

Compound for increasing efficacy of viral vectors

The field of present invention relates to compounds for increasing efficiency of non-pathogenic viral vectors, such as used in vaccines or in gene therapy.

Wild-type adeno-associated viruses (AAV) are typically non-pathogenic and only capable of replicating in the presence of helper viruses. One big advantage of this class of viral gene therapy vectors is that they maintain long term, sustained gene expression in the host cell, making them ideal for therapeutic gene delivery. Numerous natural subtypes have been isolated showing serological differences and unique tropism *in vivo* and *in vitro*. AAV vectors are well suited for targeting different cell types. Importantly, they typically do not integrate into the genome of the host cell (Colella et al, 2017).

To date, many different serotypes and variants are well studied including AAV2, AAV5 or AAV8. New gene therapy compositions such e.g. Voretigene neparvove (Luxturna®; based on AAV2) or onasemnogene abeparvovec-xioi (Zolgensma®; based on AAV9) were successfully tested and approved, reflecting the dynamic progress in this field. Li (Li et al, 2020) provides an extensive review about AAV vectors. New concepts of improving gene expression, tissue specificity, genome stability, combined with capsid engineering can be found in Domenger (Domenger et al, 2019).

Much effort was invested into engineering improved AAV capsid variants to change their biological properties including tropism and safety. However, susceptibility to antibody neutralization by preexisting antibodies of the patient remains a major challenge, see e.g. Costa Verdera et al, 2020.

Kruzik et al, 2019, investigated the prevalence of neutralizing antibodies against various AAV serotypes in different patient cohorts. It was found, for example, that neutralizing antibodies against AAV2 were most abundant at levels up to 74% of the population. Antibodies against AAV8 were found for example in up to 63%. Natural antibodies against AAV5 (up to 59%) and AAV1 (27%) were less abundant. Interestingly, most people tested exhibited antibodies against more than one

serotype. A comprehensive review was published by Ronzitti et al, 2020.

The consequences were for example that a hemophilia B gene therapy trial with an AAV vector turned out to be problematic because of pre-existing neutralizing antibodies against AAV in patients that did not respond to the therapy. Manno et al., 2006, showed for example that even low titers of neutralizing antibodies could block the effectivity of gene therapy by blocking virus function by opsonization.

Tseng et al, 2014, reviewed epitopes of anti-AAV antibodies found with human serum and monoclonal antibodies. The interaction between preexisting or induced anti-AAV antibodies and virus capsid proteins has mainly been investigated by mutation analysis, by peptide insertions or by peptide scanning and several approaches were tested to develop AAV variants that improve tropism and that escape humoral immune response. These strategies include directed evolution, structure-based approaches, the engineering of chimeric AAV vectors (for example Bennett et al, 2020) or by displaying peptides of the surface of AAV vectors (Börner et al, 2020). Other proposed strategies to avoid the negative impact of neutralizing antibodies include modifying the route of administration (Mimuro et al, 2013), the discovery of new serotypes and variants (Salganik et al, 2015), the reduction of immunogenicity by PEGylation or polymer technologies (Balakrishnan et al, 2019) or the use of capsid decoys intra- (Mingozzi et al, 2013) or extracorporeally (Bertin et al, 2020). Mechanisms of immunogenicity and their clinical impact were extensively reviewed by Monahan et al, 2021.

US 2013/0259885 A1 relates to immunomodulation with peptides containing epitopes recognized by CD4+ natural killer T cells. This is taught to be suitable for increasing efficiency of gene therapy. WO 2005/023848 A2 discloses administration of peptides to patients for increasing efficiency of an adenoviral vector.

WO 2019/018439 A1 relates to the removal of AAV-neutralizing antibodies from a subject by apheresis prior to administering recombinant AAV comprising a heterologous polynucleotide to the subject. Bertin et al, 2020, discloses a similar apheresis approach. Further along similar lines, WO 00/20041 A2 relates to

methods of enhancing the effectiveness of therapeutic viral agents by extracorporeal removal of anti-AdV-antibodies with affinity columns based on AdV subunits (i.e. selective apheresis).

However, each of these approaches have disadvantages on their own.

Neutralizing antibodies are not only problematic with respect to AAV-based gene therapy or vaccine vectors. To date, Adenovirus (AdV) serotype 5 (Ad5), as the prototypic adenoviral vector, was tested in more than 400 clinical trials. Remarkably, up to 80% of the population carries neutralizing antibodies against Ad5 which has a negative impact on transgene expression or on the efficacy of vaccines against pathogens or cancer.

Importantly, neutralizing antibodies have recently turned out to be problematic in a clinical trial with a vaccine against SARS-CoV-2: Zhu (Zhu et al, 2020) concluded that pre-existing Ad5 antibodies might have hampered the immune response against the SARS-CoV-2 vaccine. It was further concluded that there was also a negative impact on the duration of the immune response elicited by the vaccine because of pre-existing neutralizing antibodies against the viral vaccine vector.

Neutralizing antibodies and epitopes against all types of AdV and other viral vectors for vaccination and gene therapy were previously described e.g. in Tian et al, 2018; Wang et al, 2019; Fausther-Bovendo et al, 2014; and Mok et al, 2020). As with AAV vectors, much effort was made to circumvent pre-existing anti vector immunity by engineering and fine mapping of epitopes of adenoviral vectors (Roberts et al, 2006).

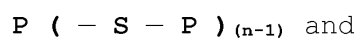
Since such strategies are cumbersome and expensive, new approaches are needed to address the problem of viral vector neutralization.

It is thus an object of the present invention to provide compounds and methods which inhibit viral vector neutralization. Thereby, efficiency of non-pathogenic viral vectors (such as used in vaccines or in gene therapy) is typically increased.

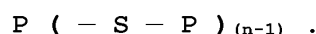
The present invention provides a compound comprising

- a biopolymer scaffold and at least

- a first peptide n-mer of the general formula:



- a second peptide n-mer of the general formula:



Independently for each occurrence, P is a peptide with a sequence length of 6-13 amino acids, and S is a non-peptide spacer. Independently for each of the peptide n-mers, n is an integer of at least 1, preferably of at least 2, more preferably of at least 3, especially of at least 4. Each of the peptide n-mers is bound to the biopolymer scaffold, preferably via a linker each. Further, independently for each occurrence, P has an amino-acid sequence comprising a sequence fragment with a length of at least six, preferably at least seven, more preferably at least eight, especially at least 9 (or 10, 11, 12 or 13) amino acids of a capsid protein sequence of a (non-pathogenic) viral vector (such as AAV or AdV), in particular of an AdV hexon protein sequence, an AdV fiber protein sequence, an AdV penton protein sequence, an AdV IIIa protein sequence, an AdV VI protein sequence, an AdV VIII protein sequence or an AdV IX protein sequence or of any one of the capsid protein sequences identified in Fig. 10 and Fig. 11 or of any one of the capsid protein sequences listed in Cearley et al., 2008. Optionally at most three, preferably at most two, most preferably at least one amino acid of the sequence fragment is independently substituted by any other amino acid.

Preferably, at least one occurrence of P is P_a and/or at least one occurrence of P is P_b . P_a is a defined peptide (i.e. a peptide of defined sequence) with a sequence length of 6-13 amino acids, preferably 7-11 amino acids, more preferably 7-9 amino acids. P_b is a defined peptide (i.e. a peptide of defined sequence) with a sequence length of 6-13 amino acids, preferably 7-11 amino acids, more preferably 7-9 amino acids.

The present invention also provides a compound comprising

- a biopolymer scaffold and at least
- a first peptide n-mer which is a peptide dimer of the formula $P_a - S - P_a$ or $P_a - S - P_b$, wherein P_a is a defined peptide (i.e. a peptide of defined sequence) with a sequence

length of 6-13 amino acids, preferably 7-11 amino acids, more preferably 7-9 amino acids, P_b is a defined peptide (i.e. a peptide of defined sequence) with a sequence length of 6-13 amino acids, preferably 7-11 amino acids, more preferably 7-9 amino acids, and S is a non-peptide spacer, wherein the first peptide n-mer is bound to the biopolymer scaffold, preferably via a linker. P_a has an amino-acid sequence comprising a sequence fragment with a length of at least six, preferably at least seven, more preferably at least eight, especially at least 9 (or 10, 11, 12 or 13) amino acids of a capsid protein sequence of a (non-pathogenic) viral vector, in particular of an AdV hexon protein sequence, an AdV fiber protein sequence, an AdV penton protein sequence, an AdV IIIa protein sequence, an AdV VI protein sequence, an AdV VIII protein sequence or an AdV IX protein sequence or of any one of the capsid protein sequences identified in Fig. 10 and Fig. 11 or of any one of the capsid protein sequences listed in Cearley et al., 2008. Optionally at most three, preferably at most two, most preferably at least one amino acid of the sequence fragment is independently substituted by any other amino acid.

This compound preferably comprises a second peptide n-mer which is a peptide dimer of the formula $P_b - S - P_b$ or $P_a - S - P_b$, wherein the second peptide n-mer is bound to the biopolymer scaffold, preferably via a linker. P_b has an amino-acid sequence comprising a sequence fragment with a length of at least six, preferably at least seven, more preferably at least eight, especially at least 9 (or 10, 11, 12 or 13) amino acids of a capsid protein sequence of a (non-pathogenic) viral vector, in particular of an AdV hexon protein sequence, an AdV fiber protein sequence, an AdV penton protein sequence, an AdV IIIa protein sequence, an AdV VI protein sequence, an AdV VIII protein sequence or an AdV IX protein sequence or of any one of the capsid protein sequences identified in Fig. 10 and Fig. 11 or of any one of the capsid protein sequences listed in Cearley et al., 2008. Optionally at most three, preferably at most two, most preferably at least one amino acid of the sequence fragment is independently substituted by any other amino acid.

Furthermore, the present invention provides a pharmaceutical composition comprising any one of the aforementioned compounds

and at least one pharmaceutically acceptable excipient. Preferably, this pharmaceutical composition is for use in therapy, in particular in combination with a vaccination or gene therapy.

In another aspect, the present invention provides a method of sequestering (or depleting) one or more antibodies present in an individual, comprising obtaining a pharmaceutical composition as defined herein, the composition being non-immunogenic in the individual, where the one or more antibodies present in the individual are specific for at least one occurrence of P, or for peptide P_a and/or peptide P_b; and administering the pharmaceutical composition to the individual.

In yet another aspect, the present invention relates to a pharmaceutical composition (i.e. a vaccine or gene therapy composition), comprising the compound defined herein and further comprising the viral vector and optionally at least one pharmaceutically acceptable excipient. The viral vector typically comprises a peptide fragment with a sequence length of at least six, preferably at least seven, more preferably at least eight, especially at least 9 amino acids. The sequence of at least one occurrence of peptide P, or peptide P_a and/or peptide P_b, of the compound is at least 70% identical, preferably at least 75% identical, more preferably at least 80% identical, yet more preferably at least 85% identical, even more preferably at least 90% identical, yet even more preferably at least 95% identical, especially completely identical to the sequence of said peptide fragment. Preferably, this pharmaceutical composition is for use in vaccination or gene therapy and/or for use in prevention or inhibition of an undesirable immune reaction against the viral vector.

In even yet another aspect, the present invention provides a method of inhibiting a (undesirable) - especially humoral - immune reaction to a treatment with a vaccine or gene therapy composition in an individual in need of treatment with the vaccine or gene therapy composition or of inhibiting neutralization of a viral vector in a vaccine or gene therapy composition for an individual in need of treatment with the vaccine or gene therapy composition, comprising obtaining said vaccine or gene therapy composition; wherein the compound of the

vaccine or gene therapy composition is non-immunogenic in the individual, and administering the vaccine or gene therapy composition to the individual.

In the course of the present invention, a compound was developed which is able to deplete (or sequester) antibodies against viral vectors in vivo and is therefore suitable to increase the efficiency of viral vectors.

Further, it was surprisingly found that the approach which is also used in the invention is particularly effective in reducing titres of undesired antibodies in an individual. In particular, the compound achieved especially good results with regard to selectivity, duration of titre reduction and/or level of titre reduction in an in vivo model (see experimental examples).

The detailed description given below relates to all of the above aspects of the invention unless explicitly excluded.

In general, antibodies are essential components of the humoral immune system, offering protection from infections by foreign organisms including bacteria, viruses, fungi or parasites. However, under certain circumstances - including autoimmune diseases, organ transplantation, blood transfusion or upon administration of biomolecular drugs or gene delivery vectors - antibodies can target the patient's own body (or the foreign tissue or cells or the biomolecular drug or vector just administered), thereby turning into harmful or disease-causing entities. Certain antibodies can also interfere with probes for diagnostic imaging. In the following, such antibodies are generally referred to as "undesired antibodies" or "undesirable antibodies".

With few exceptions, selective removal of undesired antibodies has not reached clinical practice. It is presently restricted to very few indications: One of the known techniques for selective antibody removal (although not widely established) is immunoapheresis. In contrast to immunoapheresis (which removes immunoglobulin), selective immunoapheresis involves the filtration of plasma through an extracorporeal, selective antibody-adsorber cartridge that will deplete the undesired antibody based on selective binding to its antigen binding site.

Selective immunoapheresis has for instance been used for removing anti-A or anti-B antibodies from the blood prior to ABO-incompatible transplantation or with respect to indications in transfusion medicine (Teschner et al). Selective apheresis was also experimentally applied in other indications, such as neuroimmunological indications (Tetala et al) or myasthenia gravis (Lazaridis et al), but is not yet established in the clinical routine. One reason that selective immunoapheresis is only hesitantly applied is the fact that it is a cost intensive and cumbersome intervention procedure that requires specialized medical care. Moreover, it is not known in the prior art how to deplete undesired antibodies rapidly and efficiently.

Unrelated to apheresis, Morimoto et al. discloses dextran as a generally applicable multivalent scaffold for improving immunoglobulin-binding affinities of peptide and peptidomimetic ligands such as the FLAG peptide. WO 2011/130324 A1 relates to compounds for prevention of cell injury. EP 3 059 244 A1 relates to a C-met protein agonist.

As mentioned, apheresis is applied extracorporeally. By contrast, also several approaches to deplete undesirable antibodies intracorporeally were proposed in the prior art, mostly in connection with certain autoimmune diseases involving autoantibodies or anti-drug antibodies:

Lorentz et al discloses a technique whereby erythrocytes are charged in situ with a tolerogenic payload driving the deletion of antigen-specific T cells. This is supposed to ultimately lead to reduction of the undesired humoral response against a model antigen. A similar approach is proposed in Pishesha et al. In this approach, erythrocytes are loaded ex vivo with a peptide-antigen construct that is covalently bound to the surface and reinjected into the animal model for general immunotolerance induction.

WO 92/13558 A1 relates to conjugates of stable nonimmunogenic polymers and analogs of immunogens that possess the specific B cell binding ability of the immunogen and which, when introduced into individuals, induce humoral anergy to the immunogen. Accordingly, these conjugates are disclosed to be useful for treating antibody-mediated pathologies that are

caused by foreign- or self-immunogens. In this connection, see also EP 0 498 658 A2.

Taddeo et al discloses selectively depleting antibody producing plasma cells using anti-CD138 antibody derivatives fused to an ovalbumin model antigen thereby inducing receptor crosslinking and cell suicide in vitro selectively in those cells that express the antibody against the model antigen.

Apitope International NV (Belgium) is presently developing soluble tolerogenic T-cell epitope peptides which may lead to expression of low levels of co-stimulatory molecules from antigen presenting cells inducing tolerance, thereby suppressing antibody response (see e.g. Jansson et al). These products are currently under preclinical and early clinical evaluation, e.g. in multiple sclerosis, Grave's disease, intermediate uveitis, and other autoimmune conditions as well as Factor VIII intolerance.

Similarly, Selecta Biosciences, Inc. (USA) is currently pursuing strategies of tolerance induction by so-called Synthetic Vaccine Particles (SVPs). SVP-Rapamycin is supposed to induce tolerance by preventing undesired antibody production via selectively inducing regulatory T cells (see Mazor et al).

Mingozzi et al discloses decoy adeno-associated virus (AAV) capsids that adsorb antibodies but cannot enter a target cell.

WO 2015/136027 A1 discloses carbohydrate ligands presenting the minimal Human Natural Killer-1 (HNK-1) epitope that bind to anti-MAG (myelin-associated glycoprotein) IgM antibodies, and their use in diagnosis as well as for the treatment of anti-MAG neuropathy. WO 2017/046172 A1 discloses further carbohydrate ligands and moieties, respectively, mimicking glycoepitopes comprised by glycosphingolipids of the nervous system which are bound by anti-glycan antibodies associated with neurological diseases. The document further relates to the use of these carbohydrate ligands/moieties in diagnosis as well as for the treatment of neurological diseases associated with anti-glycan antibodies.

US 2004/0258683 A1 discloses methods for treating systemic lupus erythematosus (SLE) including renal SLE and methods of reducing risk of renal flare in individuals with SLE, and

methods of monitoring such treatment. One disclosed method of treating SLE including renal SLE and reducing risk of renal flare in an individual with SLE involves the administration of an effective amount of an agent for reducing the level of anti-double-stranded DNA (dsDNA) antibody, such as a dsDNA epitope as in the form of an epitope-presenting carrier or an epitope-presenting valency platform molecule, to the individual.

US patent no. 5,637,454 relates to assays and treatments of autoimmune diseases. Agents used for treatment might include peptides homologous to the identified antigenic, molecular mimicry sequences. It is disclosed that these peptides could be delivered to a patient in order to decrease the amount of circulating antibody with a particular specificity.

US 2007/0026396 A1 relates to peptides directed against antibodies, which cause cold-intolerance, and the use thereof. It is taught that by using the disclosed peptides, in vivo or ex vivo neutralization of undesired autoantibodies is possible. A comparable approach is disclosed in WO 1992/014150 A1 or in WO 1998/030586 A2.

WO 2018/102668 A1 discloses a fusion protein for selective degradation of disease-causing or otherwise undesired antibodies. The fusion protein (termed "Seldeg") includes a targeting component that specifically binds to a cell surface receptor or other cell surface molecule at near-neutral pH, and an antigen component fused directly or indirectly to the targeting component. Also disclosed is a method of depleting a target antigen-specific antibody from a patient by administering to the patient a Seldeg having an antigen component configured to specifically bind the target antigen-specific antibody.

WO 2015/181393 A1 concerns peptides grafted into sunflower-trypsin-inhibitor- (SFTI-) and cyclotide-based scaffolds. These peptides are disclosed to be effective in autoimmune disease, for instance citrullinated fibrinogen sequences that are grafted into the SFTI scaffold have been shown to block autoantibodies in rheumatoid arthritis and inhibit inflammation and pain. These scaffolds are disclosed to be non-immunogenic.

Erlandsson et al discloses in vivo clearing of idiotypic antibodies with anti-idiotypic antibodies and their derivatives.

Berlin Cures Holding AG (Germany) has proposed an intravenous broad spectrum neutralizer DNA aptamer (see e.g. WO 2016/020377 A1 and WO 2012/000889 A1) for the treatment of dilated cardiomyopathy and other GPCR-autoantibody related diseases that in high dosage is supposed to block autoantibodies by competitive binding to the antigen binding regions of autoantibodies. In general, aptamers did not yet achieve a breakthrough and are still in a preliminary stage of clinical development. The major concerns are still biostability and bioavailability, constraints such as nuclease sensitivity, toxicity, small size and renal clearance. A particular problem with respect to their use as selective antibody antagonists are their propensity to stimulate the innate immune response.

WO 00/33887 A2 discloses methods for reducing circulating levels of antibodies, particularly disease-associated antibodies. The methods entail administering effective amounts of epitope-presenting carriers to an individual. In addition, ex vivo methods for reducing circulating levels of antibodies are disclosed which employ epitope-presenting carriers.

US 6,022,544 A relates to a method for reducing an undesired antibody response in a mammal by administering to the mammal a non-immunogenic construct which is free of high molecular weight immunostimulatory molecules. The construct is disclosed to contain at least two copies of a B cell membrane immunoglobulin receptor epitope bound to a pharmaceutically acceptable non-immunogenic carrier.

However, the approaches to deplete undesirable antibodies intracorporeally disclosed in the prior art have many shortcomings. In particular, neither of them has been approved for regular clinical use.

The biopolymer scaffold used in the present invention may be a mammalian biopolymer such as a human biopolymer, a non-human primate biopolymer, a sheep biopolymer, a pig biopolymer, a dog biopolymer or a rodent biopolymer. In particular the biopolymer scaffold is a protein, especially a (non-modified or non-modified with respect to its amino-acid sequence) plasma protein. Preferably, the biopolymer scaffold is a mammalian protein such as a human protein, a non-human primate protein, a

sheep protein, a pig protein, a dog protein or a rodent protein. Typically, the biopolymer scaffold is a non-immunogenic and/or non-toxic protein that preferably circulates in the plasma of healthy (human) individuals and can e.g. be efficiently scavenged or recycled by scavenging receptors, such as e.g. present on myeloid cells or on liver sinusoidal endothelial cells (reviewed by Sorensen et al 2015).

According to a particular preference, the biopolymer scaffold is a (preferably human) globulin, preferably selected from the group consisting of immunoglobulins, alpha1-globulins, alpha2-globulins and beta-globulins, in particular immunoglobulin G, haptoglobin and transferrin. Haptoglobin in particular has several advantageous properties, as shown in Examples 5-9, especially an advantageous safety profile.

The biopolymer scaffold may also be (preferably human) albumin, hemopexin, alpha-1-antitrypsin, C1 esterase inhibitor, lactoferrin or non-immunogenic (i.e. non-immunogenic in the individual to be treated) fragments of all of the aforementioned proteins, including the globulins.

In another preference, the biopolymer scaffold is an anti-CD163 antibody (i.e. an antibody specific for a CD163 protein) or CD163-binding fragment thereof.

Human CD163 (Cluster of Differentiation 163) is a 130 kDa membrane glycoprotein (formerly called M130) and prototypic class I scavenger receptor with an extracellular portion consisting of nine scavenger receptor cysteine-rich (SRCR) domains that are responsible for ligand binding. CD163 is an endocytic receptor present on macrophages and monocytes, it removes hemoglobin/haptoglobin complexes from the blood but it also plays a role in anti-inflammatory processes and wound healing. Highest expression levels of CD163 are found on tissue macrophages (e.g. Kupffer cells in the liver) and on certain macrophages in spleen and bone marrow. Because of its tissue- and cell-specific expression and entirely unrelated to depletion of undesirable antibodies, CD163 is regarded as a macrophage target for drug delivery of e.g. immunotoxins, liposomes or other therapeutic compound classes (Skytte et al., 2020).

Monoclonal anti-CD163 antibodies and the SRCR domains they are binding are for instance disclosed in Madsen et al., 2004, in particular Fig. 7. Further anti-CD163 antibodies and fragments thereof are e.g. disclosed in WO 2002/032941 A2 or WO 2011/039510 A2. At least two structurally different binding sites for ligands were mapped by using domain-specific antibodies such as e.g. monoclonal antibody (mAb) EDhu1 (see Madsen et al., 2004). This antibody binds to the third SRCR of CD163 and competes with hemoglobin/haptoglobin binding to CD163. Numerous other antibodies against different domains of CD163 were previously described in the literature, including Mac2-158, KiM8, GHI/61 and RM3/1, targeting SRCR domains 1, 3, 7 and 9, respectively. In addition, conserved bacterial binding sites were mapped and it was demonstrated that certain antibodies were able to inhibit either bacterial binding but not hemoglobin/haptoglobin complex binding and vice versa. This points to different modes of binding and ligand interactions of CD163 (Fabriek et al., 2009; see also citations therein).

Entirely unrelated to depletion of undesirable antibodies, CD163 was proposed as a target for cell-specific drug delivery because of its physiological properties. Tumor-associated macrophages represent one of the main targets where the potential benefit of CD163-targeting is currently explored. Remarkably, numerous tumors and malignancies were shown to correlate with CD163 expression levels, supporting the use of this target for tumor therapy. Other proposed applications include CD163 targeting by anti-drug conjugates (ADCs) in chronic inflammation and neuroinflammation (reviewed in Skytte et al., 2020). Therefore, CD163-targeting by ADCs notably with dexamethasone or stealth liposome conjugates represents therapeutic principle which is currently studied (Graversen et al., 2012; Etzerodt et al., 2012).

In that context, there are references indicating that anti-CD163 antibodies can be rapidly internalized by endocytosis when applied *in vivo*. This was shown for example for monoclonal antibody (mAb) Ed-2 (Dijkstra et al., 1985; Graversen et al., 2012) or for mAb Mac2-158 / KN2/NRY (Granfeldt et al., 2013). Based on those observations in combination with observations made in the course of the present invention (see in particular

example section), anti-CD163 antibodies and CD163-binding turned out to be highly suitable biopolymer scaffolds for depletion/sequestration of undesirable antibodies.

Numerous anti-CD163 antibodies and CD163-binding fragments thereof are known in the art (see e.g. above). These are suitable to be used as a biopolymer scaffold for the present invention. For instance, any anti-CD163 antibody or fragment thereof mentioned herein or in WO 2011/039510 A2 (which is included herein by reference) may be used as a biopolymer scaffold in the invention. Preferably, the biopolymer scaffold of the inventive compound is antibody Mac2-48, Mac2-158, 5C6-FAT, BerMac3, or E10B10 as disclosed in WO 2011/039510, in particular humanised Mac2-48 or Mac2-158 as disclosed in WO 2011/039510 A2.

In a preferred embodiment, the anti-CD163 antibody or CD163-binding fragment thereof comprises a heavy-chain variable (V_H) region comprising one or more complementarity-determining region (CDR) sequences selected from the group consisting of SEQ ID NOs: 11-13 of WO 2011/039510 A2.

In addition, or alternatively thereto, in a preferred embodiment, the anti-CD163 antibody or CD163-binding fragment thereof comprises a light-chain variable (V_L) region comprising one or more CDR sequences selected from the group consisting of SEQ ID NOs: 14-16 of WO 2011/039510 A2 or selected from the group consisting of SEQ ID NOs: 17-19 of WO 2011/039510 A2.

In a further preferred embodiment, the anti-CD163 antibody or CD163-binding fragment thereof comprises a heavy-chain variable (V_H) region comprising or consisting of the amino acid sequence of SEQ ID NO: 20 of WO 2011/039510 A2.

In addition, or alternatively thereto, in a preferred embodiment, the anti-CD163 antibody or CD163-binding fragment thereof comprises a light-chain variable (V_L) region comprising or consisting of the amino acid sequence of SEQ ID NO: 21 of WO 2011/039510 A2.

In a further preferred embodiment, the anti-CD163 antibody or CD163-binding fragment thereof comprises a heavy-chain variable (V_H) region comprising or consisting of the amino acid sequence of SEQ ID NO: 22 of WO 2011/039510 A2.

In addition, or alternatively thereto, in a preferred embodiment, the anti-CD163 antibody or CD163-binding fragment thereof comprises a light-chain variable (V_L) region comprising or consisting of the amino acid sequence of SEQ ID NO: 23 of WO 2011/039510 A2.

In a further preferred embodiment, the anti-CD163 antibody or CD163-binding fragment thereof comprises a heavy-chain variable (V_H) region comprising or consisting of the amino acid sequence of SEQ ID NO: 24 of WO 2011/039510 A2.

In addition, or alternatively thereto, in a preferred embodiment, the anti-CD163 antibody or CD163-binding fragment thereof comprises a light-chain variable (V_L) region comprising or consisting of the amino acid sequence of SEQ ID NO: 25 of WO 2011/039510 A2.

In the context of the present invention, the anti-CD163 antibody may be a mammalian antibody such as a humanized or human antibody, a non-human primate antibody, a sheep antibody, a pig antibody, a dog antibody or a rodent antibody. In embodiments, the anti-CD163 antibody may be monoclonal.

According to a preference, the anti-CD163 antibody is selected from IgG, IgA, IgD, IgE and IgM.

According to a further preference, the CD163-binding fragment is selected from a Fab, a Fab', a F(ab)2, a Fv, a single-chain antibody, a nanobody and an antigen-binding domain.

CD163 amino acid sequences are for instance disclosed in WO 2011/039510 A2 (which is included here by reference). In the context of the present invention, the anti-CD163 antibody or CD163-binding fragment thereof is preferably specific for a human CD163, especially with the amino acid sequence of any one of SEQ ID NOs: 28-31 of WO 2011/039510 A2.

In a further preferred embodiment, the anti-CD163 antibody or CD163-binding fragment thereof is specific for the extracellular region of CD163 (e.g. for human CD163: amino acids 42-1050 of UniProt Q86VB7, sequence version 2), preferably for an SRCR domain of CD163, more preferably for any one of SRCR domains 1-9 of CD163 (e.g. for human CD163: amino acids 51-152, 159-259, 266-366, 373-473, 478-578, 583-683, 719-819, 824-926 and 929-1029, respectively, of UniProt Q86VB7, sequence version

2), even more preferably for any one of SRCR domains 1-3 of CD163 (e.g. for human CD163: amino acids 51-152, 159-259, 266-366, and 373-473, respectively, of UniProt Q86VB7, sequence version 2), especially for SRCR domain 1 of CD163 (in particular with the amino acid sequence of any one of SEQ ID NOs: 1-8 of WO 2011/039510 A2, especially SEQ ID NO: 1 of WO 2011/039510 A2).

In a particular preference, the anti-CD163 antibody or CD163-binding fragment thereof is capable of competing for binding to (preferably human) CD163 with a (preferably human) hemoglobin-haptoglobin complex (e.g. in an ELISA).

In another particular preference, the anti-CD163 antibody or CD163-binding fragment thereof is capable of competing for binding to human CD163 with any of the anti-human CD163 mAbs disclosed herein, in particular Mac2-48 or Mac2-158 as disclosed in WO 2011/039510 A2.

In yet another particular preference, the anti-CD163 antibody or CD163-binding fragment thereof is capable of competing for binding to human CD163 with an antibody having a heavy chain variable (VH) region consisting of the amino acid sequence

DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIQFPGNKLEWMGYIT
YSGITNYPNPSLKSQISITRDTSKNQFFLQLNSVTTEDTATYYCVSGTYYFDYW
GQGTTLTVSS (SEQ ID NO: 1),

and having a light-chain variable (VL) region consisting of the amino acid sequence

SVVMTQTPKSLISIGDRVTITCKASQSVSSDVAWFQKPGQSPKPLIYYASNRY
TGVPDRFTGSGYGTDFTFTISSVQAEDLAVYFCGQDYTSPTFTGGGKLEIKRA (SEQ ID NO: 2) (e.g. in an ELISA).

Details on competitive binding experiments are known to the person of skilled in the art (e.g. based on ELISA) and are for instance disclosed in WO 2011/039510 A2 (which is included herein by reference).

The epitopes of antibodies E10B10 and Mac2-158 as disclosed in WO 2011/039510 were mapped (see example section). These epitopes are particularly suitable for binding of the anti-CD163 antibody (or CD163-binding fragment thereof) of the inventive compound.

Accordingly, in particularly preferred embodiment, the anti-CD163 antibody or CD163-binding fragment thereof is specific for peptide consisting of 7-25, preferably 8-20, even more preferably 9-15, especially 10-13 amino acids, wherein the peptide comprises the amino acid sequence

CSGRVEVKVQEEWGTVCNNGWSMEA (SEQ ID NO: 3) or a 7-24 amino-acid fragment thereof. Preferably, this peptide comprises the amino acid sequence GRVEVKVQEEW (SEQ ID NO: 4), WGTVCNNGWS (SEQ ID NO: 5) or WGTVCNNGW (SEQ ID NO: 6). More preferably, the peptide comprises an amino acid sequence selected from EWGTVCNNGWSME (SEQ ID NO: 7), QEEWGTVCNNGWS (SEQ ID NO: 8), WGTVCNNGWSMEA (SEQ ID NO: 9), EEWGTVCNNGWSM (SEQ ID NO: 10), VQEEWGTVCNNGW (SEQ ID NO: 11), EWGTVCNNGW (SEQ ID NO: 12) and WGTVCNNGWS (SEQ ID NO: 5). Even more preferably, the peptide consists of an amino acid sequence selected from EWGTVCNNGWSME (SEQ ID NO: 7), QEEWGTVCNNGWS (SEQ ID NO: 8), WGTVCNNGWSMEA (SEQ ID NO: 9), EEWGTVCNNGWSM (SEQ ID NO: 10), VQEEWGTVCNNGW (SEQ ID NO: 11), EWGTVCNNGW (SEQ ID NO: 12) and WGTVCNNGWS (SEQ ID NO: 5), optionally with an N-terminal and/or C-terminal cysteine residue.

Accordingly, in another particularly preferred embodiment, the anti-CD163 antibody or CD163-binding fragment thereof is specific for a peptide consisting of 7-25, preferably 8-20, even more preferably 9-15, especially 10-13 amino acids, wherein the peptide comprises the amino acid sequence DHVSCRGNESALWDCKHDGWG (SEQ ID NO: 13) or a 7-20 amino-acid fragment thereof. Preferably, this peptide comprises the amino acid sequence ESALW (SEQ ID NO: 14) or ALW. More preferably, the peptide comprises an amino acid sequence selected from ESALWDC (SEQ ID NO: 15), RGNESALWDC (SEQ ID NO: 16), SCRGNESALW (SEQ ID NO: 17), VSCRGNESALWDC (SEQ ID NO: 18), ALWDCKHDGW (SEQ ID NO: 19), DHVSCRGNESALW (SEQ ID NO: 20), CRGNESALWD (SEQ ID NO: 21), NESALWDCKHDGW (SEQ ID NO: 22) and ESALWDCKHDGWG (SEQ ID NO: 23). Even more preferably, the peptide consists of an amino acid sequence selected from ESALWDC (SEQ ID NO: 15), RGNESALWDC (SEQ ID NO: 16), SCRGNESALW (SEQ ID NO: 17), VSCRGNESALWDC (SEQ ID NO: 18), ALWDCKHDGW (SEQ ID NO: 19), DHVSCRGNESALW (SEQ ID NO: 20), CRGNESALWD (SEQ ID NO: 21), NESALWDCKHDGW (SEQ ID NO: 22)

and ESALWDCKHDGWG (SEQ ID NO: 23), optionally with an N-terminal and/or C-terminal cysteine residue.

Accordingly, in another particularly preferred embodiment, the anti-CD163 antibody or CD163-binding fragment thereof is specific for a peptide consisting of 7-25, preferably 8-20, even more preferably 9-15, especially 10-13 amino acids, wherein the peptide comprises the amino acid sequence SSLGGTDKELRLVDGENKCS (SEQ ID NO: 24) or a 7-19 amino-acid fragment thereof. Preferably, this peptide comprises the amino acid sequence SSLGGTDKELR (SEQ ID NO: 25) or SSLGG (SEQ ID NO: 26). More preferably, the peptide comprises an amino acid sequence selected from SSLGGTDKELR (SEQ ID NO: 25), SSLGGTDKEL (SEQ ID NO: 27), SSLGGTDKE (SEQ ID NO: 28), SSLGGTDK (SEQ ID NO: 29), SSLGGTD (SEQ ID NO: 30), SSLGGT (SEQ ID NO: 31) and SSLGG (SEQ ID NO: 26). Even more preferably, the peptide consists of an amino acid sequence selected from SSLGGTDKELR (SEQ ID NO: 25), SSLGGTDKEL (SEQ ID NO: 27), SSLGGTDKE (SEQ ID NO: 28), SSLGGTDK (SEQ ID NO: 29), SSLGGTD (SEQ ID NO: 30), SSLGGT (SEQ ID NO: 31) and SSLGG (SEQ ID NO: 26), optionally with an N-terminal and/or C-terminal cysteine residue.

The peptides (or peptide n-mers) are preferably covalently conjugated (or covalently bound) to the biopolymer scaffold via a (non-immunogenic) linker known in the art such as for example amine-to-sulphydryl linkers and bifunctional NHS-PEG-maleimide linkers or other linkers known in the art. Alternatively, the peptides (or peptide n-mers) can be bound to the epitope carrier scaffold e.g. by formation of a disulfide bond between the protein and the peptide (which is also referred to as "linker" herein), or using non-covalent assembly techniques, spontaneous isopeptide bond formation or unnatural amino acids for bio-orthogonal chemistry via genetic code expansion techniques (reviewed by Howarth et al 2018 and Lim et al 2016). Covalent and non-covalent bioconjugation strategies suitable for the present invention are also discussed e.g. in Sunasee et al, 2014.

The compound of the present invention may comprise e.g. at least two, preferably between 3 and 40 copies of one or several different peptides (which may be present in different forms of peptide n-mers as disclosed herein). The compound may comprise

one type of epitopic peptide (in other words: antibody-binding peptide or paratope-binding peptide), however the diversity of epitopic peptides bound to one biopolymer scaffold molecule can be a mixture of e.g. up to 8 different epitopic peptides.

Typically, since the peptides present in the inventive compound specifically bind to selected undesired antibodies, their sequence is usually selected and optimized such that they provide specific binding in order to guarantee selectivity of undesired antibody depletion from the blood. For this purpose, the peptide sequence of the peptides typically corresponds to the entire epitope sequence or portions of the undesired antibody epitope. The peptides used in the present invention can be further optimized by exchanging one, two or up to four amino-acid positions, allowing e.g. for modulating the binding affinity to the undesired antibody that needs to be depleted. Such single or multiple amino-acid substitution strategies that can provide "mimotopes" with increased binding affinity and are known in the field and were previously developed using phage display strategies or peptide microarrays. In other words, the peptides used in the present invention do not have to be completely identical to the native epitope sequences of the undesired antibodies.

Typically, the peptides used in the compound of the present invention (e.g. peptide P or P_a or P_b) are composed of one or more of the 20 amino acids commonly present in mammalian proteins. In addition, the amino acid repertoire used in the peptides may be expanded to post-translationally modified amino acids e.g. affecting antigenicity of proteins such as post translational modifications, in particular oxidative post translational modifications (see e.g. Ryan 2014) or modifications to the peptide backbone (see e.g. Müller 2018), or to non-natural amino acids (see e.g. Meister et al 2018). These modifications may also be used in the peptides e.g. to adapt the binding interaction and specificity between the peptide and the variable region of an undesired antibody. In particular, epitopes (and therefore the peptides used in the compound of the present invention) can also contain citrulline as for example in autoimmune diseases. Furthermore, by introducing modifications into the peptide sequence the propensity of binding to an HLA

molecule may be reduced, the stability and the physicochemical characteristics may be improved or the affinity to the undesired antibody may be increased.

In many cases, the undesired antibody that is to be depleted is oligo- or polyclonal (e.g. autoantibodies, ADAs or alloantibodies are typically poly- or oligoclonal), implying that undesired (polyclonal) antibody epitope covers a larger epitopic region of a target molecule. To adapt to this situation, the compound of the present invention may comprise a mixture of two or several epitopic peptides (in other words: antibody-binding peptides or paratope-binding peptides), thereby allowing to adapt to the polyclonality or oligoclonality of an undesired antibody.

Such poly-epitopic compounds of the present invention can effectively deplete undesired antibodies and are more often effective than mono-epitopic compounds in case the epitope of the undesired antibody extends to larger amino acid sequence stretches.

It is advantageous if the peptides used for the inventive compound are designed such that they will be specifically recognized by the variable region of the undesired antibodies to be depleted. The sequences of peptides used in the present invention may e.g. be selected by applying fine epitope mapping techniques (i.e. epitope walks, peptide deletion mapping, amino acid substitution scanning using peptide arrays such as described in Carter et al 2004, and Hansen et al 2013) on the undesired antibodies.

According to a preferred embodiment, the viral vector is an AdV vector or an AAV vector, preferably specific for a human host.

In another preference, the sequence fragment as used herein comprises an epitope or epitope part (e.g. at least six, especially at least seven or even at least eight amino acids) of an AdV capsid protein or of an AAV capsid protein (see e.g. Example 10), in particular wherein the AAV is one of AAV-8, AAV-9, AAV-6, AAV-2 or AAV-5, or of one of the following viral proteins identified by their UniProt accession code:

A9RAI0, B5SUY7, O41855, O56137, O56139, P03135, P04133, P04882, P08362, P10269, P12538, P69353, Q5Y9B2, Q5Y9B4, Q65311, Q6JC40, Q6VGT5, Q8JQF8, Q8JQG0, Q98654, Q9WBP8, Q9YIJ1,

or of an AdV hexon protein, an AdV fiber protein, an AdV penton protein, an AdV IIIa protein, an AdV VI protein, an AdV VIII protein or an AdV IX protein or of any one of the capsid proteins identified in Fig. 10 and Fig. 11 or of any one of the capsid proteins listed in Cearley et al., 2008.

Particularly suitable epitopes for depleting neutralizing antibodies (against AAV and AdV) were found in epitope screens and screens of human sera (see in particular Examples 14-21). Accordingly, in a preferment, the sequence fragment as used herein comprises a sequence of at least 4 or at least 5 or at least 6, preferably at least 7, more preferably at least 8, even more preferably at least 9, yet even more preferably at least 10 consecutive amino acids selected from:

the group of AdV sequences ETGPPTVPFLTPPF (SEQ ID NO: 32), HDSKLSIATQGPL (SEQ ID NO: 33), LNLRLGQGPLFINSAHNLDINY (SEQ ID NO: 34), VDPMDPEPTLLYVLFEVFDVV (SEQ ID NO: 35), MKRRARPS EDTFNPVYPYD (SEQ ID NO: 36), ISGTVQSAHLIIRFD (SEQ ID NO: 37), LGQGPLFINSAHNLDINY NKGLYLF (SEQ ID NO: 38), SYPFDAQNQLNLRLGQGPLFIN (SEQ ID NO: 39), GDTTPSAYSMSFSWDWSGHNYIN (SEQ ID NO: 40), VLLNNSFLDPEYWNFRN (SEQ ID NO: 41), HNYINEIFATSSYTFSYIA (SEQ ID NO: 42), DEATALEINLEEEEDDDNEDEVDEQAEQQKTH (SEQ ID NO: 43), INLEEEEDDDNEDEVDEQAEQ (SEQ ID NO: 44), DNEDEVDEQAEQQKTHVF (SEQ ID NO: 45), EWDEATALEINLEE (SEQ ID NO: 46), PKVVLYSEDVDIETPDTHISYMP (SEQ ID NO: 47), YIPESYKDRMYSFFRN (SEQ ID NO: 48), DSIGDRTRYFSMW (SEQ ID NO: 49), SYKDRMYSFFRN (SEQ ID NO: 50), and FLVQMLANYNIGYQGFY (SEQ ID NO: 51), or

the group of AAV sequences WQNRDVYLQGPIWAKIP (SEQ ID NO: 52), DNTYFGYSTPWGYFDNRFHC (SEQ ID NO: 53), MANQAKNWLPGPCY (SEQ ID NO: 54), LPYVLGSAHQGCLPPFP (SEQ ID NO: 55), NGSQAVGRSSFYCLEYF (SEQ ID NO: 56), PLIDQYLYYL (SEQ ID NO: 57), EERFFPSNGILIF (SEQ ID NO: 58), ADGVGSSSGNWHC (SEQ ID NO: 59), SEQ ID NOs: 383-1891 (see Table 1) - preferably group III of Table 1, more preferably group II of Table 1, especially group I of Table 1 - and SEQ ID NOs: 1892-2063 (see Table 2) - preferably group I of Table 2 -

and sequences of group II or III of Table 3 (in particular SEQ ID NOs: 2064-2103), more preferably sequences of group I of Table 3,

or the group of sequences of Table 4, in particular the group of sequences identified by SEQ ID NOs: 2104-2190.

It is particularly preferred that P_a and/or P_b or, independently for each occurrence, P comprises a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences consisting of GPPTVPFLTP (SEQ ID NO: 60), ETGPPTVPFLTPP (SEQ ID NO: 61), TGPPTVPFLT (SEQ ID NO: 62), PTPPFLTPPF (SEQ ID NO: 63), HDSKLSIATQGGL (SEQ ID NO: 64), SIATQGP (SEQ ID NO: 65), NLRLGQGGLF (SEQ ID NO: 66), QGGLFINSAH (SEQ ID NO: 67), PLFINSAHNLD (SEQ ID NO: 68), LGQGGLF (SEQ ID NO: 69), LNLRLGQGGL (SEQ ID NO: 70), GQGGLFI (SEQ ID NO: 71), NLRLGQGGLFINS (SEQ ID NO: 72), LFINSAHNLDINY (SEQ ID NO: 73), FINSAHNLDI (SEQ ID NO: 74), LRLGQGGLFI (SEQ ID NO: 75), GPLFINSAHN (SEQ ID NO: 76), DEPTLLYVLFEVF (SEQ ID NO: 77), TLLYVLFEVF (SEQ ID NO: 78), DEPTLLYVLF (SEQ ID NO: 79), TLLYVLFEVFDVV (SEQ ID NO: 80), TLLYVLF (SEQ ID NO: 81), MDEPTLLYVLFEV (SEQ ID NO: 82), EPTLLYVLFE (SEQ ID NO: 83), DPMDEPTLLYVLF (SEQ ID NO: 84), LLYVLFEVFD (SEQ ID NO: 85), YVLFEVFDVV (SEQ ID NO: 86), PTLLYVLFEV (SEQ ID NO: 87), PTLLYVLFEVFDV (SEQ ID NO: 88), LYVLFEVFDV (SEQ ID NO: 89), EPTLLYVLFEVFD (SEQ ID NO: 90), LYVLFEV (SEQ ID NO: 91), PMDEPTLLYVLFE (SEQ ID NO: 92), LLYVLFE (SEQ ID NO: 93), VDPMDPTLLYVL (SEQ ID NO: 94), YVLFEVF (SEQ ID NO: 95), PTLLYVL (SEQ ID NO: 96), MKRARPSEDTF (SEQ ID NO: 97), KRARPSEDTF (SEQ ID NO: 98), MKRARPSED (SEQ ID NO: 99), MKRARPSEDTFN (SEQ ID NO: 100), ARPSEDTFNP (SEQ ID NO: 101), RARPSEDTFN (SEQ ID NO: 102), RPSEDTF (SEQ ID NO: 103), MKRARPSEDTFNP (SEQ ID NO: 104), RARPSEDTFNPVY (SEQ ID NO: 105), ARPSED (SEQ ID NO: 106), EDTFNPVYPY (SEQ ID NO: 107), RPSEDTFNPVYPY (SEQ ID NO: 108), KRARPSEDTFNPV (SEQ ID NO: 109), DTFNPVY (SEQ ID NO: 110), RPSEDTFNPV (SEQ ID NO: 111), PSEDTFNPVY (SEQ ID NO: 112), DTFNPVYPYD (SEQ ID NO: 113), VQSAHLIIRF (SEQ ID NO: 114), AHLIIRF (SEQ ID NO: 115), SGTVQSAHLIIRF (SEQ ID NO: 116),

TVQSAHLIIR (SEQ ID NO: 117), HLIIRFD (SEQ ID NO: 118), SAHLIIR (SEQ ID NO: 119), QSAHLIIRFD (SEQ ID NO: 120), ISGTVQSAHLIIR (SEQ ID NO: 121), GTVQSAHLII (SEQ ID NO: 122), GTVQSAHLIIRFD (SEQ ID NO: 123), QSAHLII (SEQ ID NO: 124), HNLDINY (SEQ ID NO: 125), LFINSAHNLDINY (SEQ ID NO: 126), NLDINYNKGLYLF (SEQ ID NO: 127), FVSPNG (SEQ ID NO: 128), NYINEIF (SEQ ID NO: 129), NKGLYLF (SEQ ID NO: 130), INYNKGLYLF (SEQ ID NO: 131), NSAHNLDINY (SEQ ID NO: 132), WDWSGHNYINEIF (SEQ ID NO: 133), SGHNYINEIF (SEQ ID NO: 134), LGTGLSF (SEQ ID NO: 135), PFLTPPF (SEQ ID NO: 136), LGQGPLF (SEQ ID NO: 137), NLRLQGQPLF (SEQ ID NO: 138), NQLNLRLQGQPLF (SEQ ID NO: 139), GQGPLFI (SEQ ID NO: 140), QLNLRRLQGQPLFI (SEQ ID NO: 141), SYPFDAQNQLNLR (SEQ ID NO: 142), YPFDAQNQLNLRL (SEQ ID NO: 143), LRLQGQPLFI (SEQ ID NO: 144), NQLNLRL (SEQ ID NO: 145), FDAQNQLNLR (SEQ ID NO: 146), QNQLNLR (SEQ ID NO: 147), QGPLFIN (SEQ ID NO: 148), PFDAQNQLNLRLG (SEQ ID NO: 149), DAQNQLNLRL (SEQ ID NO: 150), RLGQGPLFIN (SEQ ID NO: 151), QLNLRRLG (SEQ ID NO: 152), FDAQNQLNLRLGQ (SEQ ID NO: 153), LNLRLQGQPLFIN (SEQ ID NO: 154), AQNQLNLRLG (SEQ ID NO: 155), AQNQLNL (SEQ ID NO: 156), LNLRLGQ (SEQ ID NO: 157), SYPFDAQNQL (SEQ ID NO: 158), PFDAQNQLNL (SEQ ID NO: 159), YSMSFSW (SEQ ID NO: 160), TPSAYSMSFSWDW (SEQ ID NO: 161), MSFSWDW (SEQ ID NO: 162), PSAYSMSFSW (SEQ ID NO: 163), DTPSAYSMSFSW (SEQ ID NO: 164), TTPSAYSMSF (SEQ ID NO: 165), YSMSFSWDWS (SEQ ID NO: 166), TGDTPSAYSMSF (SEQ ID NO: 167), FSWDWSGHNY (SEQ ID NO: 168), SFSWDWS (SEQ ID NO: 169), SAYSMSF (SEQ ID NO: 170), SFSWDWSGHN (SEQ ID NO: 171), SAYSMSFSWD (SEQ ID NO: 172), SMSFSWD (SEQ ID NO: 173), SWDWSGHNYI (SEQ ID NO: 174), AYSMSFS (SEQ ID NO: 175), SMSFSWDWSGHNY (SEQ ID NO: 176), FSWDWSG (SEQ ID NO: 177), SWDWSGH (SEQ ID NO: 178), FLDPEYWNFR (SEQ ID NO: 179), SFLDPEYWNF (SEQ ID NO: 180), PEYWNFR (SEQ ID NO: 181), LNNSFLDPEYWNF (SEQ ID NO: 182), NNSFLDPEYWNFR (SEQ ID NO: 183), FLDPEYW (SEQ ID NO: 184), DPEYWNF (SEQ ID NO: 185), NNSFLDPEYW (SEQ ID NO: 186), VLLNNSFLDPEYW (SEQ ID NO: 187), EYWNFRN (SEQ ID NO: 188), LNNSFLDPEY (SEQ ID NO: 189), LDPEYWNFRN (SEQ ID NO: 190), LNNSFLD (SEQ ID NO: 191), NSFLDPEYWN (SEQ ID NO: 192), SSYTFSY (SEQ ID NO: 193), FATSSYTFSY (SEQ ID NO: 194), YINEIFATSSYTF (SEQ ID NO: 195), SYTFSYI (SEQ ID NO: 196), ATSSYTF (SEQ ID NO: 197), EIFATSSYTF (SEQ ID NO: 198), NEIFATSSYTF (SEQ ID NO: 199), ATSSYTFSYI (SEQ ID NO: 200),

HNYINEIFATSSY (SEQ ID NO: 201), IFATSSY (SEQ ID NO: 202),
INEIFATSSY (SEQ ID NO: 203), NYINEIFATSSYT (SEQ ID NO: 204),
YINEIFA (SEQ ID NO: 205), YTFSYIA (SEQ ID NO: 206),
EIFATSSYTFSYI (SEQ ID NO: 207), ALEINLEEEDDDN (SEQ ID NO: 208),
ATALEINLEEEDD (SEQ ID NO: 209), EAATALEINLEEE (SEQ ID NO: 210),
LEINLEE (SEQ ID NO: 211), TALEINLEEEDDD (SEQ ID NO: 212),
EINLEEE (SEQ ID NO: 213), ALEINLEEED (SEQ ID NO: 214),
LEINLEEEDD (SEQ ID NO: 215), TALEINLEEE (SEQ ID NO: 216),
DEAATALEINLEE (SEQ ID NO: 217), LEINLEEEDDDNE (SEQ ID NO: 218),
AATALEINLEEED (SEQ ID NO: 219), EINLEEEDDD (SEQ ID NO: 220),
ATALEINLEE (SEQ ID NO: 221), INLEEEDDDN (SEQ ID NO: 222),
NLEEEDDDNE (SEQ ID NO: 223), DEVDEQA (SEQ ID NO: 224),
EDDDNEDEVDEQA (SEQ ID NO: 225), DDNEDEVDEQAEQ (SEQ ID NO: 226),
EVDEQAE (SEQ ID NO: 227), DNEDEVDEQA (SEQ ID NO: 228), VDEQAEQ
(SEQ ID NO: 229), EDEVDEQAEQQKT (SEQ ID NO: 230), EDEVDEQAEQ
(SEQ ID NO: 231), DEVDEQAEQQKTH (SEQ ID NO: 232), NEDEVDEQAEQQK
(SEQ ID NO: 233), DEVDEQAEQQ (SEQ ID NO: 234), EINLEEEDDDNED
(SEQ ID NO: 235), NLEEEDDDNEDEV (SEQ ID NO: 236), INLEED (SEQ
ID NO: 237), LEEEDDDNED (SEQ ID NO: 238), INLEEEDDDNEDE (SEQ ID
NO: 239), DDDNEDEVDEQAE (SEQ ID NO: 240), LEEEDDDNEDEV (SEQ ID
NO: 241), DDNEDEVDEQ (SEQ ID NO: 242), EDDDNED (SEQ ID NO: 243),
NLEEEDD (SEQ ID NO: 244), DDNEDEV (SEQ ID NO: 245), DDDNEDEVDE
(SEQ ID NO: 246), DDDNEDE (SEQ ID NO: 247), EEEDDDNEDE (SEQ ID
NO: 248), EEEDDDNE (SEQ ID NO: 249), EDDDNEDVD (SEQ ID NO: 250),
EDEVDEQ (SEQ ID NO: 251), EEEDDDNEDEVDEQ (SEQ ID NO: 252),
EEEDDDNEDEV (SEQ ID NO: 253), EEEDDDNEDEVDE (SEQ ID NO: 254),
EVDEQAEQQK (SEQ ID NO: 255), DNEDEVDEQAEQQ (SEQ ID NO: 256),
VDEQAEQQKT (SEQ ID NO: 257), EVDEQAEQQKTHV (SEQ ID NO: 258),
VDEQAEQQKTHVF (SEQ ID NO: 259), ALEINLE (SEQ ID NO: 260),
WDEAATALEINLE (SEQ ID NO: 261), AATALEINLE (SEQ ID NO: 262),
EWDEAATALEINL (SEQ ID NO: 263), EAATALEINL (SEQ ID NO: 264),
LYSEDVDIET (SEQ ID NO: 265), LYSEDVDIETPD (SEQ ID NO: 266),
KVVLYSEDVDIET (SEQ ID NO: 267), IETPDTH (SEQ ID NO: 268),
VDIETPDTHI (SEQ ID NO: 269), VLYSEDVDIE (SEQ ID NO: 270),
DVDIETPDTHISY (SEQ ID NO: 271), VVLYSEDVDIETP (SEQ ID NO: 272),
SEDVDIETPDTHI (SEQ ID NO: 273), ETPDTHI (SEQ ID NO: 274),
VLYSEDVDIETPD (SEQ ID NO: 275), DVDIETPDTH (SEQ ID NO: 276),
DIETPDTHIS (SEQ ID NO: 277), EDVDIETPDTHIS (SEQ ID NO: 278),
IETPDTHISY (SEQ ID NO: 279), YSEDVDIETPDTH (SEQ ID NO: 280),

VDIETPDTHISYM (SEQ ID NO: 281), PKVVLISEDVDIE (SEQ ID NO: 282), DIETPDT (SEQ ID NO: 283), DIETPDTHISYMP (SEQ ID NO: 284), EDVDIETPDT (SEQ ID NO: 285), ETPDTHISYM (SEQ ID NO: 286), IETPDTHISYMP (SEQ ID NO: 287), DRMYSFFRNF (SEQ ID NO: 288), DRMYSFF (SEQ ID NO: 289), YSFFRNF (SEQ ID NO: 290), IPESYKDRMYSFF (SEQ ID NO: 291), SYKDRMYSFF (SEQ ID NO: 292), ESYKDRMYSF (SEQ ID NO: 293), KDRMYSF (SEQ ID NO: 294), YIPESYKDRMYSF (SEQ ID NO: 295), PESYKDRMYSFFR (SEQ ID NO: 296), YKDRMYSFFR (SEQ ID NO: 297), TRYFSMW (SEQ ID NO: 298), GDRTRYF (SEQ ID NO: 299), DSIGDRTRYF (SEQ ID NO: 300), DSIGDRTRYFSMW (SEQ ID NO: 301), GDRTRYFSMW (SEQ ID NO: 302), DRMYSFFRNF (SEQ ID NO: 303), SYKDRMYSFFRNF (SEQ ID NO: 304), NYNIGYQGFY (SEQ ID NO: 305), ANYNIGYQGF (SEQ ID NO: 306), MLANYNIGYQGFY (SEQ ID NO: 307), IGYQGFY (SEQ ID NO: 308), FLVQMLANYNIGY (SEQ ID NO: 309), NIGYQGF (SEQ ID NO: 310) and QMLANYNIGYQGF (SEQ ID NO: 311), optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid.

In another preferred embodiment, P_a and/or P_b or, independently for each occurrence, P comprises a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment or even a 11-amino-acid-fragment or yet even a 12-amino-acid-fragment, especially a 13-amino-acid-fragment selected from the group of sequences consisting of SEQ ID NOs: 383-1891 (see Table 1) - preferably group III of Table 1, more preferably group II of Table 1, especially group I of Table 1 - and SEQ ID NOs: 1892-2063 (see Table 2) - preferably group I of Table 2 - and sequences of group II or III of Table 3 (in particular SEQ ID NOs: 2064-2103), more preferably sequences of group I of Table 3, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid.

In another preferred embodiment, P_a and/or P_b or, independently for each occurrence, P comprises a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment or

even a 11-amino-acid-fragment or yet even a 12-amino-acid-fragment, especially a 13-amino-acid-fragment selected from the group of sequences of Table 4, in particular the group of sequences identified by SEQ ID NOs: 2104-2190, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid.

It is further particularly preferred that P_a and/or P_b or, independently for each occurrence, P comprises a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences consisting of YLQGPIW (SEQ ID NO: 312), VYLQGP (SEQ ID NO: 313), WQNRDVY (SEQ ID NO: 314), DVYLQGP (SEQ ID NO: 315), QNRDVYL (SEQ ID NO: 316), LQGPWA (SEQ ID NO: 317), RDVYLQ (SEQ ID NO: 318), NRDVYLQ (SEQ ID NO: 319), YFGYSTPWGYFDF (SEQ ID NO: 320), FGYSTPWGYF (SEQ ID NO: 321), GYSTPWGYFD (SEQ ID NO: 322), YSTPWGYFDF (SEQ ID NO: 323), NTYFGYSTPWGYF (SEQ ID NO: 324), TPWGYFDFNRFHC (SEQ ID NO: 325), TYFGYSTPWGYFD (SEQ ID NO: 326), DNTYFGYSTPWGY (SEQ ID NO: 327), YFGYSTPWGY (SEQ ID NO: 328), FGYSTPWGYFDFN (SEQ ID NO: 329), NWLPGPC (SEQ ID NO: 330), WLPGPCY (SEQ ID NO: 331), QAKNWLPGPC (SEQ ID NO: 332), AKNWLPGPCY (SEQ ID NO: 333), MANQAKNWLPGPC (SEQ ID NO: 334), QGCLPPF (SEQ ID NO: 335), GCLPPFP (SEQ ID NO: 336), VLGSAHQGCLPPF (SEQ ID NO: 337), LPYVLGSAHQGCL (SEQ ID NO: 338), YVLGSAHQGC (SEQ ID NO: 339), CLPPFPA (SEQ ID NO: 340), SAHQGCLPPF (SEQ ID NO: 341), VLGSAHQGCL (SEQ ID NO: 342), PYVLGSAHQGCLP (SEQ ID NO: 343), GRSSFYC (SEQ ID NO: 344), AVGRSSFYCLEYF (SEQ ID NO: 345), AVGRSSFYCL (SEQ ID NO: 346), QAVGRSSFYCLEY (SEQ ID NO: 347), NGSQAVGRSSFYC (SEQ ID NO: 348), DQYLYYL (SEQ ID NO: 349), PLIDQYLYYL (SEQ ID NO: 350), IDQYLYY (SEQ ID NO: 351), FFPSNGILIF (SEQ ID NO: 352), EERFFPSNGILIF (SEQ ID NO: 353), VGSSSGNWHC (SEQ ID NO: 354) and ADGVGSSSGNWHC (SEQ ID NO: 355), optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid.

According to a further preference, P_a and/or P_b or, independently for each occurrence, P consists of a 6-amino-acid

fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences set forth in either of the four paragraphs right above, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid, optionally with an N-terminal and/or C-terminal cysteine residue.

In the entire context of the present invention, if a peptide, e.g. P_a and/or P_b or (independently for each occurrence) peptide P, contains a fragment of at least 4 consecutive amino acids selected from a sequence listed in a row of any one of Tables 1-4 (see below in the Examples section), it is preferred that this fragment is extended (N-terminally or C-terminally) such that the peptide actually contains a longer fragment (e.g. at least 6 or at least 7 or at least 8 or at least 9 or at least 10 or at least 11 or at least 12 or 13 amino acids long) of the source protein given in the same row of the table. In other words, it is preferred that the peptide contains a portion of at least 5 or at least 6 or at least 7 or at least 8 or at least 9 or at least 10 or at least 11 or at least 12 or 13 consecutive amino acids of the viral source protein of the fragment sequence (as given in Tables 1-4).

It is highly preferred that the peptides used for the inventive compound do not bind to any HLA Class I or HLA Class II molecule (i.e. of the individual to be treated, e.g. human), in order to prevent presentation and stimulation via a T-cell receptor in vivo and thereby induce an immune reaction. It is generally not desired to involve any suppressive (or stimulatory) T-cell reaction in contrast to antigen-specific immunologic tolerization approaches. Therefore, to avoid T-cell epitope activity as much as possible, the peptides of the compound of the present invention (e.g. peptide P or P_a or P_b) preferably fulfil one or more of the following characteristics:

- To reduce the probability for a peptide used in the compound of the present invention to bind to an HLA Class II or Class I molecule, the peptide (e.g. peptide P or P_a or P_b) has a

preferred length of 4-8 amino acids, although somewhat shorter or longer lengths are still acceptable.

- To further reduce the probability that such a peptide binds to an HLA Class II or Class I molecule, it is preferred to test the candidate peptide sequence by HLA binding prediction algorithms such as NetMHCII-2.3 (reviewed by Jensen et al 2018). Preferably, a peptide (e.g. peptide P or P_a or P_b) used in the compound of the present invention has (predicted) HLA binding (IC₅₀) of at least 500 nM. More preferably, HLA binding (IC₅₀) is more than 1000 nM, especially more than 2000 nM (cf. e.g. Peters et al 2006). In order to decrease the likelihood of HLA Class I binding, NetMHCpan 4.0 may also be applied for prediction (Jurtz et al 2017).

- To further reduce the probability that such a peptide binds to an HLA Class I molecule, the NetMHCpan Rank percentile threshold can be set to a background level of 10% according to Koşaloğlu-Yalçın et al, 2018. Preferably, a peptide (e.g. peptide P or P_a or P_b) used in the compound of the present invention therefore has a %Rank value of more than 3, preferably more than 5, more preferably more than 10 according to the NetMHCpan algorithm.

- To further reduce the probability that such a peptide binds to an HLA Class II molecule, it is beneficial to perform in vitro HLA-binding assays commonly used in the art such as for example refolding assays, iTopia, peptide rescuing assays or array-based peptide binding assays. Alternatively, or in addition thereto, LC-MS based analytics can be used, as e.g. reviewed by Gfeller et al 2016.

For stronger reduction of the titre of the undesired antibodies, it is preferred that the peptides used in the present invention are circularized (see also Example 4). Accordingly, in a preferred embodiment, at least one occurrence of P is a circularized peptide. Preferably at least 10% of all occurrences of P are circularized peptides, more preferably at least 25% of all occurrences of P are circularized peptides, yet more preferably at least 50% of all occurrences of P are circularized peptides, even more preferably at least 75% of all occurrences of P are circularized peptides, yet even more

preferably at least 90% of all occurrences of P are circularized peptides or even at least 95% of all occurrences of P are circularized peptides, especially all of the occurrences of P are circularized peptides. Several common techniques are available for circularization of peptides, see e.g. Ong et al 2017. It goes without saying that "circularized peptide" as used herein shall be understood as the peptide itself being circularized, as e.g. disclosed in Ong et al. (and not e.g. grafted on a circular scaffold with a sequence length that is longer than 13 amino acids). Such peptides may also be referred to as cyclopeptides herein.

Further, for stronger reduction of the titre of the undesired antibodies relative to the amount of scaffold used, in a preferred embodiment of the compound of the present invention, independently for each of the peptide n-mers, n is at least 2, more preferably at least 3, especially at least 4. Usually, in order to avoid complexities in the manufacturing process, independently for each of the peptide n-mers, n is less than 10, preferably less than 9, more preferably less than 8, even more preferably less than 7, yet even more preferably less than 6, especially less than 5. To benefit from higher avidity through divalent binding of the undesired antibody, it is highly preferred that, for each of the peptide n-mers, n is 2.

For multivalent binding of the undesired antibodies, it is advantageous that the peptide dimers or n-mers are spaced by a hydrophilic, structurally flexible, immunologically inert, non-toxic and clinically approved spacer such as (hetero-)bifunctional and -trifunctional Polyethylene glycol (PEG) spacers (e.g. NHS-PEG-Maleimide) - a wide range of PEG chains is available and PEG is approved by the FDA. Alternatives to PEG linkers such as immunologically inert and non-toxic synthetic polymers or glycans are also suitable. Accordingly, in the context of the present invention, the spacer (e.g. spacer S) is preferably selected from PEG molecules or glycans. For instance, the spacer such as PEG can be introduced during peptide synthesis. Such spacers (e.g. PEG spacers) may have a molecular weight of e.g. 10000 Dalton. Evidently, within the context of the present invention, the covalent binding of the peptide n-mers to the biopolymer scaffold via a linker each may for

example also be achieved by binding of the linker directly to a spacer of the peptide n-mer (instead of, e.g., to a peptide of the peptide n-mer).

Preferably, each of the peptide n-mers is covalently bound to the biopolymer scaffold, preferably via a linker each.

As used herein, the linker may e.g. be selected from disulphide bridges and PEG molecules.

According to a further preferred embodiment of the inventive compound, independently for each occurrence, P is P_a or P_b .

Furthermore, it is preferred when in the first peptide n-mer, each occurrence of P is P_a and, in the second peptide n-mer, each occurrence of P is P_b . Alternatively, or in addition thereto, P_a and/or P_b is circularized.

Divalent binding is particularly suitable to reduce antibody titres. According, in a preferred embodiment,

the first peptide n-mer is $P_a - S - P_a$ and the second peptide n-mer is $P_a - S - P_a$;

the first peptide n-mer is $P_a - S - P_a$ and the second peptide n-mer is $P_b - S - P_b$;

the first peptide n-mer is $P_b - S - P_b$ and the second peptide n-mer is $P_b - S - P_b$;

the first peptide n-mer is $P_a - S - P_b$ and the second peptide n-mer is $P_a - S - P_b$;

the first peptide n-mer is $P_a - S - P_b$ and the second peptide n-mer is $P_a - S - P_a$; or

the first peptide n-mer is $P_a - S - P_b$ and the second peptide n-mer is $P_b - S - P_b$.

For increasing effectivity, in a preferred embodiment the first peptide n-mer is different from the second peptide n-mer. For similar reasons, preferably, the peptide P_a is different from the peptide P_b , preferably wherein the peptide P_a and the peptide P_b are two different epitopes of the same antigen or two different epitope parts of the same epitope.

Especially for better targeting of polyclonal antibodies, it is advantageous when the peptide P_a and the peptide P_b comprise the same amino-acid sequence fragment, wherein the amino-acid

sequence fragment has a length of at least 2 amino acids, preferably at least 3 amino acids, more preferably at least 4 amino acids, yet more preferably at least 5 amino acids, even more preferably at least 6 amino acids, yet even more preferably at least 7 amino acids, especially at least 8 amino acids or even at least 9 amino acids.

Further, for stronger reduction of the titre of the undesired antibodies relative to the amount of scaffold used, the compound comprises a plurality of said first peptide n-mer (e.g. up to 10 or 20 or 30) and/or a plurality of said second peptide n-mer (e.g. up to 10 or 20 or 30).

As also illustrated above, it is highly preferred when the compound of the present invention is non-immunogenic in a mammal, preferably in a human, in a non-human primate, in a sheep, in a pig, in a dog or in a rodent.

In the context of the present invention, a non-immunogenic compound preferably is a compound wherein the biopolymer scaffold (if it is a protein) and/or the peptides (of the peptide n-mers) have an IC₅₀ higher than 100 nM, preferably higher than 500 nM, even more preferably higher than 1000 nM, especially higher than 2000 nM, against HLA-DRB1_0101 as predicted by the NetMHCII-2.3 algorithm. The NetMHCII-2.3 algorithm is described in detail in Jensen et al, which is incorporated herein by reference. The algorithm is publicly available under <http://www.cbs.dtu.dk/services/NetMHCII-2.3/>. Even more preferably, a non-immunogenic compound (or pharmaceutical composition) does not bind to any HLA and/or MHC molecule (e.g. in a mammal, preferably in a human, in a non-human primate, in a sheep, in a pig, in a dog or in a rodent; or of the individual to be treated) in vivo.

According to a further preference, the compound is for intracorporeal sequestration (or intracorporeal depletion) of at least one antibody (against the viral vector or neutralizing the viral vector) in an individual, preferably in the bloodstream of the individual and/or for reduction of the titre of at least one antibody (against the viral vector or neutralizing the viral vector) in the individual, preferably in the bloodstream of the individual.

In another preferred embodiment, the entire sequence, optionally with the exception of an N-terminal and/or C-terminal cysteine, of at least one occurrence of P, preferably of at least 10% of all occurrences of P, more preferably of at least 25% of all occurrences of P, yet more preferably of at least 50% of all occurrences of P, even more preferably of at least 75% of all occurrences of P, yet even more preferably of at least 90% of all occurrences of P or even of at least 95% of all occurrences of P, especially of all of the occurrences of P, is identical to a sequence fragment of a protein, wherein the protein is identified by one of the UniProt accession codes disclosed herein; optionally wherein the sequence fragment comprises at most five, preferably at most four, more preferably at most three, even more preferably at most two, especially at most one amino acid substitutions (e.g. for the purposes mentioned above, such as creating mimotopes).

In another preferred embodiment, the entire sequence, optionally with the exception of an N-terminal and/or C-terminal cysteine, of peptide P_a is identical to a sequence fragment of a protein, wherein the protein is identified by one of the UniProt accession codes disclosed herein; optionally wherein said sequence fragment comprises at most five, preferably at most four, more preferably at most three, even more preferably at most two, especially at most one amino acid substitutions (e.g. for the purposes mentioned above, such as creating mimotopes).

In another preferred embodiment, the entire sequence, optionally with the exception of an N-terminal and/or C-terminal cysteine, of peptide P_b is identical to a sequence fragment of a protein, wherein the protein is identified by one of the UniProt accession codes disclosed herein; optionally wherein said sequence fragment comprises at most five, preferably at most four, more preferably at most three, even more preferably at most two, especially at most one amino acid substitutions (e.g. for the purposes mentioned above, such as creating mimotopes).

In another preferred embodiment, the entire sequence, optionally with the exception of an N-terminal and/or C-terminal cysteine, of peptide P_a is identical to a sequence fragment of a protein and the entire sequence, optionally with the exception of an N-terminal and/or C-terminal cysteine, of peptide P_b is

identical to the same or another, preferably another, sequence fragment of the same protein, wherein the protein is identified by one of the UniProt accession codes listed herein; optionally wherein said sequence fragment and/or said another sequence fragment comprises at most five, preferably at most four, more preferably at most three, even more preferably at most two, especially at most one amino acid substitutions (e.g. for the purposes mentioned above, such as creating mimotopes).

In an aspect, the present invention relates to a pharmaceutical composition comprising the inventive and at least one pharmaceutically acceptable excipient.

In embodiments, the composition is prepared for intraperitoneal, subcutaneous, intramuscular and/or intravenous administration. In particular, the composition is for repeated administration (since it is typically non-immunogenic).

In a preference, the molar ratio of peptide P or P_a or P_b to biopolymer scaffold in the composition is from 2:1 to 100:1, preferably from 3:1 to 90:1, more preferably from 4:1 to 80:1, even more preferably from 5:1 to 70:1, yet even more preferably from 6:1 to 60:1, especially from 7:1 to 50:1 or even from 8:10 to 40:1.

In another aspect, the compound of the present invention is for use in therapy.

In the course of the present invention, it turned out that the in vivo kinetics of undesirable-antibody lowering by the inventive compound is typically very fast, sometimes followed by a mild rebound of the undesirable antibody. It is thus particularly preferred when the compound (or the pharmaceutical composition comprising the compound) is administered at least twice within a 96-hour window, preferably within a 72-hour window, more preferably within a 48-hour window, even more preferably within a 36-hour window, yet even more preferably within a 24-hour window, especially within a 18-hour window or even within a 12-hour window; in particular wherein this window is followed by administration of the vaccine or gene therapy composition as described herein within 24 hours, preferably within 12 hours (but typically after at least 6 hours). For instance, the pharmaceutical composition may be administered at

-24hrs and -12hrs before administration of the vaccine or gene therapy composition replacement product at 0hrs.

According to a particular preference, the compound of the present invention is for use in increasing efficacy of a vaccine in an individual, wherein the vaccine comprises the viral vector as defined herein, preferably wherein the pharmaceutical composition is administered to the individual prior to or concurrently with administration of the vaccine.

According to a further particular preference, the compound of the present invention is for use in increasing efficacy of a gene therapy composition in an individual, wherein the gene therapy composition comprises the viral vector as defined herein, preferably wherein the pharmaceutical composition is administered to the individual prior to or concurrently with administration of the gene therapy composition.

In embodiments, one or more antibodies are present in the individual which are specific for at least one occurrence of peptide P, or for peptide P_a and/or peptide P_b, preferably wherein said antibodies are neutralizing antibodies for said viral vector.

It is highly preferred that the composition is non-immunogenic in the individual (e.g. it does not comprise an adjuvant or an immunostimulatory substance that stimulates the innate or the adaptive immune system, e.g. such as an adjuvant or a T-cell epitope).

The composition of the present invention may be administered at a dose of 1-1000 mg, preferably 2-500 mg, more preferably 3-250 mg, even more preferably 4-100 mg, especially 5-50 mg, compound per kg body weight of the individual, preferably wherein the composition is administered repeatedly. Such administration may be intraperitoneally, subcutaneously, intramuscularly or intravenously.

In an aspect, the present invention relates to a method of sequestering (or depleting) one or more antibodies (preferably wherein said antibodies are neutralizing antibodies for said viral vector) present in an individual, comprising

obtaining a pharmaceutical composition as defined herein, wherein the composition is non-immunogenic in the

individual and wherein the one or more antibodies present in the individual are specific for at least one occurrence of P, or for peptide P_a and/or peptide P_b; and

administering (in particular repeatedly administering, e.g. at least two times, preferably at least three times, more preferably at least five times) the pharmaceutical composition to the individual.

In the context of the present invention, the individual (to be treated) may be a non-human animal, preferably a non-human primate, a sheep, a pig, a dog or a rodent, in particular a mouse.

Preferably, the biopolymer scaffold is autologous with respect to the individual, preferably wherein the biopolymer scaffold is an autologous protein (i.e. murine albumin is used when the individual is a mouse).

In embodiments, the individual is healthy.

In yet another aspect, the present invention relates to a pharmaceutical composition (i.e. a vaccine or gene therapy composition), comprising the compound defined herein and further comprising the viral vector and optionally at least one pharmaceutically acceptable excipient. The viral vector typically comprises a peptide fragment with a sequence length of at least six, preferably at least seven, more preferably at least eight, especially at least 9 amino acids. The sequence of at least one occurrence of peptide P, or peptide P_a and/or peptide P_b, of the compound is at least 70% identical, preferably at least 75% identical, more preferably at least 80% identical, yet more preferably at least 85% identical, even more preferably at least 90% identical, yet even more preferably at least 95% identical, especially completely identical to the sequence of said peptide fragment. Preferably, this pharmaceutical composition is for use in vaccination or gene therapy and/or for use in prevention or inhibition of an undesirable immune reaction against the viral vector.

This composition is furthermore preferably non-immunogenic in the individual.

In even yet another aspect, the present invention provides a method of inhibiting a (undesirable) – especially humoral –

immune reaction to a treatment with a vaccine or gene therapy composition in an individual in need of treatment with the vaccine or gene therapy composition as defined above or of inhibiting neutralization of a viral vector in a vaccine or gene therapy composition as defined above for an individual in need of treatment with the vaccine or gene therapy composition, comprising obtaining said vaccine or gene therapy composition ; wherein the compound of the vaccine or gene therapy composition is non-immunogenic in the individual, and administering (preferably repeatedly administering) the vaccine or gene therapy composition to the individual.

In general, screening for peptide mimotopes per se is known in the art, see for instance Shanmugam et al. Mimotope-based compounds of the invention have the following two advantages over compounds based on wild-type epitopes: First, the undesired antibodies, as a rule, have even higher affinities for mimotopes found by screening a peptide library, leading to higher clearance efficiency of the mimotope-based compound. Second, mimotopes further enable avoiding T-cell epitope activity as much as possible (as described hereinabove) in case the wild-type epitope sequence induces such T-cell epitope activity.

In a further aspect, the present invention relates to a peptide, wherein the peptide is defined as disclosed herein for any one of the at least two peptides of the inventive compound, P, P_a, or P_b.

In certain embodiments, such peptides may be used as probes for the diagnostic typing and analysis of circulating viral vector-neutralizing antibodies. The peptides can e.g. be used as part of a diagnostic vector-neutralizing antibody typing or screening device or kit or procedure, as a companion diagnostic, for patient stratification or for monitoring vector-neutralizing antibody levels prior to, during and/or after vaccination or gene therapy.

In a further aspect, the invention relates to a method for detecting and/or quantifying antibodies in a biological sample comprising the steps of

- bringing the sample into contact with the peptide defined as disclosed herein (e.g. for P, P_a, or P_b), and

- detecting the presence and/or concentration of antibodies in the sample.

The skilled person is familiar with methods for detecting and/or quantifying antibodies in biological samples. The method can e.g. be a sandwich assay, preferably an enzyme-linked immunosorbent assay (ELISA), or a surface plasmon resonance (SPR) assay.

In a preference, the peptide (especially at least 10, more preferably at least 100, even more preferably at least 1000, especially at least 10000 different peptides of the invention) is immobilized on a solid support, preferably an ELISA plate or an SPR chip or a biosensor-based diagnostic device with an electrochemical, fluorescent, magnetic, electronic, gravimetric or optical biotransducer. Alternatively, or in addition thereto, the peptide (especially at least 10, more preferably at least 100, even more preferably at least 1000, especially at least 10000 different peptides of the invention) may be coupled to a reporter or reporter fragment, such as a reporter fragment suitable for a protein-fragment complementation assay (PCA); see e.g. Li et al, 2019, or Kainulainen et al, 2021.

Preferably, the sample is obtained from a mammal, preferably a human. Preferably the sample is a blood sample, preferably a whole blood, serum, or plasma sample.

The invention further relates to the use of a peptide defined as disclosed herein (e.g. for P, P_a, or P_b) in a diagnostic assay, preferably ELISA, preferably as disclosed herein above.

A further aspect of the invention relates to a diagnostic device comprising the peptide defined as disclosed herein (e.g. for P, P_a, or P_b), preferably immobilized on a solid support. In a preference, the solid support is an ELISA plate or a surface plasmon resonance chip. In another preference, the diagnostic device is a biosensor-based diagnostic device with an electrochemical, fluorescent, magnetic, electronic, gravimetric or optical biotransducer.

In another preferred embodiment, the diagnostic device is a lateral flow assay.

The invention further relates to a diagnostic kit comprising a peptide defined as disclosed herein (e.g. for P, P_a, or P_b), preferably a diagnostic device as defined herein. Preferably the diagnostic kit further comprises one or more selected from the group of a buffer, a reagent, instructions. Preferably the diagnostic kit is an ELISA kit.

A further aspect relates to an apheresis device comprising the peptide defined as disclosed herein (e.g. for P, P_a, or P_b). Preferably the peptide is immobilized on a solid carrier. It is especially preferred if the apheresis device comprises at least two, preferably at least three, more preferably at least four different peptides defined as disclosed herein (e.g. for P, P_a, or P_b). In a preferred embodiment the solid carrier comprises the inventive compound.

Preferably, the solid carrier is capable of being contacted with blood or plasma flow. Preferably, the solid carrier is a sterile and pyrogen-free column.

In the context of the present invention, for improved bioavailability, it is preferred that the inventive compound has a solubility in water at 25°C of at least 0.1 µg/ml, preferably at least 1 µg/ml, more preferably at least 10 µg/ml, even more preferably at least 100 µg/ml, especially at least 1000 µg/ml.

The term "preventing" or "prevention" as used herein means to stop a disease state or condition from occurring in a patient or subject completely or almost completely or at least to a (preferably significant) extent, especially when the patient or subject or individual is predisposed to such a risk of contracting a disease state or condition.

The pharmaceutical composition of the present invention is preferably provided as a (typically aqueous) solution, (typically aqueous) suspension or (typically aqueous) emulsion. Excipients suitable for the pharmaceutical composition of the present invention are known to the person skilled in the art, upon having read the present specification, for example water (especially water for injection), saline, Ringer's solution, dextrose solution, buffers, Hank solution, vesicle forming compounds (e.g. lipids), fixed oils, ethyl oleate, 5% dextrose in saline, substances that enhance isotonicity and chemical

stability, buffers and preservatives. Other suitable excipients include any compound that does not itself induce the production of antibodies in the patient (or individual) that are harmful for the patient (or individual). Examples are well tolerable proteins, polysaccharides, polylactic acids, polyglycolic acid, polymeric amino acids and amino acid copolymers. This pharmaceutical composition can (as a drug) be administered via appropriate procedures known to the skilled person (upon having read the present specification) to a patient or individual in need thereof (i.e. a patient or individual having or having the risk of developing the diseases or conditions mentioned herein). The preferred route of administration of said pharmaceutical composition is parenteral administration, in particular through intraperitoneal, subcutaneous, intramuscular and/or intravenous administration. For parenteral administration, the pharmaceutical composition of the present invention is preferably provided in injectable dosage unit form, e.g. as a solution (typically as an aqueous solution), suspension or emulsion, formulated in conjunction with the above-defined pharmaceutically acceptable excipients. The dosage and method of administration, however, depends on the individual patient or individual to be treated. Said pharmaceutical composition can be administered in any suitable dosage known from other biological dosage regimens or specifically evaluated and optimised for a given individual. For example, the active agent may be present in the pharmaceutical composition in an amount from 1 mg to 10 g, preferably 50 mg to 2 g, in particular 100 mg to 1 g. Usual dosages can also be determined on the basis of kg body weight of the patient, for example preferred dosages are in the range of 0.1 mg to 100 mg/kg body weight, especially 1 to 10 mg/kg body weight (per administration session). The administration may occur e.g. once daily, once every other day, once per week or once every two weeks. As the preferred mode of administration of the inventive pharmaceutical composition is parenteral administration, the pharmaceutical composition according to the present invention is preferably liquid or ready to be dissolved in liquid such sterile, de-ionised or distilled water or sterile isotonic phosphate-buffered saline (PBS). Preferably, 1000 µg (dry-weight) of such a composition comprises or consists of 0.1-

990 µg, preferably 1-900µg, more preferably 10- 200µg compound, and option-ally 1-500 µg, preferably 1-100 µg, more preferably 5-15 µg (buffer) salts (preferably to yield an isotonic buffer in the final volume), and optionally 0.1-999.9 µg, preferably 100-999.9 µg, more preferably 200-999 µg other excipients. Preferably, 100 mg of such a dry composition is dissolved in sterile, de-ionised/distilled water or sterile isotonic phosphate-buffered saline (PBS) to yield a final volume of 0.1-100 ml, preferably 0.5-20 ml, more preferably 1-10 ml.

It is evident to the skilled person that active agents and drugs described herein can also be administered in salt-form (i.e. as a pharmaceutically acceptable salt of the active agent). Accordingly, any mention of an active agent herein shall also include any pharmaceutically acceptable salt forms thereof.

Methods for chemical synthesis of peptides used for the compound of the present invention are well-known in the art. Of course, it is also possible to produce the peptides using recombinant methods. The peptides can be produced in microorganisms such as bacteria, yeast or fungi, in eukaryotic cells such as mammalian or insect cells, or in a recombinant virus vector such as adenovirus, poxvirus, herpesvirus, Simliki forest virus, baculovirus, bacteriophage, sindbis virus or sendai virus. Suitable bacteria for producing the peptides include *E. coli*, *B. subtilis* or any other bacterium that is capable of expressing such peptides. Suitable yeast cells for expressing the peptides of the present invention include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida*, *Pichiapastoris* or any other yeast capable of expressing peptides. Corresponding means and methods are well known in the art. Also, methods for isolating and purifying recombinantly produced peptides are well known in the art and include e.g. gel filtration, affinity chromatography, ion exchange chromatography etc.

Beneficially, cysteine residues are added to the peptides at the N- and/or C-terminus to facilitate coupling to the biopolymer scaffold, especially.

To facilitate isolation of said peptides, fusion polypeptides may be made wherein the peptides are

translationally fused (covalently linked) to a heterologous polypeptide which enables isolation by affinity chromatography. Typical heterologous polypeptides are His-Tag (e.g. His₆; 6 histidine residues), GST-Tag (Glutathione-S-transferase) etc. The fusion polypeptide facilitates not only the purification of the peptides but can also prevent the degradation of the peptides during the purification steps. If it is desired to remove the heterologous polypeptide after purification, the fusion polypeptide may comprise a cleavage site at the junction between the peptide and the heterologous polypeptide. The cleavage site may consist of an amino acid sequence that is cleaved with an enzyme specific for the amino acid sequence at the site (e.g. proteases).

The coupling/conjugation chemistry used to link the peptides / peptide n-mers to the biopolymer scaffold (e.g. via heterobifunctional compounds such as GMBS and of course also others as described in "Bioconjugate Techniques", Greg T. Hermanson) or used to conjugate the spacer to the peptides in the context of the present invention can also be selected from reactions known to the skilled in the art. The biopolymer scaffold itself may be recombinantly produced or obtained from natural sources.

Herein, the term "specific for" - as in "molecule A specific for molecule B" - means that molecule A has a binding preference for molecule B compared to other molecules in an individual's body. Typically, this entails that molecule A (such as an antibody) has a dissociation constant (also called "affinity") in regard to molecule B (such as the antigen, specifically the binding epitope thereof) that is lower than (i.e. "stronger than") 1000 nM, preferably lower than 100 nM, more preferably lower than 50 nM, even more preferably lower than 10 nM, especially lower than 5 nM.

Herein, "UniProt" refers to the Universal Protein Resource. UniProt is a comprehensive resource for protein sequence and annotation data. UniProt is a collaboration between the European Bioinformatics Institute (EMBL-EBI), the SIB Swiss Institute of Bioinformatics and the Protein Information Resource (PIR). Across the three institutes more than 100 people are involved

through different tasks such as database curation, software development and support. Website: <http://www.uniprot.org/>

Entries in the UniProt databases are identified by their accession codes (referred to herein e.g. as "UniProt accession code" or briefly as "UniProt" followed by the accession code), usually a code of six alphanumeric letters (e.g. "Q1HVF7"). If not specified otherwise, the accession codes used herein refer to entries in the Protein Knowledgebase (UniProtKB) of UniProt. If not stated otherwise, the UniProt database state for all entries referenced herein is of 23 September 2020 (UniProt/UniProtKB Release 2020_04).

In the context of the present application, sequence variants (designated as "natural variant" in UniProt) are expressly included when referring to a UniProt database entry.

"Percent (%) amino acid sequence identity" or "X% identical" (such as "70% identical") with respect to a reference polypeptide or protein sequence is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the reference polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2, Megalign (DNASTAR) or the "needle" pairwise sequence alignment application of the EMBOSS software package. Those skilled in the art can determine appropriate parameters for aligning sequences, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are calculated using the sequence alignment of the computer programme "needle" of the EMBOSS software package (publicly available from European Molecular Biology Laboratory; Rice et al., 2000).

The needle programme can be accessed under the web site http://www.ebi.ac.uk/Tools/psa/emboss_needle/ or downloaded for

local installation as part of the EMBOSS package from <http://emboss.sourceforge.net/>. It runs on many widely-used UNIX operating systems, such as Linux.

To align two protein sequences, the needle programme is preferably run with the following parameters:

```
Commandline: needle -auto -stdout -asequence
SEQUENCE_FILE_A -bsequence SEQUENCE_FILE_B -datafile EBLOSUM62 -
gapopen 10.0 -gapextend 0.5 -endopen 10.0 -endextend 0.5 -
aformat3 pair -sprotein1 -sprotein2 (Align_format: pair
Report_file: stdout)
```

The % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program needle in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. In cases where "the sequence of A is more than N% identical to the entire sequence of B", Y is the entire sequence length of B (i.e. the entire number of amino acid residues in B). Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the needle computer program.

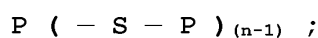
The present invention further relates to the following embodiments:

Embodiment 1. A compound comprising

- a biopolymer scaffold and at least
- a first peptide n-mer of the general formula:

$P(-S-P)_{(n-1)}$ and

- a second peptide n-mer of the general formula:



wherein, independently for each occurrence, P is a peptide with a sequence length of 6-13 amino acids, and S is a non-peptide spacer,

wherein, independently for each of the peptide n-mers, n is an integer of at least 1, preferably of at least 2, more preferably of at least 3, especially of at least 4,

wherein each of the peptide n-mers is bound to the biopolymer scaffold, preferably via a linker each,

wherein, independently for each occurrence, P has an amino-acid sequence comprising a sequence fragment with a length of at least six (preferably at least 7, more preferably at least 8, especially at least 9) amino acids of a capsid protein sequence of a viral vector, in particular of an AdV hexon protein sequence, an AdV fiber protein sequence, an AdV penton protein sequence, an AdV IIIa protein sequence, an AdV VI protein sequence, an AdV VIII protein sequence or an AdV IX protein sequence or of any one of the capsid protein sequences identified in Fig. 10 and Fig. 11 or of any one of the capsid protein sequences listed in Cearley et al., 2008,

optionally wherein at most three, preferably at most two, most preferably at least one amino acid of the sequence fragment is independently substituted by any other amino acid.

Embodiment 2. The compound of embodiment 1, wherein at least one occurrence of P is a circularized peptide, preferably wherein at least 10% of all occurrences of P are circularized peptides, more preferably wherein at least 25% of all occurrences of P are circularized peptides, yet more preferably wherein at least 50% of all occurrences of P are circularized peptides, even more preferably wherein at least 75% of all occurrences of P are circularized peptides, yet even more preferably wherein at least 90% of all occurrences of P are circularized peptides or even wherein at least 95% of all occurrences of P are circularized peptides, especially wherein all of the occurrences of P are circularized peptides.

Embodiment 3. The compound of embodiment 1 or 2, wherein, independently for each of the peptide n-mers, n is at least 2, more preferably at least 3, especially at least 4.

Embodiment 4. The compound of any one of embodiments 1 to 3, wherein, independently for each of the peptide n-mers, n is less than 10, preferably less than 9, more preferably less than 8, even more preferably less than 7, yet even more preferably less than 6, especially less than 5.

Embodiment 5. The compound of any one of embodiments 1 to 4, wherein, for each of the peptide n-mers, n is 2.

Embodiment 6. The compound of any one of embodiments 1 to 5, wherein at least one occurrence of P is P_a and/or at least one occurrence of P is P_b ,

wherein P_a is a peptide with a sequence length of 6-13 amino acids, preferably 7-11 amino acids, more preferably 7-9 amino acids,

wherein P_b is a peptide with a sequence length of 6-13 amino acids, preferably 7-11 amino acids, more preferably 7-9 amino acids.

Embodiment 7. The compound of any one of embodiments 1 to 6, wherein, independently for each occurrence, P is P_a or P_b .

Embodiment 8. The compound of any one of embodiments 1 to 7, wherein, in the first peptide n-mer, each occurrence of P is P_a and, in the second peptide n-mer, each occurrence of P is P_b .

Embodiment 9. The compound of any one of embodiments 1 to 8, wherein

the first peptide n-mer is $P_a - S - P_a$ and the second peptide n-mer is $P_a - S - P_a$; or

the first peptide n-mer is $P_a - S - P_a$ and the second peptide n-mer is $P_b - S - P_b$;

the first peptide n-mer is $P_b - S - P_b$ and the second peptide n-mer is $P_b - S - P_b$;

the first peptide n-mer is $P_a - S - P_b$ and the second peptide n-mer is $P_a - S - P_b$;

the first peptide n-mer is $P_a - S - P_b$ and the second peptide n-mer is $P_a - S - P_a$; or

the first peptide n-mer is $P_a - S - P_b$ and the second peptide n-mer is $P_b - S - P_b$.

Embodiment 10. A compound comprising

- a biopolymer scaffold and at least
- a first peptide n-mer which is a peptide dimer of the formula $P_a - S - P_a$ or $P_a - S - P_b$,

wherein P_a is a peptide with a sequence length of 6-13 amino acids, preferably 7-11 amino acids, more preferably 7-9 amino acids, P_b is a peptide with a sequence length of 6-13 amino acids, preferably 7-11 amino acids, more preferably 7-9 amino acids, and S is a non-peptide spacer,

wherein the first peptide n-mer is bound to the biopolymer scaffold, preferably via a linker,

wherein P_a has an amino-acid sequence comprising a sequence fragment with a length of at least six, preferably at least seven, more preferably at least eight, especially at least 9 (or 10, 11, 12 or 13) amino acids of a capsid protein sequence of a (non-pathogenic) viral vector, in particular of an AdV hexon protein sequence, an AdV fiber protein sequence, an AdV penton protein sequence, an AdV IIIa protein sequence, an AdV VI protein sequence, an AdV VIII protein sequence or an AdV IX protein sequence or of any one of the capsid protein sequences identified in Fig. 10 and Fig. 11 or of any one of the capsid protein sequences listed in Cearley et al., 2008, optionally wherein at most three, preferably at most two, most preferably at least one amino acid of the sequence fragment is independently substituted by any other amino acid.

Embodiment 11. The compound of embodiment 10, further comprising a second peptide n-mer which is a peptide dimer of the formula $P_b - S - P_b$ or $P_a - S - P_b$,

wherein the second peptide n-mer is bound to the biopolymer scaffold, preferably via a linker,

wherein P_b has an amino-acid sequence comprising a sequence fragment with a length of at least six, preferably at least seven, more preferably at least eight, especially at least 9 (or 10, 11, 12 or 13) amino acids of a capsid protein sequence of a (non-pathogenic) viral vector, in particular of an AdV hexon

protein sequence, an AdV fiber protein sequence, an AdV penton protein sequence, an AdV IIIa protein sequence, an AdV VI protein sequence, an AdV VIII protein sequence or an AdV IX protein sequence or of any one of the capsid protein sequences identified in Fig. 10 and Fig. 11 or of any one of the capsid protein sequences listed in Cearley et al., 2008, optionally wherein at most three, preferably at most two, most preferably at least one amino acid of the sequence fragment is independently substituted by any other amino acid.

Embodiment 12. The compound of any one of embodiments 1 to 9 and 11, wherein the first peptide n-mer is different from the second peptide n-mer.

Embodiment 13. The compound of any one of embodiments 6 to 12, wherein the peptide P_a is different from the peptide P_b, preferably wherein the peptide P_a and the peptide P_b are two different epitopes of the same capsid antigen or two different epitope parts of the same capsid epitope.

Embodiment 14. The compound of any one of embodiments 6 to 13, wherein the peptide P_a and the peptide P_b comprise the same amino-acid sequence fragment, wherein the amino-acid sequence fragment has a length of at least 2 amino acids, preferably at least 3 amino acids, more preferably at least 4 amino acids, yet more preferably at least 5 amino acids, even more preferably at least 6 amino acids, yet even more preferably at least 7 amino acids, especially at least 8 amino acids or even at least 9 amino acids.

Embodiment 15. The compound of any one of embodiments 6 to 14, wherein P_a and/or P_b is circularized.

Embodiment 16. The compound of any one of embodiments 1 to 15, wherein the compound comprises a plurality of said first peptide n-mer and/or a plurality of said second peptide n-mer.

Embodiment 17. The compound of any one of embodiments 1 to 16, wherein the biopolymer scaffold is a protein, preferably a mammalian protein such as a human protein, a non-human primate protein, a sheep protein, a pig protein, a dog protein or a rodent protein.

Embodiment 18. The compound of embodiment 17, wherein the biopolymer scaffold is a globulin.

Embodiment 19. The compound of embodiment 18, wherein the biopolymer scaffold is selected from the group consisting of immunoglobulins, alpha1-globulins, alpha2-globulins and beta-globulins.

Embodiment 20. The compound of embodiment 19, wherein the biopolymer scaffold is selected from the group consisting of immunoglobulin G, haptoglobin and transferrin.

Embodiment 21. The compound of embodiment 20, wherein the biopolymer scaffold is haptoglobin.

Embodiment 22. The compound of embodiment 17, wherein the biopolymer scaffold is an albumin.

Embodiment 23. The compound of any one of embodiments 1 to 22, wherein the compound is non-immunogenic in a mammal, preferably in a human, in a non-human primate, in a sheep, in a pig, in a dog or in a rodent.

Embodiment 24. The compound of any one of embodiments 1 to 23, wherein the compound is for intracorporeal sequestration (or intracorporeal depletion) of at least one antibody (against the viral vector or neutralizing the viral vector) in an individual, preferably in the bloodstream of the individual and/or for reduction of the titre of at least one antibody (against the viral vector or neutralizing the viral vector) in the individual, preferably in the bloodstream of the individual.

Embodiment 25. The compound of any one of embodiments 1 to 24, wherein the viral vector is an adenovirus (AdV) vector or an adeno-associated virus (AAV) vector.

Embodiment 26. The compound of any one of embodiments 1 to 25, wherein the entire sequence, optionally with the exception of an N-terminal and/or C-terminal cysteine, of at least one occurrence of P, preferably of at least 10% of all occurrences of P, more preferably of at least 25% of all occurrences of P, yet more preferably of at least 50% of all occurrences of P, even more preferably of at least 75% of all occurrences of P, yet even more preferably of at least 90% of all occurrences of P or even of at least 95% of all occurrences of P, especially of all of the occurrences of P, is identical to a sequence fragment of a protein, wherein the protein is identified by one of the following UniProt accession codes:

A9RAI0, B5SUY7, O41855, O56137, O56139, P03135, P04133, P04882, P08362, P10269, P12538, P69353, Q5Y9B2, Q5Y9B4, Q65311, Q6JC40, Q6VGT5, Q8JQF8, Q8JQG0, Q98654, Q9WBP8, Q9YIJ1, or of an AdV hexon protein, an AdV fiber protein, an AdV penton protein, an AdV IIIa protein, an AdV VI protein, an AdV VIII protein or an AdV IX protein or of any one of the capsid proteins identified in Fig. 10 and Fig. 11 or of any one of the capsid proteins listed in Cearley et al., 2008;

optionally wherein the sequence fragment comprises at most three, even more preferably at most two, especially at most one amino acid substitutions.

Embodiment 27. The compound of any one of embodiments 1 to 26, wherein the entire sequence, optionally with the exception of an N-terminal and/or C-terminal cysteine, of peptide P_a is identical to a sequence fragment of a protein, wherein the protein is identified by one of the UniProt accession codes listed in embodiment 26;

optionally wherein the sequence fragment comprises at most three, even more preferably at most two, especially at most one amino acid substitutions.

Embodiment 28. The compound of any one of embodiments 1 to 27, wherein the entire sequence, optionally with the exception of an N-terminal and/or C-terminal cysteine, of peptide P_b is identical to a sequence fragment of a protein, wherein the protein is identified by one of the UniProt accession codes listed in embodiment 26;

optionally wherein the sequence fragment comprises at most three, even more preferably at most two, especially at most one amino acid substitutions.

Embodiment 29. The compound of any one of embodiments 1 to 28, wherein the entire sequence, optionally with the exception of an N-terminal and/or C-terminal cysteine, of peptide P_a is identical to a sequence fragment of a protein and the entire sequence, optionally with the exception of an N-terminal and/or C-terminal cysteine, of peptide P_b is identical to the same or another, preferably another, sequence fragment of the same protein, wherein the protein is identified by one of the UniProt accession codes listed in embodiment 26;

optionally wherein the sequence fragment comprises at most three, even more preferably at most two, especially at most one amino acid substitutions.

Embodiment 30. The compound of any one of embodiments 1 to 29, wherein said sequence fragment comprises a sequence of at least 4 or at least 5 or at least 6, preferably at least 7, more preferably at least 8, even more preferably at least 9, yet even more preferably at least 10 consecutive amino acids selected from:

the group of AdV sequences ETGPPTVPFLTPPF (SEQ ID NO: 32), HDSKLSIATQGGL (SEQ ID NO: 33), LNLRLGQGGLFINSAHNLDINY (SEQ ID NO: 34), VDPMDPEPTLLYVLFVFDVV (SEQ ID NO: 35), MKRARPSEDTFNPVYPYD (SEQ ID NO: 36), ISGTVQSAHLIIRFD (SEQ ID NO: 37), LGQGGLFINSAHNLDINYNGGLYLF (SEQ ID NO: 38), SYPFDAQNLNRLRGQGLFIN (SEQ ID NO: 39), GDTTPSAYSMSFSWDWSGHNIN (SEQ ID NO: 40), VLLNNSFLDPEYWNFRN (SEQ ID NO: 41), HNYINEIFATSSYTFSYIA (SEQ ID NO: 42), DEATALEINLEEEEDDDNEDEVDEQAEQQKTH (SEQ ID NO: 43), INLEEEEDDDNEDEVDEQAEQ (SEQ ID NO: 44), DNEDEVDEQAEQQKTHVF (SEQ ID NO: 45), EWDEATALEINLEE (SEQ ID NO: 46), PKVVLISEDVDIETPDTHISYMP (SEQ ID NO: 47), YIPESYKDRMYSFFRNF (SEQ ID NO: 48), DSIGDRTRYFSMW (SEQ ID NO: 49), SYKDRMYSFFRNF (SEQ ID NO: 50), and FLVQMLANYNIGYQGFY (SEQ ID NO: 51), or

the group of AAV sequences WQNRDVYLQGPWAKIP (SEQ ID NO: 52), DNTYFGYSTPWGYFDFNRFHC (SEQ ID NO: 53), MANQAKNWLPGPCY (SEQ ID NO: 54), LPYVLGSAHQGLPPFP (SEQ ID NO: 55), NGSQAVGRSSFYCLEYF (SEQ ID NO: 56), PLIDQYLYYL (SEQ ID NO: 57), EERFFPSNGILIF (SEQ ID NO: 58) ADGVGSSSGNWHC (SEQ ID NO: 59), SEQ ID NOs: 383-1891 (see Table 1) - preferably group III of Table 1, more preferably group II of Table 1, especially group I of Table 1 - and SEQ ID NOs: 1892-2063 (see Table 2) - preferably group I of Table 2 - and sequences of group II or III of Table 3 (in particular SEQ ID NOs: 2064-2103), more preferably sequences of group I of Table 3, or

the group of sequences of Table 4, in particular the group of sequences identified by SEQ ID NOs: 2104-2190;

optionally wherein at most three, preferably at most two, most preferably at least one amino acid of the sequence fragment is independently substituted by any other amino acid.

Embodiment 31. The compound of any one of embodiments 1 to 30, wherein, independently for each occurrence, P comprises a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences consisting of GPPTVPFLTP (SEQ ID NO: 60), ETGPPTVPFLTPP (SEQ ID NO: 61), TGPPTVPFLT (SEQ ID NO: 62), PTVPFLTPPF (SEQ ID NO: 63), HDSKLSIATQGGL (SEQ ID NO: 64), SIATQGP (SEQ ID NO: 65), NLRLGQGGLF (SEQ ID NO: 66), QGGLFINSAH (SEQ ID NO: 67), PLFINSAHNLD (SEQ ID NO: 68), LGQGGLF (SEQ ID NO: 69), LNLRLGQGGL (SEQ ID NO: 70), GQGGLFI (SEQ ID NO: 71), NLRLGQGGLFINS (SEQ ID NO: 72), LFINSAHNLDINY (SEQ ID NO: 73), FINSAHNLDI (SEQ ID NO: 74), LRLGQGGLFI (SEQ ID NO: 75), GPLFINSAHN (SEQ ID NO: 76), DEPTLLYVLFEVF (SEQ ID NO: 77), TLLYVLFEVF (SEQ ID NO: 78), DEPTLLYVLF (SEQ ID NO: 79), TLLYVLFEVFDVV (SEQ ID NO: 80), TLLYVLF (SEQ ID NO: 81), MDEPTLLYVLFEV (SEQ ID NO: 82), EPTLLYVLFE (SEQ ID NO: 83), DPMDEPTLLYVLF (SEQ ID NO: 84), LLYVLFEVFD (SEQ ID NO: 85), YVLFEVFDVV (SEQ ID NO: 86), PTLLYVLFEV (SEQ ID NO: 87), PTLLYVLFEVFDV (SEQ ID NO: 88), LYVLFEVFDV (SEQ ID NO: 89), EPTLLYVLFEVFD (SEQ ID NO: 90), LYVLFEV (SEQ ID NO: 91), PMDEPTLLYVLFE (SEQ ID NO: 92), LLYVLFE (SEQ ID NO: 93), VDPMDEPTLLYVL (SEQ ID NO: 94), YVLFEVF (SEQ ID NO: 95), PTLLYVL (SEQ ID NO: 96), MKRARPS EDTF (SEQ ID NO: 97), KRARPS EDTF (SEQ ID NO: 98), MKRARPS EDT (SEQ ID NO: 99), MKRARPS EDTFN (SEQ ID NO: 100), ARPS EDTFNP (SEQ ID NO: 101), RARPS EDTFN (SEQ ID NO: 102), RPS EDTF (SEQ ID NO: 103), MKRARPS EDTFNP (SEQ ID NO: 104), RARPS EDTFNPVY (SEQ ID NO: 105), ARPS EDT (SEQ ID NO: 106), EDTFNPVYPY (SEQ ID NO: 107), RPS EDTFNPVYPY (SEQ ID NO: 108), KRARPS EDTFNPV (SEQ ID NO: 109), DTFNPVY (SEQ ID NO: 110), RPS EDTFNPV (SEQ ID NO: 111), PS EDTFNPVY (SEQ ID NO: 112), DTFNPVYPYD (SEQ ID NO: 113), VQSAHLIIRF (SEQ ID NO: 114), AHLIIRF (SEQ ID NO: 115), SGT VQSAHLIIRF (SEQ ID NO: 116), TVQSAHLIIR (SEQ ID NO: 117), HLIIRFD (SEQ ID NO: 118), SAHLIIR (SEQ ID NO: 119), QSAHLIIRFD (SEQ ID NO: 120), ISGT VQSAHLIIR

(SEQ ID NO: 121), GTVQSAHLII (SEQ ID NO: 122), GTVQSAHLIIRFD
(SEQ ID NO: 123), QSAHLII (SEQ ID NO: 124), HNLDINY (SEQ ID NO:
125), LFINSAHNLDINY (SEQ ID NO: 126), NLDINYNKGLYLF (SEQ ID NO:
127), FVSPNG (SEQ ID NO: 128), NYINEIF (SEQ ID NO: 129), NKGLYLF
(SEQ ID NO: 130), INYNKGLYLF (SEQ ID NO: 131), NSAHNLDINY (SEQ
ID NO: 132), WDWSGHNYINEIF (SEQ ID NO: 133), SGHNYINEIF (SEQ ID
NO: 134), LGTGLSF (SEQ ID NO: 135), PFLTPPF (SEQ ID NO: 136),
LGQGPLF (SEQ ID NO: 137), NLRLGQGPLF (SEQ ID NO: 138),
NQLNLRLGQGPLF (SEQ ID NO: 139), GQGPLFI (SEQ ID NO: 140),
QLNLRLGQGPLFI (SEQ ID NO: 141), SYPFDAQNQLNLR (SEQ ID NO: 142),
YPFDAQNQLNLRL (SEQ ID NO: 143), LRLGQGPLFI (SEQ ID NO: 144),
NQLNLRL (SEQ ID NO: 145), FDAQNQLNLR (SEQ ID NO: 146), QNQLNLR
(SEQ ID NO: 147), QGPLFIN (SEQ ID NO: 148), PFDAQNQLNLRLG (SEQ
ID NO: 149), DAQNQLNLRL (SEQ ID NO: 150), RLGQGPLFIN (SEQ ID NO:
151), QLNLRG (SEQ ID NO: 152), FDAQNQLNLRLGQ (SEQ ID NO: 153),
LNLRLGQGPLFIN (SEQ ID NO: 154), AQNQLNLRLG (SEQ ID NO: 155),
AQNQLNL (SEQ ID NO: 156), LNLRLGQ (SEQ ID NO: 157), SYPFDAQNQL
(SEQ ID NO: 158), PFDAQNQLNL (SEQ ID NO: 159), YSMSFSW (SEQ ID
NO: 160), TPSAYSMSFSWDW (SEQ ID NO: 161), MSFSWDW (SEQ ID NO:
162), PSAYSMSFSW (SEQ ID NO: 163), DTPSAYSMSFSW (SEQ ID NO:
164), TTPSAYSMSF (SEQ ID NO: 165), YSMSFSWDWS (SEQ ID NO: 166),
TGDTPSAYSMSF (SEQ ID NO: 167), FSWDWSGHNY (SEQ ID NO: 168),
SFSWDWS (SEQ ID NO: 169), SAYSMSF (SEQ ID NO: 170), SFSWDWSGHN
(SEQ ID NO: 171), SAYSMSFSWD (SEQ ID NO: 172), SMSFSWD (SEQ ID
NO: 173), SWDWSGHNYI (SEQ ID NO: 174), AYSMSFS (SEQ ID NO: 175),
SMSFSWDWSGHNY (SEQ ID NO: 176), FSWDWSG (SEQ ID NO: 177),
SWDWSGH (SEQ ID NO: 178), FLDPEYWNFR (SEQ ID NO: 179),
SFLDPEYWNF (SEQ ID NO: 180), PEYWNFR (SEQ ID NO: 181),
LNNSFLDPEYWNF (SEQ ID NO: 182), NNSFLDPEYWNFR (SEQ ID NO: 183),
FLDPEYW (SEQ ID NO: 184), DPEYWNF (SEQ ID NO: 185), NNSFLDPEYW
(SEQ ID NO: 186), VLLNNSFLDPEYW (SEQ ID NO: 187), EYWNFRN (SEQ
ID NO: 188), LNNSFLDPEY (SEQ ID NO: 189), LDPEYWNFRN (SEQ ID NO:
190), LNNSFLD (SEQ ID NO: 191), NSFLDPEYWN (SEQ ID NO: 192),
SSYTFSY (SEQ ID NO: 193), FATSSYTFSY (SEQ ID NO: 194),
YINEIFATSSYTF (SEQ ID NO: 195), SYTFSYI (SEQ ID NO: 196),
ATSSYTF (SEQ ID NO: 197), EIFATSSYTF (SEQ ID NO: 198),
NEIFATSSYTFSY (SEQ ID NO: 199), ATSSYTFSYI (SEQ ID NO: 200),
HNYINEIFATSSY (SEQ ID NO: 201), IFATSSY (SEQ ID NO: 202),
INEIFATSSY (SEQ ID NO: 203), NYINEIFATSSYT (SEQ ID NO: 204),

YINEIFA (SEQ ID NO: 205), YTFSYIA (SEQ ID NO: 206),
EIFATSSYTFYSI (SEQ ID NO: 207), ALEINLEEEDDDN (SEQ ID NO: 208),
ATALEINLEEEDD (SEQ ID NO: 209), EAATALEINLEEE (SEQ ID NO: 210),
LEINLEE (SEQ ID NO: 211), TALEINLEEEDDD (SEQ ID NO: 212),
EINLEEE (SEQ ID NO: 213), ALEINLEEED (SEQ ID NO: 214),
LEINLEEEDD (SEQ ID NO: 215), TALEINLEEE (SEQ ID NO: 216),
DEAATALEINLEE (SEQ ID NO: 217), LEINLEEEDDDNE (SEQ ID NO: 218),
AATALEINLEEED (SEQ ID NO: 219), EINLEEEDDD (SEQ ID NO: 220),
ATALEINLEE (SEQ ID NO: 221), INLEEEDDDN (SEQ ID NO: 222),
NLEEEDDDNE (SEQ ID NO: 223), DEVDEQA (SEQ ID NO: 224),
EDDDNEDEVDEQA (SEQ ID NO: 225), DDNEDEVDEQAEQ (SEQ ID NO: 226),
EVDEQAE (SEQ ID NO: 227), DNEDEVDEQA (SEQ ID NO: 228), VDEQAEQ
(SEQ ID NO: 229), EDEVDEQAEQQKT (SEQ ID NO: 230), EDEVDEQAEQ
(SEQ ID NO: 231), DEVDEQAEQQKTH (SEQ ID NO: 232), NEDEVDEQAEQQK
(SEQ ID NO: 233), DEVDEQAEQQ (SEQ ID NO: 234), EINLEEEDDDNED
(SEQ ID NO: 235), NLEEEDDDNEDEV (SEQ ID NO: 236), INLEEED (SEQ
ID NO: 237), LEEEDDDNED (SEQ ID NO: 238), INLEEEDDDNEDE (SEQ ID
NO: 239), DDDNEDEVDEQAE (SEQ ID NO: 240), LEEEDDDNEDEV (SEQ ID
NO: 241), DDNEDEVDEQ (SEQ ID NO: 242), EDDDNED (SEQ ID NO: 243),
NLEEEDD (SEQ ID NO: 244), DDNEDEV (SEQ ID NO: 245), DDDNEDEVDE
(SEQ ID NO: 246), DDDNEDE (SEQ ID NO: 247), EEEDDDNEDE (SEQ ID
NO: 248), EEEDDDNE (SEQ ID NO: 249), EDDDNED (SEQ ID NO: 250),
EDEVDEQ (SEQ ID NO: 251), EEEDDDNEDEVDEQ (SEQ ID NO: 252),
EEEDDDNEDEV (SEQ ID NO: 253), EEEDDDNEDEVDE (SEQ ID NO: 254),
EVDEQAEQQK (SEQ ID NO: 255), DNEDEVDEQAEQQ (SEQ ID NO: 256),
VDEQAEQQKT (SEQ ID NO: 257), EVDEQAEQQKTHV (SEQ ID NO: 258),
VDEQAEQQKTHVF (SEQ ID NO: 259), ALEINLE (SEQ ID NO: 260),
WDEAATALEINLE (SEQ ID NO: 261), AATALEINLE (SEQ ID NO: 262),
EWDEAATALEINL (SEQ ID NO: 263), EAATALEINL (SEQ ID NO: 264),
LYSEDVDIET (SEQ ID NO: 265), LYSEDVDIETPDT (SEQ ID NO: 266),
KVVLYSEDVDIET (SEQ ID NO: 267), IETPDTH (SEQ ID NO: 268),
VDIETPDTHI (SEQ ID NO: 269), VLYSEDVDIE (SEQ ID NO: 270),
DVDIETPDTHISY (SEQ ID NO: 271), VVLYSEDVDIETP (SEQ ID NO: 272),
SEDVDIETPDTHI (SEQ ID NO: 273), ETPDTHI (SEQ ID NO: 274),
VLYSEDVDIETPD (SEQ ID NO: 275), DVDIETPDTH (SEQ ID NO: 276),
DIETPDTHIS (SEQ ID NO: 277), EDVDIETPDTHIS (SEQ ID NO: 278),
IETPDTHISY (SEQ ID NO: 279), YSEDVDIETPDTH (SEQ ID NO: 280),
VDIETPDTHISYM (SEQ ID NO: 281), PKVVLYSEDVDIE (SEQ ID NO: 282),
DIETPDT (SEQ ID NO: 283), DIETPDTHISYM (SEQ ID NO: 284),

EDVDIETPDT (SEQ ID NO: 285), ETPDTHISYM (SEQ ID NO: 286), IETPDTHISYMP (SEQ ID NO: 287), DRMYSFFRNF (SEQ ID NO: 288), DRMYSFF (SEQ ID NO: 289), YSFFRNF (SEQ ID NO: 290), IPESYKDRMYSFF (SEQ ID NO: 291), SYKDRMYSFF (SEQ ID NO: 292), ESYKDRMYSF (SEQ ID NO: 293), KDRMYSF (SEQ ID NO: 294), YIPESYKDRMYSF (SEQ ID NO: 295), PESYKDRMYSFFR (SEQ ID NO: 296), YKDRMYSFFR (SEQ ID NO: 297), TRYFSMW (SEQ ID NO: 298), GDRTRYF (SEQ ID NO: 299), DSIGDRTRYF (SEQ ID NO: 300), DSIGDRTRYFSMW (SEQ ID NO: 301), GDRTRYFSMW (SEQ ID NO: 302), DRMYSFFRNF (SEQ ID NO: 303), SYKDRMYSFFRNF (SEQ ID NO: 304), NYNIGYQGFY (SEQ ID NO: 305), ANYNIGYQGF (SEQ ID NO: 306), MLANYNIGYQGFY (SEQ ID NO: 307), IGYQGFY (SEQ ID NO: 308), FLVQMLANYNIGY (SEQ ID NO: 309), NIGYQGF (SEQ ID NO: 310) and QMLANYNIGYQGF (SEQ ID NO: 311), , optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid.

Embodiment 32. The compound of any one of embodiments 1 to 30, wherein, independently for each occurrence, P comprises a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences consisting of YLQGPIW (SEQ ID NO: 312), VYLQGPI (SEQ ID NO: 313), WQNRDVY (SEQ ID NO: 314), DVYLQGP (SEQ ID NO: 315), QNRDVYL (SEQ ID NO: 316), LQGPIWA (SEQ ID NO: 317), RDVYLQG (SEQ ID NO: 318), NRDVYLQ (SEQ ID NO: 319), YFGYSTPWGYFDF (SEQ ID NO: 320), FGYSTPWGYF (SEQ ID NO: 321), GYSTPWGYFD (SEQ ID NO: 322), YSTPWGYFDF (SEQ ID NO: 323), NTYFGYSTPWGYF (SEQ ID NO: 324), TPWGYFDFNRFHC (SEQ ID NO: 325), TYFGYSTPWGYFD (SEQ ID NO: 326), DNTYFGYSTPWGY (SEQ ID NO: 327), YFGYSTPWGY (SEQ ID NO: 328), FGYSTPWGYFDFN (SEQ ID NO: 329), NWLPGPC (SEQ ID NO: 330), WLPGPCY (SEQ ID NO: 331), QAKNWLPGPC (SEQ ID NO: 332), AKNWLPGPCY (SEQ ID NO: 333), MANQAKNWLPGPC (SEQ ID NO: 334), QGCLPPF (SEQ ID NO: 335), GCLPPFP (SEQ ID NO: 336), VLGSAHQGCLPPF (SEQ ID NO: 337), LPYVLGSAHQGCL (SEQ ID NO: 338), YVLGSAHQGC (SEQ ID NO: 339), CLPPFPA (SEQ ID NO: 340), SAHQGCLPPF (SEQ ID NO: 341), VLGSAHQGCL (SEQ ID NO: 342), PYVLGSAHQGCLP (SEQ ID NO: 343), GRSSFYC (SEQ ID NO: 344), AVGRSSFYCLEYF (SEQ ID NO: 345), AVGRSSFYCL (SEQ ID NO: 346),

QAVGRSSFYCLEY (SEQ ID NO: 347), NGSQAVGRSSFYC (SEQ ID NO: 348), DQYLYYL (SEQ ID NO: 349), PLIDQYLYYL (SEQ ID NO: 350), IDQYLYY (SEQ ID NO: 351), FFPSNGILIF (SEQ ID NO: 352), EERFFPSNGILIF (SEQ ID NO: 353), VGSSSGNWHC (SEQ ID NO: 354) and ADGVGSSSGNWHC (SEQ ID NO: 355), optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid; or wherein, independently for each occurrence, P comprises a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment or even a 11-amino-acid-fragment or yet even a 12-amino-acid-fragment, especially a 13-amino-acid-fragment selected from the group of sequences consisting of SEQ ID NOs: 383-1891 (see Table 1) - preferably group III of Table 1, more preferably group II of Table 1, especially group I of Table 1 - and SEQ ID NOs: 1892-2063 (see Table 2) - preferably group I of Table 2 - and sequences of group II or III of Table 3 (in particular SEQ ID NOs: 2064-2103), more preferably sequences of group I of Table 3, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid; or wherein, independently for each occurrence, P comprises a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment or even a 11-amino-acid-fragment or yet even a 12-amino-acid-fragment, especially a 13-amino-acid-fragment selected from the group of sequences of Table 4, in particular the group of sequences identified by SEQ ID NOs: 2104-2190, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid.

Embodiment 33. The compound of any one of embodiments 1 to 32, wherein, independently for each occurrence, P consists of a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences set forth in embodiment 31 or selected from the

group of sequences set forth in embodiment 32, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid, optionally with an N-terminal and/or C-terminal cysteine residue.

Embodiment 34. The compound of any one of embodiments 1 to 33, wherein each of the peptide n-mers is covalently bound to the biopolymer scaffold, preferably via a linker each.

Embodiment 35. The compound of any one of embodiments 1 to 34, wherein at least one of said linkers is selected from disulphide bridges and PEG molecules.

Embodiment 36. The compound of any one of embodiments 1 to 35, wherein at least one of the spacers S is selected from PEG molecules or glycans.

Embodiment 37. The compound of any one of embodiments 1 to 36, wherein P_a comprises a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences set forth in embodiment 31, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid.

Embodiment 38. The compound of any one of embodiments 1 to 37, wherein P_b comprises a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences set forth in embodiment 31, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid.

Embodiment 39. The compound of any one of embodiments 1 to 36, wherein P_a comprises a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences set forth in

embodiment 32, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid.

Embodiment 40. The compound of any one of embodiments 1 to 37, wherein P_b comprises a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences set forth in embodiment 32, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid.

Embodiment 41. The compound of any one of embodiments 6 to 40, wherein the first peptide n-mer is $P_a - S - P_b$ and the second peptide n-mer is $P_a - S - P_b$.

Embodiment 42. The compound of any one of embodiments 6 to 41, wherein the peptide P_a and the peptide P_b comprise the same amino-acid sequence fragment, wherein the amino-acid sequence fragment has a length of at least 5 amino acids, even more preferably at least 6 amino acids, yet even more preferably at least 7 amino acids, especially at least 8 amino acids or even at least 9 amino acids.

Embodiment 43. The compound of any one of embodiments 1 to 42, wherein P_a consists of a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences set forth in embodiment 31, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid, optionally with an N-terminal and/or C-terminal cysteine residue.

Embodiment 44. The compound of any one of embodiments 1 to 43, wherein P_b consists of a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences set forth in

embodiment 31, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid, optionally with an N-terminal and/or C-terminal cysteine residue.

Embodiment 45. The compound of any one of embodiments 1 to 42, wherein P_a consists of a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences set forth in embodiment 32, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid, optionally with an N-terminal and/or C-terminal cysteine residue.

Embodiment 46. The compound of any one of embodiments 1 to 43, wherein P_b consists of a 6-amino-acid fragment, preferably a 7-amino-acid-fragment, more preferably a 8-amino-acid-fragment, even more preferably a 9-amino-acid fragment, yet even more preferably a 10-amino-acid fragment, especially an entire sequence selected from the group of sequences set forth in embodiment 32, optionally wherein at most three, preferably at most two, most preferably at least one amino acid is independently substituted by any other amino acid, optionally with an N-terminal and/or C-terminal cysteine residue

Embodiment 47. The compound of embodiments 1 to 46, wherein the first peptide n-mer is $P_a - S - P_b$ and the second peptide n-mer is $P_a - S - P_b$.

Embodiment 48. The compound of embodiments 1 to 47, wherein the peptide P_a and the peptide P_b comprise the same amino-acid sequence fragment, wherein the amino-acid sequence fragment has a length of at least 5 amino acids, even more preferably at least 6 amino acids, yet even more preferably at least 7 amino acids, especially at least 8 amino acids or even at least 9 amino acids.

Embodiment 49. The compound of any one of embodiments 1 to 48, wherein the viral vector is non-pathogenic (in the individual to be treated).

Embodiment 50. The compound of any one of embodiments 1 to 49, wherein the biopolymer scaffold is an anti-CD163 antibody (i.e. an antibody specific for a CD163 protein) or CD163-binding fragment thereof.

Embodiment 51. The compound of embodiment 50, wherein the anti-CD163 antibody or CD163-binding fragment thereof is specific for human CD163 and/or is specific for the extracellular region of CD163, preferably for an SRCR domain of CD163, more preferably for any one of SRCR domains 1-9 of CD163, even more preferably for any one of SRCR domains 1-3 of CD163, especially for SRCR domain 1 of CD163.

Embodiment 52. The compound of embodiment 50 or 51, wherein the anti-CD163 antibody or CD163-binding fragment thereof is specific for one of the following peptides:

a peptide consisting of 7-25, preferably 8-20, even more preferably 9-15, especially 10-13 amino acids, wherein the peptide comprises the amino acid sequence CSGRVEVKVQEEWGTVCNNGWSMEA (SEQ ID NO: 3) or a 7-24 amino-acid fragment thereof,

a peptide consisting of 7-25, preferably 8-20, even more preferably 9-15, especially 10-13 amino acids, wherein the peptide comprises the amino acid sequence DHVSCRGNESALWDCKHDGWG (SEQ ID NO: 13) or a 7-20 amino-acid fragment thereof, or

a peptide consisting of 7-25, preferably 8-20, even more preferably 9-15, especially 10-13 amino acids, wherein the peptide comprises the amino acid sequence SSLGGTDKELRLVDGENKCS (SEQ ID NO: 24) or a 7-19 amino-acid fragment thereof.

Embodiment 53. The compound of embodiment 50 or 51, wherein the anti-CD163 antibody or CD163-binding fragment thereof is specific for a peptide comprising the amino acid sequence ESALW (SEQ ID NO: 14) or ALW.

Embodiment 54. The compound of embodiment 50 or 51, wherein the anti-CD163 antibody or CD163-binding fragment thereof is specific for a peptide comprising the amino acid sequence GRVEVKVQEEW (SEQ ID NO: 4), WGTVCNNGWS (SEQ ID NO: 5) or WGTVCNNGW (SEQ ID NO: 6).

Embodiment 55. The compound of embodiment 50 or 51, wherein the anti-CD163 antibody or CD163-binding fragment thereof is specific for a peptide comprising the amino acid sequence SSLGGTDKELR (SEQ ID NO: 25) or SSLGG (SEQ ID NO: 26).

Embodiment 56. The compound of any one of embodiments 1 to 55, wherein the viral vector is AAV1, AAV2, AAV3, AAV5, AAV7 or AAV8.

Embodiment 57. The compound of any one of embodiments 1 to 55, wherein the viral vector is AAV8.

Embodiment 58. The compound of any one of embodiments 1 to 55, wherein the viral vector is Ad5.

Embodiment 59. The compound of any one of embodiments 58, wherein the viral vector is AdHu5.

Embodiment 60. The compound of any one of embodiments 1 to 59, wherein the viral vector is a viral vector specific for a mammal, in particular a human.

Embodiment 61. The compound of any one of embodiments 1 to 60, wherein the biopolymer scaffold is selected from human immunoglobulins and human transferrin.

Embodiment 62. The compound of embodiment any one of embodiments 1 to 61, wherein the biopolymer scaffold is human transferrin.

Embodiment 63. The compound of any one of embodiments 49 to 62, wherein at least one of the at least two peptides is circularized.

Embodiment 64. The compound of any one of embodiments 1 to 63, wherein the compound is non-immunogenic in humans.

Embodiment 65. A pharmaceutical composition comprising the compound of any one of embodiments 1 to 64 and at least one pharmaceutically acceptable excipient.

Embodiment 66. The pharmaceutical composition of embodiment 65, wherein the composition is prepared for intraperitoneal, subcutaneous, intramuscular and/or intravenous administration and/or wherein the composition is for repeated administration.

Embodiment 67. The pharmaceutical composition of any one of embodiments 1 to 66, wherein the molar ratio of peptide P to biopolymer scaffold in the composition is from 2:1 to 100:1,

preferably from 3:1 to 90:1, more preferably from 4:1 to 80:1, even more preferably from 5:1 to 70:1, yet even more preferably from 6:1 to 60:1, especially from 7:1 to 50:1 or even from 8:10 to 40:1.

Embodiment 68. The pharmaceutical composition of any one of embodiments 6 to 67, wherein the molar ratio of peptide P_a to biopolymer scaffold in the composition is from 2:1 to 100:1, preferably from 3:1 to 90:1, more preferably from 4:1 to 80:1, even more preferably from 5:1 to 70:1, yet even more preferably from 6:1 to 60:1, especially from 7:1 to 50:1 or even from 8:10 to 40:1.

Embodiment 69. The pharmaceutical composition of any one of embodiments 6 to 68, wherein the molar ratio of peptide P_b to biopolymer scaffold in the composition is from 2:1 to 100:1, preferably from 3:1 to 90:1, more preferably from 4:1 to 80:1, even more preferably from 5:1 to 70:1, yet even more preferably from 6:1 to 60:1, especially from 7:1 to 50:1 or even from 8:10 to 40:1.

Embodiment 70. The pharmaceutical composition of any one of embodiments 65 to 69 for use in therapy.

Embodiment 71. The pharmaceutical composition for use according to embodiment 70, for use in increasing efficacy of a vaccine in an individual, wherein the vaccine comprises the viral vector, preferably wherein the pharmaceutical composition is administered to the individual prior to or concurrently with administration of the vaccine.

Embodiment 72. The pharmaceutical composition for use according to embodiment 71, wherein the pharmaceutical composition is administered at least twice within a 96-hour window, preferably within a 72-hour window, more preferably within a 48-hour window, even more preferably within a 36-hour window, yet even more preferably within a 24-hour window, especially within a 18-hour window or even within a 12-hour window; preferably wherein this window is followed by administration of the vaccine within 24 hours, preferably within 12 hours.

Embodiment 73. The pharmaceutical composition for use according to embodiment 70, for use in increasing efficacy of a gene therapy composition in an individual, wherein the gene therapy

composition comprises the viral vector, preferably wherein the pharmaceutical composition is administered to the individual prior to or concurrently with administration of the gene therapy composition.

Embodiment 74. The pharmaceutical composition for use according to embodiment 73, wherein the pharmaceutical composition is administered at least twice within a 96-hour window, preferably within a 72-hour window, more preferably within a 48-hour window, even more preferably within a 36-hour window, yet even more preferably within a 24-hour window, especially within a 18-hour window or even within a 12-hour window; preferably wherein this window is followed by administration of the gene therapy composition within 24 hours, preferably within 12 hours.

Embodiment 75. The pharmaceutical composition for use according to any one of embodiments 71 to 74, wherein the individual is human.

Embodiment 76. The pharmaceutical composition for use according to any one of embodiments 70 to 75, wherein one or more antibodies are present in the individual which are specific for at least one occurrence of peptide P, or for peptide P_a and/or peptide P_b, preferably wherein said antibodies are neutralizing antibodies for said viral vector.

Embodiment 77. The pharmaceutical composition for use according to any one of embodiments 70 to 76, wherein the composition is non-immunogenic in the individual.

Embodiment 78. The pharmaceutical composition for use according to any one of embodiments 70 to 77, wherein the composition is administered at a dose of 1-1000 mg, preferably 2-500 mg, more preferably 3-250 mg, even more preferably 4-100 mg, especially 5-50 mg, compound per kg body weight of the individual.

Embodiment 79. The pharmaceutical composition for use according to any one of embodiments 70 to 78, wherein the composition is administered intraperitoneally, subcutaneously, intramuscularly or intravenously.

Embodiment 80. A method of sequestering (or depleting) one or more antibodies present in an individual, comprising

obtaining a pharmaceutical composition as defined in any one of embodiments 65 to 69, wherein the composition is non-immunogenic in the individual and wherein the one or more antibodies present in the individual are specific for at least one occurrence of P, or for peptide P_a and/or peptide P_b; and

administering the pharmaceutical composition to the individual.

Embodiment 81. The method of embodiment 80, wherein the individual is a non-human animal, preferably a non-human primate, a sheep, a pig, a dog or a rodent, in particular a mouse.

Embodiment 82. The method of embodiments 80 or 81, wherein the biopolymer scaffold is autologous with respect to the individual, preferably wherein the biopolymer scaffold is an autologous protein.

Embodiment 83. The method of any one of embodiments 80 to 82, wherein the individual is administered a vaccine or gene therapy composition comprising a viral vector prior to, concurrent with and/or subsequent to said administering of the pharmaceutical composition.

Embodiment 84. The method of any one of embodiments 80 to 83, wherein the individual is a non-human animal.

Embodiment 85. The method of any one of embodiments 80 to 82, wherein the individual is administered a vaccine or gene therapy composition comprising a viral vector and wherein the one or more antibodies present in the individual are specific for said viral vector, preferably wherein said administering of the vaccine or gene therapy composition is prior to, concurrent with and/or subsequent to said administering of the pharmaceutical composition.

Embodiment 86. The method of embodiment 85, wherein the viral vector contains genetic material.

Embodiment 87. The method of any one of embodiments 80 to 86, wherein the individual is healthy.

Embodiment 88. The method of any one of embodiments 80 to 87, wherein the composition is administered intraperitoneally, subcutaneously, intramuscularly or intravenously.

Embodiment 89. A vaccine or gene therapy composition, comprising the compound of any one of embodiments 1 to 64 and further comprising the viral vector (typically wherein the viral vector contains genetic material) and optionally at least one pharmaceutically acceptable excipient;

preferably wherein the viral vector comprises a peptide fragment with a sequence length of 6-13 amino acids, preferably 7-11 amino acids, more preferably 7-9 amino acids, and

wherein the sequence of at least one occurrence of peptide P, or peptide P_a and/or peptide P_b, of the compound is at least 70% identical, preferably at least 75% identical, more preferably at least 80% identical, yet more preferably at least 85% identical, even more preferably at least 90% identical, yet even more preferably at least 95% identical, especially completely identical to the sequence of said peptide fragment.

Embodiment 90. The vaccine or gene therapy composition of embodiment 89, wherein the viral vector is AdV or AAV.

Embodiment 91. The vaccine of embodiment 89 or 90, wherein the vaccine further comprises an adjuvant.

Embodiment 92. The gene therapy composition of any one of embodiments 89 to 90, wherein the composition is prepared for intravenous administration.

Embodiment 93. The pharmaceutical composition of any one of embodiments 89 to 92, wherein the composition is an aqueous solution.

Embodiment 94. The pharmaceutical composition of any one of embodiments 89 to 93 for use in inhibition of an immune reaction, preferably an antibody-mediated immune reaction, against the active agent.

Embodiment 95. The pharmaceutical composition for use according to embodiment 94, wherein the composition is non-immunogenic in the individual.

Embodiment 96. A method of inhibiting an immune reaction to a treatment with an active agent in an individual in need of treatment with the active agent, comprising

obtaining a pharmaceutical composition as defined in any one of embodiments 89 to 95; wherein the compound of the

pharmaceutical composition is non-immunogenic in the individual, and

administering the pharmaceutical composition to the individual.

Embodiment 97. The method of embodiment 96, wherein the individual is human.

Embodiment 98. The method of embodiment 96 or 97, wherein the biopolymer scaffold is autologous with respect to the individual, preferably wherein the biopolymer scaffold is an autologous protein.

Embodiment 99. The method of any one of embodiments 96 to 98, wherein the composition is administered intraperitoneally, subcutaneously, intramuscularly or intravenously.

Embodiment 100. A peptide with a sequence length of 6 to 50 amino acids, more preferably 6 to 25 amino acids, even more preferably 6 to 20 amino acids, yet more preferably 6 to 13 amino acids, wherein the peptide comprises a sequence of at least 4 or at least 5 or at least 6, preferably at least 7, more preferably at least 8, even more preferably at least 9, yet even more preferably at least 10 consecutive amino acids selected from:

the group of AdV sequences ETGPPTVPFLTPPF (SEQ ID NO: 32), HDSKLSIATQGGL (SEQ ID NO: 33), LNLRLGQGGLFINSAHNLDINY (SEQ ID NO: 34), VDPMDPEPTLLYVLFEVFDVV (SEQ ID NO: 35), MKRRARPS EDTFNPVYPYD (SEQ ID NO: 36), ISGTVQSAHLIIRFD (SEQ ID NO: 37), LGQGGLFINSAHNLDINY NKGlyLF (SEQ ID NO: 38), SYPFDAQNLNLRLGQGGLFIN (SEQ ID NO: 39), GDTTPSAYSMSFSWDWSGHNYIN (SEQ ID NO: 40), VLLNNSFLDPEYWNFRN (SEQ ID NO: 41), HNYINEIFATSSYTFSYIA (SEQ ID NO: 42), DEAATALEINLEEEEDDNEDEVDEQAEQQKTH (SEQ ID NO: 43), INLEEEEDDNEDEVDEQAEQ (SEQ ID NO: 44), DNEDEVDEQAEQQKTHVF (SEQ ID NO: 45), EWDEAATALEINLEE (SEQ ID NO: 46), PKVVLySEDVDIETPDTHISYMP (SEQ ID NO: 47), YIPESYKDRMYSFFRNF (SEQ ID NO: 48), DSIGDRTRYFSMW (SEQ ID NO: 49), SYKDRMYSFFRNF (SEQ ID NO: 50), and FLVQMLANYNIGYQGFY (SEQ ID NO: 51), or the group of AAV sequences WQNRDVYLQGPIWAKIP (SEQ ID NO: 52), DNTYFGYSTPWGYFDNRFHC (SEQ ID NO: 53), MANQAKNWLPGPCY (SEQ ID NO: 54), LPYVLGSAHQGCLPPFP (SEQ ID NO: 55), NGSQAVGRSSFYCLEYF

(SEQ ID NO: 56), PLIDQYLYYL (SEQ ID NO: 57), EERFFPSNGILIF (SEQ ID NO: 58), ADGVGSSSGNWHC (SEQ ID NO: 59), SEQ ID NOs: 383-1891 (see Table 1) - preferably group III of Table 1, more preferably group II of Table 1, especially group I of Table 1 - and SEQ ID NOs: 1892-2063 (see Table 2) - preferably group I of Table 2 - and sequences of group II or III of Table 3 (in particular SEQ ID NOs: 2064-2103), more preferably sequences of group I of Table 3, or

the group of sequences of Table 4, in particular the group of sequences identified by SEQ ID NOs: 2104-2190,

optionally wherein at most three, preferably at most two, most preferably at least one amino acid of the sequence is independently substituted by any other amino acid;

preferably wherein the peptide is a peptide as defined in embodiment 31, 32 or 33.

Embodiment 101. A method for detecting and/or quantifying AdV- or AAV-neutralizing antibodies in a biological sample comprising the steps of

- bringing the sample into contact with the peptide of embodiment 100, and
- detecting the presence and/or concentration of the antibodies in the sample.

Embodiment 102. The method of embodiment 101, wherein the peptide is immobilized on a solid support, in particular a biosensor-based diagnostic device with an electrochemical, fluorescent, magnetic, electronic, gravimetric or optical biotransducer and/or wherein the peptide is coupled to a reporter or reporter fragment, such as a reporter fragment suitable for a PCA.

Embodiment 103. The method of embodiment 101 or 102, wherein the method is a sandwich assay, preferably an enzyme-linked immunosorbent assay (ELISA).

Embodiment 104. The method of any one of embodiments 101 to 103, wherein the sample is obtained from a mammal, preferably a human.

Embodiment 105. The method of any one of embodiment 101 to 104, wherein the sample is a blood sample, preferably whole blood, serum, or plasma.

Embodiment 106. Use of the peptide according to embodiment 100 in an enzyme-linked immunosorbent assay (ELISA), preferably for a method as defined in any one of embodiments 101 to 105.

Embodiment 107. Diagnostic device comprising the peptide according to embodiment 100 wherein the peptide is immobilized on a solid support and/or wherein the peptide is coupled to a reporter or reporter fragment, such as a reporter fragment suitable for a PCA.

Embodiment 108. Diagnostic device according to embodiment 107, wherein the solid support is an ELISA plate or a surface plasmon resonance chip.

Embodiment 109. Diagnostic device according to embodiment 107, wherein the diagnostic device is a lateral flow assay device or a biosensor-based diagnostic device with an electrochemical, fluorescent, magnetic, electronic, gravimetric or optical biotransducer.

Embodiment 110. A diagnostic kit comprising a peptide according to embodiment 100, preferably diagnostic device according to any one of embodiment 107 to 109, and preferably one or more selected from the group of a buffer, a reagent, instructions.

Embodiment 111. An apheresis device comprising the peptide according to embodiment 100, preferably immobilized on a solid carrier.

Embodiment 112. The apheresis device according to embodiment 111, wherein the solid carrier is capable of being contacted with blood or plasma flow.

Embodiment 113. The apheresis device according to embodiment 111 or 112, wherein the solid carrier comprises the compound according to any one of embodiments 1 to 64.

Embodiment 114. The apheresis device according to any one of embodiment 111 to 113, wherein the solid carrier is a sterile and pyrogen-free column.

Embodiment 115. The apheresis device according to any one of embodiments 111 to 114, wherein the apheresis device comprises at least two, preferably at least three, more preferably at least four different peptides according to embodiment 100.

The present invention is further illustrated by the following figures and examples, without being restricted thereto. In the context of the following figures and examples the compound on which the inventive approach is based is also referred to as "Selective Antibody Depletion Compound" (SADC).

Fig. 1: SADCs successfully reduce the titre of undesired antibodies. Each SADC was applied at time point 0 by i.p. injection into Balb/c mice pre-immunized by peptide immunization against a defined antigen. Each top panel shows anti-peptide titers (0.5x dilution steps; X-axis shows log(X) dilutions) against OD values (y-axis) according to a standard ELISA detecting the corresponding antibody. Each bottom panel shows titers LogIC50 (y-axis) before injection of each SADC (i.e. titers at -48h and -24h) and after application of each SADC (i.e. titers +24h, +48h and +72h after injection; indicated on the x-axis). **(A)** Compound with albumin as the biopolymer scaffold that binds to antibodies directed against EBNA1 (associated with pre-eclampsia). The mice were pre-immunized with a peptide vaccine carrying the EBNA-1 model epitope. **(B)** Compound with albumin as the biopolymer scaffold that binds to antibodies directed against a peptide derived from the human AChR protein MIR (associated with myasthenia gravis). The mice were pre-immunized with a peptide vaccine carrying the AChR MIR model epitope. **(C)** Compound with immunoglobulin as the biopolymer scaffold that binds to antibodies directed against EBNA1 (associated with pre-eclampsia). The mice were pre-immunized with a peptide vaccine carrying the EBNA-1 model epitope. **(D)** Compound with haptoglobin as the biopolymer scaffold that binds to antibodies directed against EBNA1 (associated with pre-eclampsia). The mice were pre-immunized with a peptide vaccine carrying the EBNA-1 model epitope. **(E)** Demonstration of selectivity using the same immunoglobulin-based

SADC binding to antibodies directed against EBNA1 that was used in the experiment shown in panel C. The mice were pre-immunized with an unrelated amino acid sequence. No titre reduction occurred, demonstrating selectivity of the compound.

Fig. 2: SADCs are non-immunogenic and do not induce antibody formation after repeated injection into mice. Animals C1-C4 as well as animals C5-C8 were treated i.p. with two different SADCs. Control animal C was vaccinated with a KLH-peptide derived from the human AChR protein MIR. Using BSA-conjugated peptide probes T3-1, T9-1 and E005 (grey bars, as indicated in the graph), respectively, for antibody titer detection by standard ELISA at a dilution of 1:100, it could be demonstrated that antibody induction was absent in animals treated with an SADC, when compared to the vaccine-treated control animal C (y-axis, OD450 nm).

Fig. 3: Successful in vitro depletion of antibodies using SADCs carrying multiple copies of monovalent or divalent peptides. SADCs with mono- or divalent peptides were very suitable to adsorb antibodies and thereby deplete them. "Monovalent" means that peptide monomers are bound to the biopolymer scaffold (i.e. n=1) whereas "divalent" means that peptide dimers are bound to the biopolymer scaffold (i.e. n=2). In the present case, the divalent peptides were "homodivalent", i.e. the peptide n-mer of the SADC is E006 - spacer - E006).

Fig. 4: Rapid, selective antibody depletion in mice using various SADC biopolymer scaffolds. Treated groups exhibited rapid and pronounced antibody reduction already at 24hrs (in particular SADC-TF) when compared to the mock treated control group SADC-CTL (containing an unrelated peptide). SADC with albumin scaffold - SADC-ALB, SADC with immunoglobulin scaffold - SADC-IG, SADC with haptoglobin scaffold - SADC-HP, and SADC with transferrin scaffold - SADC-TF.

Fig. 5: Detection of SADCs in plasma via their peptide moieties 24hrs after SADC injection. Both haptoglobin-scaffold-based SADCs (SADC-HP and SADC-CTL) exhibited a relatively shorter plasma half life which represents an advantage over SADCs with other biopolymer scaffolds such as SADC-ALB, SADC-IG oder SADC-TF. SADC with albumin scaffold - SADC-ALB, SADC with

immunoglobulin scaffold - SADC-IG, SADC with haptoglobin scaffold - SADC-HP, and SADC with transferrin scaffold - SADC-TF.

Fig. 6: Detection of SADC-IgG complexes in plasma 24hrs after SADC injection. Haptoglobin based SADCs were subject to accelerated clearance when compared to SADCs with other biopolymer scaffolds. SADC with albumin scaffold - SADC-ALB, SADC with immunoglobulin scaffold - SADC-IG, SADC with haptoglobin scaffold - SADC-HP, and SADC with transferrin scaffold - SADC-TF.

Fig. 7: In vitro analysis of SADC-IgG complex formation. Animals SADC-TF and -ALB showed pronounced immunocomplex formation and binding to C1q as reflected by the strong signals and by sharp signal lowering in case 1000ng/ml SADC-TF due to the transition from antigen-antibody equilibrium to antigen excess. In contrast, in vitro immunocomplex formation with SADC-HP or SADC-IG were much less efficient when measured in the present assay. These findings corroborate the finding that haptoglobin scaffolds are advantageous over other SADC biopolymer scaffolds because of the reduced propensity to activate the complement system. SADC with albumin scaffold - SADC-ALB, SADC with immunoglobulin scaffold - SADC-IG, SADC with haptoglobin scaffold - SADC-HP, and SADC with transferrin scaffold - SADC-TF.

Fig. 8: Determination of IgG capturing by SADCs in vitro. SADC-HP showed markedly less antibody binding capacity in vitro when compared to SADC-TF or SADC-ALB. SADC with albumin scaffold - SADC-ALB, SADC with immunoglobulin scaffold - SADC-IG, SADC with haptoglobin scaffold - SADC-HP, and SADC with transferrin scaffold - SADC-TF.

Fig. 9: Blood clearance of an anti-CD163-antibody-based biopolymer scaffold. In a mouse model, mAb E10B10 (specific for murine CD163) is much more rapidly cleared from circulation than mAb Mac2-158 (specific for human CD163 but not for murine CD163, thus serving as negative control in this experiment).

Fig. 10: AdV capsid protein sequences for use in the present invention. Databases accession numbers (in particular UniProt or GenBank accession numbers) are listed.

Fig. 11: AAV capsid protein sequences for use in the present invention. Databases accession numbers (in particular UniProt or GenBank accession numbers are listed), as well as references to sequences in patent publications.

EXAMPLES

Examples 1-3, 5-8 and 11-13 demonstrate that SADCs are very well suited for selective removal of undesirable antibodies. Examples 4, 10 and 14-21 contain more details on the inventive compounds with respect to antibodies against viral vectors and corresponding peptide epitopes.

Example 1: SADCs effectively reduce the titre of undesired antibodies.

Animal models: In order to provide *in vivo* models with measurable titers of prototypic undesired antibodies in human indications, BALB/c mice were immunized using standard experimental vaccination with KLH-conjugated peptide vaccines derived from established human autoantigens or anti-drug antibodies. After titer evaluation by standard peptide ELISA, immunized animals were treated with the corresponding test SADCs to demonstrate selective antibody lowering by SADC treatment. All experiments were performed in compliance with the guidelines by the corresponding animal ethics authorities.

Immunization of mice with model antigens: Female BALB/c mice (aged 8-10 weeks) were supplied by Janvier (France), maintained under a 12h light/12h dark cycle and given free access to food and water. Immunizations were performed by s.c. application of KLH carrier-conjugated peptide vaccines injected 3 times in biweekly intervals. KLH conjugates were generated with peptide T3-2 (SEQ ID NO. 356: CGRPQKRPSCIGCKG), which represents an example for molecular mimicry between a viral antigen (EBNA-1) and an endogenous human receptor antigen, namely the placental GPR50 protein, that was shown to be relevant to preeclampsia (Elliott et al.). In order to confirm the generality of this approach, a larger antigenic peptide derived from the autoimmune condition myasthenia gravis was used for immunization of mice with a human autoepitope. In analogy to peptide T3-2, animals were immunized with peptide T1-1 (SEQ ID NO. 357: LKWNPDYGGVKKIHIPSEKGC), derived from the MIR (main immunogenic region) of the human AChR protein which plays a fundamental role in pathogenesis of the disease (Luo et al.). The T1-1 peptide

was used for immunizing mice with a surrogate partial model epitope of the human AChR autoantigen. The peptide T8-1 (SEQ ID NO. 358: DHTLYTPYHTHPG) was used to immunize control mice to provide a control titer for proof of selectivity of the system. For vaccine conjugate preparation, KLH carrier (Sigma) was activated with sulfo-GMBS (Cat. Nr. 22324 Thermo), according to the manufacturer's instructions, followed by addition of either N- or C-terminally cysteinylated peptides T3-2 and T1-1 and final addition of Alhydrogel® before injection into the flank of the animals. The doses for vaccines T3-2 and T1-1 were 15µg of conjugate in a volume of 100ul per injection containing Alhydrogel® (InvivoGen VAC-Alu-250) at a final concentration of 1% per dose.

Generation of prototypic SADCs: For testing selective antibody lowering activity by SADCs of T3-2 and T1-1 immunized mice, SADCs were prepared with mouse serum albumin (MSA) or mouse immunoglobulin (mouse-Ig) as biopolymer scaffold in order to provide an autologous biopolymer scaffold, that will not induce any immune reaction in mice, or non-autologous human haptoglobin as biopolymer scaffold (that did not induce an allogenic reaction after one-time injection within 72 hours). N-terminally cysteinylated SADC peptide E049 (SEQ ID NO. 359: GRPQKRPSICG) and/or C-terminally cysteinylated SADC peptide E006 (SEQ ID NO. 360: VKKIHIPSEKG) were linked to the scaffold using sulfo-GMBS (Cat. Nr. 22324 Thermo)-activated MSA (Sigma; Cat. Nr. A3559) or -mouse-Ig (Sigma, I5381) or -human haptoglobin (Sigma H0138) according to the instructions of the manufacturer, thereby providing MSA-, Ig- and haptoglobin-based SADCs with the corresponding cysteinylated peptides, that were covalently attached to the lysines of the corresponding biopolymer scaffold. Beside conjugation of the cysteinylated peptides to the lysines via a bifunctional amine-to-sulfhydryl crosslinker, a portion of the added cysteinylated SADC peptides directly reacted with sulfhydryl groups of cysteins of the albumin scaffold protein, which can be detected by treating the conjugates with DTT followed by subsequent detection of free peptides using mass spectrometry or any other analytical method that detects free peptide. Finally, these SADC conjugates were dialysed against water using Pur-A-Lyzer™ (Sigma) and

subsequently lyophilized. The lyophilized material was resuspended in PBS before injection into animals.

In vivo functional testing of SADCs: Prototypic SADCs, SADC-E049 and SADC-E006 were injected intraperitoneally (i.p.; as a surrogate for an intended intravenous application in humans and larger animals) into the mice that had previously been immunized with peptide vaccine T3-2 (carrying the EBNA-1 model epitope) and peptide vaccine T1-1 (carrying the AChR MIR model epitope). The applied dose was 30µg SADC conjugate in a volume of 50µl PBS. Blood takes were performed by submandibular vein puncture, before (-48h, -24h) and after (+24h,+48h,+72h, etc.) i.p. SADC injections, respectively, using capillary micro-hematocrit tubes. Using ELISA analysis (see below), it was found that both prototypic SADCs were able to clearly reduce the titers over a period of at least 72 hrs in the present animal model. It could therefore be concluded that SADCs can be used to effectively reduce titers *in vivo*.

Titer analysis: Peptide ELISAs were performed according to standard procedures using 96-well plates (Nunc Medisorp plates; Thermofisher, Cat Nr 467320) coated for 1h at RT with BSA-coupled peptides (30nM, dissolved in PBS) and incubated with the appropriate buffers while shaking (blocking buffer, 1% BSA, 1x PBS; washing buffer, 1xPBS / 0,1% Tween; dilution buffer, 1xPBS / 0.1% BSA / 0,1% Tween). After serum incubation (dilutions starting at 1:50 in PBS; typically in 1:3 or 1:2 titration steps), bound antibodies were detected using Horseradish Peroxidase-conjugated goat anti-mouse IgG (Fc) from Jackson immunoresearch (115-035-008). After stopping the reaction, plates were measured at 450nm for 20min using TMB. EC50 were calculated from readout values using curve fitting with a 4-parameter logistic regression model (GraphPad Prism) according to the procedures recommended by the manufacturer. Constraining parameters for ceiling and floor values were set accordingly, providing curve fitting quality levels of $R^2 > 0.98$.

Figure 1A shows an *in vivo* proof of concept in a mouse model for *in vivo* selective plasma-lowering activity of a prototypic albumin-based SADC candidate that binds to antibodies directed against EBNA1, as a model for autoantibodies and mimicry in preeclampsia (Elliott et al.). For these mouse experiments,

mouse albumin was used, in order to avoid any reactivity against a protein from a foreign species. Antibody titers were induced in 6 months old Balb/c mice by standard peptide vaccination. The bottom panel demonstrates that titers LogIC₅₀ (y-axis) before SADC injection (i.e. titers at -48h and -24h) were higher than titers LogIC₅₀ after SADC application (i.e. titers +24h, +48h and +72h after injection; indicated on the x-axis).

A similar example is shown in Figure 1B, using an alternative example of a peptidic antibody binding moiety for a different disease indication. Antibody lowering activity of an albumin-based SADC in a mouse model that was pre-immunized with a different peptide derived from the human AChR protein MIR region (Luo et al.) in order to mimic the situation in myasthenia gravis. The induced antibody titers against the AChR-MIR region were used as surrogate for anti-AChR-MIR autoantibodies known to play a causative role in myasthenia gravis (reviewed by Vincent et al.). A clear titer reduction was seen after SADC application.

Figures 1C and 1D demonstrate the functionality of SADC variants comprising alternative biopolymer scaffolds. Specifically, Figure 1C shows that an immunoglobulin scaffold can be successfully used whereas Figure 1D demonstrates the use of a haptoglobin-scaffold for constructing an SADC. Both examples show an *in vivo* proof of concept for selective antibody lowering by an SADC, carrying covalently bound example peptide E049.

The haptoglobin-based SADC was generated using human Haptoglobin as a surrogate although the autologous scaffold protein would be preferred. In order to avoid formation of anti-human-haptoglobin antibodies, only one single SADC injection per mouse of the non-autologous scaffold haptoglobin was used for the present experimental conditions. As expected, under the present experimental conditions (i.e. one-time application), no antibody reactivity was observed against the present surrogate haptoglobin homologue.

Figure 1E demonstrates the selectivity of the SADC system. The immunoglobulin-based SADC carrying the peptide E049 (i.e. the same as in Figure 1C) cannot reduce the Ig-titer that was

induced by a peptide vaccine with an unrelated, irrelevant amino acid sequence, designated peptide T8-1 (SEQ ID NO. 358: DHTLYTPYHTHPG). The example shows an *in vivo* proof of concept for the selectivity of the system. The top panel shows anti-peptide T8-1 titers (0,5x dilution steps starting from 1:50 to 1:102400; X-axis shows log(X) dilutions) against OD values (y-axis) according to a standard ELISA. T8-1-titers are unaffected by administration of SADC-Ig-E049 after application. The bottom panel demonstrates that the initial titers LogIC50 (y-axis) before SADC injection (i.e. titers at -48h and -24h) are unaffected by administration of SADC-Ig-E049 (arrow) when compared to the titers LogIC50 after SADC application (i.e. titers +24h, +48h and +72h; as indicated on the x-axis), thereby demonstrating the selectivity of the system.

Example 2: Immunogenicity of SADCs.

In order to exclude immunogenicity of SADCs, prototypic candidate SADCs were tested for their propensity to induce antibodies upon repeated injection. Peptides T3-1 and T9-1 were used for this test. T3-1 is a 10-amino acid peptide derived from a reference epitope of the Angiotensin receptor, against which agonistic autoantibodies are formed in a pre-eclampsia animal model (Zhou et al.); T9-1 is a 12-amino acid peptide derived from a reference anti-drug antibody epitope of human IFN gamma (Lin et al.). These control SADC conjugates were injected 8 x every two weeks i.p. into naïve, non-immunized female BALB/c mice starting at an age of 8-10 weeks.

Animals C1-C4 were treated i.p. (as described in example 1) with SADC T3-1. Animals C5-C8 were treated i.p. with an SADC carrying the peptide T9-1. As a reference signal for ELISA analysis, plasma from a control animal that was vaccinated 3 times with KLH-peptide T1-1 (derived from the AChR-MIR, explained in Example 1) was used. Using BSA-conjugated peptide probes T3-1, T9-1 and E005 (SEQ ID NO. 361: GGVKKIHIPSEK), respectively, for antibody titer detection by standard ELISA at a dilution of 1:100, it could be demonstrated that antibody induction was absent in SADC-treated animals, when compared to the vaccine-treated control animal C (see Figure 2). The plasmas

were obtained by submandibular blood collection, 1 week after the 3rd vaccine injection (control animal C) and after the last of 8 consecutive SADC injections in 2-weeks intervals (animals C1-C8), respectively. Thus it was demonstrated that SADCs are non-immunogenic and do not induce antibody formation after repeated injection into mice.

Example 3: Successful in vitro depletion of antibodies using SADCs carrying multiple copies of monovalent or divalent peptides.

Plasma of E006-KLH (VKKIHIPSEKG (SEQ ID NO: 360) with C-terminal cysteine, conjugated to KLH) vaccinated mice was diluted 1:3200 in dilution buffer (PBS + 0.1% w/v BSA + 0.1% Tween20) and incubated (100 μ l, room temperature) sequentially (10 min/well) four times on single wells of a microtiter plate that was coated with 2.5 μ g/ml (250 ng/well) of SADC or 5 μ g/ml (500 ng/well) albumin as negative control.

In order to determine the amount of free, unbound antibody present before and after incubation on SADC coated wells, 50 μ l of the diluted serum were taken before and after the depletion and quantified by standard ELISA using E006-BSA coated plates (10 nM peptide) and detection by goat anti mouse IgG bio (Southern Biotech, diluted 1:2000). Subsequently, the biotinylated antibody was detected with Streptavidin-HRP (Thermo Scientific, diluted 1:5000) using TMB as substrate. Development of the signal was stopped with 0.5 M sulfuric acid.

ELISA was measured at OD450nm (y-axis). As a result, the antibody was efficiently adsorbed by either coated mono- or divalent SADCs containing peptide E006 with C-terminal cysteine (sequence VKKIHIPSEKGC, SEQ ID NO: 362) (before=non-depleted starting material; mono- divalent corresponds to peptides displayed on the SADC surface; neg. control was albumin; indicated on the x-axis). See Fig. 3. ("Monovalent" means that peptide monomers are bound to the biopolymer scaffold (i.e. n=1) whereas "divalent" means that peptide dimers are bound to the biopolymer scaffold (i.e. n=2). In the present case, the divalent peptides were "homodivalent", i.e. the peptide n-mer of the SADC is E006 - S - E006.)

This demonstrates that SADCs with mono- or divalent peptides are very suitable to adsorb antibodies and thereby deplete them.

Example 4: Generation of mimotope-based SADCs

mAb 4D2 is a mouse IgG2a mAb targeting the adenovirus fiber epitope peptide (NCBI Reference Sequence: AP_000226.1). It represents a prototype neutralizing antibody that was generated from UV irradiated Ad2 virus (Krasnykh et al, 1998).

Linear and circular peptides derived from wild-type or modified peptide amino acid sequences can be used for the construction of specific SADCs for the selective removal of neutralizing antibodies against viral vectors. In case of a particular epitope, linear peptides or constrained peptides such as cyclopeptides containing portions of an epitope or variants thereof, where for example, one or several amino acids have been substituted or chemically modified in order to improve affinity to an antibody (mimotopes), can be used for constructing SADCs. A peptide screen can be performed with the aim of identifying peptides with optimized affinity to neutralizing antibodies. The flexibility of structural or chemical peptide modification provided a solution to minimize the risk of immunogenicity, in particular of binding of the peptide to HLA and thus the risk of unwanted immune stimulation.

Therefore, wild-type as well as modified linear and circular peptide sequences are derived from an epitope of a viral capsid protein as disclosed herein, e.g. the epitopic sequence LNLRLQGGLFINSAHNLDINY (SEQ ID NO: 34) of mAb 4D2 found in the course of the present invention (see example further below). Peptides of various length and positions are systematically permuted by amino acid substitutions and synthesized on a peptide array. This allows screening of 60000 circular and linear wild-type and mimotope peptides derived from these sequences. The peptide arrays are incubated with mAb 4D2. This antibody is therefore used to screen the 60000 peptides and 100 circular and 100 linear peptide hits are selected based on their relative binding strength to the antibody. Of these 200 peptides, 51 sequences are identical between the circular and the linear peptide group. All of the best peptides identified

have at least one amino acid substitution when aligned to the original sequences, respectively and are therefore regarded as mimotopes. Also, higher binding strengths can be achieved with circularized peptides.

These newly identified peptides, preferentially those with high relative binding values, are used to generate SADCs for increasing efficacy of AdV-based vector vaccines.

Example 5: Rapid, selective antibody depletion in mice using various SADC biopolymer scaffolds.

10 µg of model undesired antibody mAb anti V5 (Thermo Scientific) was injected i.p. into female Balb/c mice (5 animals per treatment group; aged 9-11 weeks) followed by intravenous injection of 50 µg SADC (different biopolymer scaffolds with tagged V5 peptides bound, see below) 48hrs after the initial antibody administration. Blood was collected at 24hrs intervals from the submandibular vein. Blood samples for time point 0 hrs were taken just before SADC administration.

Blood was collected every 24 hrs until time point 120 hrs after the SADC administration (x-axis). The decay and reduction of plasma anti-V5 IgG levels after SADC administration was determined by anti V5 titer readout using standard ELISA procedures in combination with coated V5-peptide-BSA (peptide sequence IPNPLLGLDC - SEQ ID NO: 561) and detection by goat anti mouse IgG bio (Southern Biotech, diluted 1:2000) as shown in Fig. 4. In addition, SADC levels (see Example 6) and immunocomplex formation (see Example 7) were analyzed.

EC50[OD450] values were determined using 4 parameter logistic curve fitting and relative signal decay between the initial level (set to 1 at time point 0) and the following time points (x-axis) was calculated as ratio of the EC50 values (y-axis, fold signal reduction EC50). All SADC peptides contained tags for direct detection of SADC and immunocomplexes from plasma samples; peptide sequences used for SADCs were: IPNPLLGLDGGSGDYKDDDDKGGK (SEQ ID NO: 363)-(BiotinAca)GC (SADC with albumin scaffold - SADC-ALB, SADC with immunoglobulin scaffold - SADC-IG, SADC with haptoglobin scaffold - SADC-HP, and SADC with transferrin scaffold - SADC-TF) and unrelated peptide

VKKIHIPSEKGGSGDYKDDDDKGGK (SEQ ID NO: 364)-(BiotinAca)GC as negative control SADC (SADC-CTR).

The SADC scaffolds for the different treatment groups of 5 animals are displayed in black/grey shades (see inset of Fig. 4).

Treated groups exhibited rapid and pronounced antibody reduction already at 24hrs (in particular SADC-TF) when compared to the mock treated control group SADC-CTL. SADC-CTR was used as reference for a normal antibody decay since it has no antibody lowering activity because its peptide sequence is not recognized by the administered anti V5 antibody. The decay of SADC-CTR is thus marked with a trend line, emphasizing the antibody level differences between treated and mock treated animals.

In order to determine the effectivity of selective antibody lowering under these experimental conditions, a two-way ANOVA test was performed using a Dunnett's multiple comparison test. 48 hrs after SADC administration, the antibody EC50 was highly significantly reduced in all SADC groups ($p < 0.0001$) compared to the SADC-CTR reference group (trend line). At 120 hrs after SADC administration, antibody decrease was highly significant in the SADC-ALB and SADC-TF groups (both $p < 0.0001$) and significant in the SADC-HP group ($p = 0.0292$), whereas the SADC-IG group showed a trend towards an EC50 reduction ($p = 0.0722$) 120 hrs after SADC administration. Of note, selective antibody reduction was highly significant ($p < 0.0001$) in the SADC-ALB and SADC-TF groups at all tested time-points after SADC administration.

It is concluded that all SADC biopolymer scaffolds were able to selectively reduce antibody levels. Titer reduction was most pronounced with SADC-ALB and SADC-TF and no rebound or recycling of antibody levels was detected towards the last time points suggesting that undesired antibodies are degraded as intended.

Example 6: Detection of SADCs in plasma 24hrs after SADC injection.

Plasma levels of different SADC variants at 24hrs after i.v. injection into Balb/c mice. Determination of Plasma levels (y-axis) of SADC-ALB, -IG, -HP, -TF and the negative control SADC-CTR (x-axis), were detected in the plasmas from the animals

already described in example 5. Injected plasma SADC levels were detected by standard ELISA whereby SADCs were captured via their biotin moieties of their peptides in combination with streptavidin coated plates (Thermo Scientific). Captured SADCs were detected by mouse anti Flag-HRP antibody (Thermo Scientific, 1:2,000 diluted) detecting the Flag-tagged peptides (see also example 7):

Assuming a theoretical amount in the order of 25 µg/ml in blood after injecting 50 µg SADC i.v., the detectable amount of SADC ranged between 799 and 623 ng/ml for SADC-ALB or SADC-IG and up to approximately 5000 ng/ml for SADC-TF, 24 hrs after SADC injection. However surprisingly and in contrast, SADC-HP and control SADC-CTR (which is also a SADC-HP variant, however carrying the in this case unrelated negative control peptide E006, see previous examples), had completely disappeared from circulation 24hrs after injection, and were not detectable anymore. See Fig. 5.

This demonstrates that both Haptoglobin scaffold-based SADCs tested in the present example ((namely SADC-HP and SADC-CTR) exhibit a relatively shorter plasma half-life which represents an advantage over SADCs such as SADC-ALB, SADC-IG oder SADC-TF in regard of their potential role in complement-dependent vascular and renal damage due to the in vivo risk of immunocomplex formation. Another advantage of SADC-HP is the accelerated clearance rate of their unwanted target antibody from blood in cases where a rapid therapeutic effect is needed. The present results demonstrate that Haptoglobin-based SADC scaffolds (as represented by SADC-HP and SADC-CTR) are subject to rapid clearance from the blood, regardless of whether SADC-binding antibodies are present in the blood, thereby minimizing undesirable immunocomplex formation and showing rapid and efficient clearance. Haptoglobin-based SADCs such as SADC-HP in the present example thus provide a therapeutically relevant advantage over other SADC biopolymer scaffolds, such as demonstrated by SADC-TF or SADC-ALB, both of which are still detectable 24hrs after injection under the described conditions, in contrast to SADC-HP or SADC-CTR which both are completely cleared 24hrs after injection.

Example 7: Detection of SADC-IgG complexes in plasma 24hrs after SADC injection.

In order to determine the amount IgG bound to SADCs in vivo, after i.v. injection of 10 µg anti V5 IgG (Thermo Scientific) followed by injection of SADC-ALB, -HP, -TF and -CTR (50 µg) administered i.v. 48h after antibody injection, plasma was collected from the submandibular vein, 24hrs after SADC injection, and incubated on streptavidin plates for capturing SADCs from plasma via their biotinylated SADC-V5-peptide [IPNPLLGLDGGSGDYKDDDDKGGK (SEQ ID NO: 363) (BiotinAca)GC or in case of SADC-CTR the negative control peptide VKKIHIPSEKGGSGDYKDDDDKGGK (SEQ ID NO: 364) (BiotinAca)GC]. IgG bound to the streptavidin-captured SADCs was detected by ELISA using a goat anti mouse IgG HRP antibody (Jackson Immuno Research, diluted 1:2,000) for detection of the SADC-antibody complexes present in plasma 24hrs after SADC injection. OD450nm values (y-axis) obtained for a negative control serum from untreated animals were subtracted from the OD450nm values of the test groups (x-axis) for background correction.

As shown in Fig. 6, pronounced anti-V5 antibody signals were seen in case of SADC-ALB and SADC-TF injected mice (black bars represent background corrected OD values at a dilution of 1:25, mean value of 5 mice; standard deviation error bars), whereas no antibody signal could be detected in plasmas from SADC-HP or control SADC-CTR injected animals (SADC-CTR is a negative control carrying the irrelevant peptide bio-FLG-E006 [VKKIHIPSEKGGSGDYKDDDDKGGK (SEQ ID NO: 364) (BiotinAca)GC] that is not recognized by any anti V5 antibody). This demonstrates the absence of detectable amounts of SADC-HP/IgG complexes in the plasma 24hrs after i.v. SADC application.

SADC-HP is therefore subject to accelerated clearance in anti V5 pre-injected mice when compared to SADC-ALB or SADC-TF.

Example 8: In vitro analysis of SADC-immunoglobulin complex formation

SADC-antibody complex formation was analyzed by pre-incubating 1 µg/ml of human anti V5 antibody (anti V5 epitope tag [SV5-P-K], human IgG3, Absolute Antibody) with increasing

concentrations of SADC-ALB, -IG, -HP, -TF and -CTR (displayed on the x-axis) in PBS +0.1% w/v BSA + 0.1% v/v Tween20 for 2 hours at room temperature in order to allow for immunocomplex formation in vitro. After complex formation, samples were incubated on ELISA plates that had previously been coated with 10 µg/ml of human C1q (CompTech) for 1 h at room temperature, in order to allow capturing of in vitro formed immunocomplexes. Complexes were subsequently detected by ELISA using anti human IgG (Fab specific)-Peroxidase (Sigma, diluted 1:1,000). Measured signals at OD450 nm (y-axis) reflect Antibody-SADC complex formation in vitro.

As shown in Fig. 7, SADC-TF and -ALB showed pronounced immunocomplex formation and binding to C1q as reflected by the strong signals and by sharp signal lowering in case 1000ng/ml SADC-TF due to the transition from antigen-antibody equilibrium to antigen excess. In contrast, in vitro immunocomplex formation with SADC-HP or SADC-IG were much less efficient when measured in the present assay.

Together with the in vivo data (previous examples), these findings corroborate the finding that haptoglobin scaffolds are advantageous over other SADC biopolymer scaffolds because of the reduced propensity to activate the complement system. In contrast, SADC-TF or SADC-ALB show higher complexation, and thereby carry a certain risk of activating the C1 complex with initiation of the classical complement pathway (a risk which may be tolerable in some settings, however).

Example 9: Determination of IgG capturing by SADCs in vitro

Immunocomplexes were allowed to form in vitro, similar to the previous example, using 1 µg/ml mouse anti V5 antibody (Thermo Scientific) in combination with increasing amounts of SADCs (displayed on the x-axis). SADC-antibody complexes were captured on a streptavidin coated ELISA plate via the biotinylated SADC-peptides (see previous examples), followed by detection of bound anti-V5 using anti mouse IgG-HRP (Jackson Immuno Research, diluted 1:2,000).

Under these assay conditions, SADC-HP showed markedly less antibody binding capacity in vitro when compared to SADC-TF or

SADC-ALB (see Fig. 8, A). The calculated EC50 values for IgG detection on SADCs were 7.0 ng/ml, 27.9 ng/ml and 55.5 ng/ml for SADC-TF, -ALB and -HP, respectively (see Fig. 8, B).

This in vitro finding is consistent with the observation (see previous examples) that SADC-HP has a lower immunocomplex formation capacity when compared to SADC-TF or SADC-ALB which is regarded as a safety advantage with respect to its therapeutic use for the depletion of unwanted antibodies.

Example 10: SADCs to reduce undesired antibodies against AAV-8

Three SADCs are provided to reduce AAV-8-neutralizing antibodies which hamper gene therapy (see Gurda et al. for the epitopes used; see also AAV-8 capsid protein sequence UniProt Q8JQF8, sequence version 1):

- (a) SADC-a with Mac2-158 (as disclosed in WO 2011/039510 A2) as biopolymer scaffold and at least two peptides with the sequence YLQGPIW (SEQ ID NO: 312) covalently bound to the scaffold,
- (b) SADC-b with human transferrin as biopolymer scaffold and at least two peptides with the sequence YFGYSTPWGYFDF (SEQ ID NO: 320) covalently bound to the scaffold, and
- (c) SADC-c with human albumin as biopolymer scaffold and at least two peptides with the sequence QGCLPPF (SEQ ID NO: 335) covalently bound to the scaffold.

These SADCs are administered to an individual who will undergo gene therapy with AAV-8 as vector in order to increase efficiency of the gene therapy.

Example 11: In-vivo function of anti-CD163-antibody-based SADC biopolymer scaffold

Rapid *in vivo* blood clearance of anti-mouse-CD163 mAb E10B10 (as disclosed in WO 2011/039510 A2). mAb E10B10 was resynthesized with a mouse IgG2a backbone. 50 µg mAb E10B10 and Mac2-158 (human-specific anti-CD163 mAb as disclosed in WO 2011/039510 A2, used as negative control in this example since it does not bind to mouse CD163) were injected i.v. into mice

and measured after 12, 24, 36, 48 , 72, 96 hours in an ELISA to determine the blood clearance.

mAb E10B10 was much more rapidly cleared from circulation than control mAb Mac2-158 was, as shown in Fig. 9, since E10B10 binds to the mouse CD163 whereas Mac2-158 is human-specific, although both were expressed as mouse IgG2a isotypes for direct comparison.

In conclusion, anti-CD163 antibodies are highly suitable as SADC scaffold because of their clearance profile. SADCs with such scaffolds will rapidly clear undesirable antibodies from circulation.

Detailed methods: 50 ug of biotinylated monoclonal antibodies E10B10 and biotinylated Mac2-158 were injected i.v. into mice and measured after 12, 24, 36, 48, 72, 96 hours to determine the clearance by ELISA: Streptavidin plates were incubated with plasma samples diluted in PBS + 0.1%BSA + 0.1% Tween20 for 1 h at room temperature (50 µl/well). After washing (3x with PBS + 0.1% Tween20), bound biotinylated antibodies were detected with anti-mouse IgG+IgM-HRP antibody at a 1:1000 dilution. After washing, TMB substrate was added and development of the substrate was stopped with TMB Stop Solution. The signal at OD450 nm was read. The EC50 values were calculated by non-linear regression using 4 parametric curve fitting with constrained curves and least squares regression. EC50 values at time-point T12 (this was the first measured time-point after antibody injection) was set at 100%, all other EC50 values were compared to the levels at T12.

Example 12: Epitope mapping of anti-CD163 mAbs

mAb E10B10 provides CD163-mediated, accelerated in vivo clearance from blood in mice (see example 11). The epitope of this antibody was fine mapped using circular peptide arrays, whereby the peptides were derived from mouse CD163. As a result, a peptide cluster that is recognized by mAb E10B10 was identified (see example 13).

The same epitope mapping procedure using circularized peptides was performed with mAb Mac2-158 (as disclosed in WO 2011/039510 A2). Epitope mapping results for mAb Mac2-158

yielded two peptide clusters (see example 13) which allowed further demarcation of CD163 epitope regions that are especially relevant to internalization of ligands and antibodies that bind to the receptor.

These newly characterized epitopes for Mac2-158 and E10B10 thus revealed three preferred binding regions for antibodies against CD163. Based on the fine epitope mapping work, linear or preferentially circular peptides are synthesized and used for the induction, production and selection of polyclonal or monoclonal antibodies or other CD163-binding SADC scaffolds that target CD163.

Example 13: Epitope mapping of anti-CD163 mAbs

Peptides aligned to SRCR domain 1 of human CD163 were selected from the top 20 peptide hits of mAb Mac2-158 circular epitope mapping peptides and the most preferred sequences were selected from two peptide alignment clusters at the N-terminus and at the C-terminus of SRCR-1 of human CD163. As a result, the following sequences (as well as motifs derived therefrom) are highly suitable epitopes anti-CD163 antibodies and fragments thereof used as SADC biopolymer scaffold:

Peptide cluster 1:

04	-----EWGTVCNNGWSME-----	(SEQ ID NO: 7)
07	-----CSGRVEVKVQEEW-----	(SEQ ID NO: 365)
09	-----QEEWGTVCNNGWS-----	(SEQ ID NO: 8)
12	-----WGTVCNNGWSMEA-----	(SEQ ID NO: 9)
14	-----EEWGTVCNNGWSM-----	(SEQ ID NO: 10)
18	-----VQEEWGTVCNNGW-----	(SEQ ID NO: 11)
19	-----EWGTVCNNGW-----	(SEQ ID NO: 12)
20	-----WGTVCNNGWS-----	(SEQ ID NO: 5)
huCD163-domain 1-3	DGENKCSGRVEVKVQEEWGTVCNNGWSMEAVSVICN	(SEQ ID NO: 366)

Peptide cluster 2:

01	-----ESALWDC-----	(SEQ ID NO: 15)
02	-----RGNESALWDC-----	(SEQ ID NO: 16)
03	-----SCRGNESALW-----	(SEQ ID NO: 17)
05	-----VSCRGNESALWDC-----	(SEQ ID NO: 18)
06	-----ALWDCKHDGW-----	(SEQ ID NO: 19)
08	-----DHVSCRGNESALW-----	(SEQ ID NO: 20)
11	-----CRGNESALWD-----	(SEQ ID NO: 21)
13	-----NESALWDCKHDGW-----	(SEQ ID NO: 22)
17	-----ESALWDCKHDGWG-----	(SEQ ID NO: 23)
huCD163-domain1-3	RIWMDHVSCRGNESALWDCKHDGWGKHSNCTHQ	(SEQ ID NO: 367)

Fine epitope mapping of mAb E10B10 was performed as for Mac2-158. 1068 circular peptides (sized 7, 10 and 13 amino acids) and derived from SRCR-1 to -3 of the mouse CD163 sequence (UniProtKB Q2VLH6.2) were screened with mAb E10B10 and the following top binding peptides were obtained (ranked by relative signal strength). The human CD163 sequence was aligned to this cluster of mouse CD163 sequences, revealing another highly suitable epitope:

Peptide cluster 3:

01	-----VTNAPGEMKKELR-----	(SEQ ID NO: 368)
02	-----ASAVTNAPGEMKK-----	(SEQ ID NO: 369)
03	-----VTNAPGEMKK-----	(SEQ ID NO: 370)
04	-----VTNAPGE-----	(SEQ ID NO: 371)
05	-----GSASAVTNAPGEM-----	(SEQ ID NO: 372)
06	-----AVTNAPGEMKKEL-----	(SEQ ID NO: 373)
07	-----SASAVTNAPGEMK-----	(SEQ ID NO: 374)
08	-----SGSASAVTNAPGE-----	(SEQ ID NO: 375)
09	-----AVTNAPGEMK-----	(SEQ ID NO: 376)
10	-----SAVTNAPGEM-----	(SEQ ID NO: 377)
11	-----ASAVTNAPGE-----	(SEQ ID NO: 378)
12	-----SAVTNAPGEMKKE-----	(SEQ ID NO: 379)
13	-----TNAPGEMKKE-----	(SEQ ID NO: 380)
mCD163(SRCR-1, N-terminus)	VTNAPGEMKKELRLAGGENNCS	(SEQ ID NO: 75)
hCD163(SRCR-1, N-terminus)	SSLGGTDKELRLVDGENKCS	(SEQ ID NO: 24)

The human homologues of mouse peptides 01 - 13 from cluster 3 have the following sequences of the N-terminal portion of the mature human CD163 protein (UniProtKB: Q86VB7):

Cluster 3 peptides (mouse):	human homologues:	
01	SSLGGTDKELR	(SEQ ID NO: 25)
06	SSLGGTDKEL	(SEQ ID NO: 27)
12,13	SSLGGTDKE	(SEQ ID NO: 28)
02,03	SSLGGTDK	(SEQ ID NO: 29)
07,09	SSLGGTD	(SEQ ID NO: 30)
05,10	SSLGGT	(SEQ ID NO: 31)

04,08,11
hCD163(SRCR-1)

SSLGG
SSLGGTDKELRLVDGENKCS

(SEQ ID NO: 26)
(SEQ ID NO: 24)

These homologue peptides represent further highly suitable epitopes for the anti-CD163 antibody-based biopolymer scaffold.

Example 14: Epitope mapping of mAb 4D2 against AdV

mAb 4D2 is a mouse IgG2a mAb targeting the adenovirus fiber epitope peptide (NCBI Reference Sequence: AP_000226.1). It represents a prototype neutralizing antibody that was generated from UV irradiated Ad2 virus (Krasnykh et al, 1998). In order to obtain cyclic antibody binding peptides from the virus neutralizing epitope, mAb 4D2 was mapped against aligned cyclic peptides derived from the fiber sequence. The sequence at amino acid positions 1 to 581 of NCBI Reference Sequence: AP_000226.1 was used as a starting sequence for designing 7mer, 10mer and 13mer cyclic peptides that were then synthesized and circularized directly on a peptide microarray and subsequently incubated with various concentrations of the antibody. The binding signal of monoclonal antibody 4D2 to the peptides yielded several binding hits that were aligned against the sequence of the protein and subsequently clustered. The resulting clusters were designated cluster1 (length=14 amino acids), cluster2 (length=13 amino acids) and cluster3 (length=22 amino acids). Below are the alignments of the corresponding new peptides that are able to bind the mAb 4D2 paratope. The number of the peptide names corresponds to the rank of the binding signal of the antibody to the microarray (i.e. peptide 01 binds strongest, 02 second strongest, etc.). A selection of top candidate binding peptides out of the top 50 top binders was aligned against the corresponding protein sequence (first line).

```
cluster1      ETGPPTVPFLTPPF (SEQ ID NO: 32)
08            --GPPTVPFLTP-- (SEQ ID NO: 60)
10            ETGPPTVPFLTPP- (SEQ ID NO: 61)
21            -TGPPTVPFLT--- (SEQ ID NO: 62)
34            ----PTVPFLTPPF (SEQ ID NO: 63)

cluster2      HDSKLSIATQGGL (SEQ ID NO: 64)
03            HDSKLSIATQGGL (SEQ ID NO: 64)
11            -----SIATQGP- (SEQ ID NO: 65)
```

```

cluster3      LNLRLGQGPLFINSAHNLDINY (SEQ ID NO: 34)
02            -NLRLGQGPLF----- (SEQ ID NO: 66)
12            -----QGPLFINSAH----- (SEQ ID NO: 67)
13            -----PLFINSAHNLD--- (SEQ ID NO: 68)
15            ----LGQGPLF----- (SEQ ID NO: 69)
17            LNLRLGQGPL----- (SEQ ID NO: 70)
19            ----GQGPLFI----- (SEQ ID NO: 71)
29            -NLRLGQGPLFINS----- (SEQ ID NO: 72)
32            -----LFINSAHNLDINY (SEQ ID NO: 73)
33            -----FINSAHNLDI-- (SEQ ID NO: 74)
37            --LRLGQGPLFI----- (SEQ ID NO: 75)
39            -----GPLFINSAHN----- (SEQ ID NO: 76)

```

The above peptides/sequences are highly suitable as peptides for SADCs which reduce neutralization of AdV vectors.

Example 15: Epitope mapping of monoclonal antibody 9C12 against AdV

Monoclonal antibody 9C12 (alias mAB TC31-9C12.C9-s) was generated by immunizing mice with the hexon protein (Uniprot ID: P04133 which corresponds to GenBank: BAG48782.1). This neutralizing antibody is directed against the hexon protein and the neutralizing activity of this antibody was demonstrated by Varghese (Varghese et al, 2004). In brief, diluted antibody was incubated with GFP-expressing replication-defective Ad vector and subsequently added to HeLa cells followed by fluorescence readout. In order to map a region from which paratope binding peptides could be derived, the sequence at amino acid positions 1 to 952 of GenBank: BAG48782.1 was used as a starting sequence for designing cyclic 7mer, 10mer and 13mer peptides that were then synthesized and circularized on a peptide microarray, and subsequently incubated with various concentrations of the antibody. The binding signal of mAb 9C12 to the peptides yielded several candidates that could be aligned and clustered against the protein. An epitopic cluster region of 20 amino acids was identified from which paratope binding peptides can be preferentially derived. Below are the alignments of the corresponding peptide hits from this screen. The number of the peptide names corresponds to the ranked binding signal obtained from the microarray (i.e. peptide 01 binds strongest, 02 second strongest, etc.). Cyclic peptides were selected out of up to 50 top binders in this experiment.

```

cluster1 VDPMDEPTLLYVLFEVFDVV (SEQ ID NO: 35)
01      ----DEPTLLYVLFEVF--- (SEQ ID NO: 77)
02      -----TLLYVLFEVF--- (SEQ ID NO: 78)
03      ----DEPTLLYVLF----- (SEQ ID NO: 79)
04      -----TLLYVLFEVFDVV (SEQ ID NO: 80)
05      -----TLLYVLF----- (SEQ ID NO: 81)
06      ---MDEPTLLYVLFEV---- (SEQ ID NO: 82)
07      -----EPTLLYVLFE----- (SEQ ID NO: 83)
08      -DPMDEPTLLYVLF----- (SEQ ID NO: 84)
09      -----LLYVLFEVFD-- (SEQ ID NO: 85)
10      -----YVLFEVFDVV (SEQ ID NO: 86)
11      -----PTLLYVLFEV---- (SEQ ID NO: 87)
12      -----PTLLYVLFEVFDV- (SEQ ID NO: 88)
13      -----LYVLFEVFDV- (SEQ ID NO: 89)
14      -----EPTLLYVLFEVFD-- (SEQ ID NO: 90)
15      -----LYVLFEV---- (SEQ ID NO: 91)
16      --PMDEPTLLYVLFE----- (SEQ ID NO: 92)
17      -----LLYVLFE----- (SEQ ID NO: 93)
18      VDPMDEPTLLYVL----- (SEQ ID NO: 94)
19      -----YVLFEVF--- (SEQ ID NO: 95)
20      -----PTLLYVL----- (SEQ ID NO: 96)

```

The above peptides/sequences are highly suitable as peptides for SADCs which reduce neutralization of AdV vectors.

Example 16: Epitope mapping of polyclonal antibody ab6982 against AdV

Polyclonal antibody ab6982 (Abcam) was generated by immunizing rabbits with purified AdV. It reacts with all capsid proteins of Ad5 including hexon, fiber and penton. It was shown that the antibody neutralizes Ad5 infection in a bioassay at 1000 adenovirus 5 particles / ml, a 50 % inactivation of the adenovirus can be achieved at a 1/25,000 dilution of the antibody. In order to identify epitopic regions that could contain peptides for ab6982 paratope binding, the antibody was mapped against the sequences of fiber (NCBI Reference Sequence: AP_000226.1) and hexon protein (GenBank: BAG48782.1). The fiber-sequence at amino acid positions 1 to 581 of (NCBI Reference Sequence: AP_000226.1), and the hexon-sequence (GenBank: BAG48782.1) at amino acid positions 1 to 952 were used as a starting sequence for designing 7mer, 10mer and 13mer cyclic peptides synthesized on a peptid array. The binding signal of this antibody to the array yielded several peptides that were aligned and clustered against the sequence of the protein. The peptide clusters were named cluster1-7 (fiber protein) and clusters8-16 (hexon protein) according to their ranked order of

cyclic peptide hits (i.e. cluster contains the strongest binders, cluster2 the second strongest etc.). Below are the alignments of the corresponding peptides that bind to polyclonal antibody ab6982. The number of the peptide names corresponds to the antibody binding signal ranking from the microarray experiment, the numbers of the clusters 1-7 and clusters 8-16 are ranked by the content of top binding peptides, respectively.

```

Cluster1      MKRARPSEDTFNPVYPYD (SEQ ID NO: 36)
001           MKRARPSEDTF----- (SEQ ID NO: 97)
002           -KRARPSEDTF----- (SEQ ID NO: 98)
003           MKRARPSEDT----- (SEQ ID NO: 99)
005           MKRARPSEDTFN----- (SEQ ID NO: 100)
010           ---ARPSEDTFNP----- (SEQ ID NO: 101)
019           --RARPSEDTFN----- (SEQ ID NO: 102)
024           ----RPSEDTF----- (SEQ ID NO: 103)
035           MKRARPSEDTFNP----- (SEQ ID NO: 104)
040           --RARPSEDTFNPVY--- (SEQ ID NO: 105)
041           ---ARPSEDT----- (SEQ ID NO: 106)
052           -----EDTFNPVYPY- (SEQ ID NO: 107)
061           ----RPSEDTFNPVYPY- (SEQ ID NO: 108)
129           -KRARPSEDTFNPV---- (SEQ ID NO: 109)
130           -----DTFNPVY--- (SEQ ID NO: 110)
150           ----RPSEDTFNPV---- (SEQ ID NO: 111)
153           -----PSEDTFNPVY--- (SEQ ID NO: 112)
163           -----DTFNPVYPYD (SEQ ID NO: 113)

Cluster2      ISGTVQSAHLIIRFD (SEQ ID NO: 37)
004           ----VQSAHLIIRF- (SEQ ID NO: 114)
006           -----AHLIIRF- (SEQ ID NO: 115)
015           -SGTVQSAHLIIRF- (SEQ ID NO: 116)
056           ---TVQSAHLIIR-- (SEQ ID NO: 117)
060           -----HLIIRFD (SEQ ID NO: 118)
065           -----SAHLIIR-- (SEQ ID NO: 119)
076           ----QSAHLIIRFD (SEQ ID NO: 120)
085           ISGTVQSAHLIIR-- (SEQ ID NO: 121)
118           --GTVQSAHLII--- (SEQ ID NO: 122)
123           --GTVQSAHLIIRFD (SEQ ID NO: 123)
126           -----QSAHLII--- (SEQ ID NO: 124)

Cluster3      LGQGPLFINSAHNLDINYNKGLYLF (SEQ ID NO: 38)
009           -----HNLDINY----- (SEQ ID NO: 125)
011           ----LFINSAHNLDINY----- (SEQ ID NO: 126)
012           -----NLDINYNKGLYLF (SEQ ID NO: 127)
013           -----FVSPNG----- (SEQ ID NO: 128)
016           -----NYINEIF-- (SEQ ID NO: 129)
020           -----NKGLYLF (SEQ ID NO: 130)
021           -----INYNKGLYLF (SEQ ID NO: 131)
023           -----NSAHNLDINY----- (SEQ ID NO: 132)
032           -----WDWSGH----NYINEIF-- (SEQ ID NO: 133)
039           -----SGH----NYINEIF-- (SEQ ID NO: 134)
044           --LGTGLSF----- (SEQ ID NO: 135)
047           PFLTPPF----- (SEQ ID NO: 136)

Cluster4      SYPFDAQNQLNRLRGQGPLFIN (SEQ ID NO: 39)
027           -----LGQGPLF-- (SEQ ID NO: 137)
029           -----NRLRGQGPLF-- (SEQ ID NO: 138)
030           -----NQLNRLRGQGPLF-- (SEQ ID NO: 139)
058           -----GQGPLFI- (SEQ ID NO: 140)

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059      -----QLNLRRLQGGLFI- (SEQ ID NO: 141)
062      SYPFDAQNQLNLR----- (SEQ ID NO: 142)
066      -YPFDAQNQLNLR----- (SEQ ID NO: 143)
070      -----LRLGQGGLFI- (SEQ ID NO: 144)
072      -----NQLNLR----- (SEQ ID NO: 145)
073      ---FDAQNQLNLR----- (SEQ ID NO: 146)
082      -----QNQLNLR----- (SEQ ID NO: 147)
093      -----QGGLFIN (SEQ ID NO: 148)
102      --PFDAQNQLNLRGL----- (SEQ ID NO: 149)
112      ----DAQNQLNLR----- (SEQ ID NO: 150)
117      -----RLGQGGLFIN (SEQ ID NO: 151)
136      -----QLNLRGL----- (SEQ ID NO: 152)
147      ---FDAQNQLNLRGLQ----- (SEQ ID NO: 153)
148      -----LNLRLQGGLFIN (SEQ ID NO: 154)
169      ----AQNQLNLRGL----- (SEQ ID NO: 155)
172      ----AQNQLNL----- (SEQ ID NO: 156)
173      -----LNLRLGLQ----- (SEQ ID NO: 157)
178      SYPFDAQNQL----- (SEQ ID NO: 158)
197      --PFDAQNQLNL----- (SEQ ID NO: 159)

Cluster5      GDTPPSAYSMSFSWDWSGHNYIN (SEQ ID NO: 40)
008      -----YSMSFSW----- (SEQ ID NO: 160)
014      ----TPSAYSMSFSWDW----- (SEQ ID NO: 161)
022      -----MSFSWDW----- (SEQ ID NO: 162)
028      ----PSAYSMSFSW----- (SEQ ID NO: 163)
049      --DTPPSAYSMSFSW----- (SEQ ID NO: 164)
078      ---TTPSAYSMSF----- (SEQ ID NO: 165)
079      -----YSMSFSWDWS----- (SEQ ID NO: 166)
091      TGDTTPSAYSMSF----- (SEQ ID NO: 167)
095      -----FSWDWSGHNY- (SEQ ID NO: 168)
100      -----SFSWDWS----- (SEQ ID NO: 169)
108      ----SAYSMSF----- (SEQ ID NO: 170)
134      -----SFSWDWSGHN-- (SEQ ID NO: 171)
143      ----SAYSMSFSWD----- (SEQ ID NO: 172)
144      -----SMSFSWD----- (SEQ ID NO: 173)
149      -----SWDWSGHNYI (SEQ ID NO: 174)
167      ----AYSMSFS----- (SEQ ID NO: 175)
176      -----SMSFSWDWSGHNY- (SEQ ID NO: 176)
186      -----FSWDWSG----- (SEQ ID NO: 177)
193      -----SWDWSGH--- (SEQ ID NO: 178)

Cluster6      VLLNNSFLDPEYWNFRN (SEQ ID NO: 41)
017      -----FLDPEYWNFR- (SEQ ID NO: 179)
018      ----SFLDPEYWNF-- (SEQ ID NO: 180)
031      -----PEYWNFR- (SEQ ID NO: 181)
033      --LNNSFLDPEYWNF-- (SEQ ID NO: 182)
034      ---NNSFLDPEYWNFR- (SEQ ID NO: 183)
050      -----FLDPEYW---- (SEQ ID NO: 184)
053      -----DPEYWNF-- (SEQ ID NO: 185)
068      ---NNSFLDPEYW---- (SEQ ID NO: 186)
088      VLLNNSFLDPEYW--- (SEQ ID NO: 187)
113      -----EYWNFRN (SEQ ID NO: 188)
114      --LNNSFLDPEY---- (SEQ ID NO: 189)
155      -----LDPEYWNFRN (SEQ ID NO: 190)
180      --LNNSFLD----- (SEQ ID NO: 191)
187      ----NSFLDPEYWN--- (SEQ ID NO: 192)

Cluster7      HNYINEIFATSSYTFSYIA (SEQ ID NO: 42)
042      -----SSYTFSY-- (SEQ ID NO: 193)
043      -----FATSSYTFSY-- (SEQ ID NO: 194)
055      --YINEIFATSSYTF--- (SEQ ID NO: 195)
064      -----SYTFSYI- (SEQ ID NO: 196)
080      -----ATSSYTF--- (SEQ ID NO: 197)
089      ----EIFATSSYTF--- (SEQ ID NO: 198)
092      ----NEIFATSSYTFSY-- (SEQ ID NO: 199)

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097      -----ATSSYTFSYI- (SEQ ID NO: 200)
099      HNYINEIFATSSY----- (SEQ ID NO: 201)
104      -----IFATSSY----- (SEQ ID NO: 202)
110      ---INEIFATSSY----- (SEQ ID NO: 203)
119      -NYINEIFATSSYT----- (SEQ ID NO: 204)
168      --YINEIFA----- (SEQ ID NO: 205)
181      -----YTFSYIA (SEQ ID NO: 206)
200      -----EIFATSSYTFSYI- (SEQ ID NO: 207)

Cluster8      DEATALEINLEEEEDDDNEDEVDEQAEQQKTH (SEQ ID NO: 43)
01      ----ALEINLEEEEDDDN----- (SEQ ID NO: 208)
02      ---ATALEINLEEEEDD----- (SEQ ID NO: 209)
03      -EAATALEINLEEE----- (SEQ ID NO: 210)
04      -----LEINLEE----- (SEQ ID NO: 211)
05      ---TALEINLEEEEDDD----- (SEQ ID NO: 212)
06      -----EINLEEE----- (SEQ ID NO: 213)
07      ----ALEINLEEEED----- (SEQ ID NO: 214)
08      -----LEINLEEEED----- (SEQ ID NO: 215)
09      ---TALEINLEEE----- (SEQ ID NO: 216)
11      DEATALEINLEE----- (SEQ ID NO: 217)
13      -----LEINLEEEEDDDNE----- (SEQ ID NO: 218)
14      --AATALEINLEEEED----- (SEQ ID NO: 219)
15      -----EINLEEEEDDD----- (SEQ ID NO: 220)
19      ---ATALEINLEE----- (SEQ ID NO: 221)
23      -----INLEEEEDDDN----- (SEQ ID NO: 222)
27      -----NLEEEEDDDNE----- (SEQ ID NO: 223)
10      -----DEVDEQA----- (SEQ ID NO: 224)
12      -----EDDDNEDEVDEQA----- (SEQ ID NO: 225)
16      -----DDNEDEVDEQAEQ----- (SEQ ID NO: 226)
17      -----EVDEQAE----- (SEQ ID NO: 227)
18      -----DNEDEVDEQA----- (SEQ ID NO: 228)
20      -----VDEQAEQ----- (SEQ ID NO: 229)
21      -----EDEVDEQAEQQKT----- (SEQ ID NO: 230)
22      -----EDEVDEQAEQ----- (SEQ ID NO: 231)
24      -----DEVDEQAEQQKTH (SEQ ID NO: 232)
25      -----NEDEVDEQAEQQK----- (SEQ ID NO: 233)
26      -----DEVDEQAEQQ----- (SEQ ID NO: 234)

Cluster9      INLEEEEDDDNEDEVDEQAEQ (SEQ ID NO: 44)
028      EINLEEEEDDDNED----- (SEQ ID NO: 235)
029      --NLEEEEDDDNEDEV----- (SEQ ID NO: 236)
032      -INLEEEED----- (SEQ ID NO: 237)
034      ---LEEEEDDDNED----- (SEQ ID NO: 238)
035      -INLEEEEDDDNEDE----- (SEQ ID NO: 239)
037      -----DDNEDEVDEQAE (SEQ ID NO: 240)
053      ---LEEEEDDDNEDEV----- (SEQ ID NO: 241)
057      -----DDNEDEVDEQ----- (SEQ ID NO: 242)
063      -----EDDDNED----- (SEQ ID NO: 243)
065      --NLEEEED----- (SEQ ID NO: 244)
078      -----DDNEDEV----- (SEQ ID NO: 245)
087      -----DDNEDEVDE----- (SEQ ID NO: 246)
096      -----DDNEDE----- (SEQ ID NO: 247)
097      ---EEEDDDNEDE----- (SEQ ID NO: 248)
108      -----EEEDDDNE----- (SEQ ID NO: 249)
121      -----EDDDNEDEV----- (SEQ ID NO: 250)
126      -----EDEVDEQ----- (SEQ ID NO: 251)
148      -----EEEDDDNEDEVDEQ----- (SEQ ID NO: 252)
185      -----EEEDDDNEDEV----- (SEQ ID NO: 253)
188      ---EEEDDDNEDEVDE----- (SEQ ID NO: 254)

Cluster10     DNEDEVDEQAEQQKTHVF (SEQ ID NO: 45)
030      ----EVDEQAEQQK----- (SEQ ID NO: 255)
031      DNEDEVDEQAEQQ----- (SEQ ID NO: 256)
036      -----VDEQAEQQKT----- (SEQ ID NO: 257)
038      ----EVDEQAEQQKTHV----- (SEQ ID NO: 258)
041      -----VDEQAEQQKTHVF (SEQ ID NO: 259)

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Cluster11 EWDEAATALEINLEE (SEQ ID NO: 46)
033 -----ALEINLE (SEQ ID NO: 260)
042 --WDEAATALEINLE (SEQ ID NO: 261)
043 -----AATALEINLE (SEQ ID NO: 262)
112 EWDEAATALEINL-- (SEQ ID NO: 263)
124 ---EAATALEINL-- (SEQ ID NO: 264)

Cluster12 PKVVLVLYSEDVDIETPDTHISYMP (SEQ ID NO: 47)
039 ----LYSEDVDIET----- (SEQ ID NO: 265)
040 ----LYSEDVDIETPD----- (SEQ ID NO: 266)
044 -KVVLYSEDVDIET----- (SEQ ID NO: 267)
045 -----IETPDTH----- (SEQ ID NO: 268)
046 -----VDIETPDTHI----- (SEQ ID NO: 269)
047 ---VLYSEDVDIE----- (SEQ ID NO: 270)
048 -----DVDIETPDTHISY-- (SEQ ID NO: 271)
049 --VVLYSEDVDIETP----- (SEQ ID NO: 272)
050 -----SEDVDIETPDTHI----- (SEQ ID NO: 273)
051 -----ETPDTHI----- (SEQ ID NO: 274)
052 ---VLYSEDVDIETPD----- (SEQ ID NO: 275)
054 -----DVDIETPDTH----- (SEQ ID NO: 276)
055 -----DIETPDTHIS--- (SEQ ID NO: 277)
056 -----EDVDIETPDTHIS--- (SEQ ID NO: 278)
058 -----IETPDTHISY-- (SEQ ID NO: 279)
059 -----YSEDVDIETPDTH----- (SEQ ID NO: 280)
060 -----VDIETPDTHISYM- (SEQ ID NO: 281)
061 PKVVLVLYSEDVDIE----- (SEQ ID NO: 282)
062 -----DIETPDTH----- (SEQ ID NO: 283)
064 -----DIETPDTHISYMP (SEQ ID NO: 284)
070 -----EDVDIETPDTH----- (SEQ ID NO: 285)
071 -----ETPDTHISYM- (SEQ ID NO: 286)
159 -----IETPDTHISYMP (SEQ ID NO: 287)

Cluster13 YIPESYKDRMYSFFRNF (SEQ ID NO: 48)
072 -----DRMYSFFRNF (SEQ ID NO: 288)
086 -----DRMYSFF--- (SEQ ID NO: 289)
104 -----YSFFRNF (SEQ ID NO: 290)
107 -IPESYKDRMYSFF--- (SEQ ID NO: 291)
120 ----SYKDRMYSFF--- (SEQ ID NO: 292)
127 ---ESYKDRMYSF--- (SEQ ID NO: 293)
143 -----KDRMYSF----- (SEQ ID NO: 294)
152 YIPESYKDRMYSF--- (SEQ ID NO: 295)
153 --PESYKDRMYSFFR-- (SEQ ID NO: 296)
160 -----YKDRMYSFFR-- (SEQ ID NO: 297)

Cluster14 DSIGDRTRYFSMW (SEQ ID NO: 49)
073 -----TRYFSMW (SEQ ID NO: 298)
080 ---GDRTRYF--- (SEQ ID NO: 299)
095 DSIGDRTRYF--- (SEQ ID NO: 300)
100 DSIGDRTRYFSMW (SEQ ID NO: 301)
101 ---GDRTRYFSMW (SEQ ID NO: 302)

Cluster15 SYKDRMYSFFRNF (SEQ ID NO: 50)
072 ---DRMYSFFRNF (SEQ ID NO: 303)
099 SYKDRMYSFFRNF (SEQ ID NO: 304)

Cluster16 FLVQMLANYNIGYQGFY (SEQ ID NO: 51)
106 -----NYNIGYQGFY (SEQ ID NO: 305)
122 -----ANYNIGYQGF- (SEQ ID NO: 306)
123 ----MLANYNIGYQGFY (SEQ ID NO: 307)
136 -----IGYQGFY (SEQ ID NO: 308)
184 FLVQMLANYNIGY---- (SEQ ID NO: 309)
187 -----NIGYQGF- (SEQ ID NO: 310)

190 ---QMLANYNIGYQGF- (SEQ ID NO: 311)

The above peptides/sequences are highly suitable as peptides for SADCs which reduce neutralization of AdV vectors. Importantly, binding of these peptides to the paratope of unwanted antibodies can be even further improved by mutating 1, 2 or 3 amino acids in order to generate mimotopes with improved antibody binding properties.

Example 17: Epitope mapping of mAb ADK8 against AAV

Monoclonal antibody ADK8 was generated by immunizing mice with AAV8 capsids. It is directed against the assembled AAV8 capsid (Sonntag et al, 2011). The neutralizing function of the antibody was previously demonstrated (Gurda et al, 2012). In brief, AAV8 was pre-incubated with ADK8 which lead to a decline in the number of virus particles present in the cytoplasm. Moreover, the binding of AAV8 to the nuclear membrane as well as the nuclear entry were abrogated following neutralization by ADK8. This suggests that ADK8 neutralization might interfere either with the cellular entry and / or the transport to the nucleus. ADK8 also cross-reacts with capsid proteins from other AAV serotypes such as AAV1, AAV3, AAV7 (Mietzsch et al, 2014) and was therefore chosen as an example from which general conclusions about the present invention can be drawn.

As for the other antibodies (see examples above), several clusters were identified, delineating regions from which preferred peptides can be deduced. Most preferably, the peptides aligned below according to their binding strengths can be used for selective antibody depletion and detection as hereinabove.

```
Cluster1  WQNRDVYLQGPIWAKIP (SEQ ID NO: 52)
01      -----YLQGPIW---- (SEQ ID NO: 312)
02      -----VYLQGPI----- (SEQ ID NO: 313)
03      WQNRDVY----- (SEQ ID NO: 314)
05      ----DVYLQGP----- (SEQ ID NO: 315)
08      -QNRDVYL----- (SEQ ID NO: 316)
12      -----LQGPIWA--- (SEQ ID NO: 317)
20      ---RDVYLQG----- (SEQ ID NO: 318)
50      --NRDVYLQ----- (SEQ ID NO: 319)

Cluster2  DNTYFGYSTPWGYFDFNRFHC (SEQ ID NO: 53)
07      ---YFGYSTPWGYFDF----- (SEQ ID NO: 320)
09      ----FGYSTPWGYF----- (SEQ ID NO: 321)
10      -----GYSTPWGYFD----- (SEQ ID NO: 322)
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11      -----YSTPWGYFDF----- (SEQ ID NO: 323)
17      -NTYFGYSTPWGYF----- (SEQ ID NO: 324)
18      -----TPWGYFDFNRFHC (SEQ ID NO: 325)
23      --TYFGYSTPWGYFD----- (SEQ ID NO: 326)
26      DNTYFGYSTPWGY----- (SEQ ID NO: 327)
28      ---YFGYSTPWGY----- (SEQ ID NO: 328)
34      ----FGYSTPWGYFDFN---- (SEQ ID NO: 329)

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Cluster3  MANQAKNWLPGPCY (SEQ ID NO: 54)
04      -----NWLPGPC- (SEQ ID NO: 330)
15      -----WLPGPCY (SEQ ID NO: 331)
16      ---QAKNWLPGPC- (SEQ ID NO: 332)
21      ----AKNWLPGPCY (SEQ ID NO: 333)
25      MANQAKNWLPGPC- (SEQ ID NO: 334)

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Cluster4  LPYVLGSAHQGCLPPFP (SEQ ID NO: 55)
06      -----QGCLPPFP- (SEQ ID NO: 335)
13      -----GCLPPFP (SEQ ID NO: 336)
27      ---VLGSAHQGCLPPFP- (SEQ ID NO: 337)
32      LPYVLGSAHQGCL---- (SEQ ID NO: 338)
37      -YVLGSAHQGC----- (SEQ ID NO: 339)
38      -----CLPPFPA (SEQ ID NO: 340)
39      -----SAHQGCLPPFP-- (SEQ ID NO: 341)
45      --VLGSAHQGCL----- (SEQ ID NO: 342)
46      PYVLGSAHQGCLP---- (SEQ ID NO: 343)

```

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Cluster5  NGSQAVGRSSFYCLEYF (SEQ ID NO: 56)
14      -----GRSSFYC---- (SEQ ID NO: 344)
22      ----AVGRSSFYCLEYF (SEQ ID NO: 345)
24      ----AVGRSSFYCL--- (SEQ ID NO: 346)
33      ---QAVGRSSFYCLEY- (SEQ ID NO: 347)
35      NGSQAVGRSSFYC---- (SEQ ID NO: 348)

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Cluster6  PLIDQYLYYL (SEQ ID NO: 57)
19      ---DQYLYYL (SEQ ID NO: 349)
29      PLIDQYLYYL (SEQ ID NO: 350)
36      --IDQYLYY- (SEQ ID NO: 351)

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Cluster7  EERFFPSNGILIF (SEQ ID NO: 58)
31      ---FFPSNGILIF (SEQ ID NO: 352)
49      EERFFPSNGILIF (SEQ ID NO: 353)

```

```

Cluster8  ADGVGSSSGNWHC (SEQ ID NO: 59)
42      ---VGSSSGNWHC (SEQ ID NO: 354)
48      ADGVGSSSGNWHC (SEQ ID NO: 355)

```

Example 18: Screen for anti-AAV antibodies in human sera

2452 linear peptides derived from the sequences of 16 different AAVs used in gene therapy and with a sequence length of 15 amino-acids each were synthesized.

Samples obtained from human donors were screened for antibodies against these AAV-derived peptides immobilized on microarrays. To this end, IgG was prepared from blood obtained from the human donors by protein G purification. Each IgG sample was incubated with the peptide microarrays and Ig binding signals were detected by fluorescence. All antibody binding signals to the peptides on the arrays were background subtracted

and ranked for each sample and a deduplicated aggregate of the respective top 250 peptide hits for each donor with the corresponding protein sequence of origin (as obtained from UniProt or other sources) was compiled (designated as group IV). Further, the deduplicated aggregate of the respective top 50 peptide hits for each donor was compiled and designated as group III. Further, the deduplicated aggregate of the respective top 25 peptide hits for each donor was compiled and designated as group II. Finally, the deduplicated aggregate of the respective top 10 peptide hits for each donor was compiled and designated as group I.

Detailed results are shown in Table 1 below. Altogether, group I contains 110 distinct peptide hits (assigned to the corresponding AAV vectors in Table 1), group II contains 289 distinct peptide hits, group III contains 428 distinct peptide hits and group IV contains 1271 distinct peptide hits. Evidently, group I is a subset of group II which in turn is a subset of group III which in turn is a subset of group IV. Groups I-IV correspond to the top 4.4%, 10.5%, 17.5% and 51.8%, respectively, of all peptides screened.

Thus, all listed peptides, preferably peptides belonging to group III, even more preferably belonging to group II and most preferably belonging to group I (i.e. to the top 4.4%), provide sequences from which shorter peptide sequences can be derived for antibody depletion according to the present invention. Furthermore, also other peptide sequences (or fragments) from the proteins from which the peptides of Table 1 were derived (preferably from group III, more preferably however from group II, most preferably from group I), are suited to be used for SADCs according to the present invention. In addition, these peptides can also be used as probes for the diagnostic detection of anti-AAV antibodies in biological samples such as human sera.

Table 1

This table lists the detailed results of a screen for linear peptides as a basis for the construction of anti-AAV antibody depleting SADCs according to the present invention. These peptides are also suitable for typing neutralizing antibodies

directed against AAV gene therapy vectors. If not stated otherwise, the peptides represent fragments from different AAV VP1 proteins. Source given is either UniProt ID, GenBank ID, PDB ID or AAV strain name.

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1	383	LRTGNNFEFSYQFED	X	X	X	X	AAO88201.1
2	384	TGNNFEFSYQFEDVP	X	X	X	X	AAO88201.1
3	385	VATEQYGVVADNLQQ	X	X	X	X	AAO88201.1
4	386	FEFSYFEDVPFHSSY	X	X	X	X	AAV-Rh74 c
5	387	RTGNFEFSYFEDVPF	X	X	X	X	AAV-Rh74 c
6	388	MLRTGNFEFSYFEDV	X	X	X	X	AAV-Rh74 c
7	389	PVPADPPTTFNQAKL	X	X	X	X	AAV-Rh74 c
8	390	TQSTGGTAGTQQLLF	X	X	X	X	AAV-Rh74 c
9	391	EEEIKTTNPVATEQY	X	X	X	X	AAV-Rh74 c
10	392	SSVMLTSEEEIKTTN	X	X	X	X	AAV-Rh74 c
11	393	VDFAVNTEGTYSEPR	X	X	X	X	AAV-Rh74 c
12	394	SVPDPQPIGEPPAGP	X	X	X	X	AAV-Rh74 c
13	395	EEIKTTNPVATEQYG	X	X	X	X	AAV-Rh74 c
14	396	PIGEPPAGPSGLGSG	X	X	X	X	AAV-Rh74 c
15	397	VNTEGTYSEPRPIGT	X	X	X	X	AAV-Rh74 c
16	398	YSSVMLTSEEEIKTT	X	X	X	X	AAV-Rh74 c
17	399	VATNHQSAQTLAVPF	X	X	X	X	ALU85156.1
18	400	VSTNLQRGNLALGET	X	X	X	X	AOD99651.1
19	401	ALGETTRPATAAQTQ	X	X	X	X	AOD99656.1
20	402	TQTTGGTTNTQTLGF	X	X	X	X	pdb3J1QA
21	403	DDEEKFFPQSGVLIF	X	X	X	X	P03135
22	404	EEEIRTTNPVATEQY	X	X	X	X	P03135
23	405	PVEPDSSSGTGKAGQ	X	X	X	X	P03135
24	406	IQYTSNYNKSVNVDF	X	X	X	X	P03135
25	407	TDEEEIRTTNPVATE	X	X	X	X	P03135
26	408	VDFTVDTNGVYSEPR	X	X	X	X	P03135
27	409	VDTNGVYSEPRPIGT	X	X	X	X	P03135
28	410	TMATGSGAPMADNNE	X	X	X	X	P03135
29	411	TSTVQVFTDSEYQLP	X	X	X	X	P03135
30	412	LYLSRTNTPSGTTT	X	X	X	X	P03135
31	413	TADVNTQGVLPGMVW	X	X	X	X	P03135
32	414	GSEKTNVDIEKVMIT	X	X	X	X	P03135
33	415	TNTMATGSGAPMADN	X	X	X	X	P03135
34	416	WNPEIQYTSNYNKSV	X	X	X	X	P03135
35	417	SYTFEDVPFHSSYAH	X	X	X	X	O56137
36	418	EDVPFHSSYAHSQL	X	X	X	X	O56137
37	419	SSTDPATGDVHVMGA	X	X	X	X	O56137
38	420	ATERFGTVAVNLQSS	X	X	X	X	O56137

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
39	421	WLEDNLSEGIREWWD	X	X	X	X	O56137
40	422	EEEIKATNPVATERF	X	X	X	X	O56137
41	423	LEDNLSEGIREWWDL	X	X	X	X	O56137
42	424	DAEFQERLQEDTSFG	X	X	X	X	O56137
43	425	EWELQKENS KRWNPE	X	X	X	X	O56137
44	426	SFITQYSTGQVSVEI	X	X	X	X	O56137
45	427	EIEWELQKENS KRWN	X	X	X	X	O56137
46	428	ITQYSTGQVSVEIEW	X	X	X	X	O56137
47	429	TDEEEKATNPVATE	X	X	X	X	O56137
48	430	EEGAKTAPGKKRPVE	X	X	X	X	O56137
49	431	IQVKEVTTNDGVTTI	X	X	X	X	O56137
50	432	SDSEYQLPYVLGSAH	X	X	X	X	O56137
51	433	PLGEPPATPAAVGPT	X	X	X	X	O56137
52	434	SSASTGASNDNHYFG	X	X	X	X	O56137
53	435	PVDQSPQEPDSSSGV	X	X	X	X	O56139
54	436	EEAAKTAPGKKRPVD	X	X	X	X	O56139
55	437	APGKKRPVDQSPQEP	X	X	X	X	O56139
56	438	ILEPLGLVEEAAKTA	X	X	X	X	O56139
57	439	TRTVNDQGALPGMVW	X	X	X	X	O56139
58	440	KRPVDQSPQEPDSSS	X	X	X	X	O56139
59	441	PLGEPPAAPTSLGSN	X	X	X	X	O56139
60	442	GKKRPVDQSPQEPDS	X	X	X	X	O56139
61	443	KTAPGKKRPVDQSPQ	X	X	X	X	O56139
62	444	SNAELDNVMITDEEE	X	X	X	X	O56139
63	445	WLEDNLSEGIREWWA	X	X	X	X	Q6JC40
64	446	PVPADPPTAFNKDKL	X	X	X	X	Q6JC40
65	447	EFENVPFHSSYAHSQ	X	X	X	X	Q6JC40
66	448	FQERLKEDTSFGGNL	X	X	X	X	Q6JC40
67	449	PQILIKNTPVPADPP	X	X	X	X	Q6JC40
68	450	ADAEFQERLKEDTSF	X	X	X	X	Q6JC40
69	451	EEIKTTNPVATESYG	X	X	X	X	Q6JC40
70	452	VEFAVNTEGVYSEPR	X	X	X	X	Q6JC40
71	453	AEFQERLKEDTSFGG	X	X	X	X	Q6JC40
72	454	EPDSSAGIGKSGAQP	X	X	X	X	Q6JC40
73	455	LIKNTVPVPADPPTAF	X	X	X	X	Q6JC40
74	456	VMITNEEEIKTTNPV	X	X	X	X	Q6JC40
75	457	VNTEGVYSEPRPIGT	X	X	X	X	Q6JC40
76	458	DKLNSFITQYSTGQV	X	X	X	X	Q6JC40
77	459	VATESYGQVATNHQS	X	X	X	X	Q6JC40
78	460	DDEERFFPSNGILIF	X	X	X	X	Q8JQF8
79	461	EEEIKTTNPVATEEY	X	X	X	X	Q8JQF8
80	462	PVPADPPTTFNQSKL	X	X	X	X	Q8JQF8
81	463	LIKNTVPVPADPPTTF	X	X	X	X	Q8JQF8
82	464	SSSGNWHCDSTWLGD	X	X	X	X	Q8JQF8

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
83	465	TSVDFAVNTEGVYSE	X	X	X	X	Q8JQF8
84	466	TTTGQNNNSNFAWTA	X	X	X	X	Q8JQF8
85	467	VDFAVNTEGVYSEPR	X	X	X	X	Q8JQF8
86	468	VSTTTGQNNNSNFAW	X	X	X	X	Q8JQF8
87	469	KTAPGKKRPVEPSQ	X	X	X	X	Q8JQF8
88	470	TQTTGGTANTQTLGF	X	X	X	X	Q8JQF8
89	471	VLEPLGLVEEGAKTA	X	X	X	X	Q8JQF8
90	472	EEVGEGFLREFLGLEA	X	X	X	X	Q9YIJ1
91	473	DAEFQEKLADDTSGF	X	X	X	X	Q9YIJ1
92	474	SFVDHPPDWLEEVGE	X	X	X	X	Q9YIJ1
93	475	EWELKKENSKRWNP	X	X	X	X	Q9YIJ1
94	476	EMEWELKKENSKRW	X	X	X	X	Q9YIJ1
95	477	TNNYNDPQFVDFAPD	X	X	X	X	Q9YIJ1
96	478	FEEVPFHSSFAPSQN	X	X	X	X	Q9YIJ1
97	479	QYTNNYNDPQFVDFA	X	X	X	X	Q9YIJ1
98	480	TSTVQVFTDDDYQLP	X	X	X	X	Q9YIJ1
99	481	EDSKPSTSSDAEAGP	X	X	X	X	Q9YIJ1
100	482	EEGAKTAPTGKRIDD	X	X	X	X	Q9YIJ1
101	483	EVFPFHSSFAPSQNL	X	X	X	X	Q9YIJ1
102	484	SSFITQYSTGQVTVE	X	X	X	X	Q9YIJ1
103	485	ELEGASYQVPPQPNG	X	X	X	X	Q9YIJ1
104	486	ERDVYLQGPWAKIP	X	X	X	X	Q9YIJ1
105	487	PQYGYATLNDRNTEN	X	X	X	X	Q9YIJ1
106	488	QVTVEMEWELKKENS	X	X	X	X	Q9YIJ1
107	489	VTVQDSTTTIANLNT	X	X	X	X	Q9YIJ1
108	490	YNEQLEAGDNPYLKY	X	X	X	X	Q9YIJ1
109	491	YNNHQYREIKSGSVD	X	X	X	X	Q9YIJ1
110	492	TSSDAEAGPSGSQQL	X	X	X	X	Q9YIJ1
111	493	FEFSYQFEDVPFHSS		X	X	X	AAO88201.1
112	494	NNFEFSYQFEDVPFH		X	X	X	AAO88201.1
113	495	YQFEDVPFHSSYAHS		X	X	X	AAO88201.1
114	496	QGAGKDNVDYSSVML		X	X	X	AAO88201.1
115	497	TPVPADPPTTFQAK		X	X	X	AAO88201.1
116	498	IKTTNPVATEQYGVV		X	X	X	AAO88201.1
117	499	GNFEFSYFEDVPFHS		X	X	X	AAV-Rh74 c
118	500	FSYFEDVPFHSSYAH		X	X	X	AAV-Rh74 c
119	501	YFEDVPFHSSYAHSQ		X	X	X	AAV-Rh74 c
120	502	EYFPSQMLRTGNFEF		X	X	X	AAV-Rh74 c
121	503	EIKTTNPVATEQYGW		X	X	X	AAV-Rh74 c
122	504	RTQSTGGTAGTQQLL		X	X	X	AAV-Rh74 c
123	505	DNVDYSSVMLTSEEE		X	X	X	AAV-Rh74 c
124	506	DEERFFPSSGVLMFG		X	X	X	AAV-Rh74 c
125	507	TNVDFAVNTEGTYSE		X	X	X	AAV-Rh74 c
126	508	EIQYTSNYYKSTNVD		X	X	X	AAV-Rh74 c

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
127	509	RVSTTLSQNNNSNFA		X	X	X	AAV-Rh74 c
128	510	SESVDPDPQIGEPPIA		X	X	X	AAV-Rh74 c
129	511	QRVSTTLSQNNNSNF		X	X	X	AAV-Rh74 c
130	512	VDYSSVMLTSEEEIK		X	X	X	AAV-Rh74 c
131	513	PQPIGEPPAGPSGLG		X	X	X	AAV-Rh74 c
132	514	QQRVSTTLSQNNNSN		X	X	X	AAV-Rh74 c
133	515	VSTTLSQNNNSNFAW		X	X	X	AAV-Rh74 c
134	516	TTRPATAPQIGTVNS		X	X	X	AOD99652.1
135	517	EYGAVAINNQAAANLA		X	X	X	AOD99654.1
136	518	TTRPATAAQTVVNN		X	X	X	AOD99656.1
137	519	NQSLALGETTRPAST		X	X	X	AOD99659.1
138	520	GQMATNNQSLALGET		X	X	X	AOD99659.1
139	521	MATNNQSLALGETTR		X	X	X	AOD99659.1
140	522	TNNQSLALGETTRPA		X	X	X	AOD99659.1
141	523	DSVPDPQPIGEPPAA		X	X	X	pdb3J1QA
142	524	TGDADSVDPQPIGE		X	X	X	pdb3J1QA
143	525	SLTMAAGGGAPMADN		X	X	X	pdb3J1QA
144	526	TTGGTTNTQTLGFSQ		X	X	X	pdb3J1QA
145	527	LYLSRTQTGGTTN		X	X	X	pdb3J1QA
146	528	SRTQTGGTTNTQTL		X	X	X	pdb3J1QA
147	529	YLSRTQTGGTTNTQ		X	X	X	pdb3J1QA
148	530	DGYLPDWLEDLSEG		X	X	X	P03135
149	531	PPFPADVFMVPQYGY		X	X	X	P03135
150	532	GEPVNEADAAALEHD		X	X	X	P03135
151	533	VNVDFTVDTNGVYSE		X	X	X	P03135
152	534	EEKFFPQSGVLIFGK		X	X	X	P03135
153	535	PDWLEDLSEGIRQW		X	X	X	P03135
154	536	PVNEADAAALEHDKA		X	X	X	P03135
155	537	TNVDIEKVMITDEEE		X	X	X	P03135
156	538	VDIEKVMITDEEEIR		X	X	X	P03135
157	539	PEIQYTSNYNKSNNV		X	X	X	P03135
158	540	VEEPVKTAPGKKRPV		X	X	X	P03135
159	541	ASHKDDEEKFFPQSG		X	X	X	P03135
160	542	EPVNEADAAALEHDK		X	X	X	P03135
161	543	ERHKDDSRGLVLPY		X	X	X	P03135
162	544	GNSSGNWHCDSTWVG		X	X	X	P03135
163	545	PVPANPSTTFSAKF		X	X	X	P03135
164	546	AAALEHDKAYDRQLD		X	X	X	P03135
165	547	FNGLDKGEVNEADA		X	X	X	P03135
166	548	YTSNYNKSNNVDFTV		X	X	X	P03135
167	549	EDTLSEGIRQWWKLK		X	X	X	P03135
168	550	EPDSSSGTGKAGQQP		X	X	X	P03135
169	551	NNSEYSWTGATKYHL		X	X	X	P03135
170	552	SNYNKSVNVDFTVDT		X	X	X	P03135

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
171	553	SSQSGASNDNHYFGY		X	X	X	P03135
172	554	KRWNPEIQYTSNYNK		X	X	X	P03135
173	555	YLSRTNTPSGTTTQS		X	X	X	P03135
174	556	YTFEDVPFHSSYAHS		X	X	X	O56137
175	557	FEDVPFHSSYAHSQS		X	X	X	O56137
176	558	QSSSTD PATGDVHVM		X	X	X	O56137
177	559	PDWLEDNLSEGIREW		X	X	X	O56137
178	560	DWLEDNLSEGIREWW		X	X	X	O56137
179	561	QYSTGQVSVEIEWEL		X	X	X	O56137
180	562	DGYLPDWLEDNLSEG		X	X	X	O56137
181	563	EDNLSEGIREWWDLK		X	X	X	O56137
182	564	DNHYFGYSTPWGYFD		X	X	X	O56137
183	565	PVEQSPQEPDSSSGI		X	X	X	O56137
184	566	ADGYLPDWLEDNLSE		X	X	X	O56137
185	567	GDESVPDPQPLGEP		X	X	X	O56137
186	568	GEPVNAADAAALEHD		X	X	X	O56137
187	569	EDTSFGGNLGRAVFQ		X	X	X	O56137
188	570	GCLPPFPADVFMIPQ		X	X	X	O56137
189	571	PVPANPPAEFSATKF		X	X	X	O56137
190	572	SESVPDPQPLGEPPA		X	X	X	O56137
191	573	EFQERLQEDTSFGGN		X	X	X	O56137
192	574	DAAALEHDKAYDQQL		X	X	X	O56137
193	575	EPVNAADAAALEHDK		X	X	X	O56137
194	576	QRVSKTKTDNNNSNF		X	X	X	O56137
195	577	DSESVPDPQPLGEPP		X	X	X	O56137
196	578	EHDKAYDQQLKAGDN		X	X	X	O56137
197	579	LPGMVWQDRDVYLQG		X	X	X	O56137
198	580	VSVEIEWELQKENS		X	X	X	O56137
199	581	DSEYQLPYVLGSAHQ		X	X	X	O56137
200	582	PQPLGEPPATPAAVG		X	X	X	O56137
201	583	VEIEWELQKENS		X	X	X	O56137
202	584	EYFPSQMLRTGNNFT		X	X	X	O56137
203	585	PLIDQYLYLNRTQN		X	X	X	O56137
204	586	QVSVEIEWELQKENS		X	X	X	O56137
205	587	ASNDNHYFGYSTPWG		X	X	X	O56137
206	588	EIKATNPVATERFGT		X	X	X	O56137
207	589	GSAHQGCLPPFPADV		X	X	X	O56137
208	590	SSSGIGKTGQQPAKK		X	X	X	O56137
209	591	AAALEHDKAYDQQLK		X	X	X	O56137
210	592	NNFQFSYTFEDVPFH		X	X	X	O56139
211	593	TGNNFQFSYTFEDVP		X	X	X	O56139
212	594	LRTGNNFQFSYTFED		X	X	X	O56139
213	595	EADAAALEHDKAYDQ		X	X	X	O56139
214	596	PQPLGEPPAAPTSLG		X	X	X	O56139

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
215	597	SSSGVGKSGKQPARK		X	X	X	O56139
216	598	DDEEKFFPMHGNLIF		X	X	X	O56139
217	599	QRLSKTANDNNNSNF		X	X	X	O56139
218	600	TTS GTTNQSRLLFSQ		X	X	X	O56139
219	601	SYEFENVPFHSSYAH		X	X	X	Q6JC40
220	602	QFSYEFENVPFHSSY		X	X	X	Q6JC40
221	603	ERLKEDTSFGGNLGR		X	X	X	Q6JC40
222	604	ESVPDPQPIGEPPAA		X	X	X	Q6JC40
223	605	NNVEFAVNTEGVYSE		X	X	X	Q6JC40
224	606	NEEEIKTTNPVATES		X	X	X	Q6JC40
225	607	SLIFGKQGTGRDNVD		X	X	X	Q6JC40
226	608	EDNLSEGIREWWALK		X	X	X	Q6JC40
227	609	NSFITQYSTGQVSVE		X	X	X	Q6JC40
228	610	SSNDNAYFGYSTPWG		X	X	X	Q6JC40
229	611	TPVPADPPTAFNKDK		X	X	X	Q6JC40
230	612	VEEAAKTAPGKKRPV		X	X	X	Q6JC40
231	613	IKNTPVPADPPTAFN		X	X	X	Q6JC40
232	614	IKTTNPVATESYGQV		X	X	X	Q6JC40
233	615	IQYTSNYYKSNNVEF		X	X	X	Q6JC40
234	616	QILIKNTPVPADPPT		X	X	X	Q6JC40
235	617	AFNKDKLNSFITQYS		X	X	X	Q6JC40
236	618	EYFPSQMLRTGNNFQ		X	X	X	Q6JC40
237	619	ITNEEEIKTTNPVAT		X	X	X	Q6JC40
238	620	LKEDTSFGGNLGRAV		X	X	X	Q6JC40
239	621	VATNHQSAQAQAQTG		X	X	X	Q6JC40
240	622	DADKVMITNEEEIKT		X	X	X	Q6JC40
241	623	SLTMASGGGAPVADN		X	X	X	Q6JC40
242	624	NKDKLNSFITQYSTG		X	X	X	Q6JC40
243	625	QPIGEPPAAPSGVGS		X	X	X	Q6JC40
244	626	DNADYSDVMLTSEEE		X	X	X	Q8JQF8
245	627	TYTFEDVPFHSSYAH		X	X	X	Q8JQF8
246	628	ARDNADYSDVMLTSE		X	X	X	Q8JQF8
247	629	IGTVNSQGALPGMVW		X	X	X	Q8JQF8
248	630	EEYGIVADNLQQQNT		X	X	X	Q8JQF8
249	631	QRVSTTTGQNNNSNF		X	X	X	Q8JQF8
250	632	DGVGSSSGNWHCDST		X	X	X	Q8JQF8
251	633	IKNTPVPADPPTTFN		X	X	X	Q8JQF8
252	634	ILIKNTPVPADPPTT		X	X	X	Q8JQF8
253	635	STIQVFTDSEYQLPY		X	X	X	Q8JQF8
254	636	CYRQQRVSTTTGQNN		X	X	X	Q8JQF8
255	637	HDKAYDQQLQAGDNP		X	X	X	Q8JQF8
256	638	LYLSRTQTGGGTAN		X	X	X	Q8JQF8
257	639	TFNQSKLNSFITQYS		X	X	X	Q8JQF8
258	640	VTQNEGKTIANNLT		X	X	X	Q8JQF8

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
259	641	QYLYLSRTQTTGGT		X	X	X	Q8JQF8
260	642	SRTQTTGGTANTQTL		X	X	X	Q8JQF8
261	643	NTYFGYSTPWGYFDF		X	X	X	Q8JQF8
262	644	PVEPSPQRSPDSSTG		X	X	X	Q8JQF8
263	645	SVPDPQPLGEPPAAP		X	X	X	Q8JQF8
264	646	EPSPQRSPDSSTGIG		X	X	X	Q8JQF8
265	647	NNFEFTYNFEEVPFH		X	X	X	Q9YIJ1
266	648	PDWLEEVGEGREFL		X	X	X	Q9YIJ1
267	649	TGNNFEFTYNFEEVP		X	X	X	Q9YIJ1
268	650	LRTGNNFEFTYNFEE		X	X	X	Q9YIJ1
269	651	EPVNRADDEVAREHDI		X	X	X	Q9YIJ1
270	652	TEEDSKPSTSSDAEA		X	X	X	Q9YIJ1
271	653	TQYSTGQVTVEMEW		X	X	X	Q9YIJ1
272	654	ESETQPVNRYAYNVG		X	X	X	Q9YIJ1
273	655	NLTSTVQVFTDDDDYQ		X	X	X	Q9YIJ1
274	656	EIQYTNNYNNDPQFVD		X	X	X	Q9YIJ1
275	657	PVPGNITSFSDVPVS		X	X	X	Q9YIJ1
276	658	TVEMEWELKKENSKR		X	X	X	Q9YIJ1
277	659	EFQEKLADDTSFGGN		X	X	X	Q9YIJ1
278	660	EQLEAGDNPYLKYNH		X	X	X	Q9YIJ1
279	661	NYNDPQFVDFAPDST		X	X	X	Q9YIJ1
280	662	SSLGADTMSAGGGGP		X	X	X	Q9YIJ1
281	663	SKPSTSSDAEAGPSG		X	X	X	Q9YIJ1
282	664	FITQYSTGQVTVEME		X	X	X	Q9YIJ1
283	665	EFLGLEAGPPKPKPN		X	X	X	Q9YIJ1
284	666	NVGGQMATNNQSSTT		X	X	X	Q9YIJ1
285	667	PSKMLRTGNNFEFTY		X	X	X	Q9YIJ1
286	668	VLEPFGLVEEGAKTA		X	X	X	Q9YIJ1
287	669	AQPASSLGADTMSAG		X	X	X	Q9YIJ1
288	670	VQDSTTTIANNLTST		X	X	X	Q9YIJ1
289	671	YLEGNMLITSESETQ		X	X	X	Q9YIJ1
290	672	NVDFAVNTDGTSEP			X	X	AAO88201.1
291	673	KDNVDYSSVMLTSEE			X	X	AAO88201.1
292	674	HDDEERFFPSSGVLM			X	X	AAV-Rh74 c
293	675	SQMLRTGNFEFSYFE			X	X	AAV-Rh74 c
294	676	GDSVSPDPQPIGEP			X	X	AAV-Rh74 c
295	677	DNPYLRYHADAEFQE			X	X	AAV-Rh74 c
296	678	NTPVPADPPTTFNQA			X	X	AAV-Rh74 c
297	679	DSLVNPGVAMATHDD			X	X	AAV-Rh74 c
298	680	PLGLVESPVKTAPGK			X	X	AAV-Rh74 c
299	681	SRTQSTGGTAGTQQL			X	X	AAV-Rh74 c
300	682	TFNQAKLASFITQYS			X	X	AAV-Rh74 c
301	683	STTLSQNNNSNFAWT			X	X	AAV-Rh74 c
302	684	SSTGIGKKGQQPAKK			X	X	AAV-Rh74 c

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
303	685	KSTNVDFAVNTEGTY			X	X	AAV-Rh74 c
304	686	TYSEPRPIGTRYLTR			X	X	AAV-Rh74 c
305	687	EYGIVADNLQQQNLA			X	X	AOD99652.1
306	688	RPATAPQIGTVNSQG			X	X	AOD99652.1
307	689	GETTRPATAAQTQVV			X	X	AOD99656.1
308	690	EYGIVSSNLQAANLA			X	X	AOD99656.1
309	691	SNLQAANLALGETTR			X	X	AOD99656.1
310	692	DADSVDPDPQIGPEPP			X	X	pdb3J1QA
311	693	QGVLPGMVWQDRDVY			X	X	P03135
312	694	NEADAALEHDKAYD			X	X	P03135
313	695	QGCLPPFPADVFMVP			X	X	P03135
314	696	EHDKAYDRQLDSGDN			X	X	P03135
315	697	PFPADVFMVPQYGYL			X	X	P03135
316	698	EPVKTAPGKKRPVEH			X	X	P03135
317	699	HKDDEEKFFPQSGVL			X	X	P03135
318	700	DKGEPVNEADAAALE			X	X	P03135
319	701	EQYGSVSTNLQRGNR			X	X	P03135
320	702	GPPPPKPAERHKDDS			X	X	P03135
321	703	IEKVMITDEEEIRTT			X	X	P03135
322	704	KSVNVDFTVDTNGVY			X	X	P03135
323	705	RPVEHSPVEPDSSSG			X	X	P03135
324	706	SDIRDQSRNWLPGPC			X	X	P03135
325	707	DNNEGADGVGNSSGN			X	X	P03135
326	708	PVATEQYGSVSTNLQ			X	X	P03135
327	709	QVKEVTQNDGTTTIA			X	X	P03135
328	710	STVQVFTDSEYQLPY			X	X	P03135
329	711	DADSVDPDPQLGQPP			X	X	P03135
330	712	DSGDNPYLKYNHADA			X	X	P03135
331	713	DSLVPNGPAMASHKD			X	X	P03135
332	714	ISSQSGASNDNHYFG			X	X	P03135
333	715	MITDEEEIRTTNPVA			X	X	P03135
334	716	RQWWKLKPGPPPKP			X	X	P03135
335	717	VKEVTQNDGTTTIAN			X	X	P03135
336	718	VTQNDGTTTIANNLT			X	X	P03135
337	719	ADNNEGADGVGNSSG			X	X	P03135
338	720	PLGLVEEPVKTAPGK			X	X	P03135
339	721	GNNFTFSYTFEDVPF			X	X	O56137
340	722	FSYTFEDVPFHSSYA			X	X	O56137
341	723	TFSYTFEDVPFHSSY			X	X	O56137
342	724	DDKDKFFPMSGVMIF			X	X	O56137
343	725	TFEDVPFHSSYAHSQ			X	X	O56137
344	726	TGDVHVMGALPGMVW			X	X	O56137
345	727	HVMGALPGMVWQDRD			X	X	O56137
346	728	TVAVNLQSSSTDPAT			X	X	O56137

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
347	729	AVNLQSSSTDPATGD			X	X	056137
348	730	NHYFGYSTPWGYFDF			X	X	056137
349	731	GSQAVGRSSFYCLEY			X	X	056137
350	732	TQYSTGQVSVEIEWE			X	X	056137
351	733	YLPDWLEDNLSEGIR			X	X	056137
352	734	SNTALDNVMITDEEE			X	X	056137
353	735	TPWGYFDFNRFHCHF			X	X	056137
354	736	YFDFNRFHCHFSPRD			X	X	056137
355	737	GYLPDWLEDNLSEGI			X	X	056137
356	738	YSTGQVSVEIEWELQ			X	X	056137
357	739	SLDRLMNPLIDQYLY			X	X	056137
358	740	STVQVFSDEYQLPY			X	X	056137
359	741	SVPDPQPLGEPPATP			X	X	056137
360	742	EFSATKFAFITQYS			X	X	056137
361	743	YSTPWGYFDFNRFHC			X	X	056137
362	744	AHQGCLPPFPADVFM			X	X	056137
363	745	ASFITQYSTGQVSVE			X	X	056137
364	746	EWWDLPKPGAPKPKAN			X	X	056137
365	747	GEPPATPAAVGPTTM			X	X	056137
366	748	MVWQDRDVYLQGPW			X	X	056137
367	749	DKGEPVNAADAAALE			X	X	056137
368	750	ERLQEDTSFGGNLGR			X	X	056137
369	751	EYQLPYVLGSAHQGC			X	X	056137
370	752	FITQYSTGQVSVEIE			X	X	056137
371	753	MITDEEEIKATNPVA			X	X	056137
372	754	AADAAALEHDKAYDQ			X	X	056137
373	755	AVGPTTMASGGGAPM			X	X	056137
374	756	DSTWLGDRVITTSTR			X	X	056137
375	757	ATPAAVGPTTMASGG			X	X	056137
376	758	DNNEGADGVGNASGN			X	X	056137
377	759	EQSPQEPDSSSGIGK			X	X	056137
378	760	FNIQVKEVTTNDGVT			X	X	056137
379	761	PAAVGPTTMASGGGA			X	X	056137
380	762	SSYAHSQSLDRLMNP			X	X	056137
381	763	TAPGKKRPVEQSPQE			X	X	056137
382	764	FHSSYAHSQSLDRLM			X	X	056137
383	765	FNGLDKGEPVNAADA			X	X	056137
384	766	HSSYAHSQSLDRLMN			X	X	056137
385	767	TTSTRTWALPTYNNH			X	X	056137
386	768	VKEVTTNDGVTTIAN			X	X	056137
387	769	DGVGNSSGNWHCDSQ			X	X	056139
388	770	NSSGNWHCDSQWLGD			X	X	056139
389	771	AKKRILEPLGLVEEA			X	X	056139
390	772	PVPANPPTTFSPAKF			X	X	056139

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
391	773	NNSNFPWTAASKYHL			X	X	O56139
392	774	PDSSSGVGKSGKQPA			X	X	O56139
393	775	QSSNTAPTTRTVNDQ			X	X	O56139
394	776	TVANNLQSSNTAPTT			X	X	O56139
395	777	AELDNVMITDEEEIR			X	X	O56139
396	778	EEKFFPMHGNLIFGK			X	X	O56139
397	779	GNNFQFSYEFENVPF			X	X	Q6JC40
398	780	NVEFAVNTEGVYSEP			X	X	Q6JC40
399	781	MLRTGNNFQFSYEF			X	X	Q6JC40
400	782	RTGNNFQFSYEFENV			X	X	Q6JC40
401	783	STVQVFTDSYQLPY			X	X	Q6JC40
402	784	DGSQAVGRSSFYCLE			X	X	Q6JC40
403	785	EFAVNTEGVYSEPRP			X	X	Q6JC40
404	786	EFAWPGASSWALNGR			X	X	Q6JC40
405	787	DTESVPDPQPIGEPP			X	X	Q6JC40
406	788	NNNSEFAWPGASSWA			X	X	Q6JC40
407	789	NTPVPADPPTAFNKD			X	X	Q6JC40
408	790	STTVTQNNNSEFAWP			X	X	Q6JC40
409	791	EIQYTSNYYKSNNVE			X	X	Q6JC40
410	792	ENVPFHSSYAHSQSL			X	X	Q6JC40
411	793	ILIKNTPVPADPPTA			X	X	Q6JC40
412	794	RVSTTVTQNNNSEFA			X	X	Q6JC40
413	795	SDYQLPYVLGSAHEG			X	X	Q6JC40
414	796	GNGLDKGEPVNAADA			X	X	Q6JC40
415	797	KSNNVEFAVNTEGVY			X	X	Q6JC40
416	798	LNSFITQYSTGQVSV			X	X	Q6JC40
417	799	QQTLKFSVAGPSNMA			X	X	Q6JC40
418	800	SSGNWHCDSQWLGD			X	X	Q6JC40
419	801	ADNNEGADGVGSSSG			X	X	Q6JC40
420	802	ASGGGAPVADNNEGA			X	X	Q6JC40
421	803	IGEPPAAPSGVGSLT			X	X	Q6JC40
422	804	PLGLVEEAAKTAPGK			X	X	Q6JC40
423	805	SAGIGKSGAQPAKKR			X	X	Q6JC40
424	806	ENSKRWNPEIQYTSN			X	X	Q6JC40
425	807	ELQKENSkrwnPEIQ			X	X	Q6JC40
426	808	GNNFQFTYTFEDVPF			X	X	Q8JQF8
427	809	EERFFPSNGILIFGK			X	X	Q8JQF8
428	810	PVATEEYGIVADNLQ			X	X	Q8JQF8
429	811	QFTYTFEDVPFHSSY			X	X	Q8JQF8
430	812	NTPVPADPPTTFNQ			X	X	Q8JQF8
431	813	EIKTTNPVATEEYGI			X	X	Q8JQF8
432	814	GSSGNWHCDSTWLG			X	X	Q8JQF8
433	815	RTGNNFQFTYTFEDV			X	X	Q8JQF8
434	816	TNPVATEEYGIVADN			X	X	Q8JQF8

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
435	817	TSEEEIKTTNPVATE			X	X	Q8JQF8
436	818	GPCYRQQRVSTTTGQ			X	X	Q8JQF8
437	819	LPGPCYRQQRVSTTT			X	X	Q8JQF8
438	820	TTGGTANTQTLGFSQ			X	X	Q8JQF8
439	821	KQISNGTSGGATNDN			X	X	Q8JQF8
440	822	KQNAARDNADYSVDM			X	X	Q8JQF8
441	823	NAARDNADYSDVMLT			X	X	Q8JQF8
442	824	SKLNSFITQYSTGQV			X	X	Q8JQF8
443	825	VKEVTQNEGKTIAN			X	X	Q8JQF8
444	826	VNSQGALPGMVWQNR			X	X	Q8JQF8
445	827	NNSNFAWTAGTKYHL			X	X	Q8JQF8
446	828	QQQNTAPQIGTVNSQ			X	X	Q8JQF8
447	829	YNNHLYKQISNGTSG			X	X	Q8JQF8
448	830	YSDVMLTSEEEIKTT			X	X	Q8JQF8
449	831	DNTYFGYSTPWGYFD			X	X	Q8JQF8
450	832	TYFGYSTPWGYFDFN			X	X	Q8JQF8
451	833	ESVPDPQPLGEPPAA			X	X	Q8JQF8
452	834	STGIGKKKGQQPARKR			X	X	Q8JQF8
453	835	FGYSTPWGYFDFNRF			X	X	Q9YIJ1
454	836	YFGYSTPWGYFDFNR			X	X	Q9YIJ1
455	837	NAYFGYSTPWGYFDF			X	X	Q9YIJ1
456	838	HPPDWLEEVGEGFRE			X	X	Q9YIJ1
457	839	TENPTERSSFFCLEY			X	X	Q9YIJ1
458	840	WLEEVGEGFLREFLGL			X	X	Q9YIJ1
459	841	YSTGQVTVEMEWELK			X	X	Q9YIJ1
460	842	FVDFAPDSTGEYRTT			X	X	Q9YIJ1
461	843	QEIVPGSVWMERDVY			X	X	Q9YIJ1
462	844	TPWGYFDFNRFHSHW			X	X	Q9YIJ1
463	845	ANAYFGYSTPWGYFD			X	X	Q9YIJ1
464	846	DDDYQLPYVVGNGTE			X	X	Q9YIJ1
465	847	DEVAREHDISYNEQL			X	X	Q9YIJ1
466	848	ELKKENSKRWNPEIQ			X	X	Q9YIJ1
467	849	GNASGDWHCDSTWMG			X	X	Q9YIJ1
468	850	GYNYLPGNGLDGRGE			X	X	Q9YIJ1
469	851	TSFSDVPVSSFITQY			X	X	Q9YIJ1
470	852	ANNLTSTVQVFTDDD			X	X	Q9YIJ1
471	853	DQYLYRFVSTNNTGG			X	X	Q9YIJ1
472	854	EYRTTRPIGTRYLTR			X	X	Q9YIJ1
473	855	IFNIQVKEVTVQDST			X	X	Q9YIJ1
474	856	ENSKRWNPEIQYTNN			X	X	Q9YIJ1
475	857	AGPPKPKPNQQHQDQ			X	X	Q9YIJ1
476	858	PSTSSDAEAGPSGSQ			X	X	Q9YIJ1
477	859	TGQVTVEMEWELKKE			X	X	Q9YIJ1
478	860	VKIFNIQVKEVTVQD			X	X	Q9YIJ1

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
479	861	DSTTTIANNLTSTVQ			X	X	Q9YIJ1
480	862	ISYNEQLEAGDNPYL			X	X	Q9YIJ1
481	863	LGLEAGPPKPKPNQQ			X	X	Q9YIJ1
482	864	TAPATGTYNLQEIVP			X	X	Q9YIJ1
483	865	TMSAGGGGGLGDNNQ			X	X	Q9YIJ1
484	866	FSYQFEDVPFHSSYA				X	AAO88201.1
485	867	VLMFGKQGAGKDNDVD				X	AAO88201.1
486	868	DFAVNTDGTSEPRP				X	AAO88201.1
487	869	DGTSEPRPIGTRYL				X	AAO88201.1
488	870	GAVNSQGALPGMVWQ				X	AAO88201.1
489	871	QMLRTGNNFEFSYQF				X	AAO88201.1
490	872	MFGKQGAGKDNDVYS				X	AAO88201.1
491	873	APIVGAVNSQGALPG				X	AAO88201.1
492	874	IVGAVNSQGALPGMV				X	AAO88201.1
493	875	LQQQNAAPIVGAVNS				X	AAO88201.1
494	876	NTDGTSEPRPIGTR				X	AAO88201.1
495	877	STNVDFAVNTDGTYS				X	AAO88201.1
496	878	KDDEERFFPSSGVLM				X	AAO88201.1
497	879	THKDDEERFFPSSGV				X	AAO88201.1
498	880	VNPGVAMATHKDDEE				X	AAO88201.1
499	881	KNTPVPADPPTFSQ				X	AAO88201.1
500	882	MATHKDDEERFFPSS				X	AAO88201.1
501	883	NPVATEQYGVVADNL				X	AAO88201.1
502	884	PGVAMATHKDDEERF				X	AAO88201.1
503	885	RDSLVPVAMATHK				X	AAO88201.1
504	886	TTNPVATEQYGVVAD				X	AAO88201.1
505	887	VPADPPTFSQAKLA				X	AAO88201.1
506	888	YFPSQMLRTGNNFEF				X	AAO88201.1
507	889	PSQMLRTGNNFEFSY				X	AAO88201.1
508	890	VLMFGKQGAGDNDVDY				X	AAV-Rh74 c
509	891	AGDNPYLRYHADAEF				X	AAV-Rh74 c
510	892	AGDNDYSSVMLTSE				X	AAV-Rh74 c
511	893	FPSQMLRTGNFEFSY				X	AAV-Rh74 c
512	894	IVGAVSQGALPGMVW				X	AAV-Rh74 c
513	895	NWGFPRPKRLNLFNI				X	AAV-Rh74 c
514	896	PVATEQYGWADNLQQ				X	AAV-Rh74 c
515	897	EQYGWADNLQQQNAA				X	AAV-Rh74 c
516	898	GPFNGLDKGEPVAAD				X	AAV-Rh74 c
517	899	LVNPGVAMATHDDEE				X	AAV-Rh74 c
518	900	LYLSRTQSTGGTAG				X	AAV-Rh74 c
519	901	NNMSAQAKNWLPGPC				X	AAV-Rh74 c
520	902	YLGPFNGLDKGEPVA				X	AAV-Rh74 c
521	903	ATEQYGWADNLQQQN				X	AAV-Rh74 c
522	904	ATHDDEERFFPSSGV				X	AAV-Rh74 c

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
523	905	CLEYFPSQMLRTGNF				X	AAV-Rh74 c
524	906	DKGEPVAADAAALEH				X	AAV-Rh74 c
525	907	FLFNIQVKEVTQNEG				X	AAV-Rh74 c
526	908	GEPVAADAAALEHDK				X	AAV-Rh74 c
527	909	LRYHADAEFQERLQE				X	AAV-Rh74 c
528	910	NPGVAMATHDDEERF				X	AAV-Rh74 c
529	911	PVAADAAALEHDKAY				X	AAV-Rh74 c
530	912	QTGDSESVDPQPIG				X	AAV-Rh74 c
531	913	YHADAEFQERLQEDT				X	AAV-Rh74 c
532	914	DPPTTFNQAKLASFI				X	AAV-Rh74 c
533	915	GFRPKRLNLFNIQV				X	AAV-Rh74 c
534	916	GPNNMSAQAKNWLPG				X	AAV-Rh74 c
535	917	GVAMATHDDEERFFP				X	AAV-Rh74 c
536	918	KTTNPVATEQYGWAD				X	AAV-Rh74 c
537	919	LEPLGLVESPVKTAP				X	AAV-Rh74 c
538	920	LNFLFNIQVKEVTQN				X	AAV-Rh74 c
539	921	NNNWGFRPKRLNLF				X	AAV-Rh74 c
540	922	PSSGVL MFGKQGAGD				X	AAV-Rh74 c
541	923	PYLR YHADAEFQERL				X	AAV-Rh74 c
542	924	RVLEPLGLVESPVKT				X	AAV-Rh74 c
543	925	SPVKTAPGKKRPVEP				X	AAV-Rh74 c
544	926	SQAGPNNMSAQAKNW				X	AAV-Rh74 c
545	927	STGGTAGTQQLFSQ				X	AAV-Rh74 c
546	928	TGGTAGTQQLFSQA				X	AAV-Rh74 c
547	929	TNPVATEQYGWADNL				X	AAV-Rh74 c
548	930	VESPVKTAPGKKRPV				X	AAV-Rh74 c
549	931	VKTAPGKKRPVEPSP				X	AAV-Rh74 c
550	932	VSQGALPGMVWQNRD				X	AAV-Rh74 c
551	933	YLSRTQSTGGTAGTQ				X	AAV-Rh74 c
552	934	YLSRTQSTGGTAGT				X	AAV-Rh74 c
553	935	NMSAQAKNWLPGPCY				X	AAV-Rh74 c
554	936	GEPPAGPSGLSGSTM				X	AAV-Rh74 c
555	937	SEEEIKTTNPVATEQ				X	AAV-Rh74 c
556	938	NVDYSSVMLTSEEEI				X	AAV-Rh74 c
557	939	FAVNTEGTYSEPRPI				X	AAV-Rh74 c
558	940	SNYYKSTNVDFAVNT				X	AAV-Rh74 c
559	941	TEGTYSEPRPIGTRY				X	AAV-Rh74 c
560	942	ERFFPSSGVL MFGKQ				X	AAV-Rh74 c
561	943	HLYKQISNGTSGGST				X	AAV-Rh74 c
562	944	IGKKGQQPAKKRLNF				X	AAV-Rh74 c
563	945	MSAQAKNWLPGPCYR				X	AAV-Rh74 c
564	946	PDPQPIGEPPAGPSG				X	AAV-Rh74 c
565	947	QYLYLSRTQSTGGT				X	AAV-Rh74 c
566	948	SVMLTSEEEIKTTNP				X	AAV-Rh74 c

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
567	949	TLSQNNNSNFAWTGA				X	AAV-Rh74 c
568	950	YYKSTNVDFAVNTEG				X	AAV-Rh74 c
569	951	AGPSGLSGGTMAAGG				X	AAV-Rh74 c
570	952	AQAKNWLPGPCYRQQ				X	AAV-Rh74 c
571	953	CYRQQRVSTTLSQNN				X	AAV-Rh74 c
572	954	DQYLYLSRTQSTGG				X	AAV-Rh74 c
573	955	DYSSVMLTSEEEIKT				X	AAV-Rh74 c
574	956	GLSGGTMAAGGGAPM				X	AAV-Rh74 c
575	957	GRDSLVPNGVAMATH				X	AAV-Rh74 c
576	958	IDQYLYLSRTQSTG				X	AAV-Rh74 c
577	959	IQYTSNYYKSTNVDF				X	AAV-Rh74 c
578	960	KKGQQPAKKRLNFGQ				X	AAV-Rh74 c
579	961	KLASFITQYSTGQVS				X	AAV-Rh74 c
580	962	KYHLNGRDSLVPNGV				X	AAV-Rh74 c
581	963	LNGRDSLVPNGVAMA				X	AAV-Rh74 c
582	964	NPEIQYTSNYYKSTN				X	AAV-Rh74 c
583	965	PEIQYTSNYYKSTNV				X	AAV-Rh74 c
584	966	PLIDQYLYLSRTQS				X	AAV-Rh74 c
585	967	QAKLASFITQYSTGQ				X	AAV-Rh74 c
586	968	QISNGTSGGSTNDNT				X	AAV-Rh74 c
587	969	QYTSNYYKSTNVDF				X	AAV-Rh74 c
588	970	RQQRVSTTLSQNNNS				X	AAV-Rh74 c
589	971	SNGTSGGSTNDNTYF				X	AAV-Rh74 c
590	972	SQNNNSNFAWTGATK				X	AAV-Rh74 c
591	973	TGIGKKGQQPAKKRL				X	AAV-Rh74 c
592	974	TSNYYKSTNVDFAVN				X	AAV-Rh74 c
593	975	TTLSQNNNSNFAWTG				X	AAV-Rh74 c
594	976	YKQISNGTSGGSTND				X	AAV-Rh74 c
595	977	YRQQRVSTTLSQNNN				X	AAV-Rh74 c
596	978	NNSNFAWTGATKYHL				X	AAV-Rh74 c
597	979	GSTNDNTYFGYSTPW				X	AAV-Rh74 c
598	980	DNGRGLVLPGYKYL				X	AAV-Rh74 c
599	981	NNNSNFAWTGATKYH				X	AAV-Rh74 c
600	982	PKPKANQQKQDNDRG				X	AAV-Rh74 c
601	983	QQKQDNDRGLVLPGY				X	AAV-Rh74 c
602	984	SNFAWTGATKYHLNG				X	AAV-Rh74 c
603	985	LAVPFKAQAQTGWVQ				X	ALU85156.1
604	986	QTLAVPFKAQAQTGW				X	ALU85156.1
605	987	SRTINGSGQNQQTLK				X	ALU85156.1
606	988	GETTRPARQAATADV				X	AOD99651.1
607	989	ALGETTRPARQAATA				X	AOD99651.1
608	990	GSVSTNLQRGNLALG				X	AOD99651.1
609	991	QYGSVSTNLQRGNLA				X	AOD99651.1
610	992	RPARQAATADVNTQG				X	AOD99651.1

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
611	993	TTRPARQAATADVNT				X	AOD99651.1
612	994	DNLQQQNLALGETTR				X	AOD99652.1
613	995	GETTRPATAPQIGTV				X	AOD99652.1
614	996	GIVADNLQQQNLALG				X	AOD99652.1
615	997	VADNLQQQNLALGET				X	AOD99652.1
616	998	RPATQAQTGLVHNQG				X	AOD99654.1
617	999	VADNLQQLALGETTR				X	AOD99655.1
618	1000	GETTRPAANTGPIVG				X	AOD99655.1
619	1001	RPAANTGPIVGNVNS				X	AOD99655.1
620	1002	TEQYGVVADNLQQLA				X	AOD99655.1
621	1003	TTRPAANTGPIVGNV				X	AOD99655.1
622	1004	VSSNLQAANLALGET				X	AOD99656.1
623	1005	GIVSSNLQAANLALG				X	AOD99656.1
624	1006	RPATAAQTQVVNNQG				X	AOD99656.1
625	1007	GETTRPASTTAPATG				X	AOD99659.1
626	1008	SLALGETTRPASTTA				X	AOD99659.1
627	1009	TTRPASTTAPATGTY				X	AOD99659.1
628	1010	VGGQMATNNQSLALG				X	AOD99659.1
629	1011	EAAKTAPGKKRPVEH				X	pdb3J1QA
630	1012	APSGVGSLTMAAGGG				X	pdb3J1QA
631	1013	GGTTNTQTLGFSQGG				X	pdb3J1QA
632	1014	VGSLTMAAGGGAPMA				X	pdb3J1QA
633	1015	GADGVGNSSGNWHCD				X	P03135
634	1016	ADAAALEHDKAYDRQ				X	P03135
635	1017	CLPPFPADVFMVPQY				X	P03135
636	1018	DKAYDRQLDSGDNPY				X	P03135
637	1019	EGADGVGNSSGNWHC				X	P03135
638	1020	NNEGADGVGNSSGNW				X	P03135
639	1021	YLPDWLEDTLSEGIR				X	P03135
640	1022	ALEHDKAYDRQLDSG				X	P03135
641	1023	DVNTQGVLPGMVWQD				X	P03135
642	1024	GPAMASHKDDEEKFF				X	P03135
643	1025	LPPFPADVFMVPQYG				X	P03135
644	1026	QRVSKTSADNNNSEY				X	P03135
645	1027	AADGYLPDWLEDTLS				X	P03135
646	1028	SSGNWHCDSTWMGDR				X	P03135
647	1029	FPADVFMVPQYGYLT				X	P03135
648	1030	GPFNGLDKGEPVNEA				X	P03135
649	1031	GVGNSSGNWHCDSTW				X	P03135
650	1032	NNLTSTVQVFTDSEY				X	P03135
651	1033	NPGPAMASHKDDEEK				X	P03135
652	1034	TAPGKKRPVEHSPVE				X	P03135
653	1035	VLPGMVWQDRDVYLQ				X	P03135
654	1036	VSKTSADNNNSEYSW				X	P03135

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
655	1037	AMASHKDDEEKFFPQ				X	P03135
656	1038	ATEQYGSVSTNLQRG				X	P03135
657	1039	DNNNSEYSWTGATKY				X	P03135
658	1040	DSVPDPQPLGQPPAA				X	P03135
659	1041	EKTNVVDIEKVMITDE				X	P03135
660	1042	EVTQNDGTTTIANNL				X	P03135
661	1043	GNWHCDSTWMGDRVI				X	P03135
662	1044	KKRPEHSPVEPDSS				X	P03135
663	1045	KPGPPPKPAERHKD				X	P03135
664	1046	KTSADNNNSEYSWTG				X	P03135
665	1047	NEGADGVGNSSGNWH				X	P03135
666	1048	NLTSTVQVFTDSEYQ				X	P03135
667	1049	NTQGVLPGMVWQDRD				X	P03135
668	1050	RLNFGQTGDADSVDP				X	P03135
669	1051	SRLQFSQAGASDIRD				X	P03135
670	1052	TVQVFTDSEYQLPYV				X	P03135
671	1053	VQVFTDSEYQLPYVL				X	P03135
672	1054	WLEDTLSEGIRQWWK				X	P03135
673	1055	YNKSVNVDFTVDTNG				X	P03135
674	1056	ADGVGNSSGNWHCDS				X	P03135
675	1057	ADVFMVPQYGYLTN				X	P03135
676	1058	ANNLTSTVQVFTDSE				X	P03135
677	1059	APSGLTNTMATGSG				X	P03135
678	1060	FKLFNIQVKEVTQND				X	P03135
679	1061	GCLPPFPADVFMVPQ				X	P03135
680	1062	GIRQWWKLKPGPPPP				X	P03135
681	1063	GLDKGEPVNEADAAA				X	P03135
682	1064	KKRVLEPLGLVEEPV				X	P03135
683	1065	KQGSEKTNVDIEKVM				X	P03135
684	1066	KVMITDEEEIRTNP				X	P03135
685	1067	LTSTVQVFTDSEYQL				X	P03135
686	1068	MADNNEGADGVGNSS				X	P03135
687	1069	PARKRLNFGQTGDAD				X	P03135
688	1070	PPPKPAERHKDDSRG				X	P03135
689	1071	SADNNNSEYSWTGAT				X	P03135
690	1072	TLSEGIRQWWKLKPG				X	P03135
691	1073	TNGVYSEPRPIGTRY				X	P03135
692	1074	TNTPSGTTTQSRLQF				X	P03135
693	1075	WMGDRVITTSTRTWA				X	P03135
694	1076	AATADVNTQGVLPGM				X	P03135
695	1077	AYDRQLDSGDNPYLK				X	P03135
696	1078	CDSTWMGDRVITTST				X	P03135
697	1079	DDSRGLVLPGYKYLK				X	P03135
698	1080	DPQPLGQPPAAPSGL				X	P03135

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
699	1081	EIRTTNPVATEQYGS				X	P03135
700	1082	FGKQGSEKTNVDIEK				X	P03135
701	1083	FTVDTNGVYSEPRPI				X	P03135
702	1084	GASDIRDQSRNWLPG				X	P03135
703	1085	GLVEEPVKTAPGKKR				X	P03135
704	1086	GNRQAATADVNTQGV				X	P03135
705	1087	GQTGDADSVDPQPQL				X	P03135
706	1088	GRDSLVPNGPAMASH				X	P03135
707	1089	GSGAPMADNNEGADG				X	P03135
708	1090	GVLIFGKQGSEKTNV				X	P03135
709	1091	HSPVEPDSSSGTGKA				X	P03135
710	1092	IQVKEVTQNDGTTTI				X	P03135
711	1093	IRDQSRNWLPGPCYR				X	P03135
712	1094	KEVTQNDGTTTIANN				X	P03135
713	1095	KGEPVNEADAAALEH				X	P03135
714	1096	KLFNIQVKEVTQNDG				X	P03135
715	1097	KLKPGPPPPKPAERH				X	P03135
716	1098	LEPLGLVEEPVKTAP				X	P03135
717	1099	LIFGKQGSEKTNVDI				X	P03135
718	1100	LNFKLFNIQVKEVTQ				X	P03135
719	1101	NFGQTGDADSVDPDQ				X	P03135
720	1102	NLQRGNRQAATADVNI				X	P03135
721	1103	NTPVPANPSTTFSA				X	P03135
722	1104	PAAPSGLGTNTMATG				X	P03135
723	1105	PAERHKDDSRGLVLP				X	P03135
724	1106	PGKKRPVEHSPVEPD				X	P03135
725	1107	PLIDQYLYLSRTNT				X	P03135
726	1108	PMADNNEGADGVGNS				X	P03135
727	1109	PQILIKNTPVPANPS				X	P03135
728	1110	QAGASDIRDQSRNWL				X	P03135
729	1111	QISSQSGASNDNHYP				X	P03135
730	1112	QRGNRQAATADVNTQ				X	P03135
731	1113	QSGVLIFGKQGSEKT				X	P03135
732	1114	RKRLNFGQTGDADSV				X	P03135
733	1115	RQQRVSKTSADNNNS				X	P03135
734	1116	RTTNPVATEQYGSVS				X	P03135
735	1117	RVLEPLGLVEEPVKT				X	P03135
736	1118	SAAKFASFITQYSTG				X	P03135
737	1119	SEYSWTGATKYHLNG				X	P03135
738	1120	SGTTTQSRQLQFSQAG				X	P03135
739	1121	SRGLVLPGYKYLGP				X	P03135
740	1122	SSGTGKAGQQPARKR				X	P03135
741	1123	TFSAAKFASFITQYS				X	P03135
742	1124	TGDADSVDPQPQLGQ				X	P03135

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
743	1125	TNPVATEQYGSVSTN				X	P03135
744	1126	VFMVPQYGYLTNNG				X	P03135
745	1127	VNEADAAALEHDKAY				X	P03135
746	1128	VPDPQPLGQPPAAPS				X	P03135
747	1129	WWKLKPGPPPKPAE				X	P03135
748	1130	GATKYHLNGRDSLVN				X	P03135
749	1131	NFTFSYTFEDVPFHS				X	O56137
750	1132	RTGNNFTFSYTFEDV				X	O56137
751	1133	EPFGLVEEGAKTAPG				X	O56137
752	1134	PVATERFGTVAVNLQ				X	O56137
753	1135	DVHVMGALPGMVWQD				X	O56137
754	1136	ERFGTVAVNLQSSST				X	O56137
755	1137	MGGFGLKHPPPQILI				X	O56137
756	1138	AMASHKDDKDKFFPM				X	O56137
757	1139	DVPFHSSYAHSQSLD				X	O56137
758	1140	FGTVAVNLQSSSTDP				X	O56137
759	1141	FHPSPLMGGFGLKHP				X	O56137
760	1142	GLKHPPPQILIKNTP				X	O56137
761	1143	GRAVFQAKKRVLEPF				X	O56137
762	1144	HPSPLMGGFGLKHPP				X	O56137
763	1145	KDKFFPMMSGVMIFGK				X	O56137
764	1146	KHPPPQILIKNTPVP				X	O56137
765	1147	LMGGFGLKHPPPQIL				X	O56137
766	1148	NLQSSSTDPATGDVH				X	O56137
767	1149	PSPLMGGFGLKHPPP				X	O56137
768	1150	TDPATGDVHVMGALP				X	O56137
769	1151	LPPFPADVFMIPQYG				X	O56137
770	1152	FDFNRFHCHFSPRDW				X	O56137
771	1153	PPFPADVFMIPQYGY				X	O56137
772	1154	HYFGYSTPWGYDFN				X	O56137
773	1155	CLPPFPADVFMIPQY				X	O56137
774	1156	NNLTSTVQVFSSEY				X	O56137
775	1157	SQAVGRSSFYCLEYF				X	O56137
776	1158	DNLSEGIREWWDLKP				X	O56137
777	1159	LDRLMNPLIDQYLYY				X	O56137
778	1160	PFPADVFMIPQYGYL				X	O56137
779	1161	QAVGRSSFYCLEYFP				X	O56137
780	1162	QGCLPPFPADVFMIP				X	O56137
781	1163	GADGVGNASGNWHCD				X	O56137
782	1164	NLSEGIREWWDLKPG				X	O56137
783	1165	RSSFYCLEYFPSQML				X	O56137
784	1166	TDGHFHPSPLMGGFG				X	O56137
785	1167	VDFTVDNNGLYTEPR				X	O56137
786	1168	AADGYLPDWLEDNLS				X	O56137

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
787	1169	ANVDFTVDNNGLYTE				X	O56137
788	1170	FPADVFMIPQYGYLT				X	O56137
789	1171	LPDWLEDNLSEGIRE				X	O56137
790	1172	MAADGYLPDWLEDNL				X	O56137
791	1173	SNDNHYFGYSTPWGY				X	O56137
792	1174	VLPGYKYLGPFNGLD				X	O56137
793	1175	WGYFDFNRFHCHFSP				X	O56137
794	1176	EVTTNDGVTTIANNL				X	O56137
795	1177	GNWHCDSTWLGDRVI				X	O56137
796	1178	NDNHYFGYSTPWGYF				X	O56137
797	1179	PAEFSATKFASFITQ				X	O56137
798	1180	PYLRYNHADAEFQER				X	O56137
799	1181	YNHADAEFQERLQED				X	O56137
800	1182	DFNRFHCHFSPRDWQ				X	O56137
801	1183	DNPYLRYNHADAEFQ				X	O56137
802	1184	DRLMNPLIDQYLYL				X	O56137
803	1185	GRSSFYCLEYFPSQM				X	O56137
804	1186	HQGCLPPFPADVMI				X	O56137
805	1187	MGALPGMVWQDRDVY				X	O56137
806	1188	PHTDGHFHPSPLMGG				X	O56137
807	1189	QTGDSESVDPQPLG				X	O56137
808	1190	SVEIEWELQKENSQR				X	O56137
809	1191	VGRSSFYCLEYFPSQ				X	O56137
810	1192	VQVFSSEYQLPYVL				X	O56137
811	1193	YKYLGPFNGLDKGEP				X	O56137
812	1194	DGVGNASGNWHCDST				X	O56137
813	1195	GDNPYLRYNHADAEF				X	O56137
814	1196	GGGAPMADNNEGADG				X	O56137
815	1197	GQVSVEIEWELQKEN				X	O56137
816	1198	KGEPVNAADAAALEH				X	O56137
817	1199	LGPFNGLDKGEPVNA				X	O56137
818	1200	LTSTVQVFSSEYQL				X	O56137
819	1201	NASGNWHCDSTWLG				X	O56137
820	1202	NNGLYTEPRPIGTRY				X	O56137
821	1203	PDPQPLGEPPATPAA				X	O56137
822	1204	QSLDRLMNPLIDQYL				X	O56137
823	1205	SQSLDRLMNPLIDQY				X	O56137
824	1206	VEEGAKTAPGKKRPV				X	O56137
825	1207	ADAEFQERLQEDTSF				X	O56137
826	1208	ADVFMIPQYGYLTN				X	O56137
827	1209	GMVWQDRDVYLQGP				X	O56137
828	1210	IDQYLYLNRTQNTQS				X	O56137
829	1211	KLFNIQVKEVTTNDG				X	O56137
830	1212	KRPVEQSPQEPDSSS				X	O56137

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
831	1213	KTKTDNNNSNFTWTG				X	O56137
832	1214	KYLGPFNGLDKGEPV				X	O56137
833	1215	NAADAAALEHDKAYD				X	O56137
834	1216	NTPVPANPPAEFSAT				X	O56137
835	1217	PVNAADAAALEHDKA				X	O56137
836	1218	PWGYFDFNRFHCHFS				X	O56137
837	1219	QEDTSFGGNLGRAVF				X	O56137
838	1220	SAHQGCLPPFPADV				X	O56137
839	1221	SGGGAPMADNNEGAD				X	O56137
840	1222	TGQVSVEIEWELQKE				X	O56137
841	1223	VFSDSEYQLPYVLGS				X	O56137
842	1224	VSKTKTDNNNSNFTW				X	O56137
843	1225	VWQDRDVYLQGPWA				X	O56137
844	1226	YLGPFNGLDKGEPVN				X	O56137
845	1227	AALEHDKAYDQQLKA				X	O56137
846	1228	ADAAALEHDKAYDQQ				X	O56137
847	1229	AEFQERLQEDTSFGG				X	O56137
848	1230	AVGRSSFYCLEYFPS				X	O56137
849	1231	DDGRGLVLPGYKYL				X	O56137
850	1232	DNNNSNFTWTGASKY				X	O56137
851	1233	ESIINPGTAMASHKD				X	O56137
852	1234	FGQTGDSESVDPQP				X	O56137
853	1235	FNRFHCHFSRPDWQR				X	O56137
854	1236	FQERLQEDTSFGGNL				X	O56137
855	1237	FRPKRLNFKLFNIQV				X	O56137
856	1238	FSPRDWQRLINNNWG				X	O56137
857	1239	FTVDNNGLYTEPRPI				X	O56137
858	1240	FTWTGASKYNLNGRE				X	O56137
859	1241	GAPKPKANQQQDDG				X	O56137
860	1242	GAPMADNNEGADGVG				X	O56137
861	1243	GASNTALDNVMITDE				X	O56137
862	1244	GHFHPSPLMGGFGLK				X	O56137
863	1245	GLDKGEPVNAADAAA				X	O56137
864	1246	GRGLVLPGYKYLGP				X	O56137
865	1247	GYFDFNRFHCHFSR				X	O56137
866	1248	GYKYLGPFGNLDKGE				X	O56137
867	1249	IEWELQKENSkrWNP				X	O56137
868	1250	IREWWDLKPGAPKPK				X	O56137
869	1251	KIPHTDGHFHPSPLM				X	O56137
870	1252	KKRPVEQSPQEPDSS				X	O56137
871	1253	KQDDGRGLVLPGYKY				X	O56137
872	1254	KTDNNNSNFTWTGAS				X	O56137
873	1255	LDKGEPVNAADAAAL				X	O56137
874	1256	LEHDKAYDQQLKAGD				X	O56137

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
875	1257	LEYFPSQMLRTGNNF				X	O56137
876	1258	LKPGAPKPKANQQKQ				X	O56137
877	1259	MASGGGAPMADNNEG				X	O56137
878	1260	NEGADGVGNASGNWH				X	O56137
879	1261	NGLDKGEPVNAADAA				X	O56137
880	1262	NGSQAVGRSSFYCLE				X	O56137
881	1263	NNSNFTWTGASKYNL				X	O56137
882	1264	NNWGFRPKRLNFKLF				X	O56137
883	1265	NPYLRYNHADAEFQE				X	O56137
884	1266	NVMITDEEEIKATNP				X	O56137
885	1267	NWGFRPKRLNFKLFN				X	O56137
886	1268	PADVFMIPQYGYLTL				X	O56137
887	1269	PDSSSGIGKTGQQPA				X	O56137
888	1270	PFNGLDKGEPVNAAD				X	O56137
889	1271	PGKKRPVEQSPQEPD				X	O56137
890	1272	PGYKYLGPFGNLDKG				X	O56137
891	1273	PIWAKIPHTDGHFHP				X	O56137
892	1274	PQILIKNTPVPANPP				X	O56137
893	1275	QEPDSSSGIGKTGQQ				X	O56137
894	1276	QISSASTGASNDNHY				X	O56137
895	1277	QQKQDDGRGLVLPGY				X	O56137
896	1278	REWWDLKPGAPKPKA				X	O56137
897	1279	RLMNPLIDQYLYLN				X	O56137
898	1280	RLNFKLFNIQVKEVT				X	O56137
899	1281	SEYQLPYVLGSAHQG				X	O56137
900	1282	SGNWHCDSTWLGDRV				X	O56137
901	1283	SPRDWQRLINNNWGF				X	O56137
902	1284	STGQVSVEIEWELQK				X	O56137
903	1285	STPWGYFDFNRFHCH				X	O56137
904	1286	TALDNVMITDEEEIK				X	O56137
905	1287	TGDSESVDPQPPLGE				X	O56137
906	1288	VGNASGNWHCDSTWL				X	O56137
907	1289	WAKIPHTDGHFHPS				X	O56137
908	1290	WELQKENSkrwnPEV				X	O56137
909	1291	YTEPRPIGTRYLTRP				X	O56137
910	1292	AGMSVQPKNWLPGPC				X	O56137
911	1293	AHSQSLDRLMNPLID				X	O56137
912	1294	APGKKRPVEQSPQEP				X	O56137
913	1295	APKPKANQQKQDDGR				X	O56137
914	1296	CDSTWLGDRVITTST				X	O56137
915	1297	CLEYFPSQMLRTGNN				X	O56137
916	1298	DGRGLVLPGYKYLGP				X	O56137
917	1299	DKAYDQQLKAGDNPY				X	O56137
918	1300	DQQLKAGDNPYLRYN				X	O56137

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
919	1301	DRDVYLQGPWAKIP				X	O56137
920	1302	FPSQMLRTGNNFTFS				X	O56137
921	1303	GASKYNLNGRESIIN				X	O56137
922	1304	GDRVITTSTRTWALP				X	O56137
923	1305	GFRPKRLNFKLFNIQ				X	O56137
924	1306	GIREWWDLKPGAPKP				X	O56137
925	1307	GLVEEGAKTAPGKKR				X	O56137
926	1308	GLVLPGYKYLGPFGNG				X	O56137
927	1309	GLYTEPRPIGTRYLT				X	O56137
928	1310	GNLGRAVFQAKKRVL				X	O56137
929	1311	GQTGDSESVDPDQPL				X	O56137
930	1312	GRESIINPGTAMASH				X	O56137
931	1313	HADAEFQERLQEDTS				X	O56137
932	1314	HFSPRDWQRLINNNW				X	O56137
933	1315	IKNTPVPANPPAEFS				X	O56137
934	1316	KANQQKQDDGRGLVL				X	O56137
935	1317	KPGAPKPKANQQKQD				X	O56137
936	1318	KPKANQQKQDDGRGL				X	O56137
937	1319	KRLNFGQTGDSESV				X	O56137
938	1320	LDNVMITDEEEIKAT				X	O56137
939	1321	LGRAVFQAKKRVLEP				X	O56137
940	1322	LNFGQTGDSESVDP				X	O56137
941	1323	LNGRESIINPGTAMA				X	O56137
942	1324	LNNGSQAVGRSSFYC				X	O56137
943	1325	LPGYKYLGPFGGLDK				X	O56137
944	1326	LPTYNNHLYKQISSA				X	O56137
945	1327	LRYNHADAEFQERLQ				X	O56137
946	1328	LVEEGAKTAPGKKRP				X	O56137
947	1329	MLRTGNNFTFSYTFE				X	O56137
948	1330	NFKLFNIQVKEVTN				X	O56137
949	1331	NHADAEFQERLQEDT				X	O56137
950	1332	NLGRAVFQAKKRVLE				X	O56137
951	1333	PFHSSYAHSQSLDRL				X	O56137
952	1334	PKRLNFKLFNIQVKE				X	O56137
953	1335	PPATPAAVGPTTMAS				X	O56137
954	1336	PPPQILIKNTPVPAN				X	O56137
955	1337	PQYGYLTLNNGSQAV				X	O56137
956	1338	PRDWQRLINNNWGF				X	O56137
957	1339	PYVLGSAHQGCLPPF				X	O56137
958	1340	QDDGRGLVLPGYKYL				X	O56137
959	1341	QDRDVYLQGPWAKI				X	O56137
960	1342	QERLQEDTSFGGNLG				X	O56137
961	1343	QRLINNNWGFPRKRL				X	O56137
962	1344	QYLYLNRQTQNSGS				X	O56137

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
963	1345	RDVYLQGPWAKIPH				X	O56137
964	1346	RDWQRLINNNWGFRP				X	O56137
965	1347	RGSPAGMSVQPKNWL				X	O56137
966	1348	RLNFGQTGDSESPD				X	O56137
967	1349	RLQEDTSFGGNLGRA				X	O56137
968	1350	RQQRVSKTKTDNNNS				X	O56137
969	1351	SEGIREWWDLKPGAP				X	O56137
970	1352	SKYNLNGRESIINPG				X	O56137
971	1353	SNFTWTGASKYNLNG				X	O56137
972	1354	SSFYCLEYFPSQMLR				X	O56137
973	1355	STRTWALPTYNNHLY				X	O56137
974	1356	TNPVATERFGTVAVN				X	O56137
975	1357	TSTRTWALPTYNNHL				X	O56137
976	1358	TTMASGGGAPMADNN				X	O56137
977	1359	TWLGDRVITTSTRTW				X	O56137
978	1360	TYNNHLYKQISSAST				X	O56137
979	1361	VDNNGLYTEPRPIGT				X	O56137
980	1362	VFMIPQYGYLTLNNG				X	O56137
981	1363	VNAADAAALEDHKAY				X	O56137
982	1364	VPFHSSYAHSQSLDR				X	O56137
983	1365	VQYTSNYAKSANVDF				X	O56137
984	1366	WGFRPKRLNFKLFNI				X	O56137
985	1367	WLGDRVITTSTRTWA				X	O56137
986	1368	WQDRDVYLQGPWAK				X	O56137
987	1369	WQRLINNNWGFRPKR				X	O56137
988	1370	YAKSANVDFTVDNNG				X	O56137
989	1371	YGYLTLNNGSQAVGR				X	O56137
990	1372	YLNRTQNNQSGSAQNK				X	O56137
991	1373	YLRYNHADADEFQERL				X	O56137
992	1374	YNLNGRESIINPGTA				X	O56137
993	1375	FQFSYTFEDVPFHSS				X	O56139
994	1376	QGALPGMVWQDRDVY				X	O56139
995	1377	NDQGALPGMVWQDRD				X	O56139
996	1378	EIRTTNPVATEQYGT				X	O56139
997	1379	EQYGTVANNLQSSNT				X	O56139
998	1380	PGNGLDKGEPVNEAD				X	O56139
999	1381	GEPPAAPTSLGSNTM				X	O56139
1000	1382	GSNTMASGGGAPMAD				X	O56139
1001	1383	NTMASGGGAPMADNN				X	O56139
1002	1384	PTTRTVNDQGALPGM				X	O56139
1003	1385	LPGNGLDKGEPVNE				X	O56139
1004	1386	PDPQPLGEPPAPTS				X	O56139
1005	1387	PVATEQYGTVANNLQ				X	O56139
1006	1388	QSMSLQARNWLPGPC				X	O56139

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1007	1389	SGVGKSGKQPARKRL				X	O56139
1008	1390	TFSPAKFASFITQYS				X	O56139
1009	1391	TVNDQGALPGMVWQD				X	O56139
1010	1392	VGNSSGNWHCDSQWL				X	O56139
1011	1393	EWWALKPGVPQPKAN				X	O56139
1012	1394	FPWTAASKYHLNGRD				X	O56139
1013	1395	LINNNWGFPRKKLSF				X	O56139
1014	1396	MGGFGLKHPPQIMI				X	O56139
1015	1397	NPPTTFSPAKFASFI				X	O56139
1016	1398	NWGFPRPKLSFKLFN				X	O56139
1017	1399	TNPVATEQYGTVANN				X	O56139
1018	1400	AAKTAPGKKRPVDQS				X	O56139
1019	1401	AAPTSLSNTMASGG				X	O56139
1020	1402	AASKYHLNGRDSL VN				X	O56139
1021	1403	ANNLQSSNTAPTTRT				X	O56139
1022	1404	DQSPQEPDSSSGVGK				X	O56139
1023	1405	EGIREWWALKPGVPQ				X	O56139
1024	1406	GKQPARKRLNFGQTG				X	O56139
1025	1407	GPQMSLSQARNWLPG				X	O56139
1026	1408	GRAVFQAKKRILEPL				X	O56139
1027	1409	IKNTPVPANPPTTFS				X	O56139
1028	1410	IREWWALKPGVPQPK				X	O56139
1029	1411	KRILEPLGLVEEAAK				X	O56139
1030	1412	LKPGVPQPKANQQHQ				X	O56139
1031	1413	NLGRAVFQAKKRILE				X	O56139
1032	1414	PANPPTTFSPAKFAS				X	O56139
1033	1415	PQIMIKNTPVPANPP				X	O56139
1034	1416	QEPDSSSGVGKSGKQ				X	O56139
1035	1417	SKYHLNGRDSL VNPG				X	O56139
1036	1418	SLGSNTMASGGGAPM				X	O56139
1037	1419	SNTAPTTRTVNDQGA				X	O56139
1038	1420	TAPTTRTVNDQGALP				X	O56139
1039	1421	HKDDEEKFFPMHG NL				X	O56139
1040	1422	ASHKDDEEKFFPMHG				X	O56139
1041	1423	KFFPMHG NLIFGKEG				X	O56139
1042	1424	NVMITDEEEIRTTNP				X	O56139
1043	1425	AMASHKDDEEKFFPM				X	O56139
1044	1426	LDNVMITDEEEIRTT				X	O56139
1045	1427	FGKEGTTASNAELDN				X	O56139
1046	1428	KTANDNNNSNFPWTA				X	O56139
1047	1429	RQQRLSKTANDNNNS				X	O56139
1048	1430	DNNNSNFPWTAASKY				X	O56139
1049	1431	FPMHG NLIFGKEGTT				X	O56139
1050	1432	GNLIFGKEGTTASNA				X	O56139

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1051	1433	KEGTTASNAELDNVM				X	O56139
1052	1434	LSKTANDNNNSNFPW				X	O56139
1053	1435	QGTTSGTTNQSRLLF				X	O56139
1054	1436	TASNAELDNVMITDE				X	O56139
1055	1437	YLYLNRTQGTTSGT				X	O56139
1056	1438	YYLNRTQGTTSGTTN				X	O56139
1057	1439	QRLINNNWGFPRKKL				X	O56139
1058	1440	DGNFHPSPLMGGFGM				X	Q6JC40
1059	1441	GEDRFFPLSGSLIFG				X	Q6JC40
1060	1442	LEDNLSEGIREWWAL				X	Q6JC40
1061	1443	NDNAYFGYSTPWGYF				X	Q6JC40
1062	1444	NFQFSYEFENVPFHS				X	Q6JC40
1063	1445	NNLTSTVQVFTDSY				X	Q6JC40
1064	1446	QGILPGMVWQDRDVY				X	Q6JC40
1065	1447	EGVYSEPRPIGTRYL				X	Q6JC40
1066	1448	GILPGMVWQDRDVYL				X	Q6JC40
1067	1449	NSEFAWPGASSWALN				X	Q6JC40
1068	1450	PYLKYNHADAEFQER				X	Q6JC40
1069	1451	KEGEDRFFPLSGSLI				X	Q6JC40
1070	1452	PGPAMASHKEGEDRF				X	Q6JC40
1071	1453	QAKKRLLEPLGLVEE				X	Q6JC40
1072	1454	QNQGILPGMVWQDRD				X	Q6JC40
1073	1455	EGADGVGSSSGNWHC				X	Q6JC40
1074	1456	HEGCLPPFPADVMI				X	Q6JC40
1075	1457	LVEEAAKTAPGKKRP				X	Q6JC40
1076	1458	NQGILPGMVWQDRDV				X	Q6JC40
1077	1459	EVTDNNGVKTIANNL				X	Q6JC40
1078	1460	GADGVGSSSGNWHCD				X	Q6JC40
1079	1461	LTSTVQVFTDSYQL				X	Q6JC40
1080	1462	NEGADGVGSSSGNWH				X	Q6JC40
1081	1463	NPVATESYGQVATNH				X	Q6JC40
1082	1464	NVDADKVMITNEEEI				X	Q6JC40
1083	1465	PVADNNEGADGVGSS				X	Q6JC40
1084	1466	SAHEGCLPPFPADV				X	Q6JC40
1085	1467	TGDTESVPDPQPIGE				X	Q6JC40
1086	1468	TMASGGGAPVADNNE				X	Q6JC40
1087	1469	VEQSPQEPDSSAGIG				X	Q6JC40
1088	1470	VQVFTDSYQLPYVL				X	Q6JC40
1089	1471	EPLGLVEEAAKTAPG				X	Q6JC40
1090	1472	EPPAAPSGVGSLTMA				X	Q6JC40
1091	1473	FNKDKLNSFITQYST				X	Q6JC40
1092	1474	GAPVADNNEGADGVG				X	Q6JC40
1093	1475	GGGAPVADNNEGADG				X	Q6JC40
1094	1476	IFGKQGTGRDNVDAD				X	Q6JC40

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1095	1477	ILPGMVWQDRDVYLQ				X	Q6JC40
1096	1478	MGGFGMKHPPQILI				X	Q6JC40
1097	1479	PPQILIKNTPVPADP				X	Q6JC40
1098	1480	RAVFQAKKRLLEPLG				X	Q6JC40
1099	1481	RDNVDADKVMITNEE				X	Q6JC40
1100	1482	SNNVEFAVNTEGVYS				X	Q6JC40
1101	1483	TEGVYSEPRPIGTRY				X	Q6JC40
1102	1484	TSGGSSNDNAYFGYS				X	Q6JC40
1103	1485	TVTQNNNSEFAWPGA				X	Q6JC40
1104	1486	VLPGYKYLPGNGLD				X	Q6JC40
1105	1487	ADPPTAFNKDKLNSF				X	Q6JC40
1106	1488	ALNGRNSLMNPGPAM				X	Q6JC40
1107	1489	APSGVGSLTMASGGG				X	Q6JC40
1108	1490	DNLSEGIREWWALKP				X	Q6JC40
1109	1491	DPPTAFNKDKLNSFI				X	Q6JC40
1110	1492	DSQWLGDRVITTSTR				X	Q6JC40
1111	1493	DSSAGIGKSGAQPAK				X	Q6JC40
1112	1494	DVFMIPQYGYLTLND				X	Q6JC40
1113	1495	GIGKSGAQPAKKRLN				X	Q6JC40
1114	1496	GKQGTGRDNVDADKV				X	Q6JC40
1115	1497	GNFHPSPLMGGFGMK				X	Q6JC40
1116	1498	GVGSSSGNWHCDSQW				X	Q6JC40
1117	1499	ISNSTSGGSSNDNAY				X	Q6JC40
1118	1500	KLNSFITQYSTGQVS				X	Q6JC40
1119	1501	KNTPVPADPPTAFNK				X	Q6JC40
1120	1502	KYLGPGNGLDKGEPV				X	Q6JC40
1121	1503	LGRAVFQAKKRLLEP				X	Q6JC40
1122	1504	LGSAHEGCLPPFPAD				X	Q6JC40
1123	1505	MNPGPAMASHKEGED				X	Q6JC40
1124	1506	NMAVQGRNYIPGPSY				X	Q6JC40
1125	1507	NNEGADGVGSSSGNW				X	Q6JC40
1126	1508	NWHCDSQWLGDRVIT				X	Q6JC40
1127	1509	PAMASHKEGEDRFFP				X	Q6JC40
1128	1510	PEIQYTSNYYKSNNV				X	Q6JC40
1129	1511	QQRVSTTVTQNNNSE				X	Q6JC40
1130	1512	RLLEPLGLVEEAAKT				X	Q6JC40
1131	1513	RPVEQSPQEPDSSAG				X	Q6JC40
1132	1514	TAFNKDKLNSFITQY				X	Q6JC40
1133	1515	TGWVQNNQGILPGMVW				X	Q6JC40
1134	1516	TQNNNSEFAWPGASS				X	Q6JC40
1135	1517	VKEVTDNNGVKTIAN				X	Q6JC40
1136	1518	VPDPQPIGEPAAAPS				X	Q6JC40
1137	1519	VQNNQGILPGMVWQDR				X	Q6JC40
1138	1520	YFPSQMLRTGNNFQF				X	Q6JC40

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1139	1521	YVLGSAHEGCLPPFP				X	Q6JC40
1140	1522	ADGVGSSSGNWHCDS				X	Q6JC40
1141	1523	ANQQHQDNARGLVLP				X	Q6JC40
1142	1524	AQPAKKRLNFGQTGD				X	Q6JC40
1143	1525	ARGLVLPGYKYLPGP				X	Q6JC40
1144	1526	ASSWALNGRNSLMNP				X	Q6JC40
1145	1527	AVNTEGVYSEPRPIG				X	Q6JC40
1146	1528	DNNEGADGVGSSSGN				X	Q6JC40
1147	1529	DPQPIGEPPAAPSGV				X	Q6JC40
1148	1530	DRFFPLSGSLIFGKQ				X	Q6JC40
1149	1531	FGMKHPPPQILIKNT				X	Q6JC40
1150	1532	GLVLPGYKYLPGPNG				X	Q6JC40
1151	1533	GNLGRAVFQAKKRLL				X	Q6JC40
1152	1534	GPGNGLDKGEPVNAA				X	Q6JC40
1153	1535	GQTGDTEVPDPQPI				X	Q6JC40
1154	1536	GSSSGNWHCDSQWLG				X	Q6JC40
1155	1537	GWVQNQGILPGMVWQ				X	Q6JC40
1156	1538	IANNLTSTVQVFTDS				X	Q6JC40
1157	1539	KKRLLEPLGLVEEAA				X	Q6JC40
1158	1540	KKRLNFGQTGDTEV				X	Q6JC40
1159	1541	LEPLGLVEEAAKTAP				X	Q6JC40
1160	1542	LGLVEEAAKTAPGKK				X	Q6JC40
1161	1543	LKAGDNPYLKYNHAD				X	Q6JC40
1162	1544	LMGGFGMKHPPPQIL				X	Q6JC40
1163	1545	LNDGSQAVGRSSFYC				X	Q6JC40
1164	1546	LPYVLGSAHEGCLPP				X	Q6JC40
1165	1547	LSEGIREWWALKPGA				X	Q6JC40
1166	1548	MKHPPPQILIKNTPV				X	Q6JC40
1167	1549	NLSEGIREWWALKPG				X	Q6JC40
1168	1550	NSTSGGSSNDNAYFG				X	Q6JC40
1169	1551	NTEGVYSEPRPIGTR				X	Q6JC40
1170	1552	NYYKSNNVEFAVNTE				X	Q6JC40
1171	1553	PADPPTAFNKDKLNS				X	Q6JC40
1172	1554	PAKKRLNFGQTGDTE				X	Q6JC40
1173	1555	PLIDQYLYLSKTIN				X	Q6JC40
1174	1556	PLMGGFGMKHPPPQI				X	Q6JC40
1175	1557	PQEPDSSAGIGKSGA				X	Q6JC40
1176	1558	PQPKANQQHQDNARG				X	Q6JC40
1177	1559	PSPLMGGFGMKHPPP				X	Q6JC40
1178	1560	PSQMLRTGNNFQFSY				X	Q6JC40
1179	1561	PSYRQQRVSTTVTQN				X	Q6JC40
1180	1562	QNQQTLKFSVAGPSN				X	Q6JC40
1181	1563	QTGWVQNQGILPGMV				X	Q6JC40
1182	1564	QYTSNYYKSNNVEFA				X	Q6JC40

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1183	1565	RLMNPLIDQYLYLS				X	Q6JC40
1184	1566	RLNFGQTGDTEVPD				X	Q6JC40
1185	1567	RNSLMNPGPAMASHK				X	Q6JC40
1186	1568	SAQAAQQTGWVQNQG				X	Q6JC40
1187	1569	SGNWHCDSQWLGDV				X	Q6JC40
1188	1570	SHKEGEDRFFPLSGS				X	Q6JC40
1189	1571	SLMNPGPAMASHKEG				X	Q6JC40
1190	1572	SQMLRTGNNFQFSYE				X	Q6JC40
1191	1573	TDSYQLPYVLGSAH				X	Q6JC40
1192	1574	TESYGQVATNHQSAQ				X	Q6JC40
1193	1575	TLKFSVAGPSNMAVQ				X	Q6JC40
1194	1576	TSNYYKSNNVEFAVN				X	Q6JC40
1195	1577	VFTDSYQLPYVLGS				X	Q6JC40
1196	1578	VGSLTMASGGGAPVA				X	Q6JC40
1197	1579	VPADPPTAFNKDKLN				X	Q6JC40
1198	1580	WVQNQGILPGMVWQD				X	Q6JC40
1199	1581	WWALKPGAPQPKANQ				X	Q6JC40
1200	1582	YDQQLKAGDNPYLKY				X	Q6JC40
1201	1583	YKYLPGNGLDKGEP				X	Q6JC40
1202	1584	YLGPGNGLDKGEPVN				X	Q6JC40
1203	1585	YRQQRVSTTVTQNNN				X	Q6JC40
1204	1586	YYKSNNVEFAVNTEG				X	Q6JC40
1205	1587	TDGNFHPSPLMGGFG				X	Q6JC40
1206	1588	WELQKENSkrwnPEI				X	Q6JC40
1207	1589	HTDGNFHPSPLMGGF				X	Q6JC40
1208	1590	PHTDGNFHPSPLMGG				X	Q6JC40
1209	1591	AKIPHTDGNFHPSPL				X	Q6JC40
1210	1592	QKENSkrwnPEIQYT				X	Q6JC40
1211	1593	GPIWAKIPHTDGNFH				X	Q6JC40
1212	1594	GVYSEPRPIGTRYLT				X	Q6JC40
1213	1595	KENSkrwnPEIQYTS				X	Q6JC40
1214	1596	KIPHTDGNFHPSPLM				X	Q6JC40
1215	1597	LQKENSkrwnPEIQY				X	Q6JC40
1216	1598	PIWAKIPHTDGNFHP				X	Q6JC40
1217	1599	TIQVFTDSEYQLPYV				X	Q8JQF8
1218	1600	NNLTSTIQVFTDSEY				X	Q8JQF8
1219	1601	HKDDEERFFPSNGIL				X	Q8JQF8
1220	1602	SSGNWHCDSTWLGDR				X	Q8JQF8
1221	1603	ATNDNTYFGYSTPWG				X	Q8JQF8
1222	1604	NFQFTYTFEDVPFHS				X	Q8JQF8
1223	1605	TAPGKKRPVEPSPQR				X	Q8JQF8
1224	1606	AALEHDKAYDQQLQA				X	Q8JQF8
1225	1607	ADYSDVMLTSEEEIK				X	Q8JQF8
1226	1608	ATHKDDEERFFPSNG				X	Q8JQF8

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1227	1609	EPAAAPSGVGPNTMA				X	Q8JQF8
1228	1610	EWWALKPGAPKPKAN				X	Q8JQF8
1229	1611	FGKQNAARDNADYS				X	Q8JQF8
1230	1612	MAAGGGAPMADNNEG				X	Q8JQF8
1231	1613	PQIGTVNSQGALPGM				X	Q8JQF8
1232	1614	QVFTDSEYQLPYVLG				X	Q8JQF8
1233	1615	VGSSSGNWHCDSTWL				X	Q8JQF8
1234	1616	ANNLTSTIQVFTDSE				X	Q8JQF8
1235	1617	GIAMATHKDDEERFF				X	Q8JQF8
1236	1618	GVGSSSGNWHCDSTW				X	Q8JQF8
1237	1619	IDQYLYLSRTQTTG				X	Q8JQF8
1238	1620	IQVFTDSEYQLPYVL				X	Q8JQF8
1239	1621	RQQRVSTTTGQNNNS				X	Q8JQF8
1240	1622	TAPQIGTVNSQGALP				X	Q8JQF8
1241	1623	YDQQLQAGDNPYLR				X	Q8JQF8
1242	1624	ATEEYGIVADNLQQQ				X	Q8JQF8
1243	1625	EGAKTAPGKKRPVEP				X	Q8JQF8
1244	1626	EVTQNEGTKTIANNL				X	Q8JQF8
1245	1627	FKLFNIQVKEVTQNE				X	Q8JQF8
1246	1628	FPSQMLRTGNNFQFT				X	Q8JQF8
1247	1629	GPNTMANQAKNWLP				X	Q8JQF8
1248	1630	LEHDKAYDQQLQAGD				X	Q8JQF8
1249	1631	LIFGKQNAARDNADY				X	Q8JQF8
1250	1632	LTSTIQVFTDSEYQL				X	Q8JQF8
1251	1633	LYKQISNGTSGGATN				X	Q8JQF8
1252	1634	MANQAKNWLPGPCYR				X	Q8JQF8
1253	1635	NLTSTIQVFTDSEYQ				X	Q8JQF8
1254	1636	NPGIAMATHKDDEER				X	Q8JQF8
1255	1637	NQSKLNSFITQYSTG				X	Q8JQF8
1256	1638	PNTMAAGGGAPMADN				X	Q8JQF8
1257	1639	SFKLFNIQVKEVTQN				X	Q8JQF8
1258	1640	TDSEYQLPYVLGSAH				X	Q8JQF8
1259	1641	TMAAGGGAPMADNNE				X	Q8JQF8
1260	1642	AMATHKDDEERFFPS				X	Q8JQF8
1261	1643	APSGVGPNTMAAGGG				X	Q8JQF8
1262	1644	DPPTTFNQSKLNSFI				X	Q8JQF8
1263	1645	DPQPLGEPPAAPSGV				X	Q8JQF8
1264	1646	EGIREWWALKPGAPK				X	Q8JQF8
1265	1647	FPSNGILIFGKQNAA				X	Q8JQF8
1266	1648	FTDSEYQLPYVLGSA				X	Q8JQF8
1267	1649	GAKTAPGKKRPVEPS				X	Q8JQF8
1268	1650	GGTANTQTLGFSQGG				X	Q8JQF8
1269	1651	GILIFGKQNAARDNA				X	Q8JQF8
1270	1652	GTKTIANNLTSTIQV				X	Q8JQF8

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1271	1653	INNNWGFRPKRLSFK				X	Q8JQF8
1272	1654	IQYTSNYYKSTSVDF				X	Q8JQF8
1273	1655	ISNGTSGGATNDNTY				X	Q8JQF8
1274	1656	KAYDQQLQAGDNPYL				X	Q8JQF8
1275	1657	KEVTQNEGKTIANN				X	Q8JQF8
1276	1658	KLFNIQVKEVTQNEG				X	Q8JQF8
1277	1659	KSTSVDFAVNTEGVY				X	Q8JQF8
1278	1660	KTIANNLTSTIQVFT				X	Q8JQF8
1279	1661	KTTNPVATEEYGIVA				X	Q8JQF8
1280	1662	LMNPLIDQYLYLSR				X	Q8JQF8
1281	1663	LPTYNNHLYKQISNG				X	Q8JQF8
1282	1664	LTSEEEIKTTNPVAT				X	Q8JQF8
1283	1665	MADNNEGADGVGSSS				X	Q8JQF8
1284	1666	NGTSGGATNDNTYFG				X	Q8JQF8
1285	1667	NHLYKQISNGTSGGA				X	Q8JQF8
1286	1668	NIQVKEVTQNEGKT				X	Q8JQF8
1287	1669	NLQQQNTAPQIGTVN				X	Q8JQF8
1288	1670	NNHLYKQISNGTSGG				X	Q8JQF8
1289	1671	NTMANQAKNWLPGPC				X	Q8JQF8
1290	1672	PEIQYTSNYYKSTSV				X	Q8JQF8
1291	1673	PGKKRPVEPSPQRSP				X	Q8JQF8
1292	1674	PTYNNHLYKQISNGT				X	Q8JQF8
1293	1675	QGGPNTMANQAKNWL				X	Q8JQF8
1294	1676	QNEGKTIANNLTST				X	Q8JQF8
1295	1677	QNNNSNFAWTAGTKY				X	Q8JQF8
1296	1678	QNTAPQIGTVNSQGA				X	Q8JQF8
1297	1679	QPLGEPPAAPSGVGP				X	Q8JQF8
1298	1680	QTLGFSQGGPNTMAN				X	Q8JQF8
1299	1681	QVKEVTQNEGKTIA				X	Q8JQF8
1300	1682	SGVGPNTMAAGGGAP				X	Q8JQF8
1301	1683	SNFAWTAGTKYHLNG				X	Q8JQF8
1302	1684	SQGALPGMVWQNRDV				X	Q8JQF8
1303	1685	TQNEGKTIANNLTS				X	Q8JQF8
1304	1686	TSGGATNDNTYFGYS				X	Q8JQF8
1305	1687	TSTIQVFTDSEYQLP				X	Q8JQF8
1306	1688	TYNNHLYKQISNGTS				X	Q8JQF8
1307	1689	VGPNTMAAGGGAPMA				X	Q8JQF8
1308	1690	VMLTSEEEIKTTNPV				X	Q8JQF8
1309	1691	WLPGPCYRQQRVSTT				X	Q8JQF8
1310	1692	YLSRTQTTGGTANTQ				X	Q8JQF8
1311	1693	YYKSTSVDFAVNTEG				X	Q8JQF8
1312	1694	DGNFHPSPLMGGFGL				X	Q8JQF8
1313	1695	NDNTYFGYSTPWGYF				X	Q8JQF8
1314	1696	GALPGMVWQNRDVYL				X	Q8JQF8

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1315	1697	AGGGAPMADNNEGAD				X	Q8JQF8
1316	1698	RPVEPSPQRSPDSST				X	Q8JQF8
1317	1699	MVWQNRDVYLQGPIW				X	Q8JQF8
1318	1700	TNDNTYFGYSTPWGY				X	Q8JQF8
1319	1701	KRPVEPSPQRSPDSS				X	Q8JQF8
1320	1702	LPGMVWQNRDVYLQG				X	Q8JQF8
1321	1703	VPDPQPLGEPPAAPS				X	Q8JQF8
1322	1704	VWQNRDVYLQGPIWA				X	Q8JQF8
1323	1705	AAGGGAPMADNNEGA				X	Q8JQF8
1324	1706	DSSTGIGKKGQQPAR				X	Q8JQF8
1325	1707	GKKKGQQPARKRLNFG				X	Q8JQF8
1326	1708	NFHPSPLMGGFGLKH				X	Q8JQF8
1327	1709	QGALPGMVWQNRDVY				X	Q8JQF8
1328	1710	QQPARKRLNFGQTGD				X	Q8JQF8
1329	1711	ALPGMVWQNRDVYLQ				X	Q8JQF8
1330	1712	GIGKKGQQPARKRLN				X	Q8JQF8
1331	1713	GMVWQNRDVYLQGPI				X	Q8JQF8
1332	1714	GNFHPSPLMGGFGLK				X	Q8JQF8
1333	1715	KKRPVEPSPQRSPDS				X	Q8JQF8
1334	1716	PDSSTGIGKKGQQPA				X	Q8JQF8
1335	1717	PGMVWQNRDVYLQGP				X	Q8JQF8
1336	1718	QRSPDSSTGIGKKGQ				X	Q8JQF8
1337	1719	VEPSPQRSPDSSTGI				X	Q8JQF8
1338	1720	QAKKRVLEPLGLVEE				X	Q8JQF8
1339	1721	EPLGLVEEGAKTAPG				X	Q8JQF8
1340	1722	RAVFQAKKRVLEPLG				X	Q8JQF8
1341	1723	AKKRVLEPLGLVEEG				X	Q8JQF8
1342	1724	FQAKKRVLEPLGLVE				X	Q8JQF8
1343	1725	PLGLVEEGAKTAPGK				X	Q8JQF8
1344	1726	RVLEPLGLVEEGAKT				X	Q8JQF8
1345	1727	GYSTPWGYFDFNRFH				X	Q9YIJ1
1346	1728	FEFTYNFEEVPFHSS				X	Q9YIJ1
1347	1729	NPTERSFFCLEYFP				X	Q9YIJ1
1348	1730	GDWHCDSTWMGDRVV				X	Q9YIJ1
1349	1731	TVQVFTDDDYQLPYV				X	Q9YIJ1
1350	1732	FTYNFEEVPFHSSFA				X	Q9YIJ1
1351	1733	VDHPPDWLEEVGEG				X	Q9YIJ1
1352	1734	RSSFFCLEYFPSKML				X	Q9YIJ1
1353	1735	TGAHFHPSAMGGFG				X	Q9YIJ1
1354	1736	ASGDWHCDSTWMGDR				X	Q9YIJ1
1355	1737	GVGNASGDWHCDSTW				X	Q9YIJ1
1356	1738	PQFVDFAPDSTGEYR				X	Q9YIJ1
1357	1739	RGEVNRADDEVAREH				X	Q9YIJ1
1358	1740	AYFGYSTPWGYFDFN				X	Q9YIJ1

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1359	1741	DNTENPTERSFFCL				X	Q9YIJ1
1360	1742	DYQLPYVVGNTEGC				X	Q9YIJ1
1361	1743	PETGAHFHPSPAMGG				X	Q9YIJ1
1362	1744	RADEVAREHDISYNE				X	Q9YIJ1
1363	1745	TERSSFFCLEYFPSK				X	Q9YIJ1
1364	1746	EGLREFLGLEAGPPK				X	Q9YIJ1
1365	1747	NDPQFVDFAPDSTGE				X	Q9YIJ1
1366	1748	PAMGGFGLKHPPPMMLI				X	Q9YIJ1
1367	1749	VAREHDISYNEQLEA				X	Q9YIJ1
1368	1750	VNRADEVAREHDISY				X	Q9YIJ1
1369	1751	YNHADAEFQEKLADD				X	Q9YIJ1
1370	1752	EPFGLVEEGAKTAPT				X	Q9YIJ1
1371	1753	FSDVPVSSFITQYST				X	Q9YIJ1
1372	1754	FTDDDYQLPYVVGN				X	Q9YIJ1
1373	1755	HADAEFQEKLADDT				X	Q9YIJ1
1374	1756	MGGFGLKHPPPMMLI				X	Q9YIJ1
1375	1757	NGLDRGEPVNRADDEV				X	Q9YIJ1
1376	1758	NPEIQYTNNYNNDPQF				X	Q9YIJ1
1377	1759	QVFTDDDYQLPYVVG				X	Q9YIJ1
1378	1760	REHDISYNEQLEAGD				X	Q9YIJ1
1379	1761	VGEGREFLGLEAGP				X	Q9YIJ1
1380	1762	WGYFDFNRFHSHWSP				X	Q9YIJ1
1381	1763	WSPRDWQRLINNYWG				X	Q9YIJ1
1382	1764	YFDFNRFHSHWSPRD				X	Q9YIJ1
1383	1765	ADGVGNASGDWHCDS				X	Q9YIJ1
1384	1766	ARTEEDSKPSTSSDA				X	Q9YIJ1
1385	1767	ASVSATFATTNRMELE				X	Q9YIJ1
1386	1768	DFNRFHSHWSPRDWQ				X	Q9YIJ1
1387	1769	EGCLPAFPPQVFTLP				X	Q9YIJ1
1388	1770	ETQPVNRVAYNVGGQ				X	Q9YIJ1
1389	1771	FHPSPAMGGFGLKHP				X	Q9YIJ1
1390	1772	GGGGPLGDNNQGADG				X	Q9YIJ1
1391	1773	GGPLGDNNQGADGVG				X	Q9YIJ1
1392	1774	IDDHFPKRKKARTEE				X	Q9YIJ1
1393	1775	LVEEGAKTAPT GKRI				X	Q9YIJ1
1394	1776	NLQEIVPGSVWMERD				X	Q9YIJ1
1395	1777	NPYLKYNHADA EFQE				X	Q9YIJ1
1396	1778	PAFPPQVFTLPQYGY				X	Q9YIJ1
1397	1779	PASSLGADTMSAGGG				X	Q9YIJ1
1398	1780	PVSSFITQYSTGQVT				X	Q9YIJ1
1399	1781	QGADGVGNASGDWHC				X	Q9YIJ1
1400	1782	TGGVQFNKNLAGRYA				X	Q9YIJ1
1401	1783	VSAFATTNRMELEGA				X	Q9YIJ1
1402	1784	YFPSKMLRTGN NFEF				X	Q9YIJ1

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1403	1785	YNFEEVPFHSSFAPS				X	Q9YIJ1
1404	1786	AFATTNRMELEGASY				X	Q9YIJ1
1405	1787	AHFHPSPAMGGFGLK				X	Q9YIJ1
1406	1788	DFAPDSTGEYRTTRP				X	Q9YIJ1
1407	1789	DGSNANAYFGYSTPW				X	Q9YIJ1
1408	1790	DNPYLKYNHADAEFQ				X	Q9YIJ1
1409	1791	DSTGEYRTTRPIGTR				X	Q9YIJ1
1410	1792	EGNMLITSESETQPV				X	Q9YIJ1
1411	1793	FVSTNNTGGVQFNKN				X	Q9YIJ1
1412	1794	GDNPYLKYNHADAEF				X	Q9YIJ1
1413	1795	GGNLGKAVFQAKKRV				X	Q9YIJ1
1414	1796	GTEGCLPAFPPQVFT				X	Q9YIJ1
1415	1797	HDISYNEQLEAGDNP				X	Q9YIJ1
1416	1798	IVPGSVWMERDVYLQ				X	Q9YIJ1
1417	1799	KIPETGAHFHPSPAM				X	Q9YIJ1
1418	1800	KMLRTGNNFEFTYNF				X	Q9YIJ1
1419	1801	LEAGPPKPKPNQQHQ				X	Q9YIJ1
1420	1802	LEYFPSKMLRTGNNF				X	Q9YIJ1
1421	1803	LPGNGGLDRGEPVNR				X	Q9YIJ1
1422	1804	LPGYNYLPGNGGLDR				X	Q9YIJ1
1423	1805	LVDQYLYRFVSTNNT				X	Q9YIJ1
1424	1806	NIQVKEVTVQDSTTT				X	Q9YIJ1
1425	1807	NITSFSDVPVSSFIT				X	Q9YIJ1
1426	1808	NNQGADGVGNASGDW				X	Q9YIJ1
1427	1809	NRASVSATFATTNRME				X	Q9YIJ1
1428	1810	NTPVPGNITSFSDVP				X	Q9YIJ1
1429	1811	NYLPGNGGLDRGEPV				X	Q9YIJ1
1430	1812	PATGTYNLQEIVPGS				X	Q9YIJ1
1431	1813	PGNGGLDRGEPVNRAD				X	Q9YIJ1
1432	1814	PGNITSFSDVPVSSF				X	Q9YIJ1
1433	1815	PRDWQRLINNYWGFR				X	Q9YIJ1
1434	1816	PSPAMGGFGLKHPPP				X	Q9YIJ1
1435	1817	PYVVGNGTEGCLPAF				X	Q9YIJ1
1436	1818	QARGLVLPGYNYLGP				X	Q9YIJ1
1437	1819	QEKLADDTSFGGNLG				X	Q9YIJ1
1438	1820	QLPYVVGNGTEGCLP				X	Q9YIJ1
1439	1821	RMELEGASYQVPPQP				X	Q9YIJ1
1440	1822	SVWMERDVYLQGPIW				X	Q9YIJ1
1441	1823	TGEYRTTRPIGTRYL				X	Q9YIJ1
1442	1824	TTTIANNLTSTVQVF				X	Q9YIJ1
1443	1825	VVGNGTEGCLPAFPP				X	Q9YIJ1
1444	1826	WMERDVYLQGPIWAK				X	Q9YIJ1
1445	1827	WMGDRVVTKSTRTWV				X	Q9YIJ1
1446	1828	YLYRFVSTNNTGGVQ				X	Q9YIJ1

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1447	1829	ADDTSFGGNLGKAVF				X	Q9YIJ1
1448	1830	AKKRVLEPFGLVEEG				X	Q9YIJ1
1449	1831	ALENTMIFNSQPANP				X	Q9YIJ1
1450	1832	APDSTGEYRTTRPIG				X	Q9YIJ1
1451	1833	APSQNLFKLANPLVD				X	Q9YIJ1
1452	1834	APTGKRIDDFPKRK				X	Q9YIJ1
1453	1835	ASYQVPPQPNGMTNN				X	Q9YIJ1
1454	1836	ATNNQSSTTAPATGT				X	Q9YIJ1
1455	1837	DHFPKRKKARTEEDS				X	Q9YIJ1
1456	1838	DTSFGGNLGKAVFQA				X	Q9YIJ1
1457	1839	DVPVSSFITQYSTGQ				X	Q9YIJ1
1458	1840	DWQRLINNYWGFRPR				X	Q9YIJ1
1459	1841	FPPQVFTLPQYGYAT				X	Q9YIJ1
1460	1842	FQAKKRVLEPFGLVE				X	Q9YIJ1
1461	1843	GDNNQGADGVGNASG				X	Q9YIJ1
1462	1844	GDRVVTKSTRTWVLP				X	Q9YIJ1
1463	1845	GFRPRSLRVKIFNIQ				X	Q9YIJ1
1464	1846	GGQMATNNQSSTTAP				X	Q9YIJ1
1465	1847	GSGVNRASVSATFATT				X	Q9YIJ1
1466	1848	GSQQLQIPAPASSL				X	Q9YIJ1
1467	1849	GVNRASVSATFATTNR				X	Q9YIJ1
1468	1850	IKSGSVDGSNANAYF				X	Q9YIJ1
1469	1851	KEVTVQDSTTTIANN				X	Q9YIJ1
1470	1852	KKENSKRWNPFIQYT				X	Q9YIJ1
1471	1853	LDRGEPVNRADDEVAR				X	Q9YIJ1
1472	1854	LGADTMSAGGGGGLG				X	Q9YIJ1
1473	1855	LINNYWGFRPRSLRV				X	Q9YIJ1
1474	1856	LREFLGLEAGPPKPK				X	Q9YIJ1
1475	1857	LVLPGYNYLGPNGNL				X	Q9YIJ1
1476	1858	NLAGRYANTYKNWFP				X	Q9YIJ1
1477	1859	NLFKLANPLVDQYLY				X	Q9YIJ1
1478	1860	NNQSSTTAPATGTYN				X	Q9YIJ1
1479	1861	NNTGGVQFNKNLAGR				X	Q9YIJ1
1480	1862	NPLVDQYLYRFVSTN				X	Q9YIJ1
1481	1863	NRDNTENPTERSFFF				X	Q9YIJ1
1482	1864	PFHSSFAPSQNLFKL				X	Q9YIJ1
1483	1865	PIWAKIPETGAHFHP				X	Q9YIJ1
1484	1866	PLGDNNQGADGVGNNA				X	Q9YIJ1
1485	1867	PMGRTQGWNLGSGVN				X	Q9YIJ1
1486	1868	PMMLIKNTVPVGNIT				X	Q9YIJ1
1487	1869	PQPNGMTNNLQGSNT				X	Q9YIJ1
1488	1870	QGPIWAKIPETGAHF				X	Q9YIJ1
1489	1871	QGSNTYALENTMIFN				X	Q9YIJ1
1490	1872	QPVNRVAYNVGGQMA				X	Q9YIJ1

peptide #	SEQ ID NO	peptide	group I	group II	group III	group IV	source
1491	1873	QVKEVTVQDSTTTIA				X	Q9YIU1
1492	1874	REIKSGSVDGSNANA				X	Q9YIU1
1493	1875	RTTRPIGTRYLTRPL				X	Q9YIU1
1494	1876	RWNPEIQYTNNYNDP				X	Q9YIU1
1495	1877	RYANTYKNWFPGPMG				X	Q9YIU1
1496	1878	SFFCLEYFPSKMLRT				X	Q9YIU1
1497	1879	SFGGNLGKAVFQAKK				X	Q9YIU1
1498	1880	SNANAYFGYSTPWGY				X	Q9YIU1
1499	1881	SNTYALENTMIFNSQ				X	Q9YIU1
1500	1882	SQNLFKLANPLVDQY				X	Q9YIU1
1501	1883	SVDGSNANAYFGYST				X	Q9YIU1
1502	1884	TGTYNLQEIVPGSVW				X	Q9YIU1
1503	1885	TLNRDNTENPTERRS				X	Q9YIU1
1504	1886	TSESETQPVNRVAYN				X	Q9YIU1
1505	1887	TYKNWFPGPMGRTQG				X	Q9YIU1
1506	1888	YATLNRDNTENPTER				X	Q9YIU1
1507	1889	YGYATLNRDNTENPT				X	Q9YIU1
1508	1890	YRFVSTNNTGGVQFN				X	Q9YIU1
1509	1891	YSTPWGYFDFNRFHS				X	Q9YIU1

Example 19: Screen for anti-AAV antibodies in human sera based on cyclic peptides

More than 1200 cyclic peptides derived from the sequences of human and rhesus monkey AAV sequences and artificial AAV sequences according to Table 2 and with a sequence length of 14 amino-acids each were synthesized.

Samples obtained from human donors were screened for antibodies against these AAV-derived peptides immobilized on microarrays. To this end, IgG was prepared from blood obtained from the human donors by protein G purification. Each IgG sample was incubated with the peptide microarrays and Ig binding signals were detected by fluorescence. All antibody binding signals to the peptides on the arrays were background subtracted and ranked for each sample and a deduplicated aggregate of the respective top 250 peptide hits for each donor with the corresponding protein sequence of origin (as obtained from UniProt or other sources) was compiled (designated as group II). Further, the deduplicated aggregate of the respective top 50 peptide hits for each donor was compiled and designated as group I.

Detailed results are shown in Table 2 below. Altogether, group I contains 47 distinct peptide hits (assigned to the corresponding AAV vectors in Table 2) and group II yielded 172 distinct peptide hits. Evidently, group I is a subset of group II.

Thus, all listed peptides, preferably peptides belonging to group I, provide sequences from which shorter peptide sequences can be derived for antibody depletion according to the present invention. Furthermore, also other peptide sequences (or fragments) from the proteins from which the peptides of Table 2 were derived (preferably from group I), are suited to be used for SADCs according to the present invention. In addition, these peptides can also be used as probes for the diagnostic detection of anti-AAV antibodies in biological samples such as human sera.

Table 2

This table lists the detailed results of a screen for circularized peptides as a basis for the construction of anti-AAV antibody depleting SADCs according to the present invention. These peptides are also suitable for typing neutralizing antibodies directed against AAV gene therapy vectors. If not stated otherwise, the peptides represent fragments from different AAV VP1 proteins. Source given is either UniProt ID, GenBank ID, PDB ID or AAV strain name.

peptide #	SEQ ID NO	peptide	group I	group II	source
1	1892	DSQWLGDVRVTTST	X	X	AAVLK03.L125I
2	1893	DTNGVYSEPRPIGT	X	X	AAVLK03.L125I
3	1894	STNLQRGNLALGET	X	X	AOD99651.1
4	1895	ANNLTSTVQIFADS	X	X	A9RAIO
5	1896	KIFNIQVKEVTTSN	X	X	A9RAIO
6	1897	GNTSQQTDRNAFY	X	X	O41855
7	1898	LEDNLSEGIREWWD	X	X	AAO88201.1
8	1899	SESVPDPQPIGEPP	X	X	AAO88201.1
9	1900	LIKNTVPADPPTT	X	X	AAO88201.1
10	1901	PQYGYLTLNNGSQA	X	X	AAO88201.1
11	1902	DEEEIRTTNPVATE	X	X	AAVLK03.L125I
12	1903	NYNKS VNVDFTVDT	X	X	AAVLK03.L125I
13	1904	YHLNGRDSLVPNGP	X	X	AAVLK03.L125I
14	1905	TRPATAPQIGTVNS	X	X	AOD99652.1

peptide #	SEQ ID NO	peptide	group I	group II	source
15	1906	GETTRPATAAQQTQV	X	X	AOD99656.1
16	1907	IFNIQVKEVTTSNG	X	X	A9RAI0
17	1908	SNSQLIFAGPNPSG	X	X	A9RAI0
18	1909	TTSSNNLLFTSEE	X	X	A9RAI0
19	1910	FNIQVKEVTNDGV	X	X	O56137
20	1911	GQTGDSESVDPQP	X	X	AAO88201.1
21	1912	PQILIKNTPVPADP	X	X	AAO88201.1
22	1913	QLKAGDNPYLRYNH	X	X	AAO88201.1
23	1914	SFITQYSTGQVSVE	X	X	AAO88201.1
24	1915	FGKQGAGRDNDVYS	X	X	AAS99285.1
25	1916	YYKSTNVDFAVNTE	X	X	AAS99285.1
26	1917	HYFGYSTPWGYFDF	X	X	AAVLK03.L125I
27	1918	APGKKRPVDQSPQE	X	X	AAVLK03.L125I
28	1919	GKKRPVDQSPQEPD	X	X	AAVLK03.L125I
29	1920	KTAPGKKRPVDQSP	X	X	AAVLK03.L125I
30	1921	PEIQYTSNYNKS VN	X	X	AAVLK03.L125I
31	1922	SESVDPQPPLGEPP	X	X	AAVLK03.L125I
32	1923	TAPGKKRPVDQSPQ	X	X	AAVLK03.L125I
33	1924	YDQQLKAGDNPYLK	X	X	AAVLK03.L125I
34	1925	YLYLNRTQGTTS	X	X	AAVLK03.L125I
35	1926	DKAYDRQLDSGDNP	X	X	AAV2i8
36	1927	GTNTMATGSGAPMA	X	X	AAV2i8
37	1928	DKAYDQQLQAGDNP	X	X	AAV-Rh74
38	1929	TESVPDPQPIGEPP	X	X	ALU85156.1
39	1930	KNTPVPADPPTTES	X	X	AAO88201.1
40	1931	PVPADPPTTESQAK	X	X	AAO88201.1
41	1932	DEEEIKATNPVATE	X	X	O56137
42	1933	DKDKFFPMSGVMIF	X	X	O56137
43	1934	LQQQNTAPQIGTVN	X	X	Q8JQF8
44	1935	EEEIKTTNPVATEE	X	X	Q8JQF8
45	1936	GQNNNSNFAWTAGT	X	X	Q8JQF8
46	1937	DDEDKFFPMSGVMI	X	X	Q9WBP8
47	1938	PLVDQYLYRFVSTN	X	X	Q9YIJ1
48	1939	ADPPTTFSQAKLAS		X	AAO88201.1
49	1940	DAAALEHDKAYDQQ		X	AAO88201.1
50	1941	DKAYDQQLKAGDNP		X	AAO88201.1
51	1942	DSESVDPQPPIGEP		X	AAO88201.1
52	1943	DWLEDNLSEGIREW		X	AAO88201.1
53	1944	EDNLSEGIREWWDL		X	AAO88201.1
54	1945	EEIKTTNPVATEQY		X	AAO88201.1
55	1946	ENSKRWNPEIQYTS		X	AAO88201.1
56	1947	ESVPDPQPPIGEPPA		X	AAO88201.1
57	1948	EYQLPYVLGSAHQG		X	AAO88201.1
58	1949	FQERLQEDTSFGGN		X	AAO88201.1
59	1950	GDESVDPQPPIGE		X	AAO88201.1

peptide #	SEQ ID NO	peptide	group I	group II	source
60	1951	HSQSLDRLMNPLID		X	AAO88201.1
61	1952	KGEPVNAADAAALE		X	AAO88201.1
62	1953	KNTPVPADPPTFS		X	AAO88201.1
63	1954	LPYVLGSAHQGCLP		X	AAO88201.1
64	1955	LQQQNAAPIVGAVN		X	AAO88201.1
65	1956	NAADAAALEHDKAY		X	AAO88201.1
66	1957	NPGVAMATHKDDEE		X	AAO88201.1
67	1958	PGAPKPKANQQKQD		X	AAO88201.1
68	1959	PPQILIKNTPVPAD		X	AAO88201.1
69	1960	PRDWQRLINNNWGF		X	AAO88201.1
70	1961	PWGYFDFNRFHCHF		X	AAO88201.1
71	1962	QLPYVLGSAHQGCL		X	AAO88201.1
72	1963	QQRVSTTLSQNNNS		X	AAO88201.1
73	1964	SEPRPIGTRYLTRN		X	AAO88201.1
74	1965	SGGSTNDNTYFGYS		X	AAO88201.1
75	1966	SQSLDRLMNPLIDQ		X	AAO88201.1
76	1967	TGDSVDPDPQPIG		X	AAO88201.1
77	1968	TIANNLTSTIQVFT		X	AAO88201.1
78	1969	TQYSTGQVSVEIEW		X	AAO88201.1
79	1970	VTQNEGKTIANNL		X	AAO88201.1
80	1971	WLEDNLSEGIREWW		X	AAO88201.1
81	1972	YFGYSTPWGYDFN		X	AAO88201.1
82	1973	LSRTQSTGGTQGTQ		X	AAS99285.1
83	1974	TQGTQQLFSQAGP		X	AAS99285.1
84	1975	DAEFQERLKEDTSF		X	AAVLK03.L125I
85	1976	DDEEKFFPMHGNLI		X	AAVLK03.L125I
86	1977	DGHFHPSPLMGGFG		X	AAVLK03.L125I
87	1978	DSESVDPDPQLGEP		X	AAVLK03.L125I
88	1979	EEEIRTTNPVATEQ		X	AAVLK03.L125I
89	1980	EEIRTTNPVATEQY		X	AAVLK03.L125I
90	1981	FQERLKEDTSFGGN		X	AAVLK03.L125I
91	1982	GADGVGNSSGNWHC		X	AAVLK03.L125I
92	1983	GDSESVDPDPQLGE		X	AAVLK03.L125I
93	1984	GNGLDKGEPVNAAD		X	AAVLK03.L125I
94	1985	KKRPVDQSPQEPDS		X	AAVLK03.L125I
95	1986	KRPVDQSPQEPDSS		X	AAVLK03.L125I
96	1987	KSVNVDFTVDTNGV		X	AAVLK03.L125I
97	1988	LSKTANDNNNSNFP		X	AAVLK03.L125I
98	1989	MASHKDDEEKFFPM		X	AAVLK03.L125I
99	1990	NNFQFSYTFEDVPF		X	AAVLK03.L125I
100	1991	PVDQSPQEPDSSSG		X	AAVLK03.L125I
101	1992	PVPANPPTTFSPAK		X	AAVLK03.L125I
102	1993	QQRLSKTANDNNNS		X	AAVLK03.L125I
103	1994	QSSNTAPTTRTVND		X	AAVLK03.L125I
104	1995	SKTANDNNNSNFPW		X	AAVLK03.L125I

peptide #	SEQ ID NO	peptide	group I	group II	source
105	1996	SNYNKSVNVDFTV		X	AAVLK03.L125I
106	1997	TTSGETTNQSRLLFS		X	AAVLK03.L125I
107	1998	VMITDEEEIRTTNP		X	AAVLK03.L125I
108	1999	APGKKRPVEHSPVE		X	AAV2i8
109	2000	FFPQSGVLIFGKQG		X	AAV2i8
110	2001	FGKQGSEKTNVDIE		X	AAV2i8
111	2002	HKDDEEKFFPQSGV		X	AAV2i8
112	2003	KGEPVNEADAAALE		X	AAV2i8
113	2004	NEADAAALEHDKAY		X	AAV2i8
114	2005	NPVATEQYGSVSTN		X	AAV2i8
115	2006	PQILIKNTPVPANP		X	AAV2i8
116	2007	QQRVSKTSADNNNS		X	AAV2i8
117	2008	QTGDADSVDPQPL		X	AAV2i8
118	2009	ADPPTTFNQAKLAS		X	AAV-Rh74
119	2010	AGDNVDYSSVMLTS		X	AAV-Rh74
120	2011	KNTPVPADPPTTFN		X	AAV-Rh74
121	2012	KRVLEPLGLVESPV		X	AAV-Rh74
122	2013	PYLRYHADAEFQER		X	AAV-Rh74
123	2014	EEEIKTTNPVATES		X	ALU85156.1
124	2015	EFAWPGASSWALNG		X	ALU85156.1
125	2016	KSNNVEFAVNTEGV		X	ALU85156.1
126	2017	MNPGPAMASHKEGE		X	ALU85156.1
127	2018	PVPADPPTAFNKDK		X	ALU85156.1
128	2019	TVQVFTDSYQLPY		X	ALU85156.1
129	2020	NLQAANLALGETTR		X	AOD99656.1
130	2021	GGQMATNNQSLALG		X	AOD99659.1
131	2022	MATNNQSLALGETT		X	AOD99659.1
132	2023	KKRILEPLGLVEEA		X	AAB95452.1
133	2024	ADPPTTFNQSKLNS		X	3J1Q
134	2025	KSTSVDFAVNTEGV		X	3J1Q
135	2026	LQRGNRQAATADV		X	3J1Q
136	2027	PVPADPPTTFNQSK		X	3J1Q
137	2028	DDDDRFFPMHGNLI		X	QLI60567.1
138	2029	PEPADVFMIPQYGY		X	AAO88201.1
139	2030	DIYYQGPIWAKVPH		X	A9RAIO
140	2031	FEKVPFHSMYAHSQ		X	A9RAIO
141	2032	FSAARINSFLTQYS		X	A9RAIO
142	2033	HSQSLDRMMNPLLD		X	A9RAIO
143	2034	KKRILEPLGLVEEG		X	A9RAIO
144	2035	MVPQYGYCGVVTGK		X	A9RAIO
145	2036	NQTDRNAFYCLEYF		X	A9RAIO
146	2037	RDTDMFGQIADNNQ		X	A9RAIO
147	2038	RDWQRLINNNWGLR		X	A9RAIO
148	2039	TVQIFADSTYELPY		X	A9RAIO
149	2040	DIYYQGPIWAKIPH		X	O41855

peptide #	SEQ ID NO	peptide	group I	group II	source
150	2041	QIFADSSYELPYVM		X	O41855
151	2042	THSTLDGRWSALTP		X	O41855
152	2043	TVQIFADSSYELPY		X	O41855
153	2044	DKFFPMSGVMIFGK		X	O56137
154	2045	EEEIKATNPVATER		X	O56137
155	2046	EGADGVGNASGNWH		X	O56137
156	2047	LFNIQVKEVTTNDG		X	O56137
157	2048	QVKEVTTNDGVTTI		X	O56137
158	2049	RVSKTKTDNNNSNF		X	O56137
159	2050	SDSEYQLPYVLGSA		X	O56137
160	2051	HSQSLDRLMNPLLD		X	Q5Y9B2
161	2052	IEMRAAPGGNAVDA		X	Q5Y9B2
162	2053	KRLNFEEDTGAGDG		X	Q5Y9B2
163	2054	SQSLDRLMNPLLDQ		X	Q5Y9B2
164	2055	STGQVAVQIEWEIE		X	Q5Y9B2
165	2056	TTSANNLLFTSEEE		X	Q5Y9B2
166	2057	TTSGETLNQGNAAT		X	Q5Y9B2
167	2058	GESESVPDPQPIGE		X	Q5Y9B4
168	2059	GQTGESESVPDPQP		X	Q5Y9B4
169	2060	ANPGIAMATHKDDE		X	Q8JQF8
170	2061	EGASYQVPPQPNGM		X	Q9YIJ1
171	2062	EYRTTRPIGTRYLT		X	Q9YIJ1
172	2063	YNLQEIVPGSVWME		X	Q9YIJ1

Example 20: Further screen for anti-AAV antibodies in human sera

By using a cumulative gliding average signal of all sera tested over 4 consecutively aligned peptide signals along the corresponding AAV sequences, 1948 linear peptides were derived from AAV vectors AAV1, AAV2, AAV5, AAV6, AAV8, AAV9 and AAVrh.10.

Detailed results are shown in Table 3 below. 63 top candidates with the strongest signals were assigned to group I corresponding to 3.2 % of all AAV peptides analyzed by gliding average signal along the AAV VP1 sequence. The peptides of group I as well as the 135 peptides with second strongest signals were assigned to group II corresponding to 10.1 % of all AAV peptides analyzed. Additional 82 peptides (assigned to group III) were derived from the top 200 ranked peptide signals of the present screen not covered by group I and II. In summary, groups I, II and III thus contain 280 linear peptides suitable (as basis for

SADCs) to remove or to detect anti AAV antibodies, in particular antibodies directed against the AAV1, AAV2, AAV5, AAV6, AAV8, AAV9 and AAVrh.10 VP1 proteins.

Table 3

This table provides a separate compilation of suitable peptides covering stretches along the VP1 sequence of widely used AAV vectors including AAV1, AAV2, AAV5, AAV6, AAV8, AAV9 and AAVrh.10. Source given is either UniProt ID, GenBank ID, PDB ID or AAV strain name. The asterisk (*) indicates peptide sequences for which a SEQ ID NO has already been assigned in Table 1 above.

peptide #	SEQ ID NO	peptide	group I	group II	group III	source
1	*	ADPPTAFNKDKLNSF	X	X		Q6JC40
2	2064	ADTMSAGGGGPLGDN	X	X		Q9YIJ1
3	*	AEFQERLKEDTSFGG	X	X		spP03135
4	2065	AKTAPGKKRPVEPSP	X	X		Q8JQF8
5	*	APTGKRIDDHFPKPK	X	X		Q9YIJ1
6	*	DKLNSFITQYSTGQV	X	X		Q6JC40
7	2066	DVYLQGPIWAKIPET	X	X		Q9YIJ1
8	*	EEEIKTTNPVATEEY	X	X		Q8JQF8
9	*	EEEIKTTNPVATEQY	X	X		AAO88201.1
10	*	EEEIRTTNPVATEQY	X	X		spP03135
11	*	EEIKTTNPVATEQYG	X	X		AAO88201.1
12	*	EIKTTNPVATEEYGI	X	X		Q8JQF8
13	*	EIRTTNPVATEQYGS	X	X		spP03135
14	*	ELKKENSKRWNPFIQ	X	X		Q9YIJ1
15	*	EMEWELKKENSKRWNP	X	X		Q9YIJ1
16	*	ERDVYLQGPIWAKIP	X	X		Q9YIJ1
17	*	ERLKEDTSFGGNLGR	X	X		spP03135
18	*	EWELKKENSKRWNPFI	X	X		Q9YIJ1
19	*	FITQYSTGQVSVEIE	X	X		spP03135
20	*	FITQYSTGQVTVEME	X	X		Q9YIJ1
21	*	FQERLKEDTSFGGNL	X	X		spP03135
22	2067	GAKTAPTGKRIDDHF	X	X		Q9YIJ1
23	2068	GQVATNHQSAQAQAQ	X	X		Q6JC40
24	*	IKTTNPVATEQYGVV	X	X		AAO88201.1
25	*	IQYTSNYNKSVMVDF	X	X		spP03135
26	*	KKENSKRWNPFIQYT	X	X		Q9YIJ1
27	*	KLNSFITQYSTGQVS	X	X		Q6JC40
28	2069	KTAPTGKRIDDHFPK	X	X		Q9YIJ1
29	*	KTTNPVATEEYGIVA	X	X		Q8JQF8

peptide #	SEQ ID NO	peptide	group I	group II	group III	source
30	*	LKEDTSFGGNLGRAV	X	X		spP03135
31	*	LNSFITQYSTGQVSV	X	X		Q6JC40
32	2070	MNPLIDQYLYLSKT	X	X		Q6JC40
33	2071	NHQYREIKSGSVDGS	X	X		Q9YIJ1
34	*	NSFITQYSTGQVSVE	X	X		Q6JC40
35	*	NTEGVYSEPRPIGTR	X	X		Q6JC40
36	*	PADPPTAFNKDKLNS	X	X		Q6JC40
37	*	PEIQYTSNYNKSNNV	X	X		spP03135
38	*	PLIDQYLYLSKTIN	X	X		Q6JC40
39	2072	PTTFNQSKLNSFITQ	X	X		Q8JQF8
40	*	PVPADPPTAFNKDKL	X	X		Q6JC40
41	*	QGPIWAKIPETGAHF	X	X		Q9YIJ1
42	2073	QYREIKSGSVDGSNA	X	X		Q9YIJ1
43	*	REIKSGSVDGSNANA	X	X		Q9YIJ1
44	*	RTTNPVATEQYGSVS	X	X		spP03135
45	*	SEEEIKTTNPVATEQ	X	X		AAO88201.1
46	*	SFITQYSTGQVSVEI	X	X		spP03135
47	*	SSFITQYSTGQVTVE	X	X		Q9YIJ1
48	*	SSVMLTSEEEIKTTN	X	X		AAO88201.1
49	*	SSYAHQSQSLDRLMNP	X	X		spP03135
50	*	SVMLTSEEEIKTTNP	X	X		AAO88201.1
51	2074	SYAHQSQSLDRLMNPL	X	X		spP03135
52	*	TMSAGGGGGLGDNNQ	X	X		Q9YIJ1
53	*	TNPVATEEYGIVADN	X	X		Q8JQF8
54	*	TNPVATEQYGSVSTN	X	X		spP03135
55	*	TQTTGGTANTQTLGF	X	X		Q8JQF8
56	*	TTNPVATEQYGVVAD	X	X		AAO88201.1
57	*	VPADPPTAFNKDKLN	X	X		Q6JC40
58	2075	VYSEPRPIGTRYLTR	X	X		spP03135
59	*	WNPEIQYTSNYNKS	X	X		spP03135
60	2076	YLQGPIWAKIPETGA	X	X		Q9YIJ1
61	*	YNNHQYREIKSGSVD	X	X		Q9YIJ1
62	*	YSSVMLTSEEEIKTT	X	X		AAO88201.1
63	*	YTSNYNKSNNVDFTV	X	X		spP03135
64	*	ADAEFQERLKEDTSF		X		spP03135
65	*	AGPPKPKPNQQHQDQ		X		Q9YIJ1
66	*	AGPSGLGSGTMAAGG		X		AAO88201.1
67	*	ANNLTSTVQVFTDDD		X		Q9YIJ1
68	*	CYRQQRVSTTTGQNN		X		Q8JQF8
69	*	DPPTTFNQSKLNSFI		X		Q8JQF8
70	2077	DSSSGTGKAGQQPAR		X		spP03135
71	*	DSTTTIANNLTSTVQ		X		Q9YIJ1
72	*	EDTSFGGNLGRAVFQ		X		spP03135
73	*	EEGAKTAPGKKRPVE		X		Q8JQF8
74	*	EEGAKTAPTGRIDD		X		Q9YIJ1

peptide #	SEQ ID NO	peptide	group I	group II	group III	source
75	*	EEIKTTNPVATESYG		X		Q6JC40
76	*	EFENVPFHSSYAHSQ		X		Q6JC40
77	*	EGAKTAPGKKRPVEP		X		Q8JQF8
78	*	EGLREFLGLEAGPPK		X		Q9YIJ1
79	*	EIQYTSNYYKSTNVD		X		AAO88201.1
80	*	EKTNVDIEKVMITDE		X		spP03135
81	*	ELQKENSkrwnPEIQ		X		spP03135
82	*	ENSKRWNPEIQYTNN		X		Q9YIJ1
83	*	ENVPFHSSYAHSQSL		X		Q6JC40
84	*	EPDSSSGTGKAGQQP		X		spP03135
85	*	EQLEAGDNPYLKYNH		X		Q9YIJ1
86	*	EWELQKENSkrwnPE		X		spP03135
87	*	GAKTAPGKKRPVEPS		X		Q8JQF8
88	*	GEPPAGPSGLGSGTM		X		AAO88201.1
89	*	GGTANTQTLGFSQGG		X		Q8JQF8
90	*	GSEKTNVDIEKVMIT		X		spP03135
91	2078	GVVADNLQQNAAPI		X		AAO88201.1
92	*	GVYSEPRPIGTRYLT		X		spP03135
93	2079	HSSFAPSQNLFKLAN		X		Q9YIJ1
94	*	HSSYAHSQSLDRLMN		X		spP03135
95	*	IKNTPVPADPPTAFN		X		Q6JC40
96	*	IKTTNPVATESYGQV		X		Q6JC40
97	*	ILIKNTPVPADPPTA		X		Q6JC40
98	*	IQYTSNYYKSNNVEF		X		Q6JC40
99	*	IQYTSNYYKSTNVDF		X		AAO88201.1
100	*	ITNEEEIKTTNPVAT		X		Q6JC40
101	*	ITQYSTGQVSVEIEW		X		spP03135
102	2080	KDKLNSFITQYSTGQ		X		Q6JC40
103	*	KNTPVPADPPTAFNK		X		Q6JC40
104	*	KRWNPEIQYTSNYNK		X		spP03135
105	2081	KRWNPEIQYTSNYYK		X		Q6JC40
106	2082	LEAGDNPYLKYNHAD		X		Q9YIJ1
107	*	LEAGPPKPKPNQQHQ		X		Q9YIJ1
108	*	LGADTMSAGGGGPLG		X		Q9YIJ1
109	*	LGLEAGPPKPKPNQQ		X		Q9YIJ1
110	*	LIKNTPVPADPPTAF		X		Q6JC40
111	2083	LKYNHADA EFQEKLA		X		Q9YIJ1
112	*	LQKENSkrwnPEIQY		X		spP03135
113	*	LREFLGLEAGPPKPK		X		Q9YIJ1
114	*	LYLSRTNTPSGTTT		X		spP03135
115	*	NEEEIKTTNPVATES		X		Q6JC40
116	*	NKDKLNSFITQYSTG		X		Q6JC40
117	*	NNSNFAWTAGTKYHL		X		Q8JQF8
118	*	NPVATEQYGVVADNL		X		AAO88201.1
119	*	NPVATESYGQVATNH		X		Q6JC40

peptide #	SEQ ID NO	peptide	group I	group II	group III	source
120	2084	NSQGALPGMVWQNRD		X		Q8JQF8
121	*	NTPVPADPPTAFNKD		X		Q6JC40
122	*	NTPVPADPPTTFNQS		X		Q8JQF8
123	2085	PADPPTTFNQSKLNS		X		Q8JQF8
124	*	PFHSSFAPSQNLFKL		X		Q9YIJ1
125	*	PIGEPPAGPSGLGSG		X		AAO88201.1
126	2086	PPAGPSGLSGTMAA		X		AAO88201.1
127	*	PQILIKNTPVPADPP		X		Q6JC40
128	*	PQYGYATLNRDNTEN		X		Q9YIJ1
129	*	PSTSSDAEAGPSGSQ		X		Q9YIJ1
130	*	PVATEQYGSVSTNLQ		X		spP03135
131	*	PVEPDSSSGTGKAGQ		X		spP03135
132	*	PVPADPPTTFNQSKL		X		Q8JQF8
133	*	PVPGNITSFSDVPVS		X		Q9YIJ1
134	2087	PYLKYNHADAEFQEK		X		Q9YIJ1
135	*	QILIKNTPVPADPPT		X		Q6JC40
136	*	QRVSTTTGQNNNSNF		X		Q8JQF8
137	2088	QSGASNDNHYFGYST		X		spP03135
138	2089	QSTGGTAGTQQLLFS		X		AAO88201.1
139	*	QVTVEMEWELKKENS		X		Q9YIJ1
140	2090	QYGVVADNLQQQNA		X		AAO88201.1
141	*	QYTSNYYKSNNVEFA		X		Q6JC40
142	*	RQQRVSTTTGQNNNS		X		Q8JQF8
143	2091	RWNPEIQYTSNYYKS		X		Q6JC40
144	2092	SFAPSQNLFKLANPL		X		Q9YIJ1
145	*	SGNWHCDSTWLGDRV		X		Q8JQF8
146	2093	SKRWNPEIQYTSNYY		X		Q6JC40
147	*	SNYNKSVNVDFTVDT		X		spP03135
148	2094	SQSGASNDNHYFGYS		X		spP03135
149	2095	SRTNTPSGTTTQSRL		X		spP03135
150	*	SSGNWHCDSTWLGDR		X		Q8JQF8
151	*	SSGTGKAGQQPARKR		X		spP03135
152	*	SSLGADTMSAGGGGP		X		Q9YIJ1
153	*	SSQSGASNDNHYFGY		X		spP03135
154	*	SSSGNWHCDSTWLGDR		X		Q8JQF8
155	*	STGGTAGTQQLLFSQ		X		AAO88201.1
156	*	STTLSQNNNSNFAWT		X		AAO88201.1
157	2096	SYGQVATNHQSAQAQ		X		Q6JC40
158	2097	TANTQTLGFSQGGPN		X		Q8JQF8
159	*	TEGVYSEPRPIGTRY		X		Q6JC40
160	2098	TEQYGVVADNLQQQN		X		AAO88201.1
161	*	TESYGQVATNHQSAQ		X		Q6JC40
162	*	TGGTAGTQQLLFSQA		X		AAO88201.1
163	2099	TGQNNNSNFAWTAGT		X		Q8JQF8
164	*	TLNRDNTENPTERRS		X		Q9YIJ1

peptide #	SEQ ID NO	peptide	group I	group II	group III	source
165	*	TLSQNNNSNFAWTGA		X		AAO88201.1
166	*	TNGVYSEPRPIGTRY		X		spP03135
167	*	TNTPSGTTTQSRLQF		X		spP03135
168	*	TNVDIEKVMITDEEE		X		spP03135
169	*	TQSTGGTAGTQQLLF		X		AAO88201.1
170	*	TQYSTGQVSVEIEWE		X		spP03135
171	*	TQYSTGQVTVEMEWE		X		Q9YIJ1
172	*	TSNYYKSNNVEFAVN		X		Q6JC40
173	*	TSSDAEAGPSGSQQL		X		Q9YIJ1
174	*	TTGGTANTQTLGFSQ		X		Q8JQF8
175	*	TTLSQNNNSNFAWTG		X		AAO88201.1
176	2100	TTNPVATESYGQVAT		X		Q6JC40
177	*	TTTGQNNNSNFAWTA		X		Q8JQF8
178	*	TVEMEWELKKENSKR		X		Q9YIJ1
179	*	VATEQYGVVADNLQQ		X		AAO88201.1
180	*	VATESYGQVATNHQS		X		Q6JC40
181	*	VATNHQSAQAQAQTG		X		Q6JC40
182	*	VDIEKVMITDEEEIR		X		spP03135
183	*	VDTNGVYSEPRPIGT		X		spP03135
184	*	VEIEWELQKENSQRW		X		spP03135
185	*	VNTEGVYSEPRPIGT		X		Q6JC40
186	*	VQDSTTTIANLST		X		Q9YIJ1
187	*	VSTTLSQNNNSNFAW		X		AAO88201.1
188	*	VSTTTGQNNNSNFAW		X		Q8JQF8
189	*	VTVQDSTTTIANLST		X		Q9YIJ1
190	2101	WTGATKYHLNGRDSL		X		spP03135
191	2102	YAHSQSLDRLMNPLI		X		spP03135
192	*	YATLNRDNTENPTER		X		Q9YIJ1
193	*	YGYATLNRDNTENPT		X		Q9YIJ1
194	*	YLSRTNTPSGTTTQS		X		spP03135
195	*	YNKSVNVDFTVDTNG		X		spP03135
196	*	YNNHLYKQISNGTSG		X		Q8JQF8
197	*	YSTGQVTVEMEWEWK		X		Q9YIJ1
198	2103	YTSNYYKSNNVEFAV		X		Q6JC40
199	*	ASHKDDEEKFFPQSG			X	spP03135
200	*	ASNDNHYFGYSTPWG			X	spP03135
201	*	ATERFGTVAVNLQSS			X	O56137
202	*	AVNLQSSSTDPATGD			X	O56137
203	*	DAAALEHDKAYDQQL			X	Q6JC40
204	*	DAEFQERLQEDTSFG			X	Q8JQF8
205	*	DDEEKFFPQSGVLIF			X	spP03135
206	*	EDSKPSTSSDAEAGP			X	Q9YIJ1
207	*	EDVPFHSSYAHSQSL			X	spP03135
208	*	EEEIKATNPVATERF			X	Q9WBP8
209	*	EEVGEGLEFLGLEA			X	Q9YIJ1

peptide #	SEQ ID NO	peptide	group I	group II	group III	source
210	*	EEYGIVADNLQQQNT			X	Q8JQF8
211	*	EFLGLEAGPPKPKPN			X	Q9YIJ1
212	*	EHDKAYDQQLKAGDN			X	Q6JC40
213	*	EHDKAYDRQLDSGDN			X	spP03135
214	*	EIKATNPVATERFGT			X	Q9WBP8
215	*	EPDSSAGIGKSGAQP			X	Q6JC40
216	*	EPVNAADAAALEHDK			X	Q6JC40
217	*	EPVNEADAAALEHDK			X	spP03135
218	*	ERHKDDSRGLVLPGY			X	spP03135
219	*	ESVPDPQPIGEPPAA			X	Q6JC40
220	*	EVPFHSSFAPSQNLF			X	Q9YIJ1
221	*	FHSSYAHSQSLEDRM			X	spP03135
222	*	FNGLDKGEPVNAADA			X	Q8JQF8
223	*	FNGLDKGEPVNEADA			X	spP03135
224	*	GEPVNAADAAALEHD			X	Q6JC40
225	*	GEPVNEADAAALEHD			X	spP03135
226	*	GNGLDKGEPVNAADA			X	Q6JC40
227	*	GSAHQGCLPPFPADV			X	spP03135
228	*	GSSSGNWHCDSTWLG			X	Q8JQF8
229	*	IGTVNSQGALPGMVW			X	Q8JQF8
230	*	IQVKEVTTNDGVTTI			X	Q9WBP8
231	*	LIKNTVPVADPPTTF			X	Q8JQF8
232	*	LRTGNNFEFSYQFED			X	AAO88201.1
233	*	NEADAAALEHDKAYD			X	spP03135
234	*	NNNSEFAWPGASSWA			X	Q6JC40
235	*	NNSEYSWTGATKYHL			X	spP03135
236	*	NVGGQMATNNQSSTT			X	Q9YIJ1
237	*	NYNDPQFVDFAPDST			X	Q9YIJ1
238	*	PLGEPPATPAAVGPT			X	Q9WBP8
239	*	PQPLGEPPATPAAVG			X	Q9WBP8
240	*	PSKMLRTGNNFEFTY			X	Q9YIJ1
241	*	PVATEEYGIVADNLQ			X	Q8JQF8
242	*	PVEPSPQRSPPDSSTG			X	Q8JQF8
243	*	PVEQSPQEPDSSSGI			X	Q9WBP8
244	*	PVNEADAAALEHDKA			X	spP03135
245	*	PVPANPPAEFSATKF			X	Q9WBP8
246	*	QQRVSTTSLQNNNSN			X	AAO88201.1
247	*	QRVSKTKTDNNNSNF			X	Q9WBP8
248	*	QRVSTTSLQNNNSNF			X	AAO88201.1
249	*	QSSSTDPATGDVHVM			X	O56137
250	*	QYTNNYNDPQFVDFA			X	Q9YIJ1
251	*	RVSTTSLQNNNSNFA			X	AAO88201.1
252	*	SDSEYQLPYVLGSAH			X	Q9WBP8
253	*	SESVDPDPQPIGEPPA			X	AAO88201.1
254	*	SESVDPDPQLGEPPA			X	Q8JQF8

peptide #	SEQ ID NO	peptide	group I	group II	group III	source
255	*	SFVDHPPDWLEEVGE			X	Q9YIJ1
256	*	SSNDNAYFGYSTPWG			X	Q6JC40
257	*	SSSGIGKTGQQPAKK			X	Q9WBP8
258	*	STTVTQNNNSEFAWP			X	Q6JC40
259	*	SVPDPQPLGEPPAAP			X	Q8JQF8
260	*	SVPDPQPLGEPPATP			X	Q9WBP8
261	*	SYEFENVPFHSSYAH			X	Q6JC40
262	*	SYTFEDVPFHSSYAH			X	spP03135
263	*	TDEEEIKATNPVATE			X	Q9WBP8
264	*	TDEEEIRTTNPVATE			X	spP03135
265	*	TGNNFEFSYQFEDVP			X	AAO88201.1
266	*	TMATGSGAPMADNNE			X	spP03135
267	*	TNNYNDPQFVDFAPD			X	Q9YIJ1
268	*	TNTMATGSGAPMADN			X	spP03135
269	*	TPVPADPPTAFNKDK			X	Q6JC40
270	*	TPVPADPPTTFSQAK			X	AAO88201.1
271	*	TSTVQVFTDSEYQLP			X	spP03135
272	*	TSVDFAVNTEGVYSE			X	Q8JQF8
273	*	TVAVNLQSSSTDPAT			X	O56137
274	*	VDFAVNTEGVYSEPR			X	Q8JQF8
275	*	VEFAVNTEGVYSEPR			X	Q6JC40
276	*	VLEPLGLVEEGAKTA			X	Q8JQF8
277	*	VNVDFTVDTNGVYSE			X	spP03135
278	*	VSVEIEWELQKENS			X	spP03135
279	*	WLEDNLSEGIREWWD			X	Q9WBP8
280	*	YNEQLEAGDNPYLKY			X	Q9YIJ1

Example 21: Further screen for anti-vector antibodies in human sera

Out of the 3285 cyclic peptides derived from Ad5 Hexon, fiber and penton proteins P04133, P11818 and P12538, respectively, and AAV VP1 sequences P03135, Q6JC40, Q8JQF8, Q9WBP8, Q9YIJ1, O56137, AAO88201.1, O41855, O56139 and Q8JQG0, the peptides with the top 5% maximal IgG signal strength over the microarray screens were obtained, yielding a total of 164 peptides with top signals from the vector protein sequences screened. The details are shown in Table 4 below.

Table 4

This table provides another compilation of viral peptide sequences suitable as a basis for the present invention. Source

given is either UniProt ID or GenBank ID. The asterisk (*) indicates peptide sequences for which a SEQ ID NO has already been assigned in Table 2 above.

peptide #	SEQ ID NO	peptide	source
1	2104	AAEAAAPAAQPEVE	P12538
2	2105	AAAPAAQPEVEKPQ	P12538
3	2106	DASEYLSPLVQFA	P04133
4	2107	DGLEFGSPNAPNTN	P11818
5	2108	APVAAALGSPFDAP	P12538
6	2109	NLEEEDDNEDEV	P04133
7	2110	EEDDDNEDEVDEQA	P04133
8	2111	DDNEDEVDEQAEQQ	P04133
9	2112	VLQSSLGNDLRVDG	P04133
10	2113	PSEDTFNPVYPYDT	P11818
11	2114	FPVVGAEELLPVHVK	P12538
12	2115	EEIRPTNPVATEEY	Q8JQG0
13	2116	SGSGAEENSNAAAA	P12538
14	2117	YEEGPPPSYESVVS	P12538
15	2118	NAAAAAMQPVEDMN	P12538
16	2119	AAALGSPFDAPLDP	P12538
17	2120	NGVLESDIGVKFDT	P12538
18	2121	AAAMQPVEDMNDHA	P12538
19	2122	PAQPASSLGADTMS	Q9YIJ1
20	2123	TVQVFTDDDYQLPY	Q9YIJ1
21	2124	PVPGNITSFSDVPV	Q9YIJ1
22	2125	TQYSTGQVTVEMEW	Q9YIJ1
23	2126	YLGPGNGLDRGEPV	Q9YIJ1
24	2127	TSESETQPVNRVAY	Q9YIJ1
25	2128	RARPSEDTFNPVYP	P11818
26	2129	ATALEINLEEEEDD	P04133
27	2130	ENSNAAAAAAMQPVE	P12538
28	2131	YLGPFNGLDKGEPV	P03135
29	2132	NNFEFSYSFEDVPF	Q8JQG0
30	2133	SFITQYSTGQVTVE	Q9YIJ1
31	2134	YNKSVNVDFTVDTN	P03135
32	2135	LGSPFDAPLDPPFV	P12538
33	2136	PAAQPEVEKPQKKP	P12538
34	2137	ENSKRWNPEIQYTN	Q9YIJ1
35	2138	YLVDNKSTDVASLN	P12538
36	2139	PPMMLIKNTPVPGN	Q9YIJ1
37	2140	PVPADPPTTFSQAK	AAO88201.1
38	2141	DTFNPVYPYDTETG	P11818
39	2142	ITQYSTGQVTVE	Q9YIJ1
40	2143	AGNLTSQNVTTVSP	P11818

peptide #	SEQ ID NO	peptide	source
41	2144	NNFTFSYTFEDVPP	P03135
42	2145	WVLPSYNNHQYREI	Q9YIJ1
43	2146	YLGPGNGLDKGEPV	Q6JC40
44	2147	FLYSNIALYLPDKL	P04133
45	2148	NSTGNMGVLAGQAS	P04133
46	2149	YLYNHADADEFQER	P03135
47	2150	LAPKGAPNPCEWDE	P04133
48	2151	IQYTNNYNPDQFVD	Q9YIJ1
49	2152	SHGKTAKSNIVSQV	P11818
50	2153	VSAAPVAAALGSPF	P12538
51	2154	GNDRLTLPNEFEIK	P04133
52	2155	LEINLEEEDDDNED	P04133
53	2156	YLRYNHADADEFQER	Q8JQF8
54	2157	AAGGAAVEGGQGAD	O41855
55	2158	VKEVTTSNGETTVA	O41855
56	2159	EAMLRNDTNDQSFN	P04133
57	2160	DGHFHPSPLIGGFG	O41855
58	2161	NMTKDWFLVQMLAN	P04133
59	2162	VGSGTVAAGGGAPM	Q8JQG0
60	2163	EQYGTVANNLQSSN	O56139
61	2164	CLEYFPSKMLRTGN	Q9YIJ1
62	2165	AHALDMTFEVDPM	P04133
63	2166	TMANQAKNWLPGPC	Q8JQF8
64	2167	KRPVEQSPQEPDSS	Q6JC40
65	2168	KTANDNNNSNFPWT	O56139
66	2169	TQNNNSEFAWPGAS	Q6JC40
67	2170	KNTPVPADPPTAFN	Q6JC40
68	2171	TVQVFSSEYQLPY	Q9WBP8
69	2172	LDKGEPVNAADAAA	Q6JC40
70	2173	VLEPLGLVEEPVKT	P03135
71	2174	KLFNIQVKEVTTND	Q9WBP8
72	2175	LQSSNTAPTTRTVN	O56139
73	2176	SPPLKKTAKSNINLE	P11818
74	2177	LDKGEPVNEADAAA	P03135
75	2178	MLRTGNNFQFSYEF	Q6JC40
76	2179	ARKRLNFGQTGDAD	P03135
77	2180	NTYNGFSTPWGYFD	O41855
78	2181	QYGTVANNLQSSNT	O56139
79	2182	LARPPAPTITTVSE	P12538
80	2183	FPADVFMIPQYGYL	Q6JC40
81	2184	STGQVSVEIEWELQ	P03135
82	2185	LRNDTNDQSFNDYL	P04133
83	2186	NFQFSYEFENVPFH	Q6JC40
84	2187	FITQYSTGQVTVEM	Q9YIJ1
85	2188	QQPARKRLNFGQQTG	P03135

peptide #	SEQ ID NO	peptide	source
86	2189	HDSKLSIATQGPLT	P11818
87	2190	NTYFGYSTPWGYFD	Q8JQF8
88	*	ANNLTSTVQIFADS	O41855
89	*	GNTSQQQTDRNAFY	O41855
90	*	DTNGVYSEPRPIGT	P03135
91	*	KIFNIQVKEVTTSN	O41855
92	*	LIKNTVPADPPTT	Q8JQF8
93	*	DEEEIRTTNPVATE	P03135
94	*	DKAYDRQLDSGDNP	P03135
95	*	DKDKFFPMSGVMIF	O56137
96	*	LQQQNTAPQIGTVN	Q8JQF8
97	*	GTNTMATGSGAPMA	P03135
98	*	IFNIQVKEVTTSNG	O41855
99	*	DKAYDQQLQAGDNP	Q8JQF8
100	*	DSQWLGDRTVTTST	Q6JC40
101	*	DEEEIKATNPVATE	Q9WBP8
102	*	SFITQYSTGQVSVE	P03135
103	*	PLVDQYLYRFVSTN	Q9YIJ1
104	*	GKKRPVDQSPQEPD	O56139
105	*	NPVATEQYGSVSTN	P03135
106	*	DKAYDQQLKAGDNP	Q6JC40
107	*	TAPGKKRPVDQSPQ	O56139
108	*	VMITDEEEIRTTNP	P03135
109	*	FGKQGSEKTNVDIE	P03135
110	*	LQRGNRQAATADVND	P03135
111	*	KTAPGKKRPVDQSP	O56139
112	*	SESVDPQPPIGEPP	AAO88201.1
113	*	LEDNLSEGIREWWD	Q9WBP8
114	*	PEIQYTSNYNKSVDN	P03135
115	*	DKFFPMSGVMIFGK	Q9WBP8
116	*	APGKKRPVDQSPQE	O56139
117	*	NNFQFSYTFEDVPF	O56139
118	*	EFAWPGASSWALNG	Q6JC40
119	*	QSSNTAPTTRTVND	O56139
120	*	PVPADPPTTFNQSK	Q8JQF8
121	*	TQYSTGQVSVEIEW	P03135
122	*	SKTANDNNNSNFPW	O56139
123	*	TVQIFADSSYELPY	O41855
124	*	SESVDPQPPLGEPP	Q8JQF8
125	*	TESVPDPQPPIGEPP	Q6JC40
126	*	KNTVPADPPTTFS	AAO88201.1
127	*	PVPADPPTAFNKDK	Q6JC40
128	*	KKRPVDQSPQEPDS	O56139
129	*	KNTVPADPPTTFN	Q8JQF8
130	*	PRDWQRLINNNWGF	P03135

peptide #	SEQ ID NO	peptide	source
131	*	LFNIQVKEVTTNDG	Q9WBP8
132	*	TTS GTTNQSRLLFS	O56139
133	*	LSKTANDNNNSNFP	O56139
134	*	ENSKRWNPEIQYTS	P03135
135	*	DIYYQGPIWAKIPH	O41855
136	*	DDEDKFFPMSGVMI	Q9WBP8
137	*	THSTLDGRWSALTP	O41855
138	*	GADGVGNSSGNWHC	P03135
139	*	TIANNLTSTIQVFT	Q8JQF8
140	*	PQILIKNTPVPADP	Q6JC40
141	*	QLKAGDNPYLRYNH	Q9WBP8
142	*	NYNKS VNVDFTVDT	P03135
143	*	EEEIKTTNPVATEE	Q8JQF8
144	*	KGEPVNEADAAALE	P03135
145	*	KGEPVNAADAAALE	Q6JC40
146	*	DGHFHPSPLMGGFG	P03135
147	*	HYFGYSTPWGYFDF	P03135
148	*	EEIKTTNPVATEQY	AAO88201.1
149	*	FNIQVKEVTTNDGV	Q9WBP8
150	*	PWGYFDFNRFHCHF	P03135
151	*	LQQQNAAPIVGAVN	AAO88201.1
152	*	DWLEDNLSEGIREW	Q6JC40
153	*	WLEDNLSEGIREWW	Q6JC40
154	*	DSESVDPQPIGEP	AAO88201.1
155	*	KRPVDQSPQEPDSS	O56139
156	*	HSQSLDRLMNPLID	P03135
157	*	FEKVPFHSMYAHSQ	O41855
158	*	YDQQLKAGDNPYLK	Q6JC40
159	*	EDNLSEGIREWWDL	Q9WBP8
160	*	QVKEVTTNDGVTTI	Q9WBP8
161	*	PQYGYLTLNNGSQA	P03135
162	*	EEEIKTTNPVATES	Q6JC40
163	*	EGADGVGNASGNWH	Q9WBP8
164	*	DSESVDPQPPLGEP	Q8JQF8

Non-patent references

Balakrishnan, Balaji, and Ernest David. "Biopolymers augment viral vectors based gene delivery." *Journal of biosciences* 44.4 (2019): 1-8.

Bennett, Antonette, et al. "Structure comparison of the chimeric AAV2. 7m8 vector with parental AAV2." *Journal of structural biology* 209.2 (2020): 107433.

Bertin, Berangere, et al. "Capsid-specific removal of circulating antibodies to adeno-associated virus vectors." *Scientific reports* 10.1 (2020): 1-11.

Börner, Kathleen, et al. "Pre-arrayed pan-AAV peptide display libraries for rapid single-round screening." *Molecular Therapy* 28.4 (2020): 1016-1032.

Carter, John Mark, and Larry Loomis-Price. "B cell epitope mapping using synthetic peptides." *Current protocols in immunology* 60.1 (2004): 9-4.

Cearley, Cassia N., et al. "Expanded repertoire of AAV vector serotypes mediate unique patterns of transduction in mouse brain." *Molecular therapy* 16.10 (2008): 1710-1718.

Colella, Pasqualina, Giuseppe Ronzitti, and Federico Mingozzi. "Emerging issues in AAV-mediated in vivo gene therapy." *Molecular Therapy-Methods & Clinical Development* 8 (2018): 87-104.

Dijkstra, C. D., et al. "The heterogeneity of mononuclear phagocytes in lymphoid organs: distinct macrophage subpopulations in rat recognized by monoclonal antibodies ED1, ED2 and ED3." *Microenvironments in the Lymphoid System*. Springer, Boston, MA, 1985. 409-419.

Domenger, Claire, and Dirk Grimm. "Next-generation AAV vectors—do not judge a virus (only) by its cover." *Human molecular genetics* 28.R1 (2019): R3-R14.

Elliott, Serra E., et al. "A pre-eclampsia-associated Epstein-Barr virus antibody cross-reacts with placental GPR50." *Clinical Immunology* 168 (2016): 64-71.

Erlandsson, Ann, et al. "In vivo clearing of idiotypic antibodies with antiidiotypic antibodies and their derivatives." *Molecular immunology* 43.6 (2006): 599-606.

Etzerodt, Anders, et al. "Efficient intracellular drug-targeting of macrophages using stealth liposomes directed to the hemoglobin scavenger receptor CD163." *Journal of controlled release* 160.1 (2012): 72-80.

Fabrick, Babs O., et al. "The macrophage scavenger receptor CD163 functions as an innate immune sensor for bacteria." *Blood* 113.4 (2009): 887-892.

Fausther-Bovendo, Hugues, and Gary P. Kobinger. "Pre-existing immunity against Ad vectors: humoral, cellular, and innate response, what's important?." *Human vaccines & immunotherapeutics* 10.10 (2014): 2875-2884.

Garces, Jorge Carlos, et al. "Antibody-mediated rejection: a review." *The Ochsner Journal* 17.1 (2017): 46.

Gazarian, Karlen, et al. "Mimotope peptides selected from phage display combinatorial library by serum antibodies of pigs experimentally infected with *Taenia solium* as leads to developing diagnostic antigens for human neurocysticercosis." *Peptides* 38.2 (2012): 381-388.

Gfeller, David, et al. "Current tools for predicting cancer-specific T cell immunity." *Oncoimmunology* 5.7 (2016): e1177691.

Granfeldt, Asger, et al. "Targeting dexamethasone to macrophages in a porcine endotoxemic model." *Critical Care Medicine* 41.11 (2013): e309-e318.

Graversen, Jonas H., et al. "Targeting the hemoglobin scavenger receptor CD163 in macrophages highly increases the anti-inflammatory potency of dexamethasone." *Molecular Therapy* 20.8 (2012): 1550-1558.

Gurda, Brittney L., et al. "Mapping a neutralizing epitope onto the capsid of adeno-associated virus serotype 8." *Journal of virology* 86.15 (2012): 7739-7751.

Hansen, Lajla Bruntse, Soren Buus, and Claus Schafer-Nielsen. "Identification and mapping of linear antibody epitopes in human serum albumin using high-density peptide arrays." *PLoS One* 8.7 (2013): e68902.

Homma, Masayuki, et al. "A Novel Fusion Protein, AChR-Fc, Ameliorates Myasthenia Gravis by Neutralizing Antiacetylcholine

Receptor Antibodies and Suppressing Acetylcholine Receptor-Reactive B Cells." *Neurotherapeutics* 14.1 (2017): 191-198.

Howard Jr, James F. "Myasthenia gravis: the role of complement at the neuromuscular junction." *Annals of the New York Academy of Sciences* 1412.1 (2018): 113-128.

Howarth, M., & Brune, K. D. (2018). New routes and opportunities for modular construction of particulate vaccines: stick, click and glue. *Frontiers in immunology*, 9, 1432.

Jansson, Liselotte, et al. "Immunotherapy With Apitopes Blocks the Immune Response to TSH Receptor in HLA-DR Transgenic Mice." *Endocrinology* 159.9 (2018): 3446-3457.

Jensen, Kamilla Kjærgaard, et al. "Improved methods for predicting peptide binding affinity to MHC class II molecules." *Immunology* 154.3 (2018): 394-406.

Jurtz, Vanessa, et al. "NetMHCpan-4.0: improved peptide-MHC class I interaction predictions integrating eluted ligand and peptide binding affinity data." *The Journal of Immunology* 199.9 (2017): 3360-3368.

Kainulainen, Markus H., et al. "High-throughput quantitation of SARS-CoV-2 antibodies in a single-dilution homogeneous assay." *Scientific reports* 11.1 (2021): 1-9.

Koşaloğlu-Yalçın, Zeynep, et al. "Predicting T cell recognition of MHC class I restricted neoepitopes." *Oncoimmunology* 7.11 (2018): e1492508.

Krasnykh, Victor, et al. "Characterization of an adenovirus vector containing a heterologous peptide epitope in the HI loop of the fiber knob." *Journal of virology* 72.3 (1998): 1844-1852.

Kruzik, Anita, et al. "Prevalence of anti-adenovirus-associated virus immune responses in international cohorts of healthy donors." *Molecular Therapy-Methods & Clinical Development* 14 (2019): 126-133.

Lazaridis, Konstantinos, et al. "Specific removal of autoantibodies by extracorporeal immunoadsorption ameliorates experimental autoimmune myasthenia gravis." *Journal of neuroimmunology* 312 (2017): 24-30.

Leung, Nicki YH, et al. "Screening and identification of mimotopes of the major shrimp allergen tropomyosin using one-bead-one-compound peptide libraries." *Cellular & molecular immunology* 14.3 (2017): 308-318.

Li, Chengwen, and R. Jude Samulski. "Engineering adeno-associated virus vectors for gene therapy." *Nature Reviews Genetics* 21.4 (2020): 255-272.

Li, Peipei, Li Wang, and Li-jun Di. "Applications of protein fragment complementation assays for analyzing biomolecular interactions and biochemical networks in living cells." *Journal of proteome research* 18.8 (2019): 2987-2998.

Lim, Sung In, and Inchan Kwon. "Bioconjugation of therapeutic proteins and enzymes using the expanded set of genetically encoded amino acids." *Critical reviews in biotechnology* 36.5 (2016): 803-815.

Lin, Chia-Hao, et al. "Identification of a major epitope by anti-interferon- γ autoantibodies in patients with mycobacterial disease." *Nature medicine* 22.9 (2016): 994.

Lorentz, Kristen M., et al. "Engineered binding to erythrocytes induces immunological tolerance to *E. coli* asparaginase." *Science advances* 1.6 (2015): e1500112.

Luo, Jie, et al. "Main immunogenic region structure promotes binding of conformation-dependent myasthenia gravis autoantibodies, nicotinic acetylcholine receptor conformation maturation, and agonist sensitivity." *Journal of Neuroscience* 29.44 (2009): 13898-13908.

Luo, Jie, and Jon Lindstrom. "AChR-specific immunosuppressive therapy of myasthenia gravis." *Biochemical pharmacology* 97.4 (2015): 609-619.

Madsen, Mette, et al. "Molecular Characterization of the Haptoglobin· Hemoglobin Receptor CD163 ligand binding properties of the scavenger receptor cysteine-rich domain region." *Journal of Biological Chemistry* 279.49 (2004): 51561-51567.

Majowicz, Anna, et al. "Seroprevalence of pre-existing NABs against AAV1, 2, 5, 6 and 8 in the South African Hemophilia B patient population." (2019): 3353-3353.

Manno, Catherine S., et al. "Successful transduction of liver in hemophilia by AAV-Factor IX and limitations imposed by the host immune response." *Nature medicine* 12.3 (2006): 342-347.

Mazor, Ronit, et al. "Tolerogenic nanoparticles restore the antitumor activity of recombinant immunotoxins by mitigating immunogenicity." *Proceedings of the National Academy of Sciences* 115.4 (2018): E733-E742.

Meister, Daniel, S. Maryamdokht Taimoory, and John F. Trant. "Unnatural amino acids improve affinity and modulate immunogenicity: Developing peptides to treat MHC type II autoimmune disorders." *Peptide Science* 111.1 (2019): e24058.

Mietzsch, Mario, et al. "OneBac: platform for scalable and high-titer production of adeno-associated virus serotype 1-12 vectors for gene therapy." *Human gene therapy* 25.3 (2014): 212-222.

Mimuro, Jun, et al. "Minimizing the inhibitory effect of neutralizing antibody for efficient gene expression in the liver with adeno-associated virus 8 vectors." *Molecular Therapy* 21.2 (2013): 318-323.

Mingozzi, Federico, et al. "Overcoming preexisting humoral immunity to AAV using capsid decoys." *Science translational medicine* 5.194 (2013): 194ra92-194ra92.

Mingozzi, Federico, and Katherine A. High. "Overcoming the host immune response to adeno-associated virus gene delivery vectors: the race between clearance, tolerance, neutralization, and escape." *Annual review of virology* 4 (2017): 511-534.

Mok, Darren ZL, and Kuan Rong Chan. "The effects of pre-existing antibodies on live-attenuated viral vaccines." *Viruses* 12.5 (2020): 520.

Monahan, Paul E., et al. "Emerging Immunogenicity and Genotoxicity Considerations of Adeno-Associated Virus Vector Gene Therapy for Hemophilia." *Journal of Clinical Medicine* 10.11 (2021): 2471.

Morimoto et. al., *Bioconjugate Chemistry* 25 (8) (2014): 1479-1491

Moussa, Ehab M., et al. "Immunogenicity of therapeutic protein aggregates." *Journal of pharmaceutical sciences* 105.2 (2016): 417-430.

Müller, Manuel M. "Post-translational modifications of protein backbones: unique functions, mechanisms, and challenges." *Biochemistry* 57.2 (2017): 177-185.

Siang Ong, Yong, et al. "Recent advances in synthesis and identification of cyclic peptides for bioapplications." *Current topics in medicinal chemistry* 17.20 (2017): 2302-2318.

Peters, Bjoern, et al. "A community resource benchmarking predictions of peptide binding to MHC-I molecules." *PLoS computational biology* 2.6 (2006): e65.

Pishesha, Novalia, et al. "Engineered erythrocytes covalently linked to antigenic peptides can protect against autoimmune disease." *Proceedings of the National Academy of Sciences* (2017): 201701746.

Rey et al., *Clinical Immunology* 96 (3) (2000): 269-279

Rice, Peter, Ian Longden, and Alan Bleasby. "EMBOSS: the European molecular biology open software suite." *Trends in genetics* 16.6 (2000): 276-277.

Roberts, Diane M., et al. "Hexon-chimaeric adenovirus serotype 5 vectors circumvent pre-existing anti-vector immunity." *Nature* 441.7090 (2006): 239-243.

Ronzitti, Giuseppe, David-Alexandre Gross, and Federico Mingozzi. "Human immune responses to adeno-associated virus (AAV) vectors." *Frontiers in immunology* 11 (2020): 670.

Ruff, Robert L., and Robert P. Lisak. "Nature and action of antibodies in myasthenia gravis." *Neurologic clinics* 36.2 (2018): 275-291.

Rummler, Silke, et al. "Current techniques for AB0-incompatible living donor liver transplantation." *World journal of transplantation* 6.3 (2016): 548.

Runcie, Karie, et al. "Bi-specific and tri-specific antibodies-the next big thing in solid tumor therapeutics." *Molecular Medicine* 24.1 (2018): 50.

Ryan, Brent J., Ahuva Nissim, and Paul G. Winyard. "Oxidative post-translational modifications and their involvement in the pathogenesis of autoimmune diseases." *Redox biology* 2 (2014): 715-724.

Salganik, Max, Matthew L. Hirsch, and Richard Jude Samulski. "Adeno-associated virus as a mammalian DNA vector." *Mobile DNA* III (2015): 827-849.

Shanmugam, Arulkumaran, et al. "Identification of PSA peptide mimotopes using phage display peptide library." *Peptides* 32.6 (2011): 1097-1102.

Skytthe, Maria K., Jonas Heilskov Graversen, and Søren K. Moestrup. "Targeting of CD163+ Macrophages in Inflammatory and Malignant Diseases." *International Journal of Molecular Sciences* 21.15 (2020): 5497.

Sonntag, F., et al. "The assembly-activating protein promotes capsid assembly of different adeno-associated virus serotypes." *Journal of virology* 85.23 (2011): 12686-12697.

Sørensen, Karen Kristine, et al. "Liver sinusoidal endothelial cells." *Comprehensive Physiology* 5.4 (2011): 1751-1774.

Spieß, Christoph, Qianting Zhai, and Paul J. Carter. "Alternative molecular formats and therapeutic applications for bispecific antibodies." *Molecular immunology* 67.2 (2015): 95-106.

Sunasee, Rajesh, and Ravin Narain. "Covalent and noncovalent bioconjugation strategies." *Chemistry of Bioconjugates: Synthesis, Characterization, and Biomedical Applications* (2014): 1-75.

Taddeo, Adriano, et al. "Selection and depletion of plasma cells based on the specificity of the secreted antibody." *European journal of immunology* 45.1 (2015): 317-319.

Teschner, Sven, et al. "ABO-incompatible kidney transplantation using regenerative selective immunoglobulin adsorption." *Journal of clinical apheresis* 27.2 (2012): 51-60.

Tetala, Kishore KR, et al. "Selective depletion of neuropathy-related antibodies from human serum by monolithic

affinity columns containing ganglioside mimics." *Journal of medicinal chemistry* 54.10 (2011): 3500-3505.

Tian, Xingui, et al. "Broadly neutralizing monoclonal antibodies against human adenovirus types 55, 14p, 7, and 11 generated with recombinant type 11 fiber knob." *Emerging microbes & infections* 7.1 (2018): 1-12.

Tseng, Yu-Shan, and Mavis Agbandje-McKenna. "Mapping the AAV capsid host antibody response toward the development of second generation gene delivery vectors." *Frontiers in immunology* 5 (2014): 9.

Varghese, Robin, et al. "Postentry neutralization of adenovirus type 5 by an antihexon antibody." *Journal of virology* 78.22 (2004): 12320-12332.

Verdera, Helena Costa, Klaudia Kuranda, and Federico Mingozzi. "AAV vector immunogenicity in humans: a long journey to successful gene transfer." *Molecular Therapy* 28.3 (2020): 723-746.

Vincent, Angela, et al. "Serological and experimental studies in different forms of myasthenia gravis." *Annals of the New York Academy of Sciences* 1413.1 (2018): 143-153.

Wallukat, Gerd, et al. "Patients with preeclampsia develop agonistic autoantibodies against the angiotensin AT 1 receptor." *The Journal of clinical investigation* 103.7 (1999): 945-952.

Wang, Rong, et al. "A Murine Monoclonal Antibody With Potent Neutralization Ability Against Human Adenovirus 7." *Frontiers in cellular and infection microbiology* 9 (2019): 417.

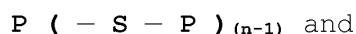
Zhou, Cissy C., et al. "Angiotensin receptor agonistic autoantibodies induce pre-eclampsia in pregnant mice." *Nature medicine* 14.8 (2008): 855.

Zhu, Feng-Cai, et al. "Safety, tolerability, and immunogenicity of a recombinant adenovirus type-5 vectored COVID-19 vaccine: a dose-escalation, open-label, non-randomised, first-in-human trial." *The Lancet* 395.10240 (2020): 1845-1854.

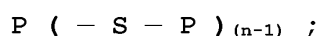
Claims

1. A compound comprising

- a biopolymer scaffold and at least
- a first peptide n-mer of the general formula:



- a second peptide n-mer of the general formula:



wherein, independently for each occurrence, P is a peptide with a sequence length of 6-13 amino acids, and S is a non-peptide spacer,

wherein, independently for each of the peptide n-mers, n is an integer of at least 1, preferably of at least 2, more preferably of at least 3, especially of at least 4,

wherein each of the peptide n-mers is bound to the biopolymer scaffold, preferably via a linker each,

wherein, independently for each occurrence, P has an amino-acid sequence comprising a sequence fragment with a length of at least six amino acids of a capsid protein sequence of a viral vector,

optionally wherein at most three, preferably at most two, most preferably at least one amino acid of the sequence fragment is independently substituted by any other amino acid.

2. The compound of claim 1, wherein the viral vector is an adenovirus (AdV) vector or an adeno-associated virus (AAV) vector.

3. The compound of claim 2, wherein said sequence fragment comprises a sequence of at least 6, preferably at least 7, more preferably at least 8, even more preferably at least 9, yet even more preferably at least 10 consecutive amino acids selected from:

the group of AdV sequences ETGPPTVPFLTPPF (SEQ ID NO: 32), HDSKLSIATQGPL (SEQ ID NO: 33), LNLRLGQGPLFINSAHNLDINY (SEQ ID

NO: 34), VDPMDEPTLLYVLFEVFDVV (SEQ ID NO: 35), MKRARPS EDTFNPVYPYD (SEQ ID NO: 36), ISGTVQSAHLIIRFD (SEQ ID NO: 37), LGQGPLFINS AHNLDINYNKGLYLF (SEQ ID NO: 38), SYPFDAQNLNLR LGQGPLFIN (SEQ ID NO: 39), GDTTPSAYSMSFSWDWSGHNYIN (SEQ ID NO: 40), VLLNNSFLDPEYWNFRN (SEQ ID NO: 41), HNYINEIFATSSYTFSYIA (SEQ ID NO: 42), DEATALEINLEEEEDDDNEDEVDEQAEQQKTH (SEQ ID NO: 43), INLEEEEDDDNEDEVDEQAEQ (SEQ ID NO: 44), DNEDEVDEQAEQQKTHVF (SEQ ID NO: 45), EWDEATALEINLEE (SEQ ID NO: 46), PKVLYSEDVDIETPDTHISYMP (SEQ ID NO: 47), YIPESYKDRMYSFFRNF (SEQ ID NO: 48), DSIGDRTRYFSMW (SEQ ID NO: 49), SYKDRMYSFFRNF (SEQ ID NO: 50), and FLVQMLANYNIGYQGFY (SEQ ID NO: 51), or

the group of AAV sequences WQNRDVYLQGPIWAKIP (SEQ ID NO: 52), DNTYFGYSTPWGYFDNRFHC (SEQ ID NO: 53), MANQAKNWLPGPCY (SEQ ID NO: 54), LPYVLGSAHQGCLPPFP (SEQ ID NO: 55), NGSQAVGRSSFYCLEYF (SEQ ID NO: 56), PLIDQYLYYL (SEQ ID NO: 57), EERFFPSNGILIF (SEQ ID NO: 58), ADGVGSSSGNWHC (SEQ ID NO: 59), SEQ ID NOS: 383-1891, SEQ ID NOS: 1892-2063 and SEQ ID NOS: 2064-2103, or

the group of sequences identified by SEQ ID NOS: 2104-2190.

4. The compound of any one of claims 1 to 3, wherein at least one occurrence of P is a circularized peptide, preferably wherein at least 10% of all occurrences of P are circularized peptides, more preferably wherein at least 25% of all occurrences of P are circularized peptides, yet more preferably wherein at least 50% of all occurrences of P are circularized peptides, even more preferably wherein at least 75% of all occurrences of P are circularized peptides, yet even more preferably wherein at least 90% of all occurrences of P are circularized peptides or even wherein at least 95% of all occurrences of P are circularized peptides, especially wherein all of the occurrences of P are circularized peptides.

5. The compound of any one of claims 1 to 4, wherein, independently for each occurrence, P is P_a or P_b,

wherein P_a has an amino-acid sequence comprising a first sequence fragment with a length of at least six amino acids of a capsid protein sequence of a viral vector, optionally wherein at

most three, preferably at most two, most preferably at least one amino acid of the sequence fragment is independently substituted by any other amino acid,

wherein P_b has an amino-acid sequence comprising a second sequence fragment with a length of at least six amino acids of a capsid protein sequence of a viral vector, optionally wherein at most three, preferably at most two, most preferably at least one amino acid of the sequence fragment is independently substituted by any other amino acid; and wherein

the first peptide n-mer is $P_a - S - P_a$ and the second peptide n-mer is $P_a - S - P_a$,

the first peptide n-mer is $P_a - S - P_a$ and the second peptide n-mer is $P_b - S - P_b$,

the first peptide n-mer is $P_b - S - P_b$ and the second peptide n-mer is $P_b - S - P_b$,

the first peptide n-mer is $P_a - S - P_b$ and the second peptide n-mer is $P_a - S - P_b$,

the first peptide n-mer is $P_a - S - P_b$ and the second peptide n-mer is $P_a - S - P_a$, or

the first peptide n-mer is $P_a - S - P_b$ and the second peptide n-mer is $P_b - S - P_b$.

6. The compound of claim 5, wherein the peptide P_a and the peptide P_b are two different epitopes of the same capsid antigen or two different epitope parts of the same capsid epitope.

7. The compound of any one of claims 1 to 6, wherein the biopolymer scaffold is selected from the group consisting of albumins, alpha1-globulins, alpha2-globulins, beta-globulins and immunoglobulins, in particular wherein the biopolymer scaffold is haptoglobin or transferrin, especially transferrin; or wherein the biopolymer scaffold is an antibody specific for a CD163 protein, or a CD163-binding fragment thereof.

8. The compound of any one of claims 1 to 7, wherein the compound is non-immunogenic in a mammal, preferably in a human,

in a non-human primate, in a sheep, in a pig, in a dog or in a rodent.

9. A pharmaceutical composition comprising the compound of any one of claims 1 to 8 and at least one pharmaceutically acceptable excipient.

10. The pharmaceutical composition of claim 9, wherein the composition is non-immunogenic in humans.

11. The pharmaceutical composition of claim 9 or 10 for use in therapy.

12. The pharmaceutical composition for use according to claim 11, for use in increasing efficacy of a vaccine in an individual, wherein the vaccine comprises the viral vector, preferably wherein the pharmaceutical composition is administered to the individual prior to or concurrently with administration of the vaccine.

13. The pharmaceutical composition for use according to claim 11, for use in increasing efficacy of a gene therapy composition in an individual, wherein the gene therapy composition comprises the viral vector, preferably wherein the pharmaceutical composition is administered to the individual prior to or concurrently with administration of the gene therapy composition.

14. A method of sequestering one or more antibodies present in an individual, comprising

obtaining a pharmaceutical composition as defined in claims 9 or 10, wherein the composition is non-immunogenic in the individual and wherein the one or more antibodies present in the individual are specific for at least one occurrence of P, or for peptide P_a and/or peptide P_b; and

administering the pharmaceutical composition to the individual.

15. A vaccine or gene therapy composition, comprising the compound of any one of claims 1 to 8 and further comprising the viral vector and optionally at least one pharmaceutically acceptable excipient.

16. A method of inhibiting an immune reaction to a treatment with a vaccine or a gene therapy composition in an individual in need of treatment with the vaccine or gene therapy composition, comprising

obtaining the vaccine or gene therapy composition as defined in claim 15; wherein the compound of the vaccine or gene therapy composition is non-immunogenic in the individual, and

administering the vaccine or gene therapy composition to the individual.