

CLAIMS:

1. Use of a homocitrullinated T cell epitope for the manufacture of a medicament for treating cancer, wherein the epitope has (i) a predicted binding score to MHC class II or MHC class I of <30 using the online IEDB prediction program (<http://www.iedb.org/>) and (ii) at least 5 consecutive amino acids that form a spiral conformational structure, and stimulates an immune response against the cancer.
2. Use of the epitope of claim 1, which is from a cytoplasmic protein.
3. Use of the epitope of claim 1 or claim 2, which comprises, consists essentially of, or consists of one or more of the following amino acid sequences, wherein one or more of the lysine (K) residues is replaced with homocitrulline:

NYIDKVRFLEQQNKILLAE	(Vimentin 116-135),
FKNTRTNEKVELQELNDRFA	(Vimentin 96-115)
TNEKVELQELNDRFANYIDKVR	(Vimentin 101-122)
KVRFLEQQNKLLAE	(Vimentin 120-134)
DVRQQYESVAAKNLQEAE	(Vimentin 271-288)
EAEWYKSKFADLSEAANRN	(Vimentin 286-305)
FSLADAINTEFKNTRTNEKVELQ	(Vimentin 86-108)
KMALDIEIATYRKLLGEE	(Vimentin 390-408)
IGGVILFHETLYQKADDGRP	(Aldolase 74-93),
KDGADFAKWRCVLKIGEH	(Aldolase 140-157)
HACTQKFSHEEIAMATVTA	(Aldolase 238-256)
DLKRCQYVTEKVLAAVYKA	(Aldolase 198-216)
AAQEEYVKRALANSLACQGK	(Aldolase 323-342)
KVLAAYKALSDHHIYLEG	(Aldolase 208-226)
YVTEKVLAAVYKALSD	(Aldolase 204-219 Hcit)
VLAAYKAL	(Aldolase 209-217Hcit)
KFASFIDKVRFLEQQNKMLE	(Cytokeratin 8 101-120)
LEQQNKMLETKWSLLQQQKT	(Cytokeratin 8 112-131)
KMLETKWSL	(Cytokeratin 8 117-125)
EINKRTEMENEFVLIKKDVDE	(Cytokeratin 8 182-202)
LREYQELMNVLALDIEI	(Cytokeratin 8 371-388)
KLALDIEIATYRKLLGEE	(Cytokeratin 8 381-399)
ETKWSLLQQQKTARSNMDNMF	(Cytokeratin 8 120-140)
EQIKSLNNKFASFIDKVRFL	(Cytokeratin 8 93-112)
ENEFVLIKKDVDEAYMNKV	(Cytokeratin 8 190-208)
GKHGDDLRRRTKTEISEM	(Cytokeratin 8 294-310)

RQLREYQELMNVKLALAI	(Cytokeratin 8 369-388)
EIEGLKGQRASLEAAIADA	(Cytokeratin 8 320-338)
EQRGELAIKDANAKLSELEA	(Cytokeratin 8 339-358)
NDPSVQQDIKFLPFKVVEKKT	(BiP 104-124)
EISAMVLTKMKETAEA	(BiP 144-159)
GEDFDQRMVMEHFILYKKKTG	(BiP 255-275)
QKLRRVEKAKRALSSQHQAR	(BiP 286-306)
EDFSETLTRAKFEELNMDLFR	(BiP 316-336)
EELNMDLFRSTMKPVQKVL	(BiP 328-346)
RIPKIQQLVKEFFNGKEPSRG	(BiP 367-387)
TVTIKVYEGERPLTKDNHLLG	(BiP 460-480)
RNELESYAYSLKNQIGDK	(BiP 562-579)
KKELEEIVQPIISKLYGSAG	(BiP 620-639)
PLRPQNYLFGCELKADK	(NPM 11-27)
EGSPIKVTLATLKMSVQPTVSL	(NPM 68-89)
EEEDVKLLSISGKRSAPGGGS	(NPM 129-149)
SKGQESFKKQEKTPKTPKG	(NPM 222-240)
GGSLPKVEAKFINYVKNCFR	(NPM 258-277)
AKFINYVKNCFRMTDQEAIQDL	(NPM 266-287)
MSILKIHAREIFDSRG	(Alpha enolase 1-16)
NDKTRYMGKGVSKAVEHI	(Alpha enolase 52-69)
TENKSKFGANAILGVSLAVCKA	(Alpha enolase 100-121)
GSHAGNKLAMQEFMILPVGAA	(Alpha enolase 156-176)
REAMRIGAEVYHNLKNVIK	(Alpha enolase 179-197)
NVIKEKYGKDATNVGDEGG	(Alpha enolase 194-212)
DVAASEFFRSGKYDLDFKSP	(Alpha enolase 245-264)
PDQLADLYKSFIKDYPVVS	(Alpha enolase 273-291)
WGAWQKFTASAGIQVVG	(Alpha enolase 301-317)
NKSCNCLLLKVNQIGSVTE	(Alpha enolase 333-352)
RSERLAKYNQLLRIEEEELGS	(Alpha enolase 400-419)
GSKAKFAGRNFRNPLAK	(Alpha enolase 418-434)
EPSQMLKHAVVNLINYQD	(Beta-Catenin 127-144)
EKLLWTTSRVLKVLSVCSSNK	(Beta-Catenin 334-354)
TLHNLLHQEGAKMAVRL	(Beta-Catenin 258-275)
AKMAVRLAGGLQKMVALLNK	(Beta-Catenin 269-288)
KTNVKFLAITTDCLQILAYG	(Beta-Catenin 288-307)
TYEKLLWTTSRVLKVLSV	(Beta-Catenin 332-349)
TSRVLKVLSVCSSNKPAIV	(Beta-Catenin 340-358)
YGLPVVVKLLHPPSHWPL	(Beta-Catenin 489-506)
HWPLIKATVGLIRNLALCPA	(Beta-Catenin 503-522)

IQRIQVAAGVLCALQDK	(Beta-Catenin 607-625)
GVATYAAAVLFRMSDKP	(Beta-Catenin 650-667)
IDLKDKYKNIGAKLVQDVAN	(HSP60 84-103)
TVLARSIAKEGFEEKISKGAN	(HSP60 117-136)
GEALSTLVNLRLKVGLQVVA	(HSP60 280-299)
TTSEYEKEKLNRLAKLS	(HSP60 381-398)
GIIDPTVKVVRTALLDAAGVA	(HSP60 517-536).

4. Use of the epitope of claim 3, which comprises, consists essentially of, or consists of one or more of the following amino acid sequences:

NYID-Hcit-VRFLEQQN-Hcit-ILLAEL	(Vimentin 116-135 Hcit),
F-Hcit-NTRTNE-Hcit-VELQELNDRFA	(Vimentin 96-115 Hcit)
TNE-Hcit-VELQELNDRFANYID-Hcit-VR	(Vimentin 101-122 Hcit)
KVRFLEQQN-Hcit-LLAE	(Vimentin 120-134 Hcit)
DVRQQYESVAA-Hcit-NLQEA	(Vimentin 271-288 Hcit)
EAEWY-Hcit-S-Hcit-FADLSEAANRN	(Vimentin 286-305 Hcit)
FSLADAINTEF-Hcit-NTRTNE-Hcit-VELQ	(Vimentin 86-108 Hcit)
Hcit-MALDIEIATYR-Hcit-LLEGEE	(Vimentin 390-408 Hcit)
IGGVILFHETLYQ-Hcit-ADDGRP	(Aldolase 74-93 Hcit),
Hcit-DGADFA-Hcit-WRCVL-Hcit-IGEH	(Aldolase 140-157 Hcit)
HACTQ-Hcit-FSHEEIAMATVTA	(Aldolase 238-256 Hcit)
DL-Hcit-RCQYVTE-Hcit-VLAAVY-Hcit-A	(Aldolase 198-216 Hcit)
AAQEEYV-Hcit-RALANSLACQG-Hcit	(Aldolase 323-342 Hcit)
Hcit-VLAAVY-Hcit-ALSDHHIYLEG	(Aldolase 208-226 Hcit)
YVTE-Hcit-VLAAVY-Hcit-ALSD	(Aldolase 204-219 Hcit)
VLAAVY-Hcit-AL	(Aldolase 209-217)
KFASFID-Hcit-VRFLEQQN-Hcit-MLE	(Cytokeratin 8 101-120 Hcit)
LEQQN-Hcit-MLET-Hcit-WSLLQQQ-Hcit-T	(Cytokeratin 8 112-131 Hcit)
Hcit-MLET-Hcit-WSL	(Cytokeratin 8 117-125)
EIN-Hcit-RTMENEFVLI-Hcit-Hcit-DVDE	(Cytokeratin 8 182-202 Hcit)
LREYQELMNH-Hcit-LALDIEI	(Cytokeratin 8 371-388 Hcit)
Hcit-LALDIEIATYR-Hcit-LLEGEE	(Cytokeratin 8 381-399 Hcit)
ET-Hcit-WSLLQQQ-Hcit-TARSNMDNMF	(Cytokeratin 8 120-140 Hcit)
EQL-Hcit-SLNN-Hcit-FASFID-Hcit-VRFL	(Cytokeratin 8 93-112 Hcit)
ENEFVLI-Hcit-Hcit-DVDEAYMN-Hcit-V	(Cytokeratin 8 190-208 Hcit)
G-Hcit-HGDDLRRRT-Hcit-TEISEM	(Cytokeratin 8 294-310 Hcit)
RQLREYQELMNH-Hcit-LALEI	(Cytokeratin 8 369-388 Hcit)
EIEGL-Hcit-GQRASLEAAIADA	(Cytokeratin 8 320-338 Hcit)
EQRGELAI-Hcit-DANA-Hcit-LSELEA	(Cytokeratin 8 339-358 Hcit)

NDPSVQQDI-Hcit-FLPF-Hcit-VVE-Hcit-Hcit-T	(BiP 104-124 Hcit)
EISAMVLT-Hcit-M-Hcit-ETAEA	(BiP 144-159 Hcit)
GEDFDQRVMEHFI-Hcit-LY-Hcit-Hcit-Hcit-TG	(BiP 255-275 Hcit)
QKLRRVEVEKAKRALSSQHQAR	(BiP 286-306 Hcit)
EDFSETLTRA-Hcit-FEELNMDLFR	(BiP 316-336 Hcit)
EELNMDLFRSTM-Hcit-PVQ-Hcit-VL	(BiP 328-346 Hcit)
RIP-Hcit-IQQLV-Hcit-EFFNG-Hcit-EPSRG	(BiP 367-387 Hcit)
TVTI-Hcit-VYEGERPLT-Hcit-DNHLLG	(BiP 460-480 Hcit)
RNELESYAYSL-Hcit-NQIGD-Hcit-	(BiP 562-579 Hcit)
Hcit-Hcit-ELEEIVQPIIS-Hcit-LYGSAG	(BiP 620-639 Hcit)
PLRPQNYLFGCEL-Hcit-AD-Hcit-	(NPM 11-27 Hcit)
EGSPIKVTLATLKMSVQPTVSL	(NPM 68-89 Hcit)
EEEDV-Hcit-LLSISG-Hcit-RSAPGGGS	(NPM 129-149 Hcit)
S-Hcit-GQESF-Hcit-Hcit-QE-Hcit-TP-Hcit-TP-Hcit-G	(NPM 222-240 Hcit)
GGSLP-Hcit-VEA-Hcit-FINYV-Hcit-NCFR	(NPM 258-277 Hcit)
A-Hcit-FINYV-Hcit-NCFRMTDQEAIQDL	(NPM 266-287 Hcit)
MSIL-Hcit-IHAREIFDSRG	(Alpha enolase 1-16 Hcit)
ND-Hcit-TRYMG-Hcit-GVS-Hcit-AVEHI	(Alpha enolase 52-69 Hcit)
TEN-Hcit-S-Hcit-FGANAILGVSLAVC-Hcit-A	(Alpha enolase 100-121 Hcit)
GSHAGN-Hcit-LAMQEFMILPVGAA	(Alpha enolase 156-176 Hcit)
REAMRIGAEVYHNL-Hcit-NVI-Hcit-	(Alpha enolase 179-197 Hcit)
NVI-Hcit-E-Hcit-YG-Hcit-DATNVGDEGG	(Alpha enolase 194-212 Hcit)
DVAASEFFRSG-Hcit-YDLDF-Hcit-SP	(Alpha enolase 245-264 Hcit)
PDQLADLY-Hcit-SFI-Hcit-DYPVVS	(Alpha enolase 273-291 Hcit)
WGAWQ-Hcit-FTASAGIQVVG	(Alpha enolase 301-317 Hcit)
N-Hcit-SCNCLLL-Hcit-VNQIGSVTE	(Alpha enolase 333-352 Hcit)
RSERLA-Hcit-YNQLLRIEEEELGS	(Alpha enolase 400-419 Hcit)
GS-Hcit-A-Hcit-FAGRNFNPLA-Hcit-	(Alpha enolase 418-434 Hcit)
EPSQML-Hcit-HAVVNLINYQD	(Beta-Catenin 127-144 Hcit)
E-Hcit-LLWTTSRVL-Hcit-VLSVCSSN-Hcit	(Beta-Catenin 334-354 Hcit)
TLHNLLHQEGA-Hcit-MAVRL	(Beta-Catenin 258-275 Hcit)
A-Hcit-MAVRLAGGLQ-Hcit-MVALLN-Hcit	(Beta-Catenin 269-288 Hcit)
-Hcit-TNV-Hcit-FLAITTDCLQILAYG	(Beta-Catenin 288-307 Hcit)
TYE-Hcit-LLWTTSRVL-Hcit-VLSV	(Beta-Catenin 332-349 Hcit)
TSRVL-Hcit-VLSVCSSN-Hcit-PAIV	(Beta-Catenin 340-358 Hcit)
YGLPVVV-Hcit-LLHPPSHWPL	(Beta-Catenin 489-506 Hcit)
HWPLI-Hcit-ATVGLIRNLALCPA	(Beta-Catenin 503-522 Hcit)
IENIQRVAAGVLCELAQD-Hcit-	(Beta-Catenin 607-625 Hcit)
GVATYAAAVLFRMSD-Hcit-P	(Beta-Catenin 650-667 Hcit)
IDLKDKYKNIGAKLVQDVAN	(HSP60 84-103 Hcit)

TVLARSIA-Hcit-EGFE-Hcit-IS-Hcit-GAN	(HSP60 117-136 Hcit)
GEALSTLVLNRL-Hcit-VGLQVVA	(HSP60 280-299 Hcit)
TTSEYE-Hcit-E-Hcit-LNERLA-Hcit-LS	(HSP60 381-398 Hcit)
GIIDPTV-Hcit-VRTALLDAAGVA	(HSP60 517-536 Hcit)

wherein "Hcit" represents homocitrulline.

5. Use of a complex of an antigen comprising a homocitrullinated T cell epitope of any preceding claim and an MHC molecule for the manufacture of a medicament for treating cancer, optionally wherein the MHC molecule is MHC class II, optionally selected from HLA-DR4, DR1 and DP4, or MHC class I, optionally HLA-A2.

6. The use of a homocitrullinated T cell epitope as defined in any one of claims 1-4 and/or a complex as defined in claim 5, formulated as a pharmaceutical composition with a pharmaceutically acceptable carrier.

7. A method of identifying a binding moiety that binds a complex as claimed in claim 5, the method comprising contacting a candidate binding moiety with the complex and determining whether the candidate binding moiety binds the complex.