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

Note

- *The submission is confidential and intended solely for the WHO/IUIS Allergen Nomenclature Sub-Committee. Please include more information rather than less.*
- *You may exclude specific members of the sub-committee from reviewing (see last page).*
- *SDS-PAGE, Western blots, ELISA, sequence data etc. are appreciated as attachments.*
- *Please review the submission guidelines outlined at https://www.allergen.org/submission.php.*
- *The sub-committee 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 ?).*

Please send the completed form and accompanying documents via e-mail to the science co-chair of the WHO/IUIS Allergen Nomenclature Sub-Committee: Maksymilian Chruszcz (chruszcz@msu.edu).

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1 Applicant information

1.1 Principal applicant

* Name

* Affiliation

* City, country

* E-mail address

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

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

1.2 Co-applicant (optional)

Name

Affiliation

City, country

E-mail address

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

I agree to have my e-mail address displayed in the database entry of the approved 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 contained in the NCBI database)

3 Submitted candidate allergen

* Biochemical or protein family name(s)

3.1 Proposed 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 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 (e.g. Der p 1, Der f 1, Blo t 1 and Tyr p 1 are all cysteine proteases).*
- *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

* 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 ☐ Skin contact ☐ Sting/bite ☐ Human autoallergen

Comments

3.4 * 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 mRNA: please provide the nucleotide and, if available, the protein sequence accession number.*
- *New sequences identified only at the protein level (e.g. Edman degradation, tandem MS de novo sequencing): please provide the protein sequence accession number.*
- *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

☐ I 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 and/or the study describing this sequence gets published.

3.5 Sequences

* Full-length amino acid sequence corresponding to the database entry (*single-letter code; including signal peptide, propeptides etc.*)

Full-length nucleotide sequence corresponding to the database entry

☐ I 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.

3.6 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

4 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

4.1 mRNA level

☐ The expression of the candidate allergen in its natural source was shown at the mRNA level

* Detection method:

☐ Transcriptome sequencing

☐ Amplification of the specific mRNA by PCR

☐ Other (please specify)

* Source material

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

Total sequence coverage (relative to the length of the sequence that encodes the expected mature protein) *

0 %

4.2 Protein level

☐ The expression of the candidate allergen in its natural source was shown on the protein level

Detection method

☐ Sequence independent detection method (e.g. Western blot; please fill in section 4.2.1)

☐ Detection of the specific sequence in a protein extract (please fill in section 4.2.2)

☐ Sequencing of the purified natural protein (please fill in section 5.2)

4.2.1 Sequence independent detection method

For example, immunoassays with a specific antibody, inhibition of binding of patients sera or specific antibodies to a protein extract by a purified recombinant protein.

* Source material

* Details (*separation and identification methods*)

4.2.2 Detection of the specific sequence in a protein extract

* Source material

* Sequencing method (*please specify the exact mass spectrometry method*)

* Analysis method (*e.g. de novo sequencing, database search – please specify the database used*)

* Total sequence coverage (relative to the length of the expected mature protein) 0 %

5 Purified natural allergen

☐ The purified natural allergen was tested for IgE binding

5.1 Purification

* Source material

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

* Estimated purity 0 %

* Method of determining the purity (*separation and detection method*)

5.2 Amino acid sequence confirmation

* Sequencing method (*please specify the exact mass spectrometry method*)

* Analysis method (*e.g. de novo sequencing, database search – please specify the database used*)

* Total sequence coverage (relative to the length of the expected mature protein) 0 %

* Confirmed sequence

Please enter the complete sequence of the mature protein with the confirmed parts in uppercase and the non-confirmed parts in lowercase. If the complete sequence is unknown, please enter the known peptides in uppercase separated by "xxx" for gaps of unknown length. If the order of the peptides is unknown (no homologous proteins in the database), just provide a list of identified peptides.

Detected diagnostic peptides that discriminate this sequence from other isoforms

6 Recombinant allergen

☐ The purified recombinant allergen was tested for IgE binding

6.1 Establishment of the nucleotide sequence

◯ The recombinant allergen was obtained using a previously published 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

6.1.1 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 within the nucleotide sequence (*Please provide the full nucleotide sequence in section 3.5 and use the base pair numbering of that sequence as a reference*)

* Forward: Start , End

* Reverse: Start , End

* Sequence of the forward primer

* Sequence of the reverse primer

* On which experiments/results was the design of the primer sequences based?

6.2 Expression system

* Expression host

* Expression vector

Modifications of the recombinant allergen compared with its natural counterpart

6.3 Purification

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

* Estimated purity 0 %

* Method of determining the purity (*separation and detection method*)

6.4 Amino acid sequence confirmation

Sequencing method (*please specify the exact mass spectrometry method*)

Analysis method (*e.g. de novo sequencing, database search – please specify the database used*)

Total sequence coverage (relative to the length of the expected mature protein) 0 %

Confirmed sequence

Please enter the complete sequence of the expressed mature protein (including tags, fusion partners and other vector-derived modifications) with the confirmed parts in uppercase and the non-confirmed parts in lowercase.

7 Biochemistry

7.1 * 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 ---	☐	☐		

7.2 Post-translational modifications

7.2.1 * Glycosylation

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

7.2.2 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*

7.3 Other relevant properties of the protein (e.g. oligomerization, stability)

8 Study population

8.1 Allergic patients

* Number of tested allergic patients 0

* Inclusion criteria

*Please provide the diagnostic methods used to demonstrate **clinically relevant allergy** (rather than sensitization alone) to the specific allergen **source** (Note: do not enter tests using the purified allergen here. Those should be entered into section 9). For each entry, please specify:*

- *the diagnostic method used;*
- *the origin and type of the source material tested (e.g. commercial extract, raw food, cooked food preparation, whole-body extract, animal fluid-derived material, fecal extract, total protein extract, soluble protein fraction, etc.);*
- *where relevant, additional details on the preparation or extraction method that may influence the diagnostic relevance of the material tested.*

8.1.1 Case history

☐ * The patients showed allergic symptoms after getting exposed to the natural source of the submitted allergen candidate.

* Type of symptoms

* Method of taking the patient's history (*e.g. unstructured interviews, questionnaire*)

Other observations that corroborate the connection between symptoms and the specific allergen source (*e.g. seasonality, connection with certain locations*)

8.1.2 Skin test

☐ A skin test was performed (*e.g. skin-prick test, prick-to-prick test, intradermal test*)

Tested material	
Type of test	

8.1.3 Challenge test

☐ A challenge test was performed (*e.g. oral food challenge, nasal challenge*)

Tested material	
Type of test	

8.1.4 *In vitro* serum sIgE test

☐ An *in vitro* serum sIgE test was performed (*e.g. commercial sIgE test, ELISA, Western blot*)

Tested material	
Type of test	

8.1.5 *In vitro* cellular test

☐ An *in vitro* cellular test was performed (*e.g. BAT, RBL assay, MAT*)

Tested material	
Type of test	

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

Details

8.2 Negative control subjects

* Number of subjects 0

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

9 Allergenicity of the purified allergen

9.1 * Tests with 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 should be entered in section 8.1.*

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

Test method

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 method

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 method

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 method

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 method

Number of allergic patients tested 0 , positive 0

Number of negative control subjects tested 0 , positive 0

Comments

9.2 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:

9.3 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*)

9.4 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

10 Additional comments

Description of additional data submitted for reviewing

Other comments

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

☐ * I acknowledge that the use of non-approved allergen names that resemble the format of official names recognized by the WHO/IUIS Allergen Nomenclature Sub-Committee is prohibited. Allergen names may be used in presentations and publications only after approval by the WHO/IUIS Allergen Nomenclature Sub-Committee.

☐ * By submitting this form, I agree that the submitted data, including my 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, I have the right to request the deletion of my personal data at any time.