The embedded sequences are depicted in bold. (e) IFN-γ ELISPOT assay of AML patient PBMC after stimulation with different HLA class II AML LiTAPs (P^{II}_{1}, PI^{II}_{2} and PI^{II}_{3}). PHA served as positive control, stimulation with $FLNA_{1669\text{-}1683}$ HLA-DR peptide as negative control. For P^{II}_{1}, PI^{II}_{2} and PI^{II}_{3} a significant increase in IFN-γ production was observed in multiple patients. Abbreviations: UPN, uniform patient number.

Figure 6 shows the results of an experiment in order to evaluate the internal heterogeneity of HLA class I ligandomes in the FLT3-ITD (n=8) versus the FLT3-WT (n=7) subsets. The inventors performed semi-quantitative similarity indexing. To enable comparison of ligandomes of different HLA types, the inventors performed the analysis on the level of HLA ligand source proteins. Semi-quantitative information was derived from analyzing spectral counts (PSMs) of representing HLA ligands. Euclidean distances were analyzed as a measure for sample-pair similarity/dissimilarity, with low values indicating high similarities and high values indicating high dissimilarities. Euclidean distances were calculated for every possible sample pair within each subset utilizing an in-house Python script (Python v3.3.3, Python Software Foundation). In brief, total PSM counts in each sample pair were normalized to the respective higher counting sample. The source protein lists were combined and the absolute values of differences in PSM counts representing the respective source proteins were summed up to yield the Euclidean distance. *** $P< 0.001$, unpaired *t* test.

EXAMPLES

EXAMPLE 1:

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

Tissue samples

Patients' tumor samples were provided by University of Tübingen, Tübingen, Germany. Written informed consents of all patients had been given. The samples were shock-frozen in liquid nitrogen immediately after surgery and stored until isolation of TUMAPs at -80°C. For ligandome analysis, PBMC from AML patients at time of diagnosis or at relapse prior to therapy (>80% AML blast count in blood), as well as PBMC and BMNC of healthy donors were isolated by density gradient centrifugation

Isolation of HLA peptides from tissue samples

HLA class I and II molecules were isolated employing standard immunoaffinity purification as described previously. In brief, snap-frozen cell pellets were lysed in 10 mM CHAPS/PBS (AppliChem, St. Louis, MO, USA/Gibco, Carlsbad, CA, USA) containing 1x protease inhibitor (Complete, Roche, Basel, Switzerland). HLA molecules were single-step purified using the pan-HLA class I specific mAb W6/32 and the pan-HLA class II specific mAb Tü39 respectively, covalently linked to CNBr-activated sepharose (GE Healthcare, Chalfont St Giles, UK). HLA:peptide complexes were eluted by repeated addition of 0.2% trifluoroacetic acid (TFA, Merck, Whitehouse Station, NJ, USA). Elution fractions E1-E8 were pooled and free HLA ligands were isolated by ultrafiltration using centrifugal filter units (Amicon, Millipore, Billerica, MA, USA). HLA ligands were extracted and desalted from the filtrate using ZipTip C18 pipette tips (Millipore). Extracted peptides were eluted in 35 µl of 80% acetonitrile (ACN, Merck)/0.2% TFA, centrifuged to complete dryness and resuspended in 25 µl of 1% ACN/0.05% TFA. Samples were stored at -20 °C until analysis by LC-MS/MS.

Analysis of HLA ligands by LC-MS/MS

Peptide samples were separated by reversed-phase liquid chromatography (nanoUHPLC, UltiMate 3000 RSLCnano, ThermoFisher, Waltham, MA, USA) and subsequently analyzed in an on-line coupled LTQ Orbitrap XL hybrid mass spectrometer (ThermoFisher). Samples were analyzed in 5 technical replicates. Sample volumes of 5 µl (sample shares of 20%) were

injected onto a 75 µm x 2 cm trapping column (Acclaim PepMap RSLC, ThermoFisher) at 4 µl/min for 5.75 min. Peptide separation was subsequently performed at 50°C and a flow rate of 175 nl/min on a 50 µm x 50 cm separation column (Acclaim PepMap RSLC, ThermoFisher) applying a gradient ranging from 2.4 to 32.0% of ACN over the course of 140 min. Eluting peptides were ionized by nanospray ionization and analyzed in the mass spectrometer implementing a top 5 CID (collision induced dissociation) method generating fragment spectra for the 5 most abundant precursor ions in the survey scans. Resolution was set to 60,000. For HLA class I ligands, the mass range was limited to 400-650 m/z with charge states 2 and 3 permitted for fragmentation. For HLA class II, a mass range of 300-1,500 m/z was analyzed with charge states ≥2 allowed for fragmentation.

Presentation profiles of exemplary over-presented peptides are shown in Figure 3.

Amplification of peptide-specific T cells

PBMC from AML patients and healthy volunteers were cultured in RPMI1640 medium (Gibco) supplemented with 10% pooled human serum (PHS, produced in-house), 100 mM β-mercaptoethanol (Roth, Karlsruhe, Germany) and 1% penicillin/streptomycin (GE). For $CD8^+$ T cell stimulation, PBMC were thawed and pulsed with 1 µg/ml per peptide. Peptide-pulsed PBMC (5-6 x 10^6 cells/ml) were cultured at 37°C and 5% CO_2 for 12 days. On day 0 and day 1, 5 ng/ml IL-4 (R&D Systems, Minneapolis, MN, USA) and 5 ng/ml IL-7 (Promokine, Heidelberg, Germany) were added to the culture medium. On days 3, 5, 7 and 9, 2 ng/ml IL-2 (R&D Systems) were added to the culture medium. Peptide-stimulated PBMC were functionally characterized by ELISPOT assays on day 12 and by intracellular cytokine staining on day 13 respectively. For $CD4^+$ T-cell stimulation, culture was performed as described for $CD8^+$ T cells with 2 modifications: pulsing was carried out with 10 µg/ml of HLA class II peptide and no IL-4 and IL-7 was added.

IFN-γ ELISPOT assay

IFN-γ ELISPOT assays were carried out as described previously (Widenmeyer M, Griesemann H, Stevanovic S, Feyerabend S, Klein R, Attig S, et al. Promiscuous survivin peptide induces robust CD4+ T-cell responses in the majority of vaccinated cancer patients. Int J Cancer. 2012 Jul 1;131(1):140-9). In brief, 96-well nitrocellulose plates (Millipore) were coated with 1 mg/ml IFN-γ mAb (Mabtech, Cincinnati, OH, USA) and incubated over night at 4 °C. Plates were blocked with 10% PHS for 2 h at 37 °C. 5 x 10^5 cells/well of pre-

stimulated PBMC were pulsed with 1 µg/ml (HLA class I) or 2.5 µg/ml (HLA class II) peptide and incubated for 24-26 h. Readout was performed according to manufacturer's instructions. Spots were counted using an ImmunoSpot S5 analyzer (CTL, Shaker Heights, OH, USA). T cell responses were considered to be positive when >15 spots/well were counted and the mean spot count per well was at least 3-fold higher than the mean number of spots in the negative control wells (according to the cancer immunoguiding program (CIP) guidelines).

Intracellular IFN-γ and TNF-α staining

The frequency and functionality of peptide-specific $CD8^+$ T cells was analyzed by intracellular IFN-γ and TNF-α staining. PBMC were pulsed with 1 µg/ml of individual peptide and incubated in the presence of 10 µg/ml Brefeldin A (Sigma, St. Louis, MO, USA) and 10 µg/ml GolgiStop (BD) for 6-8 h. Cells were labeled using Cytofix/Cytoperm (BD), CD8-PECy7 (Beckman Coulter, Fullerton, CA, USA), CD4-APC (BD Bioscience), TNF-α-PE (Beckman Coulter) and IFN-γ-FITC (BD). Samples were analyzed on a FACS Canto II.

Quantification of HLA surface expression

To allow for comparison with healthy monocytes, quantification of HLA surface expression was performed in additional patient samples containing $CD15^-$ AML blasts and at least 5% normal $CD15^+$ monocytes as defined by immunophenotyping. HLA surface expression was analyzed using the QIFIKIT® quantitative flow cytometric assay kit (Dako, Glostrup, Denmark) according to manufacturer's instructions. In brief, triplicates of each sample were stained with the pan-HLA class I specific monoclonal antibody (mAb) W6/32, HLA-DR specific mAb L243 (both produced in house) or IgG isotype control (BioLegend, San Diego, CA, USA) respectively. Secondary staining with FITC-conjugated rabbit-anti-mouse $F(ab')_2$ fragments (Dako) was subsequently carried out on PBMC, BMNC as well as QIFIKIT® quantification beads. Surface marker staining was carried out with directly labeled CD34 (BD, Franklin Lakes, NJ, USA), CD15 (BD), CD45 (BD) and CD38 (BD). 7AAD (BioLegend) was added as viability marker immediately prior to flow cytometric analysis on a LSR Fortessa cell analyzer (BD).

Results

Primary AML samples display no loss or down-regulation of HLA expression compared to autologous benign leukocytes

The HLA expression levels on AML blasts compared to corresponding benign leukocytes were determined. To this end HLA surface levels were quantified by flow cytometry in a panel of 5 patients with $CD15^-$ AML and 5 healthy BMNC donors. AML blasts were gated as $CD34^+$, $CD45^{med}$ viable cells, and their HLA expression was compared to autologous $CD15^+$normal granulocytes and monocytes. HLA levels were found to be heterogeneous with total HLA class I molecule counts ranging from 45,189-261,647 molecules/cell on AML blasts and 75,344-239,496 molecules/cell on $CD15^+$ cells. Patient individual analysis of HLA surface expression in triplicates revealed slight, albeit significant overexpression in 3/5 patients (unpaired *t* test, $P \leq 0.001$). HLA-DR expression ranged from 1,476-45,150 molecules/cell on AML blasts and 0-3,252 on $CD15^+$ cells and was significantly higher on AML blasts in all analyzed patients ($P \leq 0.001$). For reference, HLA surface molecule counts on hematopoietic stem cells (HSC, $CD34^+CD38^-$) of 5 healthy BMNC donors were analyzed. Comprehensive statistical analysis of HLA surface expression on AML compared to normal monocytes revealed no significant differences in mean HLA class I and II expression. Mean HLA class I count on normal HSC (248,587±35,351 molecules/cell) was found to be significantly higher than that on AML blasts (116,445±37,855 molecules/cell, $P=0.034$, Fig. 1c). Mean HLA class II count on normal HSC (38,373±5,159 molecules/cell) showed no significantly elevated level compared to AML blasts (17,103±7,604 molecules/cell, $P=0.053$).

LC-MS/MS identifies a vast array of naturally presented HLA class I and II ligands

Mapping the HLA class I ligandomes of 15 AML patients (Table 1) a total of 13,238 different peptides representing 6,104 source proteins was identified. The numbers of identified (cancer) unique peptides per patient ranged from 563-2,733 (mean 1,299 peptides). In the healthy cohort (30 PBMC donors, 5 BMNC donors), a total of 17,940 unique peptides were identified (17,322 peptides/7,207 source proteins on PBMC; 1,738 peptides/1,384 source proteins on BMNC, supplementary). Analysis of HLA class II ligandomes in 12 AML patients yielded a total of 2,816 unique peptides (range 104-753 peptides/patient, mean 332 peptides) representing 885 source proteins. The HLA class II healthy control cohort (13 PBMC, 2 BMNC donors) yielded 2,202 different peptides (2,046 peptides/756 source proteins on PBMC, 317 peptides/164 source proteins on BMNC). No correlation of analyzed cell numbers and number of peptide identifications was found neither for HLA class I (Spearman $r=0.27$, $P=0.33$), nor for HLA class II ($r=0.31$, $P=0.33$).

Comparative profiling of HLA class I ligandomes reveals a multitude of AML-associated antigens

To identify novel targets for peptide vaccination in AML, the HLA ligand source proteins of the AML, PBMC and BMNC cohorts were comparatively mapped. Overlap analysis of HLA source proteins revealed 1,435 proteins (23.6% of the mapped AML source proteome) to be exclusively represented in the HLA ligandomes of AML patients. AML was found to share 75.5% (4,588 proteins) of its HLA source proteins with PBMC and 19.3% (1,173 proteins) with BMNC. HLA ligand source proteins of BMNC showed 89.9% (1,173 proteins) overlap with the source proteome of PBMC. Out of this vast array of potential targets we aimed to select the most relevant and broadly applicable candidates for off-the-shelf vaccine design. Accordingly, we defined AML-exclusivity and high frequency of representation in AML ligandomes as paramount criteria for antigen selection on our platform. Ranking of HLA ligand source proteins according to these criteria identified a subset of 132 proteins (2.2% of the AML source proteome) exclusively represented in ≥20% of AML ligandomes. Within these LiTAAs (ligandome-derived tumor-associated antigens) defined by these two criteria, we identified as highest ranking the FAS associated factor 1 (FAF1), which was detected in 8/15 (53.3%) of patient ligandomes and was represented by 6 different HLA ligands (AEQFRLEQI (SEQ ID NO: 1) (B*44), FTAEFSSRY (SEQ ID NO: 2) (A*03), HHDESVLTNVF (SEQ ID NO: 3) (B*38:01), REQDEAYRL (SEQ ID NO: 4) (B*44:25), RPVMPSRQI (SEQ ID NO: 5) (B*07), VQREYNLNF (SEQ ID NO: 6) (B*15). An overview of the top 15 LiTAAs which showed representation in ≥33% of AML ligandomes is shown in Table 2. In summary, the top 132 most frequent LiTAAs alone provide a panel of 341 different naturally presented HLA ligands (LiTAPs, ligandome-derived tumor-associated peptides) of more than 25 different HLA restrictions, suited for the development of broadly applicable AML-specific peptide vaccines. In addition, the further 1,389 AML-exclusive source proteins with representation frequencies <20% represented by 1,727 different HLA ligands may serve as repositories for more individualized vaccine design approaches.

Identification of naturally presented HLA class I ligands derived from established AML-associated antigens

A secondary data mining approach focused on the identification and ranking of established AML-associated antigens (as summarized in Anguille S, Van Tendeloo VF, Berneman ZN. Leukemia-associated antigens and their relevance to the immunotherapy of acute myeloid

leukemia. Leukemia. 2012 Oct;26(10):2186-96) in the dataset of naturally presented HLA ligands. 122 different HLA ligands representing 29 of these published antigens were identified. Strikingly, it was found >80% (24/29) of these antigens also to be represented on benign PBMC and/or BMNC and thus not to be AML-specific.

AML-exclusivity with regard to HLA presentation was found for FLT3 (SELKMMTQL, B*40) (SEQ ID NO: 338), PASD1 (LLGHLPAEI, C*01:02) (SEQ ID NO: 447), HOXA9 (DAADELSVGRY, A*26:01) (SEQ ID NO: 437), AURKA (REVEIQSHL, B*49:01) (SEQ ID NO: 400) and CCNA1 (LEADPFLKY, B*18:01 (SEQ ID NO: 402); EPPAVLLL, B*51:01 (SEQ ID NO: 401)). For myeloperoxidase (MPO), a total of 19 different HLA ligands were identified and detected representation in 6/15 (40%) of AML and 0/30 PBMC ligandomes. However, analysis of normal BMNC revealed representation in 3/5 (60%) of ligandomes underlining the relevance of employing both, PBMC and BMNC for target identification. In summary, our analysis revealed that a large proportion of established AML-associated antigens do not meet the requirement of tumor-exclusive HLA-restricted representation.

Subset-specific analysis of FLT3-ITD mutated versus FLT3-WT AML HLA class I ligandomes identifies shared LiTAAs in spite of significant ligandome dissimilarity

To assess the applicability of our novel targets across different subsets of AML, the representation of LiTAAs in FMS-like tyrosine kinase 3 internal tandem duplication (FLT3-ITD, n=8) and FLT3 wild type (FLT3-WT, n=7) patient subsets was characterized. Similarity indexing of HLA class I ligandomes revealed that the FLT3-WT subset displayed significantly lower internal heterogeneity (mean 916.2±70.6, n=21) than the FLT3-TID subset (mean 1687.0±156.5, n=21, $P< 0.0001$, Figure 6). Overlap analysis of AML-exclusive HLA source proteins (FLT3-WT: 748 proteins, FLT3-ITD: 926 proteins) revealed overlaps of 32.0% (FLT3-WT/FLT3-ITD) and 25.6% (FLT3-ITD/FLT3-WT) respectively (Fig. 3d). Of note, 42/46 (91.3%) of the high ranking LiTAAs were found to be represented in both subsets (Fig. 3e). The three HLA ligand source proteins SKP1 (5/8), C16orf13 (5/8) and ERLIN1 (4/8), which were identified exclusively in the FLT3-ITD subset, reached representation frequencies of ≥50%. The FLT3-WT specific LiTAA MUL1 was represented in 4/7 (57.1%) of FLT3-WT ligandomes. Taken together, these data support the devised strategy of cohort-comprising analysis of HLA ligandomes for target selection while pointing out a small fraction of highly frequent, subset-specific targets.

Functional characterization of LiTAPs reveals AML-associated immunoreactivity

In order to evaluate the immunogenicity and specificity of our HLA-A*03 LiTAPs, the inventors next performed 12-day recall IFN-γ ELISPOT assays. PBMC obtained from 6 AML patients as well as 8 healthy individuals were stimulated with different pools (P^I_1 and P^I_2) of top ranking HLA-A*03 LiTAPs. Significant IFN-γ secretion was observed with both employed peptide pools in 2/6 AML samples (Fig. 4a). In order to confirm these findings, intracellular cytokine staining and flow cytometry for IFN-γ and TNF-α was carried out using 12-day pre-stimulated PBMC (Fig. 4b). it was confirmed P^I_1 and P^I_2 -specific $CD8^+$ T cell responses functionally characterized by IFN-γ (P^I_1: 1.6%, P^I_2: 1.7% of $CD8^+$ T cells) and TNF-α (P^I_1: 2.6%, P^I_2: 2.4% of $CD8^+$ T cells) secretion. Cross-checking ELISPOT assays using A*03 positive healthy donor PBMC stimulated with P^I_1 and P^I_2 showed no significant secretion of IFN-γ (0/8, Fig. 4c). These initial characterizations demonstrate the here defined LiTAPs to potentially function as AML-specific T cell epitopes.

HLA class II ligandome analysis provides additional targets and pinpoints potentially synergistic embedded ligands

Overlap analysis of HLA class II source proteomes identified 396 proteins (44.7%) represented by 1,079 different HLA ligands to be exclusively represented in the HLA ligandome of AML. AML was found to share 53.3% (472 proteins) and 15.1% (134 proteins) of its source proteome with PBMC and BMNC, respectively. BMNC showed 88.2% (127 proteins) source proteome overlap with PBMC. Performing comparative HLA source proteome profiling as described above for HLA class I, the inventors were able to identify 36 LiTAAs (represented by 152 different HLA class II ligands) with representation frequencies ≥20%. The highest ranking class II LiTAA (A1BG) was identified on 6/12 (50%) patients represented by 5 different ligands. In order to identify LiTAAs presented in both, the HLA class I and class II ligandomes, the inventors subsequently compared the respective AML-exclusive source proteomes. This revealed a panel of only 43 shared source proteins (3.0%/10.4% of the HLA class I/HLA class II source proteome, respectively). Mapping of the respective class I against class II ligands identified 3 HLA class II peptides containing complete embedded HLA class I ligands.

In order to functionally characterize the HLA class II LiTAPs, the inventors performed 12-day recall IFN-γ ELISPOT assays. For 3/7 of the top ranking LiTAPs significant secretion of

IFN-γ was detected in AML patients. T cell responses were detected for the peptide P^{II}_1 ($CLSTN1_{836-852}$) in 4/15 (26.7%), for P^{II}_2 ($LAB5A_{123-138}$) in 3/15 (20.0%) and for P^{II}_3 ($MBL2_{191-206}$) in 2/15 (13.3%) of AML patients. Fig. 5e shows an example of the frequency of specific T cells for peptides P^{II}_1, P^{II}_2 and P^{II}_3 in an AML patient. Cross-checking ELISPOT assays using healthy donor PBMC stimulated with P^{II}_1, P^{II}_2 and P^{II}_3 showed no significant secretion of IFN-γ (0/8). Thus, the here defined AML-specific HLA class II epitopes have the potential to complement a HLA class I peptide vaccine.

EXAMPLE 2

Expression profiling of genes encoding the peptides of the invention

Not all peptides identified AML as being presented on the surface of tumor cells by MHC molecules are suitable for immunotherapy, because the majority of these peptides are derived from normal cellular proteins expressed by many cell types. Only few of these peptides are tumor-associated and likely able to induce T cells with a high specificity of recognition for the tumor from which they were derived. In order to identify such peptides and minimize the risk for autoimmunity induced by vaccination the inventors focused on those peptides that are derived from proteins that are over-expressed on tumor cells compared to the majority of normal tissues.

The ideal peptide will be derived from a protein that is unique to the tumor and not present in any other tissue. To identify peptides that are derived from genes with an expression profile similar to the ideal one the identified peptides were assigned to the proteins and genes, respectively, from which they were derived and expression profiles of these genes were generated.

RNA sources and preparation

Surgically removed tissue specimens were provided by University of Heidelberg, Heidelberg, Germany (see Example 1) after written informed consent had been obtained from each patient. Tumor tissue specimens were snap-frozen in liquid nitrogen 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 AML are shown in Fig. 3.

EXAMPLE 3

***In vitro* immunogenicity for AML 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 9 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.

***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 Transfusion Medicine Tuebingen, Germany, after informed consent.

Isolated CD8+ lymphocytes or PBMCs were incubated until use in T-cell medium (TCM) 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 (Promo Cell, 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.

All pMHC complexes used for aAPC loading and cytometric readout were derived from UV-induced MHC ligand exchange (Rodenko B, et al. Generation of peptide-MHC class I complexes through UV-mediated ligand exchange. Nat Protoc. 2006;1(3):1120-32) with minor modifications. In order to determine the amount of pMHC monomer obtained by exchange, the inventors performed streptavidin-based sandwich ELISAs according to Rodenko B, et al., 2006..

The purified co-stimulatory mouse IgG2a anti human CD28 Ab 9.3 (Jung G, et al. Induction of cytotoxicity in resting human T lymphocytes bound to tumor cells by antibody heteroconjugates. Proc Natl Acad Sci USA. 1987 Jul;84(13):4611-5) 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 (SEQ ID NO: 606) from modified Melan-A/MART-1) and A*0201/DDX5-001 (YLLPAIVHI from DDX5 (SEQ ID NO: 607)), 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 3-4 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 3-4 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 Parallel detection of antigen-specific T cell responses by combinatorial encoding of MHC multimers. Nat Protoc. 2012 Apr 12;7(5):891-902.) 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 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 AML peptides**

For tested HLA class I peptides, *in vitro* immunogenicity can be demonstrated by generation of peptide specific T-cell lines. Exemplary flow cytometry results after TUMAP-specific multimer staining for two peptides of the invention are shown in figure 4 together with corresponding negative controls.

EXAMPLE 4

Synthesis of peptides

All peptides were synthesized using standard and well-established solid phase peptide synthesis using the Fmoc-strategy. After purification by preparative RP-HPLC, ion-exchange procedure was performed to incorporate physiological compatible counter ions (for example trifluoro-acetate, acetate, ammonium or chloride).

Identity and purity of each individual peptide have been determined by mass spectrometry and analytical RP-HPLC. After ion-exchange procedure the peptides were obtained as white to off-white lyophilizates in purities of 90% to 99.7%.

All TUMAPs are preferably administered as trifluoro-acetate salts or acetate salts, other suitable salt-forms are also possible. For the measurements of example 3, trifluoro-acetate salts of the peptides were used.

EXAMPLE 5

MHC Binding Assays – MHC class I

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 exchange 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. et al., Nat Protoc. 1 (2006): 1120-1132).

96 well MAXISorp plates (NUNC) were coated over night with 2ug/ml streptavidin in PBS at room temperature, washed 4x and blocked for 1 h 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 1 h at 37°C, washed four times, incubated with 2 µg/ml HRP conjugated anti-β2m for 1 h at 37°C, washed again and detected with TMB solution that is stopped with NH_2SO_4. Absorption was measured at 450 nm. 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.

MHC class I binding scores for the peptides as tested were; <20 % = +; 20 % - 49 % = ++; 50 % - 75 %= +++; >= 75 % = ++++

Seq ID NO.	sequence	Peptide exchange
54	AVIEAEKIAQV	++++
266	KLQEQLAQL	++++
36	SLLYKVPYV	++++
251	VLGGKAFLEHL	++++

EXAMPLE 6

MHC Binding Assays – MHC class II

HLA class II proteins are divided into three major isotypes HLA-DR, -DP, DQ which are encoded by numerous haplotypes. The combination of various α- and β- chains increases the diversity of the HLA class II proteins found in an arbitrary population. Thus, the selected HLA class II TUMAPs have to bind to several different HLA-DR molecules (i.e. show promiscuous binding ability) in order to be able to contribute to an effective T-cell response in a significant percentage of patients.

The promiscuous binding of GALNT7-001 and ERGIC1-001 to various HLA-DR haplotypes and the stability of the formed complexes was assessed in an *in vitro* binding assay.

The peptides as tested were:

Sequence ID No	Peptide ID	Sequence	length
597	GALNT7-001	GNQLFRINEANQLMQ	15
604	ERGIC1-001	FEGQFSINKVPGNFHVS	17

The seven investigated HLA-DR haplotypes are selected according to their frequencies in HLA-A*02- and HLA-A*24- positive North American populations. Data are derived from the analysis of 1.35 million HLA-typed volunteers registered in the National Marrow Donor Program (Mori M, Beatty PG, Graves M, Boucher KM, Milford EL (1997). HLA gene and haplotype frequencies in the North American population: the National Marrow Donor Program Donor Registry. Transplantation 64, 1017-1027). The analyzed population was subdivided in the following ethnic groups: Caucasian Americans (N=997,193), African Americans (N=110,057), Asian Americans (N=81,139), Latin Americans (N=100,128), and Native Americans (N=19,203).

The MHC-peptide binding assay as used determined the ability of each candidate peptide to bind to the selected HLA class II haplotype and stabilize the HLA-peptide complex. For this, the candidate peptides are assembled *in vitro* with a particular HLA class II protein.

The binding capacity of a candidate peptide to a particular HLA molecule is compared to a reference peptide with known very strong binding properties (positive control) for each HLA haplotype. Experimental standard errors derive from binding experiments of triplicated positive controls.

Besides the affinity of a peptide to a particular HLA molecule, the enduring stability of the formed HLA-peptide complex is crucial for the occurrence of an immune response. For this reason the presence of the formed HLA-peptide complex is measured after its incubation for 24 h at 37°C. The stability of the formed MHC-peptide complex is calculated as a ratio of the binding scores at 24 h and the binding scores which are received right after the refolding (accordingly at time 0) in percent.

The analysis of GALNT7-001 and ERGIC1-001 in REVEAL® MHC-peptide binding assay showed that both peptides bind to various HLA haplotypes. Both peptides were shown to

form a complex with five of seven investigated HLA haplotypes (HLA-DR1, -DR2, -DR4, -DR5, and –DR7)**Fehler! Verweisquelle konnte nicht gefunden werden.**. The detected binding scores were in the range of 0.02 to about 78.5% compared to the positive control and clearly above scores of non-binding peptides. GALNT7-001 showed promiscuous strong binding (i.e. with the binding score over 15%, the value which based on experience of the service provider is considered to reflect the strong binding) to four of seven investigated HLA haplotypes (HLA-DR1, -DR2, -DR4, -DR7). For ERGIC-001, the binding scores of two investigated HLA haplotypes were about or over 15% (HLA-DR4, -DR5). Both peptides did not bind to HLA-DR3 and HLA-DR6.

The stability analysis of the formed HLA- GALNT7-001 and HLA- ERGIC1-001 complexes revealed that 4 of 7 investigated HLA-peptide complexes were stable after 24 h at 37°C (HLA-DR1, -DR4, -DR5, -DR7).

The analysis of binding capacity of GALNT7-001 and ERGIC1-001 to the most frequent HLA-DR haplotypes using the *in vitro* binding assay revealed the promiscuous binding ability for both peptides. Both peptides formed complexes with 5 of 7 investigated HLA-DR haplotypes. Thus, the analysis showed considerable binding capacity of GALNT7-001 to at least 4 and of ERGIC1-001 to at least 2 HLA-DR haplotypes. Furthermore, 4 of 5 formed HLA-peptide complexes for each investigated peptide were stable for at least 24 h. Thus, the analysis showed that both peptides should be capable to contribute to an effective T-cell response in a significant percentage of patients.

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Claims

1. A peptide of between 9 and 100 amino acids in length, comprising an amino acid sequence that is at least 80% identical to a sequence selected from SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605, or a pharmaceutically acceptable salt thereof.

2. The peptide according to claim 1, wherein said peptide has the ability to bind to a human major histocompatibility complex (MHC) class-I molecule and/or a human major histocompatibility complex (MHC) class-II molecule.

3. The peptide according to claim 1, wherein said peptide is between 9 and 30 amino acids in length.

4. The peptide according to claim 1, comprising an N-terminal and/or C-terminal amino acid extension of no more than 10 amino acids in length.

5. The peptide according to any one of claims 1 to 3, selected from the group consisting of:
(a) a peptide consisting of an amino acid sequence that is to at least 80% identical to SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605;
(b) the peptide of (a) having an N-terminal extension of the core sequence not more than 10 amino acids in length; and
(c) the peptide of (a) or (b), having a C-terminal extension not more than 10 amino acids in length.

6. The peptide according to any of claims 1 to 5, wherein said amino acid sequence is to at least 90% identical to SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605.

7. The peptide according to any of claims 1 to 6, wherein said amino acid sequence is at least 95% identical to SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605.

8. The peptide according to any of claims 1 to 6, wherein said amino acid sequence comprises any of SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605.

9. The peptide according to claim 1 or 2, wherein said amino acid sequence consists of any of SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605.

10. The peptide according to any of Claims 1 to 9, wherein said peptide is modified and/or includes non-peptide bonds.

11. A T-cell receptor that is reactive with an HLA ligand having at least 80% identity to an amino acid sequence selected from the group consisting SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447, and SEQ ID NO: 448 to SEQ ID NO: 605.

12. The T-cell receptor according to claim 11, wherein said amino acid sequence is to least 90%, or to at least 95% identical to SEQ ID NO: 1 to SEQ ID NO: 325 or SEQ ID NO: 448 to SEQ ID NO: 605.

13. The T-cell receptor according to claim 11 or 12, wherein said amino acid sequence comprises any of SEQ ID NO: 1 to SEQ ID NO: 325 or SEQ ID NO: 448 to SEQ ID NO: 605.

14. The T-cell receptor according to any of claims 11 to 13, wherein said amino acid sequence consists of any of SEQ ID NO: 1 to SEQ ID NO: 325, SEQ ID NO: 326 to SEQ ID NO: 447 or SEQ ID NO: 448 to SEQ ID NO: 605.

15. A fusion protein, comprising
(a) an amino acid sequence that is to at least 80% identical to SEQ ID NO: 1 to SEQ ID NO: 325 or SEQ ID NO: 448 to SEQ ID NO: 605; and
(b) N-terminal amino acids 1-80 of HLA-DR antigen-associated invariant chain (Ii).

16. The fusion protein according to claim 15, wherein said amino acid sequence of (a) is at least 90%, preferably at least 95% identical to SEQ ID NO: 1 to SEQ ID NO: 325 or SEQ ID NO: 448 to SEQ ID NO: 605.

17. The fusion protein according to claim 16, wherein said amino acid sequence of (a) comprises SEQ ID NO: 1 to SEQ ID NO: 325 or SEQ ID NO: 448 to SEQ ID NO: 605.

18. A nucleic acid, encoding for:
(a) the peptide according to any of Claims 1 to 10;
(b) the T cell receptor according to any claims 11 to 14; or
(c) the fusion protein according to claims 15 to 17.

19. The nucleic acid according to Claim 18, which is DNA, cDNA, PNA, RNA, or combinations thereof.

20. An expression vector comprising a nucleic acid according to Claim 18 or 19.

21. A host cell comprising the nucleic acid according to Claim 18 or 19, or the expression vector according to Claim 20.

22. The host cell according to Claim 21 that is an antigen presenting cell, for example a dendritic cell.

23. A method for producing the peptide according to any one of Claims 1 to 10, the T cell receptor according to any of Claims 12 to 14, or the fusion protein according to any of Claims 15 to 17, said method comprising culturing the host cell according to Claim 21, and isolating said peptide, said T cell receptor, or said fusion protein from said host cell and/or its culture medium.

24. An *in vitro* method for producing activated cytotoxic T lymphocytes (CTL), the method comprising contacting *in vitro* a CTL 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 CTL in an antigen specific manner, wherein said antigen is said peptide according to any one of claims 1 to 10.

25. The method according to Claim 24, wherein said 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.

26. The method according to Claim 25, wherein said antigen-presenting cell comprises an expression vector capable of expressing said peptide according to any one of claims 1 to 9.

27. An activated cytotoxic T lymphocyte (CTL), produced by the method according to any one of Claims 24 to 26.

28. A method of killing target cancer cells in a patient, the method comprising administering to said patient an effective number of cytotoxic T lymphocytes (CTL) according to Claim 27.

29. Use of the peptide according to any one of Claims 1 to 10, the T cell receptor according to any of Claims 12 to 14, the fusion protein according to any of Claims 15 to 17, the nucleic acid according to Claim 18 or 19, the expression vector according to claim 20, the host cell according to Claims 22 or 23, or the activated cytotoxic T lymphocyte according to claim 27 as a medicament, or in the manufacture of a medicament.

30. The use according to claim 29, wherein said medicament is a vaccine.

31. The use according to Claim 29 or 30, wherein said medicament is active against cancer.

32. The use according to any of Claims 29 to 31, wherein said cancer is acute myeloid leukemia and/or chronic lymphatic leukemia.

33. 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 10, the T cell receptor according to any of Claims 12 to 14, the fusion protein according to any of Claims 15 to 17, the nucleic acid according to Claim 18 or 19, the expression vector according to claim 20, the host cell according to Claims 22 or 23, and the activated cytotoxic T lymphocyte according to claim 27, and
a pharmaceutically acceptable carrier.

34. A pharmaceutical composition comprising at least one active ingredient selected from the group consisting of

a) a peptide having the ability to bind to a human major histocompatibility complex (MHC) class-I molecule and/or a human major histocompatibility complex (MHC) class-II molecule, and wherein said peptide is derived from a protein selected from the group consisting of FAF1, PLXND1, GMNN, CPQ, ATP5L, ITGA5, SKP1, CHD1L, TGFBRAP1, NGLY1, APLP2, KIF2C, ELP3, DGKZ, MYCH2, SLC31A2, ERLIN1, SERPINB2, ABHD2, GAA, OPRL1, WDR45B, TUFM, MFAP1, ZNF543, STK4, ZKSCAN8, FNDC3B, TMEM164, THOC7, KLF2, TMEM126B, UFD1L, MUL1, VCPIP1, KIF20B, CSF3R, NOC4L, EMILIN2, SHANK3, UCK2, PHPT1, KIF15, SLC12A6, DOLK, EEF2K, PIK3R2, TMEM194A, CCS, ZNF264, LYRM1, NBN, TIPRL TIP41, RPS6KA4, RCBTB2, PAK4, ERCC1, DMD, UNG, CPA3, AZU1, ATP2B4, MARK3, HLA-DMA, NDUFS1, S100A11, HAL, PRIM1, RENBP, CCNG1, ZNF131, HRSP12, EIF6, TMPRSS3, UBE2G2, NOP14, TFCP2, TARBP1, TTL12, HLX, CBX2, ZNF638, C3AR1, TAF9, FSCN1, ZNF805, CLEC12A, SLX4IP, RLTPR, RNF19B, DDX46, LRRC8D, C16orf62, GOLGA7, RHOT1, BBS1, CEP76, GANC, ATP8B4, PPIL4, HPT1, CHTF18, DGCR8, ANKS1A, TOP1MT, PHACTR3, CCDC115, SORCS2, ACCS, ACBD6, ORAI3, SIKE1, C9orf156, EDEM2, NUP85, PANK2, SPATC1L, IKZF4, DHX33, METTL7A, QTRTD1, TMBIM4, RAVER2, SDAD1, UCKL1, STMN3, CHIC2, ODF2L, PRR12, FARSA, CTDP1, A1BG, CORO1A, RPS5, C19orf10, PLIN3, CLSTN1, HSP90B1, B4GALT1, SPN, METAP1, HSPG2, QSOX1, MANBA, CREG1, LDHA, CP, COL1A1, CRP, APRT, MBL2, IFI30, LBP, RAB5A, ICAM3, MAN1A1, RBMX, PBX2, YARS, TPM4, RBL36A, GANAB, HSP90B2P, LAIR1, GALNT7, ARRDC1, and ERGIC1;

b) a T-cell receptor reactive with a peptide according to (a);

c) a fusion protein comprising a peptide according to (a), and the N-terminal amino acids 1 to 80 of the HLA-DR antigen-associated invariant chain (Ii);

d) a nucleic acid encoding for any of a) to c) or an expression vector comprising said nucleic acid,

e) a host cell comprising the expression vector of d, and

f) an activated cytotoxic T-lymphocyte (CTL), obtained by a method comprising contacting *in vitro* CTL with a peptide according to a) expressed on the surface of a suitable antigen-presenting cell for a period of time sufficient to activate said CTL in an antigen specific manner; and

a pharmaceutically acceptable carrier.

35. A method for killing target cells in a patient, said method comprising administering to the patient an effective amount of the pharmaceutical composition according to Claim 34.

36. A method for identifying a tumor-associated peptide as suitable for inclusion in a peptide-based vaccine, said method comprising:
(a) eluting and identifying naturally presented HLA ligands from at least one primary tumor sample and from at least one corresponding normal tissue sample,
(b) generating a ligandome for said at least tumor sample and for said at least normal tissue sample based on said HLA ligands as identified; and
(c) selecting at least one HLA ligand as suitable for inclusion that a) is derived from an antigen exclusively presented by cells of said at least one tumor sample and b) exhibits a high frequency of presentation in said ligandome for said at least one tumor sample.

37. The method according to Claim 36, wherein said frequency of presentation is selected from at least 5%, at least 10%, and at least 20%.

38. The method according to Claims 36 or 37, wherein a plurality of samples is used, and a plurality of ligandomes is generated.

39. A method for identifying a tumor-associated peptide as suitable for inclusion in a personalized peptide-based vaccine, wherein a tumor sample from an individual patient is used in step (a).

40. The method according to any of Claims 36 to 39, wherein said selecting in step (c) comprises comparing said ligandome with a database of peptides that have been prescreened for immunogenicity and overpresentation in tumors as compared to corresponding non tumor tissue.

41. The method according to any of Claims 36 to 40, wherein said identifying comprises eluting bound peptides from MHC molecules from said tumor sample, and sequencing of said eluted peptides.

42. The method according to any of Claims 36 to 41, wherein said at least normal tissue sample corresponds in tissue type to the tumor sample from the patient.

43. The method according to any of Claims 39 to 42, wherein said peptides included in the database are identified by a method comprising:
1) identifying HLA ligands from said tumor material by mass spectrometry;
2) identifying genes that are over-expressed in the tumor material by comparison with a range of normal tissues using genome-wide messenger ribonucleic acid (mRNA) expression analysis using microarrays;
3) comparing the HLA ligands as identified with the gene expression data;
4) selecting peptides encoded by genes that are specifically expressed or over-expressed as detected in step b);
5) confirming the relevance of the over-expression at the mRNA level by redetection of selected HLA ligands from step c) on tumor tissue in contrast to normal tissues; and
6) performing *in vitro* immunogenicity assays using human T cells from the patient or healthy donors in order to assess, whether an induction of *in vivo* T-cell responses by the peptides as selected can be achieved.

44. The method according to any of Claims 40 to 43, wherein the immunogenicity of the peptides included in the database is determined by a method selected from the group of *in vitro* immunogenicity assays, patient immune-monitoring for individual HLA binding, MHC multimer staining, ELISPOT assays, and intracellular cytokine staining.

45. The method according to any of Claims 40 to 44, wherein the database comprises the peptides SEQ ID NO: 1 to SEQ ID NO: 605.

46. The method according to any of Claims 40 to 43, further comprising the step of identifying at least one peptide having at least one mutation that is unique for said tumor sample compared with normal corresponding tissue from said individual patient, and optionally, selecting said peptide for inclusion into the vaccine.

47. The method according to Claim 46, wherein said at least one mutation is identified by whole genome sequencing.

48. The method according to any of Claims 36 to 47, further comprising the step of producing a peptide-based vaccine comprising at least one tumor-associated peptide as selected according to (c), wherein said peptide-based vaccine is preferably personalized.