Submission of a new allergen to the WHO/IUIS Allergen Nomenclature Sub-Committee

Note

- *The submission is confidential to the WHO/IUIS Allergen Nomenclature Sub-Committee. Please include more information rather than less.*
- *SDS-PAGE, Western blots, ELISA, sequence data etc. are appreciated as attachments.*
- *We may ask for clarification after your submission and before approval.*
- *Mandatory fields are marked with an asterisk (*).*
- *Move the mouse over the text boxes to see additional hints (text boxes containing hints are labeled by ?).*

Sub-Committee members to be excluded from reviewing this submission *(see the List of sub-committee members)*

1 Submitter info

1.1 First submitter

Name *

Affiliation *

Location *

E-mail address *

I agree to have my name and affiliation displayed in the database entry of the submitted allergen at www.allergen.org ◯ Yes ◯ No

I agree to have my e-mail address displayed in the database entry of the submitted allergen at www.allergen.org ◯ Yes ◯ No

1.2 Second submitter (optional)

Name

Affiliation

Location

E-mail address

I agree to have my name and affiliation displayed in the database entry of the submitted allergen at www.allergen.org ◯ Yes ◯ No

I agree to have my e-mail address displayed in the database entry of the submitted allergen at www.allergen.org ◯ Yes ◯ No

2 Allergen Source

For taxonomic classification, please refer to the NCBI Taxonomy Database (https://www.ncbi.nlm.nih.gov/taxonomy)

Scientific name (genus and species) *

Synonymous scientific name

Common name *

Family *

Order *

NCBI Taxonomy ID (numeric) *

Other source of taxonomic data (if species not in the NCBI database)

3 Submitted candidate allergen

Biochemical or protein family name(s) *

3.1 Proposed candidate allergen name

The final decision on the allergen name will be made by the WHO/IUIS Allergen Nomenclature Sub-Committee based on related species and proteins, and may differ from the submitter's proposed name.

Naming scheme for allergens:

- *General naming scheme:* ***Ggg(g) s(s) m.nnnn (from-to)***
  - *Ggg(g): abbreviation of the genus (3-4 letters)*
  - *s(s): abbreviation of the species (1-2 letters)*
  - *m: allergen number*
  - *nnnn: isoallergen/variant number*
  - *from-to: amino acid range of a naturally occurring allergen fragment (optional)*
- *If possible, corresponding allergen numbers are assigned to homologous allergens from related species.*
- *Isoallergens share the following biochemical properties: similar molecular size and – as a guideline – an amino acid sequence identity greater than 67%. Isoallergens are numbered by the first two digits of the 4-digit isoallergen/variant number.*
- *Each isoallergen may have multiple forms of closely similar sequences (identity > 90%), which are designated as variants (also referred to as isoforms in the allergy field). Variants are numbered by the third and fourth digits of the 4-digit isoallergen/variant number.*
- *Naturally occurring fragments are designated by the amino acid range (relative to the non-processed full-length sequence) in parentheses following the isoallergen/variant number.*

Example: Ara h 1.0101 (26-84) = Arachis hypogaea allergen 1, isoallergen 1, variant 1, fragment encompassing amino acid residues 26 to 84.

Genus (first 3-4 letters) *

Species (first 1-2 letters) *

Allergen number * 0

4-digit isoallergen/variant number (*including amino acid range if an allergen fragment is submitted*) *

3.2 Justification of the proposed number

Justification * -- Please select ---

Comments (*e.g. name of the homologous allergen*)

3.3 Route(s) of allergen exposure *

☐ Airway ☐ Food ☐ Contact ☐ Sting/bite ☐ Human autoallergen

Comments

4 Sequence

4.1 Sequence and structure accession numbers

Submissions will only be accepted if they include an accession number. Please adhere to the following guidelines:

- *New sequences identified by cloning from genomic DNA or cDNA: please provide the nucleotide and, if available, the protein acc. no.*
- *New sequences identified only at the protein level (e.g. Edman degradation, tandem MS de novo sequencing): please provide the protein acc. no.*
- *Identification of previously available sequences as allergens: please provide all existing accession numbers*

	Accession number	Public
Nucleotide sequence (NCBI/ENA/DDBJ)		--- Please selec
Amino acid sequence (NCBI/ENA/DDBJ)		--- Please selec
Amino acid sequence (UniProt)		--- Please selec
Structure (PDB)		--- Please selec

☐ We agree to make these accession numbers publicly accessible on the WHO/IUIS Allergen Nomenclature website

Please inform the WHO/IUIS Allergen Nomenclature Sub-Committee as soon as non-public accession numbers get released.

4.2 Sequences

*Please provide the parts of the sequence that you have determined in your study. When there are gaps of unknown length or long gaps in the sequence use *"xxx" * (e.g MVIGPFRxxxxDSQTL).For single unknown residues, use capital X.*

Amino acid sequence (*single-letter code*) *

Nucleotide sequence

☐ We agree to make these sequences publicly accessible on the WHO/IUIS Allergen Nomenclature website

Please inform the WHO/IUIS Allergen Nomenclature Sub-Committee as soon as non-public accession numbers are released and/or the study describing this sequence gets published.

4.3 Natural allergen – amino acid sequence confirmation

☐ The sequence of the PURIFIED natural allergen was fully or partially established or confirmed (*Note: data on initial identification of the allergen in its source should be entered in section 5.1.2*)

Method	Number of amino acids	Comments
N-terminal sequencing by Edman degradation		
Edman sequencing of internal peptides		
Mass spectrometry combined with database search		
Mass spectrometry combined with *de novo* sequencing		
Other (use Comments field)		

Total sequence coverage (percentage of the expected mature protein) * 0 %

4.4 Recombinant allergen – nucleotide sequence

◯ The recombinant allergen was produced using a previously obtained nucleotide sequence

Origin of the nucleotide sequence * --- Please select ---

For mRNA sequences: tissue/organ of origin

Comments

◯ The nucleotide sequence of the allergen was newly determined in this study

Origin of the nucleotide sequence * --- Please select ---

For mRNA sequences: tissue/organ of origin

Sequencing method *

Comments

Level of sequence confirmation

☐ Multiple independent clones were analyzed and sequenced

☐ The sequence was established based on complementary sequence data from both DNA strands of each clone

Method of obtaining the clone used for producing the recombinant allergen in this study *

--- Please select ---

Details

4.4.1 PCR-derived novel sequences

The complete coding region of PCR-derived novel sequences should be confirmed independently of the PCR primers, e.g. by using primers outside the coding region or using a RACE method to confirm the sequences of the 5' and 3' ends.

☐ The complete coding sequence was determined independently of the primer sequences.

Positions of the primers (*using the provided nucleotide sequence as a reference*)

Forward: Reverse:

Sequence of the forward primer

Sequence of the reverse primer

On which data was the design of the primers based?

4.5 Recombinant allergen – amino acid sequence confirmation

☐ The amino acid sequence of the purified recombinant allergen was fully or partially confirmed

Method	Number of amino acids	Comments
N-terminal sequencing by Edman degradation		
Edman sequencing of internal peptides		
Mass spectrometry combined with database search		
Mass spectrometry combined with *de novo* sequencing		
Other (use comments field)		

Total sequence coverage (percentage of the expected mature protein) * 0 %

4.6 Sequence reference(s)

PubMed ID (separate multiple IDs by commas)

DOI (if no PubMed ID is available)

Publication or congress abstract not accessible via PubMed or DOI

Authors

Title

Congress title

Year

Journal

Volume Issue Pages

5 Biochemistry

5.1 Expression of the candidate allergen in its source

The allergen will be considered only if its expression in a tissue or organ relevant for human exposure is shown at the mRNA and/or protein level combined with IgE binding to the recombinant protein derived from that sequence or to the natural protein isolated from that specific tissue. Proof of protein expression is preferred and may also be provided by indirect methods, such as an

inhibition assay in which binding of human IgE or a specific antibody to an extract is inhibited by the recombinant allergen. Detection of the mRNA should specifically show the expression of the isoallergen that was used for IgE testing.

Tissue or organ of expression in the natural source *

5.1.1 mRNA level

☐ Expression of the allergen in its natural source was shown at the mRNA level

* Details (*source material, PCR method, sequencing method, etc.*)

Total sequence coverage (percentage of the sequence that encodes the expected mature protein) *

0 %

5.1.2 Protein level

This section refers to the identification of the allergen in its source. Data on purification and sequence confirmation of the purified allergen should be entered in sections 5.2 and 4.3

☐ Expression of the allergen in its natural source was shown on the protein level

* Details (*source material, separation and identification methods*)

Total sequence coverage (percentage of the expected mature protein) * 0 %

5.2 Allergen purified from the natural source

☐ The natural purified allergen was tested for IgE binding

Method(s) of purification (*source material, chromatography methods, etc.*) *

Estimated purity * 0 %

5.3 Recombinant allergen

☐ The recombinant allergen was tested for IgE binding

Expression system (*host, vector*) *

Modifications of the recombinant allergen compared with its natural counterpart

Method(s) of purification (*source material, chromatography methods, etc.*) *

Estimated purity * 0 %

5.4 Molecular mass of the mature protein *

Method	Natural allergen	Rec. allergen	Molecular mass (kDa)	Comments
--- Please select ---	☐	☐		
--- Please select ---	☐	☐		
--- Please select ---	☐	☐		
--- Please select ---	☐	☐		
--- Please select ---	☐	☐		
--- Please select ---	☐	☐		

5.5 Post-translational modifications

5.5.1 Glycosylation

	Natural allergen	Recombinant allergen
The allergen is glycosylated *	--- Please select ---	--- Please select ---
Type of glycosylation		
Method(s) of glycan determination		

5.5.2 Other post-translational modifications of the natural allergen

Type	Position(s) [a]	Method of determination [b]	Comments
Cleavage of signal peptide		--- Please select ---	
Removal of propeptide(s)		--- Please select ---	
Disulfide bonds		--- Please select ---	
Side chain modifications		--- Please select ---	
Other		--- Please select ---	

[a] *Amino acid position(s) in the sequence of the non-processed precursor protein*
[b] *Please provide details in the Comments field*

5.6 Other relevant properties of the protein (e.g. oligomerization)

6 Allergenicity

6.1 Study population

6.1.1 Allergic patients

Number of tested allergic patients * 0

Provide the diagnostic methods used to prove that the patients were allergic to the specific allergen SOURCE (Note: do not enter tests using the purified allergen here. Those should be entered into section 6.2). In each line, please provide details on the method and source material that were used (e.g. extract, fresh food, cooked food etc.)

Inclusion criteria *

☐ Case history *

Details

☐ Skin test (*e.g. skin-prick test, prick-to-prick test, intradermal test*)

Details

☐ Challenge test (*e.g. oral food challenge, nasal challenge*)

Details

☐ *In vitro* IgE test (*e.g. EAST, ELISA, Western blot*)

Details

☐ *In vitro* cellular test (*e.g. BAT, RBL assay, MAT*)

Details

☐ Other inclusion or exclusion criteria (*e.g. specific symptoms, age groups etc.*)

Details

Comments

6.1.2 Negative control subjects

Number of subjects * 0

Inclusion criteria (*e.g. non-atopic subjects, subjects allergic to a different source*) *

6.2 Allergenicity of the purified allergen

6.2.1 Tests of individual patients or sera *

A candidate allergen will only be accepted if it is shown to bind IgE from sera of at least five individuals allergic to the natural source of the allergen. Exceptions should be explained.

Please fill in results from at least one type of test result for the PURIFIED natural or recombinant allergen. IgE binding assays with extracts will not be accepted.

Type of test --- Please select --- Tested molecule --- Please select ---

Test details

Number of allergic patients tested 0, positive 0

Number of negative control subjects tested 0, positive 0

Comments

Type of test --- Please select --- Tested molecule --- Please select ---

Test details

Number of allergic patients tested 0 , positive 0

Number of negative control subjects tested 0 , positive 0

Comments

Type of test --- Please select --- Tested molecule --- Please select ---

Test details

Number of allergic patients tested 0 , positive 0

Number of negative control subjects tested 0 , positive 0

Comments

Type of test --- Please select --- Tested molecule --- Please select ---

Test details

Number of allergic patients tested 0 , positive 0

Number of negative control subjects tested 0 , positive 0

Comments

Type of test --- Please select --- Tested molecule --- Please select ---

Test details

Number of allergic patients tested 0 , positive 0

Number of negative control subjects tested 0 , positive 0

Comments

Type of test --- Please select --- Tested molecule --- Please select ---

Test details

Number of allergic patients tested 0 , positive 0

Number of negative control subjects tested 0 , positive 0

Comments

6.2.2 Tests using serum pools

Test with serum pools (such as inhibition assays) may add evidence of the allergenicity or significance of the submitted allergen, but cannot replace tests with individual sera.

Description of the tests and their results:

6.2.3 IgE binding of glycosylated allergens

Natural allergen:

The glycan moiety binds IgE --- Please select ---

The protein moiety binds IgE --- Please select ---

Recombinant allergen:

The glycan moiety binds IgE --- Please select ---

The protein moiety binds IgE --- Please select ---

Experiments performed (*e.g. glycan removal, inhibition tests*)

6.3 Allergenicity reference(s)

PubMed ID (separate multiple IDs by commas)

DOI (if no PubMed ID is available)

Publication or congress abstract not accessible via PubMed or DOI

Authors

Title

Congress title

Year

Journal

Volume Issue Pages

7 Additional comments

Description of additional data submitted for reviewing

Other comments

☐ * By submitting this form, we agree that the submitted data, including our personal data (name, affiliation, e-mail-address), are stored by the science co-chair of the WHO/IUIS Allergen Nomenclature Sub-Committee and forwarded to other sub-committee members for review purposes. The data will not be transferred to persons or organizations outside the WHO/IUIS Allergen Nomenclature Sub-Committee. After the completion of the submission and review process, the data will be stored for documentation purposes. However, we have the right to request the deletion of our personal data at any time.

Please send the completed form via e-mail to the science co-chair of the WHO/IUIS Allergen Nomenclature Sub-Committe: Christian Radauer (christian.radauer@muv.ac.at).