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Cinquième Session
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RÉVISION DE LA NORME ST.26 DE L'OMPI

Document établi par le Secrétariat

1. À la reprise de sa quatrième session tenue à Genève en mars 2016, le Comité des normes de l'OMPI (CWS) a adopté la norme ST.26 de l'OMPI intitulée "Recommandation de norme relative à la présentation des listages des séquences de nucléotides et d'acides aminés en langage XML (eXtensible Markup Language)". Le CWS est donc convenu de modifier la tâche n° 44 comme suit : "Tâche n° 44 : Établir des recommandations concernant des dispositions relatives au passage de la norme ST.25 à la norme ST.26 de l'OMPI; et élaborer une proposition relative à la révision de la norme ST.26 de l'OMPI, le cas échéant" (voir les paragraphes 49 à 53 et 82 à 84 du document CWS/4BIS/16.)

2. Conformément à cette nouvelle description, l'équipe d'experts SEQL a tenu des discussions sur la révision de la norme ST.26; l'Office européen des brevets (OEB), en tant que responsable de l'équipe d'experts, a établi un rapport sur l'état d'avancement des travaux menés par celle-ci, qui figure à l'annexe I du présent document.

3. À l'issue de ces discussions, l'équipe d'experts SEQL a soumis au CWS, pour examen et approbation éventuelle, une proposition finale de révision de la norme ST.26 contenant les modifications à apporter au corps du texte et aux annexes I à III de cette norme, ainsi qu'une nouvelle annexe VI (document d'orientation). Il convient de noter que les annexes IV et V de la norme ST.26 restent inchangées (c'est pourquoi elles n'ont pas été jointes au présent document). La proposition de révision qui figure à l'annexe II du présent document concerne le corps du texte de la norme ST.26 et ses annexes I et II (intitulées "annexe I de la norme ST.26" et "annexe II de la norme ST.26", respectivement); s'agissant de l'annexe III de la norme ST.26, l'équipe d'experts SEQL propose de remplacer par des minuscules les codes de langue à deux lettres en majuscules afin qu'ils soient alignés sur les codes à deux lettres définis dans la

norme ISO 639, par exemple en remplaçant le code à deux lettres “EN” pour l’anglais par “en”. Il convient de noter que si cette proposition de révision était approuvée par le CWS, la nouvelle version de la norme ST.26 deviendrait la version 1.1 (l’annexe III de la norme ST.26 n’est pas jointe au présent document).

4. Le CWS est invité

(a) à prendre note du contenu du présent document et du rapport sur l’état d’avancement des travaux menés par l’équipe d’experts SEQL qui figure à l’annexe I du présent document; et

(b) à examiner et à approuver éventuellement la proposition de révision de la norme ST.26 de l’OMPI mentionnée au paragraphe 3 ci-dessus, qui figure à l’annexe II du présent document.

[L’annexe I suit]

RAPPORT SUR LA REVISION DE LA NORME ST.26 DE L'OMPI ETABLI PAR L'ÉQUIPE D'EXPERTS SEQL

Document établi par l'Office européen des brevets (OEB)

RAPPEL

1. L'équipe d'experts chargée de la norme relative aux listages des séquences a été créée par le Comité des normes de l'OMPI (CWS) à sa première session (tenue du 25 au 29 octobre 2010) afin de mener à bien la tâche n° 44 (voir le paragraphe 29 du document CWS/1/10) :

2. "Établir une recommandation concernant la présentation des listages des séquences de nucléotides et d'acides aminés en langage XML (eXtensible Markup Language) pour adoption en tant que norme de l'OMPI. La proposition relative à l'établissement de cette nouvelle norme de l'OMPI devrait être assortie d'une étude de l'incidence de ladite norme sur la norme ST.25 actuelle de l'OMPI, indiquant notamment les modifications à apporter à la norme ST.25."

3. L'équipe d'experts a également été priée :

> "de coordonner ses travaux avec l'organe compétent du PCT en ce qui concerne l'incidence éventuelle de ladite norme sur l'annexe C des Instructions administratives du PCT".

4. L'Office européen des brevets (OEB) s'est vu confier le rôle de responsable de l'équipe d'experts et la nouvelle norme de l'OMPI, intitulée ST.26, a été officiellement adoptée lors de la reprise de la quatrième session du CWS (CWS/4BIS) en mars 2016.

5. Une version modifiée de la description de la tâche n° 44 a été approuvée par le CWS à la reprise de sa quatrième session (tenue du 21 au 24 mars 2016), qui est désormais libellée comme suit :

> "Établir des recommandations concernant des dispositions relatives au passage de la norme ST.25 à la norme ST.26 de l'OMPI ; et élaborer une proposition relative à la révision de la norme ST.26 de l'OMPI, le cas échéant".

RAPPORT SUR L'ETAT D'AVANCEMENT DES TRAVAUX

6. Comme suite à l'adoption de la norme ST.26 à la reprise de la quatrième session du CWS, l'équipe d'experts a tenu deux séries de discussions. Les discussions de la huitième série ont essentiellement porté sur la façon d'améliorer la norme adoptée afin de garantir son efficacité une fois qu'elle serait mise en œuvre et celles de la neuvième série sur les questions concernant le passage de la norme ST.25 à la norme ST.26. Au cours de cette période, l'équipe d'experts a tenu plusieurs réunions WebEx et deux réunions informelles à Genève (les 23 mars et 9 septembre 2016).

7. L'équipe d'experts a notamment travaillé sur une version révisée de la norme ST.26 adoptée, afin d'en faciliter la mise en œuvre par les déposants et les offices. La norme ST.26, soumise à la cinquième session du CWS pour approbation, comporte les principales modifications suivantes :

- explications concernant les acides nucléiques peptidiques (ANP) et les séquences variantes à l'intérieur de la norme ;

- inclusion d'un document d'orientation (annexe VI) pour promouvoir l'harmonisation des pratiques et des interprétations des offices et des déposants ;

– mise à jour de l’annexe I – Vocabulaire contrôlé – à des fins d’harmonisation avec le tableau V.10.6 des caractéristiques de l’International Nucleotide Sequence Database Collaboration (INSDC) publié en novembre 2016 ;

– ajout ou reformulation de commentaires figurant à l’annexe II (DTD) à des fins de clarification et d’harmonisation avec la syntaxe de la définition de type de document (DTD) V1.5 du tableau des caractéristiques INSDC.

– amélioration du texte général de la norme sur la base des consultations publiques effectuées par l’OEB, le JPO et l’USPTO en 2016-2017.

FEUILLE DE ROUTE

8. Obtenir l’approbation des adjonctions et des modifications à la ST.26 à la cinquième session du CWS.

9. Obtenir l’approbation des “recommandations concernant des dispositions relatives au passage de la norme ST.25 à la norme ST.26 de l’OMPI” à la cinquième session du CWS.

10. Aider le Bureau international de l’OMPI en communiquant les besoins et les informations en retour des utilisateurs concernant l’outil de création de contenus.

11. Appuyer le Bureau international dans le cadre de la révision des Instructions administratives du PCT.

12. Collaborer à toute autre révision de la norme ST.26 de l’OMPI. Il est proposé que les futures révisions de la norme soient à l’initiative des membres du CWS et non pas déterminées selon un calendrier prédéfini.

[L’annexe II suit]

NORME ST.26

RECOMMANDATION DE NORME RELATIVE À LA PRÉSENTATION DES LISTAGES DES SÉQUENCES DE NUCLÉOTIDES ET D'ACIDES AMINÉS EN LANGAGE XML (*EXTENSIBLE MARKUP LANGUAGE*)

Version ~~*1.0*~~*1.1*

Proposition présentée par l'équipe d'experts SEQL pour examen et approbation par le CWS à sa cinquième session
~~*Adopté par le Comité des normes de l'OMPI (CWS)*~~
~~*à la reprise de sa quatrième session le 24 mars 2016*~~

Note du Bureau International

Le Comité des normes de l'OMPI (CWS) est convenu de prier les offices de propriété industrielle de reporter les préparatifs en vue de la mise en œuvre de cette nouvelle norme ST.26 de l'OMPI jusqu'à ce que les recommandations relatives au passage de la norme ST.25 à la nouvelle norme ST.26 soient approuvées par le CWS à sa prochaine session, qui aura lieu en 2017. Dans l'intervalle, la norme ST.25 doit continuer d'être appliquée.

La norme est publiée à des fins d'information des offices de propriété industrielle et d'autres parties intéressées.

TABLE DES MATIÈRES

ANNEXES

NORME ST.26

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~~Adopté par le Comité des normes de l'OMPI (CWS)~~
~~à la reprise de sa quatrième session le 24 mars 2016~~

INTRODUCTION

1. La présente norme définit la manière dont des séquences de nucléotides et d'acides aminés doivent être divulguées dans une demande de brevet pour pouvoir être jointes à un listage des séquences. Elle précise ~~les caractéristiques de~~ la façon dont ces divulgations doivent être représentées et la définition de type de document (DTD) à employer lorsque le listage des séquences est effectué au format XML (*eXtensible Markup Language*). Il est recommandé que les offices de propriété industrielle acceptent tous les listages de séquences conformes à cette norme qui sont déposés en tant que partie intégrante d'une demande de brevet ou en relation avec une demande de brevet.

2. Cette norme a pour but :

(a) de permettre aux déposants d'établir, dans le cadre d'une demande de brevet, un listage des séquences unique qui soit acceptable pour les procédures internationales et nationales ou régionales;

(b) d'accroître la précision et la qualité de la présentation des séquences pour faciliter leur diffusion dans l'intérêt des déposants, du public et des examinateurs;

(c) de faciliter la recherche de données sur ces séquences; et

(d) de permettre l'échange de données sur les séquences sous forme électronique et l'incorporation de ces données dans des bases de données informatisées.

DÉFINITIONS

3. Aux fins de la présente norme, l'expression :

(a) "acide aminé" désigne tout acide aminé pouvant être représenté à l'aide des symboles indiqués dans le tableau I (voir section 3, tableau 3). Ces acides aminés comprennent notamment les acides aminés D et les acides aminés contenant des chaînes latérales modifiées ou synthétiques. Les acides aminés seront considérés comme des acides aminés L non modifiés sauf s'il est précisé dans leur description dans le tableau de caractéristiques qu'ils sont modifiés au sens du paragraphe ~~29~~30. Aux fins de la présente norme, un résidu d'acide nucléique peptidique (ANP) est considéré non pas comme un acide aminé, mais comme un nucléotide conformément à ce qui est indiqué au paragraphe 3.g)i)2);

(b) "vocabulaire contrôlé" désigne la terminologie employée dans la présente norme, qui doit être reprise dans la description des caractéristiques d'une séquence, c'est-à-dire dans les annotations de régions ou de sites présentant un intérêt particulier conformément à l'annexe I;

(c) "énumération de ses résidus" désigne la divulgation d'une séquence dans une demande de brevet sous forme de listage, dans un ordre donné, de chacun des résidus de la séquence, étant entendu que :

(i) le résidu est représenté par un nom, une abréviation, un symbole ou une structure (p. ex. HHHHHHQ ou HisHisHisHisHisGln); ou

(ii) les résidus multiples sont représentés par une formule topologique (p. ex. His_6Gln);

(d) "séquence délibérément omise" ou séquence vide désigne un espace réservé qui est destiné à préserver la numérotation des séquences dans le listage afin de garantir la cohérence de cette numérotation avec celle des divulgations jointes à la demande, par exemple lorsqu'une séquence a été supprimée dans la divulgation, pour éviter d'avoir à renuméroter les séquences à la fois dans la divulgation et dans le listage des séquences;

(e) "acide aminé modifié" désigne tout acide aminé tel que décrit au paragraphe 3.a) différent de L-alanine, L-arginine, L-asparagine, L-aspartate, L-cystéine, L-glutamine, L-glutamate, L-glycine, L-histidine, L-isoleucine, L-leucine, L-lysine, L-méthionine, L-phénylalanine, L-proline, L-pyrrolysine, L-sérine, L-sélénocystéine, L-thréonine, L-tryptophane, L-tyrosine ou L-valine;

(f) "nucléotide modifié" désigne tout nucléotide ~~ou~~tel que décrit au paragraphe 3.g) différent de la désoxyadénosine 3'-monophosphate, de la désoxyguanosine 3'-monophosphate, de la désoxycytidine 3'-monophosphate, de la désoxythymidine 3'-monophosphate, de l'adénosine 3'-monophosphate, de la guanosine 3'-monophosphate, de la cytidine 3'-monophosphate ou de l'uridine 3'-monophosphate;

(g) "~~analogue nucléotidique~~nucléotide" désigne tout nucléotide ou analogue nucléotidique qui peut être représenté à l'aide des symboles indiqués dans l'annexe I (voir section 1, tableau 1~~). Les nucléotides peuvent notamment contenir~~), le nucléotide ou analogue nucléotidique comprenant :

(i) une fraction squelette sélectionnée parmi

1) un 2' désoxyribose 5' monophosphate (la fraction squelette d'un désoxyribonucléotide) ou un ribose 5' monophosphate (la fraction squelette d'un ribonucléotide); ou

2) un analogue du 2' désoxyribose 5' monophosphate ou du ribose 5' monophosphate, qui lorsqu'il constitue le squelette d'un analogue d'acide nucléique, forme une disposition de bases azotées reproduisant celle des acides nucléiques contenant un squelette 2' désoxyribose 5' monophosphate ou ribose 5' monophosphate, l'analogue d'acide nucléique étant capable de former une paire de base avec à un acide nucléique complémentaire; on peut citer comme exemples d'analogues nucléotidiques les acides aminés dans les acides nucléiques peptidiques, les molécules de glycol dans les acides nucléiques à glycol, les molécules de sucre thréofuranosyl dans les acides nucléiques à thréose, les cycles morpholiniques et les groupes phosphorodiamidate dans les morpholinos, et les molécules cyclohexényle dans les acides nucléiques à cyclohexényle;

et

(ii) le squelette étant

1) relié à une base azotée, y compris une base azotée pyrimidique ou purine modifiée ou synthétique~~, ou un ribose ou désoxyribose modifié ou synthétique, et peuvent être reliés par une liaison inter-nucléoside de 3' à 5' modifiée ou synthétique, c'est-à-dire par toute fraction chimique assurant la même fonction structurelle que la fraction phosphate de l'ADN ou de l'ARN, par exemple la fraction phosphorothioate~~; ou

2) dépourvu d'une base azotée pyrimidique ou purine lorsque le nucléotide fait partie d'une séquence nucléotidique, soit un "site AP" ou "site abasique";

(h) "résidu" désigne tout nucléotide ou acide aminé individuel ou leurs analogues respectifs dans une séquence;

(i) "numéro d'identification de séquence" désigne un numéro unique (nombre entier) attribué à chaque séquence du listage;

(j) "listage des séquences" désigne une partie de la description, dans la demande de brevet déposée ou dans un document déposé après la demande, qui ~~présente~~ comprend la ou les séquences de nucléotides et/ou d'acides aminés divulguées, ainsi que toute autre description complémentaire, tel que prescrit par la présente norme;

(k) "spécialement défini" désigne tout nucléotide différent de ceux qui sont représentés par le symbole "n" et tout acide aminé différent de ceux qui sont représentés par le symbole "X" dans l'annexe I (voir section 1, tableau 1, et section 3, tableau 3, respectivement);

(l) "inconnu", pour un nucléotide ou un acide aminé, signifie qu'un seul nucléotide ou acide aminé est présent mais que son identité est inconnue ou non divulguée.

4. Aux fins de la présente norme,

(a) le terme "peut" indique qu'une démarche est facultative ou autorisée, mais pas obligatoire;

(b) le terme "doit" indique qu'une démarche est obligatoire selon la présente norme et que le non-respect de celle-ci peut entraîner la non-conformité de la demande;

(c) l'expression "ne doit pas" indique une interdiction au sens de la présente norme;

(d) le terme "devrait" indique qu'une démarche est fortement conseillée, mais pas obligatoire.

(e) l'expression "ne devrait pas" indique qu'une démarche est fortement déconseillée, mais pas interdite.

PORTÉE

5. La présente norme définit les exigences en matière de présentation des listages des séquences de nucléotides et d'acides aminés pour les séquences divulguées dans les demandes de brevet.

6. Un listage des séquences conforme à cette norme (ci-après "listage des séquences") contient une partie consacrée aux informations générales et une partie destinée aux données des séquences. Le listage des séquences doit être présenté dans un fichier unique qui doit être au format XML et être conforme à la définition de type de document (DTD) présentée dans l'annexe II. Les informations bibliographiques figurant dans la partie consacrée aux informations générales sont uniquement destinées à associer le listage des séquences à la demande de brevet pour laquelle le listage a été communiqué. La partie consacrée aux données des séquences se compose d'un ou plusieurs éléments de données, chacun d'eux contenant des informations sur une seule séquence. Ces éléments de données des séquences comportent différentes clés de caractérisation et des qualificateurs ultérieurs conformes aux exigences de la Collaboration internationale sur les bases de données de séquences de nucléotides (INSDC) et d'UniProt.

7. Aux fins de la présente norme, une séquence doit être intégrée dans un listage si elle est divulguée dans n'importe quelle partie d'une demande de brevet par l'énumération de ses résidus, et ~~s'il s'agit~~peut être représentée sous la forme :

(a) d'une séquence non ramifiée ou d'une ~~partie~~région linéaire d'une séquence ramifiée contenant au moins 10 nucléotides définis de manière spécifique, et dont les nucléotides adjacents ~~ont des liaisons de 3' à 5' (ou de 5' à 3'), ou~~sont reliés par :

(i) une liaison phosphodiester de 3' à 5' (ou 5' à 3'); ou

(ii) toute liaison chimique résultant en une disposition de bases azotées adjacentes qui reproduit la disposition des bases azotées des acides nucléiques existant à l'état naturel; ou

(b) d'une séquence non ramifiée ou d'une ~~partie~~région linéaire d'une séquence ramifiée contenant au moins quatre acides aminés définis de manière spécifique, et dont les acides aminés adjacents ont des liaisons peptidiques.

8. Un listage des séquences ne doit contenir, en tant que séquence disposant de son propre numéro d'identification de séquence, aucune séquence comportant moins de 10 nucléotides définis de manière spécifique ou moins de quatre acides aminés définis de manière spécifique.

RÉFÉRENCES

9. Les normes et ressources suivantes sont pertinentes à l'égard de la présente norme :

Collaboration internationale sur les bases de données de séquences de nucléotides (INSDC)	http://www.insdc.org/;
Norme internationale ISO 639−1:2002	Codes pour la représentation des noms de langue - Partie 1 : Code Alpha2;
Consortium UniProt	http://www.uniprot.org/;
Norme du W3C sur le XML 1.0	http://www.w3.org/;
Norme ST.2 de l'OMPI	Indication normalisée des dates à l'aide du calendrier grégorien;
Norme ST.3 de l'OMPI	Codes à deux lettres pour la représentation des États, autres entités et organisations intergouvernementales.
Norme ST.16 de l'OMPI	Identification de différents types de documents de brevet;
Norme ST.25 de l'OMPI	Présentation des listages des séquences de nucléotides et d'acides aminés.

~~PRÉSENTATION~~REPRÉSENTATION DES SÉQUENCES

10. À chaque séquence visée par le paragraphe 7 doit être attribué un numéro d'identification de séquence distinct, y compris en ce qui concerne les séquences qui sont identiques à une région d'une séquence plus longue. Ces numéros doivent commencer par le chiffre 1 et être incrémentés de manière consécutive par des nombres entiers. Si aucune séquence ne correspond à un numéro d'identification donné, par exemple en cas de séquence délibérément omise, il convient d'insérer la chaîne de caractères "000" à la place de la séquence (voir le paragraphe 58). Le nombre total de séquences doit être indiqué dans le listage des séquences et doit être égal au nombre total de numéros d'identification de séquence, que ces numéros soient suivis d'une séquence ou de la chaîne de caractères "000".

Séquences de nucléotides

11. Toute séquence de nucléotides doit être ~~présentée~~représentée par un seul brin de codage, dans le sens 5'-3' et de gauche à droite, ou de gauche à droite de manière à reproduire le sens 5'-3'. Les désignations 5' et 3' ou toute autre désignation similaire ne doivent pas ~~apparaître~~être incluses dans la séquence. Toute séquence de nucléotides représentée par deux brins de codage et divulguée par énumération des résidus des deux brins doit être ~~présentée~~représentée sous la forme :

(a) d'une seule séquence ou de deux séquences distinctes, chacune disposant de son propre numéro d'identification de séquence, si les deux brins distincts sont entièrement complémentaires l'un de l'autre; ou

(b) de deux séquences distinctes, chacune disposant de son propre numéro d'identification de séquence, si les deux brins ne sont pas entièrement complémentaires l'un de l'autre.

12. Aux fins de la présente norme,~~La numérotation des positions des nucléotides doit commencer par la première base de la séquence, qui portera le~~ le premier nucléotide présenté dans la séquence correspond à la position de résidu numéro 1. ~~Elle doit être continue dans toute la séquence dans le sens 5'-3'. 13. Cette méthode de numérotation~~Lorsque des séquences de nucléotides ~~s'applique aussi aux séquences de nucléotides de~~présentent une configuration circulaire~~. Dans ce cas,~~ le déposant doit choisir le nucléotide ~~correspondant au premier numéro~~à la position de résidu numéro 1. La numérotation est continue sur l'ensemble de la séquence dans le sens 5'-3', ou dans le sens qui reproduit le sens 5'-3'. Le dernier numéro de position de résidu doit correspondre au nombre de nucléotides de la séquence.

13. Tous les nucléotides d'une séquence doivent être représentés à l'aide des symboles indiqués dans l'annexe I (voir section 1, tableau 1). Seules les lettres minuscules sont autorisées. Tout symbole employé pour représenter un nucléotide ne peut être l'équivalent que d'un seul résidu.

14. Le symbole “t” désigne la thymine dans de l’ADN et l’uracile dans de l’ARN. L’uracile dans de l’ADN ou la thymine dans de l’ARN sont considérés comme des nucléotides modifiés et doivent être accompagnés d’une description supplémentaire dans le tableau de caractéristiques au sens du paragraphe ~~18~~19.

15. Lorsqu’il convient d’employer un symbole ambigu (représentant deux ~~bases~~nucléotides possibles ou plus), il faut choisir le symbole le plus restrictif indiqué à l’annexe I (voir section 1, tableau 1). Si par exemple ~~une base~~un nucléotide dans une position quelconque pouvait être désigné~~e~~ par “a” ou “g”, il faut employer “r” au lieu de “n”. Le symbole “n” sera considéré comme équivalent à l’un des symboles “a”, “c”, “g” ou “t/u”, sauf s’il est accompagné d’une description supplémentaire au sens des paragraphes 16 et 17 ou ~~20~~21. Ce symbole “n” ne peut être employé que pour représenter un nucléotide. Il peut représenter un seul nucléotide modifié ou “inconnu” s’il est accompagné d’une description supplémentaire dans le tableau de caractéristiques au sens des paragraphes 16 et 17 ou ~~20~~21. On trouvera des détails sur la représentation des variantes de séquence, par exemple des alternatives, des suppressions, des adjonctions ou des remplacements, aux paragraphes 92 à 98.

16. Les nucléotides modifiés doivent être représentés dans la séquence comme les ~~bases~~nucléotides non modifié~~e~~s correspondant~~e~~s, c’est-à-dire par “a”, “c”, “g” ou “t” chaque fois que possible. Tout nucléotide modifié apparaissant dans une séquence et ne pouvant être représenté à l’aide d’un autre symbole indiqué dans l’annexe I (voir section 1, tableau 1), c’est-à-dire un nucléotide “other”, comme par exemple un nucléotide n’existant pas à l’état naturel, doit être représenté par le symbole “n”. Lorsque ce symbole “n” est employé pour représenter un nucléotide modifié, il n’est l’équivalent que d’un seul résidu.

17. Tout nucléotide modifié doit être accompagné d’une description supplémentaire dans le tableau de caractéristiques (voir les paragraphes ~~59~~60 et suivants) comportant la clé de caractérisation “modified_base” et le qualificateur obligatoire “mod_base”. La valeur qualificative ne peut être constituée que d’une seule abréviation issue de l’annexe I (voir section 2, tableau 2). Si cette abréviation est “OTHER”, le nom complet non abrégé ~~de la base~~du nucléotide modifié~~e~~ doit être indiqué dans un qualificateur de type “note”. Pour un listage d’autres nucléotides modifiés, la valeur qualificative “OTHER” peut être utilisée conjointement avec un qualificateur de type “note” supplémentaire (voir les paragraphes 95 et 96). Les abréviations (ou les noms complets) indiquées dans l’annexe I (voir section 2, tableau 2) qui sont mentionnées ci-dessus ne doivent pas être employées dans la séquence elle-même.

18. Une séquence de nucléotides comprenant une ou plusieurs régions de nucléotides modifiés consécutifs partageant la même fraction squelette (voir le paragraphe 3.g)i)2)) doit être accompagnée d’une description supplémentaire dans le tableau de caractéristiques comme indiqué au paragraphe 17. Les nucléotides modifiés de chacune de ces régions peuvent faire l’objet d’une description commune au moyen d’un seul élément INSDFeature comme indiqué au paragraphe 22. Le nom chimique complet non abrégé le plus restrictif qui englobe tous les nucléotides modifiés de la série ou une liste des noms chimiques de tous les nucléotides de la série doit être indiqué sous forme de valeur dans le qualificateur de type “note”. Par exemple, la séquence d’un acide nucléique à glycol contenant des bases azotées “a”, “c”, “g”, ou “t” peut comporter un qualificateur de type “note” dont la valeur est “2,3-dihydroxypropyl nuclosides”. Cette même séquence peut également comporter un qualificateur de type “note” dont la valeur est “2,3-dihydroxypropyladenine, 2,3-dihydroxypropylthymine, 2,3-dihydroxypropylguanine, or 2,3-dihydroxypropylcytosine”. Lorsqu’un nucléotide modifié de la région comporte une modification supplémentaire, celui-ci doit également être accompagné d’une description supplémentaire dans le tableau de caractéristiques comme indiqué au paragraphe 17.

19. L’uracile dans de l’ADN ou la thymine dans de l’ARN sont considérés comme des nucléotides modifiés et doivent être représentés dans la séquence par un “t” et être accompagnés d’une description supplémentaire dans le tableau de caractéristiques. Cette description doit comporter la clé de caractérisation “modified_base”, le qualificateur “mod_base” dont la valeur doit être “OTHER”, et un qualificateur de type “note” dont la valeur doit être respectivement “uracil” ou “thymine”.

20. Les exemples ci-après illustrent la manière dont des nucléotides modifiés doivent être ~~présentés~~représentés pour être conformes aux paragraphes 16 ~~et 17~~à 18 ci-dessus :

Exemple 1 : Nucléotide modifié représenté par une abréviation indiquée dans l’annexe I (voir section 2, tableau 2).

```
<INSDFeature>
   <INSDFeature_key>modified_base</INSDFeature_key>
   <INSDFeature_location>15</INSDFeature_location>
   <INSDFeature_quals>
       <INSDQualifier>
           <INSDQualifier_name>mod_base</INSDQualifier_name>
           <INSDQualifier_value>i</INSDQualifier_value>
       </INSDQualifier>
   </INSDFeature_quals>
</INSDFeature>
```

Exemple 2 : Nucléotide modifié "xanthine" représenté par la valeur "OTHER" indiquée dans l'annexe I (voir section 2, tableau 2)

```
<INSDFeature>
   <INSDFeature_key>modified_base</INSDFeature_key>
   <INSDFeature_location>4</INSDFeature_location>
   <INSDFeature_quals>
       <INSDQualifier>
           <INSDQualifier_name>mod_base</INSDQualifier_name>
           <INSDQualifier_value>OTHER</INSDQualifier_value>
       </INSDQualifier>
       <INSDQualifier>
           <INSDQualifier_name>note</INSDQualifier_name>
           <INSDQualifier_value>xanthine</INSDQualifier_value>
       </INSDQualifier>
   </INSDFeature_quals>
</INSDFeature>
```

Exemple 3 : Séquence de nucléotides composée de nucléotides modifiés visés par le paragraphe 3.g)i)2) avec deux nucléotides individuels comportant une modification supplémentaire

```
<INSDFeature>
    <INSDFeature_key>modified_base</INSDFeature_key>
    <INSDFeature_location>1..954</INSDFeature_location>
    <INSDFeature_quals>
        <INSDQualifier>
            <INSDQualifier_name>mod_base</INSDQualifier_name>
            <INSDQualifier_value>OTHER</INSDQualifier_value>
        </INSDQualifier>
        <INSDQualifier>
            <INSDQualifier_name>note</INSDQualifier_name>
            <INSDQualifier_value>2,3-dihydroxypropyl nucleosides</INSDQualifier_value>
        </INSDQualifier>
    </INSDFeature_quals>
</INSDFeature>

<INSDFeature>
    <INSDFeature_key>modified_base</INSDFeature_key>
    <INSDFeature_location>439</INSDFeature_location>
    <INSDFeature_quals>
        <INSDQualifier>
            <INSDQualifier_name>mod_base</INSDQualifier_name>
            <INSDQualifier_value>i</INSDQualifier_value>
        </INSDQualifier>
    </INSDFeature_quals>
</INSDFeature>
<INSDFeature>
    <INSDFeature_key>modified_base</INSDFeature_key>
    <INSDFeature_location>684</INSDFeature_location>
    <INSDFeature_quals>
        <INSDQualifier>
            <INSDQualifier_name>mod_base</INSDQualifier_name>
            <INSDQualifier_value>OTHER</INSDQualifier_value>
        </INSDQualifier>
        <INSDQualifier>
            <INSDQualifier_name>note</INSDQualifier_name>
            <INSDQualifier_value>xanthine</INSDQualifier_value>
        </INSDQualifier>
    </INSDFeature_quals>
</INSDFeature>
```

21. Tout nucléotide "inconnu" doit être représenté par le symbole "n" dans la séquence. Un nucléotide "inconnu" doit en outre être accompagné d'une description supplémentaire dans le tableau de caractéristiques (voir les paragraphes 60 et suivants) comportant la clé de caractérisation "unsure". Le symbole "n" ne peut être l'équivalent que d'un seul résidu.

22. Toute région contenant un nombre connu de résidus "a", "c", "g", "t" ou "n" auxquels la même description s'applique peut faire l'objet d'une description commune au moyen d'un seul élément INSDFeature avec ~~de~~ la syntaxe "x..y" dans le descripteur d'emplacement de l'élément `INSDFeature_location` (voir les paragraphes ~~65~~64 à ~~72~~71). On trouvera des détails sur la ~~présentation~~représentation des variantes de séquence, par exemple des suppressions, des adjonctions ou des remplacements, aux paragraphes 92 à ~~97~~98.

23. L'exemple ci-après illustre la ~~présentation~~représentation d'une région de nucléotides modifiés faisant l'objet de la même description au sens du paragraphe ~~21~~22 ci-dessus :

```
<INSDFeature>
   <INSDFeature_key>modified_base</INSDFeature_key>
   <INSDFeature_location>358..485</INSDFeature_location>
   <INSDFeature_quals>
           <INSDQualifier>
           <INSDQualifier_name>mod_base</INSDQualifier_name>
           <INSDQualifier_value>OTHER</INSDQualifier_value>
       </INSDQualifier>
           <INSDQualifier>
           <INSDQualifier_name>note</INSDQualifier_name>
           <INSDQualifier_value>isoguanine</INSDQualifier_value>
       </INSDQualifier>
   </INSDFeature_quals>
</INSDFeature>
```

Séquences d'acides aminés

24. Les acides aminés d'une séquence ~~protéinique ou peptidique~~d'acides aminés doivent être ~~énumérés~~représentés dans le sens amino-carboxy et de gauche à droite. Les groupes amino et carboxy ne doivent pas être représentés dans la séquence.

25. Aux fins de la présente norme, ~~La numérotation des positions des acides aminés doit commencer au~~ le premier acide aminé de la séquence est dans la position de résidu numéro 1~~numéroté 1~~, en tenant compte des acides aminés précédant la protéine mature, par exemple les préséquences, les proséquences et les pré-proséquences ainsi que les séquences signal. ~~Elle doit être continue sur~~Lorsque les séquences d'acides aminés présentent une configuration circulaire, le déposant doit choisir l'acide aminé à la position de résidu numéro 1. La numérotation est continue sur l'ensemble de la séquence dans le sens amino-carboxy.

26. Tous les acides aminés d'une séquence doivent être représentés à l'aide des symboles indiqués dans l'annexe I (voir section 3, tableau 3). Seules les lettres majuscules sont autorisées. Tout symbole employé pour représenter un acide aminé ne peut être l'équivalent que d'un seul résidu.

27. Lorsqu'il convient d'employer un symbole ambigu (représentant deux acides aminés possibles ou plus), il faut choisir le symbole le plus restrictif. Si par exemple un acide aminé dans une position quelconque pouvait être de l'acide aspartique ou de l'asparagine, il faut employer le symbole "B" au lieu de "X". Le symbole "X" ne sera pas considéré comme équivalent à l'un des symboles "A", "R", "N", "D", "C", "Q", "E", "G", "H", "I", "L", "K", "M", "F", "P", "O", "S", "U", "T", "W", "Y" ou "V", sauf s'il est accompagné d'une description supplémentaire dans le tableau de caractéristiques au sens des paragraphes ~~28~~29 à ~~30~~31 ou ~~31 à~~32 et 33. Le symbole "X" ne peut être employé que pour représenter un acide aminé. Il peut représenter un seul acide aminé s'il est accompagné d'une description supplémentaire dans le tableau de caractéristiques au sens des paragraphes ~~28~~29 à ~~30~~31 ou ~~31 à~~32 et 33. On trouvera des détails sur la ~~présentation~~représentation des variantes de séquence, par exemple des alternatives, des suppressions, des adjonctions ou des remplacements, aux paragraphes 92 à ~~97~~98.

28. Les séquences d'acides aminés divulguées séparées par des~~un ou plusieurs espaces blancs ou 7~~ symboles internes de fin (représentés par exemple par "Ter", l'astérisque "*",~~ou~~ le point "." ou un espace blanc) doivent être ~~présentées~~ajoutées comme des séquences distinctes pour chaque séquence qui contient au moins quatre acides aminés définis de manière spécifique et qui est visée par le paragraphe ~~6~~7. Chacune de ces séquences distinctes doit ~~être présentée, dans le listage des séquences, avec~~ disposer de son propre numéro d'identification de séquence ~~et uniquement à l'aide des symboles indiqués dans l'annexe I (voir section 3, tableau 3)~~. Les symboles de fin et les espaces blancs ne doivent pas être ~~employés~~ajoutés dans les séquences figurant dans un listage (voir le paragraphe 57).

29. Les acides aminés modifiés, y compris les acides aminés D, doivent être représentés dans la séquence comme les acides aminés non modifiés correspondants chaque fois que possible. Tout acide aminé modifié apparaissant dans une séquence et ne pouvant être représenté à l'aide d'un autre symbole indiqué dans l'annexe I (voir section 3, tableau 3), c'est-à-dire un acide aminé "autre", doit être représenté par le symbole "X". Ce symbole "X" n'est l'équivalent que d'un seul résidu.

30. Tout acide aminé modifié doit être accompagné d'une description supplémentaire dans le tableau de caractéristiques (voir les paragraphes 60 et suivants). Le cas échéant, les clés de caractérisation "CARBOHYD" ou "LIPID" devraient être utilisées avec le qualificateur "NOTE". Il faudrait employer la clé de caractérisation "MOD_RES" et le qualificateur "NOTE" pour les acides aminés autres modifiés après traduction; autrement, la clé de caractérisation "SITE" ainsi que le qualificateur "NOTE" doivent être utilisés. La valeur du qualificateur "NOTE" doit être soit une abréviation indiquée dans l'annexe I (voir section 4, tableau 4), soit le nom complet non abrégé de l'acide aminé modifié. Les abréviations indiquées dans le tableau 4 précité ou les noms complets non abrégés ne doivent pas être employés dans la séquence elle-même.

31. Les exemples ci-après illustrent la manière dont des acides aminés modifiés doivent être ~~présentés~~représentés pour être conformes au paragraphe ~~29~~30 ci-dessus :

Exemple 1 : Acide aminé modifié après traduction.

```
<INSDFeature>
   <INSDFeature_key>MOD_RES</INSDFeature_key>
   <INSDFeature_location>3</INSDFeature_location>
   <INSDFeature_quals>
       <INSDQualifier>
           <INSDQualifier_name>NOTE</INSDQualifier_name>
           <INSDQualifier_value>~~3-Hyp~~3Hyp</INSDQualifier_value>
        </INSDQualifier>
    </INSDFeature_quals>
</INSDFeature>
~~        </INSDQualifier>~~
~~    </INSDFeature_quals>~~
~~</INSDFeature>~~
```

Exemple 2 : Acide aminé modifié différemment

```
<INSDFeature>
   <INSDFeature_key>SITE</INSDFeature_key>
   <INSDFeature_location>3</INSDFeature_location>
   <INSDFeature_quals>
       <INSDQualifier>
           <INSDQualifier_name>NOTE</INSDQualifier_name>
           <INSDQualifier_value>Orn</INSDQualifier_value>
       </INSDQualifier>
   </INSDFeature_quals>
</INSDFeature>
```

Exemple 3 : acide aminé D

```
<INSDFeature>
   <INSDFeature_key>SITE</INSDFeature_key>
   <INSDFeature_location>9</INSDFeature_location>
   <INSDFeature_quals>
       <INSDQualifier>
           <INSDQualifier_name>NOTE</INSDQualifier_name>
           <INSDQualifier_value>D-Arginine</INSDQualifier_value>
       </INSDQualifier>
   </INSDFeature_quals>
</INSDFeature>
```

32. Tout acide aminé “inconnu” ~~ou “autre” qui n’est pas visé par le paragraphe 28~~ doit être représenté par le symbole “X” dans la séquence. ~~Le symbole “X” ne peut être l’équivalent que d’un seul résidu.~~ Tout acide aminé “inconnu” désigné par “X” doit être accompagné d’une description supplémentaire dans le tableau de caractéristiques (voir les paragraphes 60 et suivants) comportant la clé de caractérisation “UNSURE” et éventuellement le qualificateur “NOTE”. ~~Tout acide aminé “autre” désigné par “X” doit être accompagné d’une description supplémentaire comportant la clé de caractérisation “SITE” ou “MOD_RES”, selon le cas, ainsi que le qualificateur “NOTE” avec le nom complet non abrégé de l’acide aminé “autre”.~~ Le symbole “X” ne peut être l’équivalent que d’un seul résidu.

33. ~~Les exemples~~L’exemple ci-après illustre~~nt~~ la manière dont ~~des~~un acide~~s~~ aminé~~s~~ “inconnu~~s~~” ~~ou “autres” doivent~~doit être ~~présentés~~représenté pour être conforme~~s~~ au~~x~~ paragraphe~~s 31 et~~ 32 ci-dessus :

~~Exemple 1 : Acide aminé “inconnu”.~~

```
<INSDFeature>
   <INSDFeature_key>UNSURE</INSDFeature_key>
   <INSDFeature_location>3</INSDFeature_location>
   <INSDFeature_quals>
       <INSDQualifier>
           <INSDQualifier_name>NOTE</INSDQualifier_name>
           <INSDQualifier_value>A or V</INSDQualifier_value>
       </INSDQualifier>
   </INSDFeature_quals>
</INSDFeature>
```

~~Exemple 2 acide aminé "autre".~~

```
~~<INSDFeature>~~
~~    <INSDFeature_key>SITE</INSDFeature_key>~~
~~    <INSDFeature_location>3</INSDFeature_location>~~
~~    <INSDFeature_quals>~~
~~        <INSDQualifier>~~
~~            <INSDQualifier_name>NOTE</INSDQualifier_name>~~
~~            <INSDQualifier_value>Homoserine</INSDQualifier_value>~~
~~        </INSDQualifier>~~
~~    </INSDFeature_quals>~~
~~</INSDFeature>~~
```

34. Toute région contenant un nombre connu de résidus "X" contigus auxquels la même description s'applique peut faire l'objet d'une description commune au moyen de la syntaxe "x..y" dans le descripteur d'emplacement de l'élément `INSDFeature_location` (voir les paragraphes ~~65~~64 à ~~71~~70). On trouvera des détails sur la ~~présentation~~représentation des variantes de séquence, par exemple des suppressions, des adjonctions ou des remplacements, aux paragraphes ~~92~~93 à ~~97~~98.

Présentation de cas particuliers

35. Toute séquence divulguée par énumération de ses résidus qui est construite comme une séquence continue et unique d'un ou plusieurs segments non contigus provenant d'une séquence plus grande ou de segments provenant de différentes séquences doit être ajoutée au listage des séquences ~~comme une séquence unique avec un~~et doit disposer de son propre numéro d'identification de séquence ~~unique~~.

36. Toute séquence ~~divulguée par énumération de ses résidus~~ qui contient des régions de résidus ~~énumérés~~définis de manière spécifique et séparés par une ou plusieurs régions de résidus "n" ou "X" contigus (voir respectivement les paragraphes 15 et ~~26~~27), et pour laquelle le nombre exact de résidus "n" ou "X" dans chaque région est divulgué, doit être ajoutée au listage des séquences comme une séquence ~~unique~~et doit disposer de son propre ~~avec un~~ numéro d'identification de séquence ~~unique~~.

37. Toute séquence ~~divulguée par énumération de ses résidus~~ qui contient des régions de résidus ~~énumérés~~définis de manière spécifique et séparés par une ou plusieurs brèches composées d'un nombre inconnu ou non divulgué de résidus ne doit pas être représentée dans le listage des séquences comme une séquence unique. Chaque région de résidus définis de manière spécifique visée par le paragraphe 7 doit être insérée dans le listage des séquences comme une ~~série de~~ séquence~~s~~ distincte~~s. Chacune de ces séquences distinctes doit comporter une région de résidus énumérés de manière spécifique et~~ et doit disposer de son propre numéro d'identification de séquence~~. Le nombre de séquences distinctes doit ainsi être égal au nombre de régions de résidus énumérés de manière spécifique. Les séquences contenant des brèches composées d'un nombre inconnu ou non divulgué de résidus ne doivent pas être ajoutées au listage des séquences en tant que séquences uniques~~.

STRUCTURE DU LISTAGE DE SÉQUENCES EN XML

38. En application du paragraphe ~~5~~6 ci-dessus, l'instance XML d'un fichier de listage des séquences conforme à la présente norme se compose des éléments suivants :

(a) une partie consacrée aux informations générales, qui contient des informations sur la demande de brevet à laquelle se rapporte le listage des séquences; et

(b) une partie consacrée aux données des séquences, qui contient un ou plusieurs éléments de données sur les séquences, chacun de ces éléments contenant des informations sur une seule séquence.

On trouvera un exemple de listage de séquences dans l'annexe III.

39. Le listage des séquences doit être présenté au format XML 1.0 en employant la DTD définie dans l'annexe II intitulée "Définition de type de document pour le listage des séquences".

(a) La première ligne de l'instance XML doit contenir la déclaration du format XML :

```
<?xml version="1.0" encoding="UTF-8"?>.
```

(b) La deuxième ligne de l'instance XML doit contenir une déclaration de type de document (DOCTYPE) :

```
<!DOCTYPE ST26SequenceListing PUBLIC "-//WIPO//DTD Sequence Listing 1.0//EN"
"ST26SequenceListing_V1_0.dtd">.
```

40. Le listage des séquences au format électronique doit être entièrement contenu dans un seul fichier. Celui-ci doit être codé selon la norme Unicode UTF-8, avec les restrictions suivantes :

(a) les informations figurant dans les éléments `ApplicantName`, `InventorName` et `InventionTitle` dans la partie consacrée aux informations générales peuvent comporter n'importe quel caractère Unicode à l'exception des caractères réservés, qui doivent être remplacés selon la méthode décrite au paragraphe 41; et

(b) les informations figurant dans tous les autres éléments de la partie consacrée aux informations générales et dans tous les éléments de la partie sur les données des séquences

- doivent être composées de caractères imprimables (y compris le caractère d'espace) indiqués dans le tableau de codes des caractères latins de base de la norme Unicode, à l'exception des caractères réservés, qui doivent être remplacés selon la méthode décrite au paragraphe 41 (c'est-à-dire que ces caractères sont limités aux points de codes Unicode 0020, 0021, 0023 jusqu'à 0026, 0028 jusqu'à 003B, 003D, et 003F jusqu'à 007E – voir l'annexe IV), et les seules entités de caractères autorisées sont les entités prédéfinies prévues au paragraphe 41.

41. Dans l'instance XML d'un listage des séquences, les caractères réservés suivants doivent être remplacés par les entités prédéfinies correspondantes lorsqu'ils sont employés pour renseigner la valeur d'un attribut ou le contenu d'un élément :

Caractère réservé	Entités prédéfinies
<	<
>	>
&	&
"	"
'	'

On trouvera un exemple au paragraphe ~~72~~71.

42. Tous les éléments obligatoires doivent être renseignés (sauf ceux qui sont indiqués au paragraphe 58 à propos des séquences délibérément omises). Les éléments facultatifs pour lesquels aucun contenu n'est disponible ne doivent pas figurer dans l'instance XML (à l'exception de ce qui est prévu au paragraphe 95 concernant la représentation d'une suppression dans une séquence dans la valeur du qualificateur "replace").

Élément racine

43. L'élément racine d'une instance XML au sens de la présente norme est l'élément `ST26SequenceListing`, dont les attributs sont les suivants :

Attribut	Description	Obligatoire/Facultatif
`dtdVersion`	Version de la DTD employée pour créer ce fichier au format "V#_#", par exemple "V1_0".	Obligatoire
`fileName`	Nom du fichier contenant le listage des séquences.	Facultatif
`softwareName`	Nom du logiciel ayant créé le fichier.	Facultatif
`softwareVersion`	Version du logiciel ayant créé le fichier.	Facultatif
`productionDate`	Date de production du fichier contenant le listage des séquences (format "SSAA-MM-JJ").	Facultatif

44. L'exemple ci-après est une illustration de l'élément racine `ST26SequenceListing` et de ses attributs dans une instance XML conforme au paragraphe 43 ci-dessus :

```
<ST26SequenceListing dtdVersion="V1_0" fileName="US11_405455_SEQL.xml"
softwareName="SEQL-software-name" softwareVersion="1.0" productionDate="2006-05-10">
     {...}*
</ST26SequenceListing>


*{...} représente la partie des informations générales et la partie des données de
séquences qui ne figurent pas dans cet exemple.
```

Partie consacrée aux informations générales

45. Les éléments de la partie consacrée aux informations générales contiennent des informations sur la demande de brevet, comme indiqué ci-après :

Élément	Description	Obligatoire/ Facultatif
`ApplicationIdentification` L'élément `ApplicationIdentification` est composé des éléments suivants :	Identification de la demande pour laquelle le listage des séquences est soumis.	Obligatoire lorsqu'un listage des séquences est remis à un moment quelconque après l'attribution d'un numéro de demande.
`IPOfficeCode`	Code ST.3 de l'office de dépôt	Obligatoire
`ApplicationNumberText`	Identification de la demande fournie par l'office de dépôt (ex : PCT/IB2013/099999)	Obligatoire
`FilingDate`	Date de dépôt de la demande de brevet pour laquelle le listage des séquences est remis (au format ST.2 "SSAA-MM-JJ", en désignant l'année civile sur 4 chiffres, le mois civil sur 2 chiffres et le jour du mois civil sur 2 chiffres, p. ex. 2015-01-31)	Obligatoire lorsqu'un listage des séquences est remis à un moment quelconque après l'attribution d'une date de dépôt.
`ApplicantFileReference`	Identificateur unique attribué par le demandeur pour désigner une demande particulière, composé de caractères définis au paragraphe 40 b).	Obligatoire lorsqu'un listage des séquences est remis à un moment quelconque avant l'attribution du numéro de demande; facultatif dans les autres cas.
`EarliestPriorityApplicationIdentification`	Identification de la première revendication de priorité dans la demande (contient également les éléments `IPOfficeCode`, `ApplicationNumberText` et `FilingDate`, voir `ApplicationIdentification` ci-dessus)	Obligatoire si une priorité est revendiquée.
`ApplicantName`	Nom du premier déposant mentionné, composé de caractères définis au paragraphe 40 a). Cet élément comporte l'attribut obligatoire `languageCode` conformément au paragraphe 47.	Obligatoire
`ApplicantNameLatin`	Si l'élément `ApplicantName` comporte des caractères différents de ceux définis au paragraphe 40 b), une traduction ou une translittération du nom du premier déposant mentionné doit être fournie et doit aussi se composer de caractères définis au paragraphe 40 b).	Obligatoire si l'élément `ApplicantName` contient des caractères non latins.
`InventorName`	Nom du premier inventeur mentionné, composé de caractères définis au paragraphe 40 a). Cet élément comporte l'attribut obligatoire `languageCode` conformément au paragraphe 47.	Facultatif

Élément	Description	Obligatoire/ Facultatif
`InventorNameLatin`	Si l'élément `InventorName` comporte des caractères différents de ceux définis au paragraphe 40 b), une traduction ou une translittération du nom du premier inventeur mentionné doit être fournie et doit aussi se composer de caractères définis au paragraphe 40 b).	Facultatif
`InventionTitle`	Titre de l'invention, composé de caractères définis au paragraphe 40 a) dans la langue de dépôt. Une traduction du titre de l'invention dans d'autres langues peut être fournie; elle doit alors se composer de caractères définis au paragraphe 40 a) et apparaître sous des éléments `InventionTitle` supplémentaires. Cet élément comporte l'attribut obligatoire `languageCode` défini au paragraphe 48. Le titre de l'invention doit comporter de préférence deux à sept mots.	Obligatoire dans la langue de dépôt. Facultatif dans d'autres langues.
`SequenceTotalQuantity`	Nombre total de toutes les séquences apparaissant dans le listage, y compris les séquences délibérément omises (également appelées séquences vides) (voir le paragraphe ~~9~~10).	Obligatoire

46. Les exemples ci-après illustrent la manière dont la partie du listage des séquences consacrée aux informations générales doit être présentée pour être conforme au paragraphe 45 ci-dessus :

Exemple 1 : Listage des séquences déposé avant l'attribution du numéro d'identification et de la date de dépôt de la demande.

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE ST26SequenceListing PUBLIC "-//WIPO//DTD Sequence Listing 1.0//EN"
"ST26SequenceListing_V1_0.dtd">
<ST26SequenceListing dtdVersion="V1_0" fileName="Invention_SEQL.xml"
softwareName="SEQL-software-name" softwareVersion="1.0" productionDate="2015-05-10">
   <ApplicantFileReference>AB123</ApplicantFileReference>
   <EarliestPriorityApplicationIdentification>
       <IPOfficeCode>IB</IPOfficeCode>
       <ApplicationNumberText>PCT/IB2013/099999</ApplicationNumberText>
           <FilingDate>2014-07-10</FilingDate>
   </EarliestPriorityApplicationIdentification>
   <ApplicantName languageCode="ENen">GENOS Co., Inc.</ApplicantName>
   <InventorName languageCode="ENen">Keiko Nakamura</InventorName>
   <InventionTitle languageCode="ENen">SIGNAL RECOGNITION PARTICLE RNA AND
PROTEINS</InventionTitle>
   <SequenceTotalQuantity>9</SequenceTotalQuantity>
   <SequenceData sequenceIDNumber="1"> {...}* </SequenceData>
   <SequenceData sequenceIDNumber="2"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="3"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="4"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="5"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="6"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="7"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="8"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="9"> {...} </SequenceData>
</ST26SequenceListing>

*{...} représente des informations pertinentes pour chaque séquence qui ne figurent
pas dans cet exemple.
```

Exemple 2 : Listage des séquences déposé après l'attribution du numéro d'identification et de la date de dépôt de la demande

```
<?xml version="1.0" encoding="UTF-8"?>
<!DOCTYPE ST26SequenceListing PUBLIC "-//WIPO//DTD Sequence Listing 1.0//EN"
"ST26SequenceListing_V1_0.dtd">
<ST26SequenceListing dtdVersion="1_0" fileName="Invention_SEQL.xml"
softwareName="SEQL-software-name" softwareVersion="1.0" productionDate="2015-05-10">
    <ApplicationIdentification>
       <IPOfficeCode>US</IPOfficeCode>
       <ApplicationNumberText>14/999,999</ApplicationNumberText>
      <FilingDate>2015-01-05</FilingDate>
   </ApplicationIdentification>
   <ApplicantFileReference>AB123</ApplicantFileReference>
   <EarliestPriorityApplicationIdentification>
       <IPOfficeCode>IB</IPOfficeCode>
       <ApplicationNumberText>PCT/IB2014/099999</ApplicationNumberText>
      <FilingDate>2014-07-10</FilingDate>
   </EarliestPriorityApplicationIdentification>
   <ApplicantName languageCode="ENen">GENOS Co., Inc.</ApplicantName>
   <InventorName languageCode="ENen">Keiko Nakamura</InventorName>
   <InventionTitle languageCode="ENen">SIGNAL RECOGNITION PARTICLE RNA AND
PROTEINS</InventionTitle>
   <SequenceTotalQuantity>9</SequenceTotalQuantity>
   <SequenceData sequenceIDNumber="1"> {...}* </SequenceData>
   <SequenceData sequenceIDNumber="2"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="3"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="4"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="5"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="6"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="7"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="8"> {...} </SequenceData>
   <SequenceData sequenceIDNumber="9"> {...} </SequenceData>
</ST26SequenceListing>

*{...} représente des informations pertinentes pour chaque séquence qui ne figurent
pas dans cet exemple.
```

47. Le nom du déposant et, à titre facultatif, le nom de l'inventeur doivent être indiqués respectivement dans les éléments `ApplicantName` et `InventorName` car ils sont généralement mentionnés dans la langue de dépôt de la demande. Le code de langue adéquat (voir la référence à la norme ISO 639-1:2002 aule paragraphe 89) doit être indiqué dans l'attribut `languageCode` pour chaque élément. Si le nom du déposant contient des caractères différents de l'alphabet latin tel que défini au paragraphe 40 b), une translittération ou une traduction de ce nom doit aussi être fournie en caractères latins dans l'élément `ApplicantNameLatin`. Si le nom de l'inventeur contient des caractères différents de l'alphabet latin, une translittération ou une traduction de ce nom doit aussi être fournie en caractères latins dans l'élément `InventorNameLatin`.

48. Le titre de l'invention doit être indiqué dans l'élément `InventionTitle` dans la langue de dépôt et peut aussi figurer dans d'autres langues en ajoutant d'autres éléments `InventionTitle` (voir le tableau du paragraphe 45). Le code de langue adéquat (voir la référence à la norme ISO 639-1:2002 aule paragraphe 89) doit être indiqué dans l'attribut `languageCode` de l'élément.

49. L'exemple ci-après illustre la manière dont les noms et le titre de l'invention doivent être présentés pour être conformes aux paragraphes 47 et 48 ci-dessus :

Exemple : Le nom du déposant et celui de l'inventeur sont présentés en caractères japonais et latins et le titre de l'invention est présenté en japonais, en anglais et en français

```
<ApplicantName languageCode="JAja">出願製□株式□社</ApplicantName>
<ApplicantNameLatin>Shutsugan Pharmaceuticals Kabushiki Kaisha</ApplicantNameLatin>
<InventorName languageCode="JA="ja">特許―太□</InventorName>
<InventorNameLatin>Taro Tokkyo</InventorNameLatin>
<InventionTitle languageCode="JA"> ja">efg タンパク質のためのをコ□ドするマウス abcd-1 遺伝子
</InventionTitle>
<InventionTitle languageCode="EN"> en">Mus musculus abcd-1 gene for efg
protein</InventionTitle>
<InventionTitle languageCode="FR"> fr">Gène abcd-1 de Mus musculus pour protéine
efg</InventionTitle>
```

Partie consacrée aux données sur les séquences

50. La partie consacrée aux données sur les séquences doit être composée d'un ou plusieurs éléments `SequenceData`, chacun d'eux contenant des informations sur une séquence.

51. Chaque élément `SequenceData` doit avoir un attribut obligatoire `sequenceIDNumber` contenant le numéro d'identification de la séquence (voir le paragraphe ~~9~~10), par exemple :

```
<SequenceData sequenceIDNumber="1">
```

52. L'élément `SequenceData` doit contenir un élément subordonné `INSDSeq` qui se compose d'autres éléments subordonnés, de la manière suivante :

Élément	Description	Obligatoire/Non indiqué	
		Séquences	Séquences délibérément omises
`INSDSeq_length`	Longueur de la séquence	Obligatoire	Obligatoire, aucune valeur indiquée
`INSDSeq_moltype`	Type de molécule	Obligatoire	Obligatoire, aucune valeur indiquée
`INSDSeq_division`	Indication du fait qu'une séquence est liée à une demande de brevet	Obligatoire avec la valeur "PAT"	Obligatoire, aucune valeur indiquée
`INSDSeq_feature-table`	Liste d'annotations de la séquence	Obligatoire	Ne doit PAS être indiqué
`INSDSeq_sequence`	Séquence	Obligatoire	Obligatoire, indiquer la valeur "000"

53. L'élément `INSDSeq_length` doit divulguer le nombre de nucléotides ou d'acides aminés de la séquence figurant dans l'élément `INSDSeq_sequence`, par exemple :

```
<INSDSeq_length>8</INSDSeq_length>
```

54. L'élément `INSDSeq_moltype` doit divulguer le type de la molécule ~~présentée~~représentée. Pour les séquences de nucléotides, y compris les séquences d'analogues nucléotidiques, le type de molécule doit être ADN ou ARN. Pour les séquences ~~protéiniques ou peptidiques~~d'acides aminés, le type de molécule doit être AA. (Cet élément est distinct des qualificateurs "mol_type" et "MOL_TYPE" mentionnés aux paragraphes 55 et ~~85~~84.) Par exemple :

```
<INSDSeq_moltype>AA</INSDSeq_moltype>
```

55. Si une séquence de nucléotides contient à la fois des fragments d'ADN et d'ARN, l'élément `INSDSeq_moltype` doit prendre la valeur "DNA". La molécule combinée d'ADN/ARN doit en outre être décrite dans le tableau de caractéristiques à l'aide de la clé de caractérisation "source", du qualificateur obligatoire "organism", qui prend la valeur "synthetic construct", et du qualificateur obligatoire "mol_type", qui prend la valeur "other DNA". Chaque fragment d'ADN et d'ARN de la molécule combinée d'ADN/ARN doit en outre être décrit par la clé de caractérisation "misc_feature" et par le qualificateur "note", ce dernier indiquant s'il s'agit d'un fragment d'ADN ou d'ARN.

56. L'exemple ci-après illustre la description d'une séquence de nucléotides contenant à la fois des fragments d'ADN et d'ARN comme le prévoit le paragraphe 55 ci-dessus :

```
<INSDSeq>
   <INSDSeq_length>120</INSDSeq_length>
   <INSDSeq_moltype>DNA</INSDSeq_moltype>
   <INSDSeq_division>PAT</INSDSeq_division>
   <INSDSeq_feature-table>
       <INSDFeature>
           <INSDFeature_key>source</INSDFeature_key>
           <INSDFeature_location>1..120</INSDFeature_location>
           <INSDFeature_quals>
               <INSDQualifier>
                   <INSDQualifier_name>organism</INSDQualifier_name>
                   <INSDQualifier_value>synthetic construct</INSDQualifier_value>
               </INSDQualifier>
               <INSDQualifier>
                   <INSDQualifier_name>mol_type</INSDQualifier_name>
                   <INSDQualifier_value>other DNA</INSDQualifier_value>
               </INSDQualifier>
           </INSDFeature_quals>
       </INSDFeature>
       <INSDFeature>
           <INSDFeature_key>misc_feature</INSDFeature_key>
```

```
            <INSDFeature_location>1..60</INSDFeature_location>
            <INSDFeature_quals>
                <INSDQualifier>
                    <INSDQualifier_name>note</INSDQualifier_name>
                    <INSDQualifier_value>DNA fragment</INSDQualifier_value>
                </INSDQualifier>
            </INSDFeature_quals>
        </INSDFeature>
        <INSDFeature>
            <INSDFeature_key>misc_feature</INSDFeature_key>
            <INSDFeature_location>61..120</INSDFeature_location>
            <INSDFeature_quals>
                <INSDQualifier>
                    <INSDQualifier_name>note</INSDQualifier_name>
                    <INSDQualifier_value>RNA fragment</INSDQualifier_value>
                </INSDQualifier>
            </INSDFeature_quals>
        </INSDFeature>
    </INSDSeq_feature-table>
<INSDSeq_sequence>cgacccacgcgtccgaggaaccaaccatcacgtttgaggacttcgtgaaggaattggataatacccgt
ccctaccaaaatggcgagcgccgactcattgctcctcgtaccgtcgagcggc</INSDSeq_sequence>
</INSDSeq>
```

57. L'élément `INSDSeq_sequence` doit divulguer la séquence. ~~Les résidus de la séquence doivent être présentés de manière contiguë à l'aide des~~Seuls les symboles adéquats indiqués dans l'annexe I (voir section 1, tableau 1 et section 3, tableau 3) doivent figurer dans la séquence. La séquence ne doit pas ~~comprendre~~contenir de chiffres, de signes de ponctuation ou d'espaces blancs.

58. Une séquence délibérément omise doit ~~être présentée~~figurer dans le listage des séquences et être représentée de la manière suivante :

(a) l'élément `SequenceData` et son attribut `sequenceIDNumber`, qui prend pour valeur le numéro d'identification de la séquence omise;

(b) les éléments `INSDSeq_length`, `INSDSeq_moltype`, `INSDSeq_division`, qui sont présents mais ne contiennent aucune valeur;

(c) l'élément `INSDSeq_feature-table` ne doit pas être indiqué; et

(d) l'élément `INSDSeq_sequence`, qui prend la valeur "000".

59. L'exemple ci-après illustre la manière dont une séquence délibérément omise doit être ~~présentée~~représentée pour être conforme au paragraphe 58 ci-dessus :

```
<SequenceData sequenceIDNumber="3">
   <INSDSeq>
       <INSDSeq_length/>
       <INSDSeq_moltype/>
       <INSDSeq_division/>
       <INSDSeq_sequence>000</INSDSeq_sequence>
   </INSDSeq>
</SequenceData>
```

Tableau de caractéristiques

60. Le tableau de caractéristiques contient des informations sur l'emplacement et les rôles des différentes régions d'une séquence particulière. Il est obligatoire de fournir un tableau de caractéristiques pour chaque séquence, sauf s'il s'agit d'une séquence délibérément omise; dans ce cas, ce tableau ne doit pas apparaître. Le tableau de caractéristiques figure dans l'élément `INSDSeq_feature-table`, qui se compose d'un ou plusieurs éléments `INSDFeature`.

61. Chaque élément `INSDFeature` contient la description d'une caractéristique et se compose d'éléments subordonnés de la manière suivante :

Élément	Description	Obligatoire/Facultatif
`INSDFeature_key`	Mot ou abréviation indiquant une caractéristique	Obligatoire
`INSDFeature_location`	Région de la séquence ~~présentée~~ correspondant à la caractéristique	Obligatoire
`INSDFeature_quals`	Qualificateur contenant des informations complémentaires sur une caractéristique	Obligatoire si la clé de caractérisation nécessite un ou plusieurs qualificateurs, p. ex. "source". Facultatif dans les autres cas.

Clés de caractérisation

62. L'annexe I contient une liste complète des clés de caractérisation qui peuvent être employées dans le cadre de la présente norme, ainsi qu'une liste complète des qualificateurs associés à ces clés, dans laquelle il est précisé si les qualificateurs sont obligatoires ou facultatifs. La section 5 de l'annexe I contient la liste complète des clés de caractérisation destinées aux séquences de nucléotides, et la section 7 contient la liste complète des clés de caractérisation destinées aux séquences d'acides aminés.

Clés de caractérisation obligatoires

63. La clé de caractérisation "source" est obligatoire pour toutes les séquences de nucléotides et la clé de caractérisation "SOURCE" est obligatoire pour toutes les séquences d'acides aminés, sauf s'il s'agit d'une séquence délibérément omise. Chaque séquence doit comporter une clé "source" ou "SOURCE" unique couvrant la séquence tout entière. Si une séquence provient de plusieurs sources, celles-ci doivent en outre être décrites dans le tableau de caractéristiques à l'aide de la clé de caractérisation "misc_feature" et du qualificateur "note" pour les séquences de nucléotides, et de la clé de caractérisation "REGION" et du qualificateur "NOTE" pour les séquences d'acides aminés.

~~64. Certaines clés de caractérisation nécessitent l'emploi d'une clé de caractérisation supplémentaire, appelée "Parent Key". Ainsi, la clé de caractérisation "C_region" doit être accompagnée de la clé "CDS" (voir annexe I, section 5).~~

Emplacement de la caractéristique

64. L'élément obligatoire `INSDFeature_location` doit contenir au moins un descripteur d'emplacement qui définit un site ou une région correspondant à une caractéristique de la séquence dans l'élément `INSDSeq_sequence`. Il peut contenir plusieurs descripteurs d'emplacement (voir les paragraphes ~~68~~67 à ~~71~~70).

65. Le descripteur d'emplacement peut être un numéro de résidu unique, un site entre deux numéros de résidus adjacents, une région délimitant une série de numéros de résidus contigus, ou un site ou une région qui s'étend au-delà du résidu ou de la série de résidus particuliers. On peut employer plusieurs descripteurs d'emplacement en conjonction avec un opérateur d'emplacement quand une caractéristique correspond à des sites ou des régions discontinus de la séquence (voir les paragraphes ~~68~~67 à ~~71~~70). Le descripteur d'emplacement ne doit pas comporter de numéros de résidus en dehors de la série indiquée pour la séquence dans l'élément `INSDSeq_sequence`.

66. La syntaxe de chaque type de descripteurs d'emplacement est indiquée dans le tableau ci-dessous, où x et y sont des numéros de résidus indiqués en nombres entiers non négatifs et inférieurs ou égaux à la longueur de la séquence dans l'élément `INSDSeq_sequence`, et où x est inférieur à y.

Type de descripteurs d'emplacement	Syntaxe	Description
Numéro de résidu unique	x	Désigne un résidu unique dans la séquence ~~présentée~~.
Numéros de résidus délimitant un ensemble dans la séquence	`x..y`	Désigne une série continue de résidus délimitée par un résidu de début et un résidu de fin, ces deux résidus étant inclus dans la série.

Résidus situés avant le premier ou après le dernier numéro de résidu indiqué	`<x`
	`>x`
	`<x..y`
	`x..>y`
		Désigne une région qui comprend un résidu ou une série de résidus indiqués et qui s'étend au-delà d'un résidu indiqué. Les symboles "<" et ">" peuvent être employés à l'égard d'un résidu unique ou des numéros du résidu de début et de fin d'une série de résidus pour signaler qu'une caractéristique s'étend au-delà du numéro de résidu indiqué.

Site s'étendant entre deux numéros de résidus adjacents	`x^y`	Désigne un site entre deux résidus adjacents, par exemple le site d'un clivage endonucléolytique. Les numéros de position des résidus adjacents sont séparés par un caret (^). Les formats autorisés pour ce descripteur sont x^x+1 (par exemple 55^56), ou pour les nucléotides circulaires, x^1, où "x" est la longueur totale de la molécule, c'est-à-dire 1000^1 pour une molécule circulaire de longueur 1000.

67. Un opérateur d'emplacement est le préfixe d'un descripteur ou d'une combinaison de descripteurs d'emplacement correspondant à une caractéristique unique mais discontinue. Il indique l'emplacement correspondant à la caractéristique dans la séquence présentée, ou comment la caractéristique est construite. Une liste d'opérateurs d'emplacement est fournie ci-après avec leur définition.

(a) Opérateur d'emplacement pour des nucléotides et des acides aminés :

Syntaxe de l'emplacement	Description de l'emplacement
`join(location,location, ... location)`	Les emplacements indiqués sont joints (placés bout à bout) pour former une seule séquence contiguë.
`order(location,location, ... location)`	Les éléments se trouvent dans l'ordre indiqué mais aucune information ne permet de déterminer s'il est raisonnable de les joindre.

(b) Opérateur d'emplacement réservé aux nucléotides :

Syntaxe de l'emplacement	Description de l'emplacement
`complement(location)`	Indique que la caractéristique se trouve sur le brin complémentaire à la série de la séquence indiquée par le descripteur d'emplacement, lorsque la séquence est lue dans le sens 5'-3', ou dans le sens qui reproduit le sens 5'-3'.

68. Les opérateurs d'emplacement assurant un rôle de jonction ou d'ordonnancement nécessitent au moins deux descripteurs d'emplacement séparés par des virgules. Les descripteurs d'emplacement concernant des sites situés entre deux résidus adjacents, c'est-à-dire x^y, ne ~~peuvent~~doivent pas être employés dans un emplacement de jonction ou d'ordonnancement. L'emploi de l'opérateur d'emplacement de jonction implique que les résidus désignés par les descripteurs d'emplacement sont physiquement mis en contact par des processus biologiques (par exemple, les exons qui contribuent à la caractéristique d'une région jouant un rôle de codage).

69. L'opérateur d'emplacement "complement" ne peut être employé que pour des nucléotides. Il peut être employé en combinaison soit avec "join" soit avec "order" dans le même emplacement. Les combinaisons de "join" et "order" ne sont pas autorisées dans un même emplacement.

70. Les exemples ci-après illustrent des emplacements de caractéristiques au sens des paragraphes ~~65~~64 à ~~70~~69 ci-dessus :

(a) emplacements pour des nucléotides et des acides aminés :

Exemple d'emplacement	Description
`467`	Désigne le résidu 467 de la séquence.
`123^124`	Désigne un site entre les résidus 123 et 124.
`340..565`	Désigne une série continue de résidus dont les bornes sont le 340 et le 565, ces bornes étant incluses dans la série.
`<1`	Désigne un emplacement de caractéristique situé avant le premier résidu.
`<345..500`	Indique que le point exact de la borne inférieure d'une caractéristique est inconnu. L'emplacement commence à un résidu situé quelque part avant le 345 et continue jusqu'au résidu 500 inclus.
`<1..888`	Indique que la caractéristique commence avant le premier résidu de la séquence et continue jusqu'au résidu 888 inclus.
`1..>888`	Indique que la caractéristique commence au premier résidu de la séquence et continue au-delà du résidu 888.
`join(12..78,134..202)`	Indique que les régions 12 à 78 et 134 à 202 devraient être jointes pour constituer une séquence contiguë.

(b) emplacements réservés aux nucléotides :

Exemple d'emplacement	Description
`complement(34..126)`	Commence ~~à la base~~au nucléotide complémentaire ~~à la base~~au nucléotide 126 et finit ~~à la base~~au nucléotide complémentaire ~~à la base~~au nucléotide 34 (la caractéristique est située sur le brin complémentaire au brin présenté).
`complement(join(2691..4571, 4918..5163))`	Joint les ~~bases~~nucléotides 2691 à 4571 et 4918 à 5163, puis complète les segments joints (la caractéristique est située sur le brin complémentaire au brin présenté).
`join(complement(4918..5163), complement(2691..4571))`	Complète les régions 4918 à 5163 et 2691 à 4571, puis joint les segments complétés (la caractéristique est située sur le brin complémentaire au brin présenté).

71. Dans une instance XML d'un listage des séquences, les caractères "<" et ">" d'un descripteur d'emplacement doivent être remplacés par les entités prédéfinies adéquates (voir le paragraphe 41), par exemple :

```
Feature location "<1" :
<INSDFeature_location>&lt;1</INSDFeature_location>

Feature location "1..>888" :
<INSDFeature_location>1..&gt;888</INSDFeature_location>
```

Qualificateurs de caractéristiques

72. Les qualificateurs permettent de fournir des informations sur les caractéristiques pour compléter les informations figurant dans la clé de caractérisation et l'emplacement de la caractéristique. La valeur des qualificateurs peut prendre trois types de formats selon le type d'informations fournies :

(a) du texte libre (voir les paragraphes ~~86~~85 et ~~87~~86);

(b) un vocabulaire contrôlé ou l'énumération de valeurs (p. ex. un nombre ou une date); et

(c) des séquences.

73. La section 6 de l'annexe I contient une liste complète des qualificateurs et la définition du format de leurs valeurs, le cas échéant, pour la clé de caractérisation de chaque nucléotide, et la section 8 contient la liste complète des qualificateurs pour la clé de caractérisation de chaque acide aminé.

74. Toute séquence prévue au paragraphe ~~6~~7 qui est indiquée à titre de valeur d'un qualificateur doit ~~être présentée~~figurer de manière distincte dans le listage des séquences et doit disposer de~~avec~~ son propre numéro d'identification de séquence.

Qualificateurs de caractéristiques obligatoires

75. Une clé de caractérisation obligatoire, en l'occurrence "source" pour les séquences de nucléotides et "SOURCE" pour les séquences d'acides aminés, doit être accompagnée de deux qualificateurs obligatoires, "organism" et "mol_type" pour les séquences de nucléotides et "ORGANISM" et "MOL_TYPE" pour les séquences d'acides aminés. Certaines clés de caractérisation facultatives nécessitent aussi des qualificateurs obligatoires.

Éléments des qualificateurs

76. L'élément `INSDFeature_quals` se compose d'un ou plusieurs éléments `INSDQualifier`. Chaque élément `INSDQualifier` représente un seul qualificateur et se compose de deux éléments subordonnés, de la manière suivante :

Élément	Description	Obligatoire/Facultatif
`INSDQualifier_name`	Nom du qualificateur (voir annexe I, sections 6 et 8)	Obligatoire
`INSDQualifier_value`	Valeur du qualificateur, le cas échéant, au format indiqué (voir annexe I, sections 6 et 8)	Obligatoire si indiqué (voir annexe I, sections 6 et 8)

77. Le qualificateur d'organisme, c'est-à-dire l'élément "organism" pour les séquences de nucléotides (voir annexe I, section 6) et "ORGANISM" pour les séquences d'acides aminés (voir annexe I, section 8) doit divulguer la source, c'est-à-dire l'organisme ou l'origine unique de la séquence~~ qui est présentée~~. Les indications d'organisme doivent être choisies parmi les éléments d'une taxonomie.

78. Si la séquence existe à l'état naturel et qu'il existe une désignation de genre et d'espèce en latin pour l'organisme source, le qualificateur doit prendre cette désignation pour valeur. Il est possible d'indiquer le nom commun anglais le plus courant à l'aide du qualificateur "note" pour les séquences de nucléotides et "NOTE" pour les séquences d'acides aminés, mais ce nom ne doit pas être employé comme valeur du qualificateur d'organisme.

79. Les exemples suivants illustrent la source ~~de séquences présentées~~d'une séquence conformément aux paragraphes ~~78~~77 et ~~79~~78 ci-dessus :

Exemple 1 : Source d'une séquence de nucléotides.

```
<INSDSeq_feature-table>
   <INSDFeature>
       <INSDFeature_key>source</INSDFeature_key>
       <INSDFeature_location>1..5164</INSDFeature_location>
       <INSDFeature_quals>
           <INSDQualifier>
               <INSDQualifier_name>organism</INSDQualifier_name>
               <INSDQualifier_value>Solanum lycopersicum</INSDQualifier_value>
           </INSDQualifier>
           <INSDQualifier>
               <INSDQualifier_name>note</INSDQualifier_name>
               <INSDQualifier_value>common name: tomato</INSDQualifier_value>
           </INSDQualifier>
           <INSDQualifier>
               <INSDQualifier_name>mol_type</INSDQualifier_name>
               <INSDQualifier_value>genomic DNA</INSDQualifier_value>
           </INSDQualifier>
       </INSDFeature_quals>
   </INSDFeature>
</INSDSeq_feature-table>
```

Exemple 2 : Source d'une séquence ~~de protéines~~d'acides aminés

```
<INSDSeq_feature-table>
   <INSDFeature>
       <INSDFeature_key>SOURCE</INSDFeature_key>
       <INSDFeature_location>1..174</INSDFeature_location>
       <INSDFeature_quals>
           <INSDQualifier>
               <INSDQualifier_name>ORGANISM</INSDQualifier_name>
               <INSDQualifier_value>Homo sapiens</INSDQualifier_value>
           </INSDQualifier>
           <INSDQualifier>
               <INSDQualifier_name>MOL_TYPE</INSDQualifier_name>
               <INSDQualifier_value>protein</INSDQualifier_value>
           </INSDQualifier>
       </INSDFeature_quals>
   </INSDFeature>
</INSDSeq_feature-table>
```

80. Si la séquence existe à l'état naturel et qu'il existe une désignation de genre en latin pour l'organisme source, mais que l'espèce n'est pas indiquée ou connue, le qualificateur d'organisme doit prendre pour valeur le genre en latin suivi de "sp.", par exemple :

```
<INSDQualifier_name>organism</INSDQualifier_name>
<INSDQualifier_value>Bacillus sp.</INSDQualifier_value>
```

81. Si la ~~source de la~~ séquence existe à l'état naturel, mais que la désignation latine de genre et d'espèce de l'organisme est inconnue, le qualificateur d'organisme doit prendre pour valeur l'indication "unidentified" et être accompagné de toute information taxonomique connue dans le qualificateur "note" pour les séquences de nucléotides et "NOTE" pour les séquences d'acides aminés, par exemple :

```
<INSDQualifier_name>organism</INSDQualifier_name>
<INSDQualifier_value>unidentified</INSDQualifier_value>
<INSDQualifier_name>note</INSDQualifier_name>
<INSDQualifier_value>bacterium B8</INSDQualifier_value>
```

82. Si la séquence existe à l'état naturel et que l'organisme source n'a pas de désignation de genre et d'espèce en latin (comme par exemple un virus), le qualificateur d'organisme peut prendre pour valeur un autre nom scientifique acceptable (ex : "adénovirus canin type 2"), par exemple :

```
<INSDQualifier_name>organism</INSDQualifier_name>
<INSDQualifier_value>Canine adenovirus type 2</INSDQualifier_value>
```

83. Si la séquence n'existe pas à l'état naturel, le qualificateur d'organisme doit prendre pour valeur "synthetic construct". On peut ajouter d'autres informations sur la manière dont la séquence a été créée à l'aide du qualificateur "note" pour les séquences de nucléotides et "NOTE" pour les séquences d'acides aminés, par exemple :

```
<INSDSeq_feature-table>
   <INSDFeature>
       <INSDFeature_key>SOURCE</INSDFeature_key>
       <INSDFeature_location>1..40</INSDFeature_location>
       <INSDFeature_quals>
           <INSDQualifier>
               <INSDQualifier_name>ORGANISM</INSDQualifier_name>
               <INSDQualifier_value>synthetic construct</INSDQualifier_value>
           </INSDQualifier>
           <INSDQualifier>
               <INSDQualifier_name>MOL_TYPE</INSDQualifier_name>
               <INSDQualifier_value>protein</INSDQualifier_value>
           </INSDQualifier>
           <INSDQualifier>
               <INSDQualifier_name>NOTE</INSDQualifier_name>
               <INSDQualifier_value>synthetic peptide used as assay for
               antibodies</INSDQualifier_value>
           </INSDQualifier>
       </INSDFeature_quals>
   </INSDFeature>
</INSDSeq_feature-table>
```

84. Le qualificateur “mol_type” pour les séquences de nucléotides (voir annexe I, section 6) et “MOL_TYPE” pour les séquences d’acides aminés (voir annexe I, section 8) doit divulguer le type de molécule représenté dans la séquence. Ces qualificateurs sont distincts de l’élément `INSDSeq_moltype` examiné au paragraphe 54 :

(a) pour des séquences de nucléotides, la valeur du qualificateur “mol_type” doit être l’un des éléments suivants : “genomic DNA”, “genomic RNA”, “mRNA”, “tRNA”, “rRNA”, “other RNA”, “other DNA”, “transcribed RNA”, “viral cRNA”, “unassigned DNA” ou “unassigned RNA”. Si la séquence n’existe pas à l’état naturel, c’est-à-dire si la valeur du qualificateur “organism” est “synthetic construct”, la valeur du qualificateur “mol_type” doit être soit “other RNA” soit “other DNA”;

(b) pour des séquences d’acides aminés, la valeur du qualificateur “MOL_TYPE” est “protein”.

Texte libre

85. Le texte libre est un format de valeur autorisé pour certains qualificateurs (comme indiqué à l’annexe I). Il s’agit d’un texte descriptif qui se présente sous forme de segments de phrases, de préférence en anglais.

86. L’emploi du texte libre doit être limité à un petit nombre de termes brefs indispensables à la compréhension d’une caractéristique de la séquence. Pour chaque qualificateur, le texte libre ne peut compter plus de 1000 caractères.

Séquences de codage

87. La clé de caractérisation “CDS” peut servir à désigner des séquences de codage, c’est-à-dire des séquences de nucléotides correspondant à la séquence d’acides aminés dans une protéine et au codon d’arrêt. L’élément `INSDFeature_location` doit indiquer l’emplacement de la caractéristique “CDS”, y compris le codon d’arrêt.

88. Les qualificateurs “transl_table” et “translation” peuvent être employés en association avec la clé de caractérisation “CDS” (voir annexe I). Si le qualificateur “transl_table” n’est pas employé, on présume que c’est le tableau de codes normalisés qui est appliqué (voir annexe I, section 9, tableau 5).

89. Le qualificateur “transl_except” doit être employé en association avec la clé de caractérisation “CDS” et le qualificateur “translation” doit être employé pour désigner un codon codant pour la pyrrolysine ou la sélénocystéine.

90. Toute séquence ~~protéinique~~d’acides aminés codée selon la séquence de codage et divulguée dans un qualificateur de type “translation” visé par le paragraphe ~~6~~7 doit figurer dans le listage des séquences et doit disposer de~~avoir~~ son propre numéro d’identification de séquence ~~et doit être présentée dans le listage des séquences~~. Le numéro d’identification de séquence attribué à la séquence ~~protéinique~~d’acides aminés doit figurer dans la valeur du qualificateur “protein_id” associé à la clé de caractérisation “CDS”. Le qualificateur “ORGANISM” associé à la clé de caractérisation “SOURCE” de la séquence ~~protéinique~~d’acides aminés doit être identique à celui de sa séquence de codage, par exemple :

```
<INSDSeq_feature-table>
   <INSDFeature>
       <INSDFeature_key>CDS</INSDFeature_key>
       <INSDFeature_location>1..507</INSDFeature_location>
       <INSDFeature_quals>
           <INSDQualifier>
               <INSDQualifier_name>transl_table</INSDQualifier_name>
               <INSDQualifier_value>11</INSDQualifier_value>
           </INSDQualifier>
           <INSDQualifier>
               <INSDQualifier_name>translation</INSDQualifier_name>
               <INSDQualifier_value>
MLVHLERTTIMFDFSSLINLPLIWGLLIAIAVLLYILMDGFDLGIGILLPFAPSDKCRDHMISSIAPFWDGNETWLVLGGGGLFAA
FPLAYSILMPAFYIPIIIMLLGLIVRGVSFEFRFKAEGKYRRLWDYAFHFGSLGAAFCQGMILGAFIHGVEVNGRNFSGGQLM
               </INSDQualifier_value>
           </INSDQualifier>
           <INSDQualifier>
                  <INSDQualifier_name>protein_id</INSDQualifier_name>
               <INSDQualifier_value>89</INSDQualifier_value>
           </INSDQualifier>
       </INSDFeature_quals>
   </INSDFeature>
</INSDSeq_feature-table>
```

Variantes

91. Toute séquence primaire et toute variante de cette séquence, chacune d’elles étant divulguée par énumération de ses résidus et visée par le paragraphe ~~6~~7, doit ~~être présentée~~figurer dans le listage des séquences ~~avec~~et doit disposer de son propre numéro d’identification de séquence.

92. Toute séquence variante, divulguée comme une séquence unique avec des résidus de variante alternatifs énumérés à une ou plusieurs positions, doit figurer dans le listage des séquences et devrait être représentée par une séquence unique, les résidus de variante alternatifs énumérés étant représentés par le symbole le plus restrictif. (voir les paragraphes 15 et 27).

93. Toute séquence ~~de~~ variante, divulguée uniquement par référence à un ou plusieurs suppressions, adjonctions ou remplacements effectués dans une séquence primaire figurant dans le listage des séquences, ~~peut être présentée~~doit figurer dans le listage des séquences. Si tel est le cas, cette séquence ~~de~~ variante :

(a) peut être ~~présentée~~représentée par annotation de la séquence primaire, si elle comporte une ou plusieurs variations à un seul emplacement ou à plusieurs emplacements distincts et que les occurrences de ces variations sont indépendantes;

(b) devrait être ~~présentée~~représentée en tant que séquence distincte ~~avec~~et devrait disposer de son propre numéro d'identification de séquence, si elle comporte des variations à plusieurs emplacements distincts et que les occurrences de ces variations sont interdépendantes; et

(c) doit être ~~présentée~~représentée en tant que séquence distincte ~~avec~~et doit disposer de son propre numéro d'identification de séquence, si elle comporte une séquence qui a été ajoutée ou remplacée et qui contient plus de 1000 résidus (voir le paragraphe ~~87~~86).

94. Le tableau ci-dessous indique le bon usage des clés de caractérisation et des qualificateurs pour des variantes d'acides nucléiques et d'acides aminés :

Type de séquence	Clé de caractérisation	Qualificateur	Usage
Acide nucléique	variation	replace or note	Mutations et polymorphismes existant à l'état naturel, p. ex. des allèles ou des polymorphismes de longueur des fragments de restriction
Acide nucléique	misc_difference	replace or note	La variabilité a été créée artificiellement, p. ex. par une manipulation génétique ou une synthèse chimique
Acide aminé	VAR_SEQ	NOTE	La variante a été produite par un épissage alternatif, l'usage de promoteurs alternatifs, une initiation alternative et un déphasage ribosomique
Acide aminé	VARIANT	NOTE	Tout type de variante pour laquelle VAR_SEQ n'est pas applicable

95. L'annotation d'une séquence ~~primaire~~ effectuée pour une variante particulière doit comporter une clé de caractérisation et un qualificateur, conformément au tableau ci-dessus, et indiquer l'emplacement de la caractéristique. La valeur du qualificateur "replace" doit correspondre uniquement à un nucléotide alternatif unique ou à une séquence de nucléotides alternatifs uniques représenté à l'aide des symboles indiqués dans la section 1 du tableau 1. Un listage des résidus de variante alternatifs peut être indiqué dans le qualificateur "note" ou "NOTE". Il convient en particulier d'indiquer un listage d'acides aminés alternatifs dans le qualificateur "NOTE" si "X" est employé dans une séquence mais représente un sous-groupe de "any one of 'A', 'R', 'N', 'D', 'C', 'Q', 'E', 'G', 'H', 'I', 'L', 'K', 'M', 'F', 'P', 'O', 'S', 'U', 'T', 'W', 'Y', ou 'V'" Toute suppression doit être représentée par une valeur de qualificateur vide pour le qualificateur "replace" ou une indication dans le qualificateur "note" ou "NOTE" selon laquelle le résidu peut être supprimé. Tout résidu ajouté ou remplacé doit être indiqué dans le qualificateur "replace", "note" ou "NOTE". La valeur du qualificateur "replace", "note" ou "NOTE" est un texte libre qui ne doit pas dépasser 1000 caractères, conformément au paragraphe ~~87~~86. Pour les séquences visées par le paragraphe ~~6~~7 qui sont présentées à titre d'adjonction ou de remplacement de la valeur d'un qualificateur, se reporter au paragraphe ~~97~~98. ~~La valeur du qualificateur peut comporter un listage des résidus alternatifs pouvant être ajoutés ou remplacés.~~

96. Les symboles indiqués dans l'annexe I (voir respectivement les sections 1 à 4, tableaux 1 à 4) peuvent être employés pour représenter des résidus de variantes, selon les besoins. ~~Si~~Pour le qualificateur "note" ou "NOTE", si un résidu de variante est un résidu modifié qui ne figure pas dans les tableaux 2 ou 4 de l'annexe I, le nom complet non abrégé du résidu modifié doit être indiqué dans la valeur du qualificateur. Les résidus modifiés doivent être accompagnés d'une description supplémentaire dans le tableau de caractéristiques comme prévu aux paragraphes 17 ou 30.

97. Les exemples ci-après illustrent la manière de ~~présenter~~représenter des variantes pour qu'elles soient conformes aux paragraphes ~~92~~93 à ~~95~~96 ci-dessus :

Exemple 1 : Clé de caractérisation “~~variation~~misc_difference” pour ~~un remplacement dans une séquence de nucléotides~~ des nucléotides de variante alternatifs énumérés. Le “n” à la position 53 de la séquence peut être un nucléotide alternatif parmi cinq nucléotides alternatifs.

~~Une cytosine remplace le nucléotide défini à la position 413 de la séquence.~~

```
<INSDFeature>
    <INSDFeature_key>variationmisc_difference</INSDFeature_key>
    <INSDFeature_location>41353</INSDFeature_location>
    <INSDFeature_quals>
        <INSDQualifier>
            <INSDQualifier_name>replacenote</INSDQualifier_name>
            <INSDQualifier_value>cw, cmnm5s2u, mam5u, mcm5s2u, or p
</INSDQualifier_value>
        </INSDQualifier>
    </INSDFeature_quals>
</INSDFeature>
<INSDFeature>
    <INSDFeature_key>modified_base</INSDFeature_key>
    <INSDFeature_location>53</INSDFeature_location>
    <INSDFeature_quals>
        <INSDQualifier>
            <INSDQualifier_name>mod_base</INSDQualifier_name>
            <INSDQualifier_value>OTHER</INSDQualifier_value>
            <INSDQualifier_name>note</INSDQualifier_name>
            <INSDQualifier_value>cmnm5s2u, mam5u, mcm5s2u, or p</INSDQualifier_value>
        </INSDQualifier>
    </INSDFeature_quals>
</INSDFeature>
```

Exemple 2 : Clé de caractérisation “misc_difference” pour une suppression dans une séquence de nucléotides.

Le nucléotide à la position 413 de la séquence est supprimé.

```
<INSDFeature>
   <INSDFeature_key>misc_difference</INSDFeature_key>
   <INSDFeature_location>413</INSDFeature_location>
   <INSDFeature_quals>
       <INSDQualifier>
           <INSDQualifier_name>replace</INSDQualifier_name>
           <INSDQualifier_value></INSDQualifier_value>
       </INSDQualifier>
   </INSDFeature_quals>
</INSDFeature>
```

Exemple 3 : Clé de caractérisation “misc_difference” pour une adjonction dans une séquence de nucléotides.

La séquence “atgccaaatat” est ajoutée entre les positions 100 et 101 de la séquence primaire.

```
<INSDFeature>
   <INSDFeature_key>misc_difference</INSDFeature_key>
   <INSDFeature_location>100^101</INSDFeature_location>
   <INSDFeature_quals>
       <INSDQualifier>
           <INSDQualifier_name>replace</INSDQualifier_name>
           <INSDQualifier_value>atgccaaatat</INSDQualifier_value>
       </INSDQualifier>
   </INSDFeature_quals>
</INSDFeature>
```

Exemple 4 : Clé de caractérisation “~~VARIANT~~variation” pour un remplacement dans une séquence ~~d'acides aminés~~nucléotidique.

~~L'acide aminé indiqué à la position 100 de la séquence peut être remplacé par~~Une cytosine remplace le nucléotide indiqué à la position 413 de la séquence.

```
      <INSDFeature>
          <INSDFeature_key>variation</INSDFeature_key>
          <INSDFeature_location>413</INSDFeature_location>
          <INSDFeature_quals>
              <INSDQualifier>
                  <INSDQualifier_name>replace</INSDQualifier_name>
                  <INSDQualifier_value>c</INSDQualifier_value>
              </INSDQualifier>
          </INSDFeature_quals>
      </INSDFeature>
```

Exemple 5 : Clé de caractérisation “VARIANT” pour un remplacement dans une séquence d'acides aminés. L'acide aminé indiqué à la position 100 de la séquence peut être remplacé par I, A, F, Y, alle, MeIle, ou Nle.

```
<INSDFeature>
    <INSDFeature_key>VARIANT</INSDFeature_key>
    <INSDFeature_location>100</INSDFeature_location>
    <INSDFeature_quals>
        <INSDQualifier>
            <INSDQualifier_name>NOTE</INSDQualifier_name>
            <INSDQualifier_value>I, A, F, Y, aIle, MeIle, or Nle
               </INSDQualifier_value>
        </INSDQualifier>
    </INSDFeature_quals>
</INSDFeature>
<INSDFeature>
    <INSDFeature_key>MOD_RES</INSDFeature_key>
    <INSDFeature_location>100</INSDFeature_location>
    <INSDFeature_quals>
        <INSDQualifier>
            <INSDQualifier_name>NOTE</INSDQualifier_name>
            <INSDQualifier_value>aIle, MeIle, or Nle</INSDQualifier_value>
        </INSDQualifier>
    </INSDFeature_quals>
</INSDFeature>
```

Exemple 6 : Clé de caractérisation “VARIANT” pour un remplacement dans une séquence d'acides aminés. L'acide aminé indiqué à la position 100 de la séquence peut être remplacé par ~~Exemple 5 : Clé de caractérisation “VARIANT” pour un remplacement dans une séquence d'acides aminés.~~

~~L'acide aminé indiqué à la position 100 de la séquence peut être remplacé par~~ tout acide aminé sauf Lys, Arg ou His.

```
<INSDFeature>
    <INSDFeature_key>VARIANT</INSDFeature_key>
    <INSDFeature_location>100</INSDFeature_location>
    <INSDFeature_quals>
        <INSDQualifier>
            <INSDQualifier_name>NOTE</INSDQualifier_name>
            <INSDQualifier_value>not K, R, or H</INSDQualifier_value>
        </INSDQualifier>
    </INSDFeature_quals>
</INSDFeature>
```

98. Toute séquence visée par le paragraphe ~~6~~7 qui est présentée à titre d'adjonction ou de remplacement dans la valeur d'un qualificateur pour une annotation de séquence primaire doit aussi ~~être présentée~~figurer dans le listage des séquences ~~avec~~et disposer de son propre numéro d'identification de séquence.

[L'annexe I à la norme ST.26 suit]

ST.26 - ANNEX I

CONTROLLED VOCABULARY

Version ~~1.0~~1.1

Proposal presented by the SEQL Task Force for consideration and approval at the CWS/5
~~Adopted by the Committee on WIPO Standards (CWS)~~
~~at its reconvened fourth session on March 24, 2016~~

Final Draft

TABLE OF CONTENTS

SECTION 1: LIST OF NUCLEOTIDES

The nucleotide base codes to be used in sequence listings are presented in Table 1. The symbol “t” will be construed as thymine in DNA and uracil in RNA when it is used with no further description. Where an ambiguity symbol (representing two or more bases in the alternative) is appropriate, the most restrictive symbol should be used. For example, if a base in a given position could be “a or g,” then “r” should be used, rather than “n”. The symbol “n” will be construed as “a or c or g or t/u” when it is used with no further description.

Table 1: List of nucleotides

Symbol	Nucleotide
a	adenine
c	cytosine
g	guanine
t	thymine in DNA/uracil in RNA (t/u)
m	a or c
r	a or g
w	a or t/u
s	c or g
y	c or t/u
k	g or t/u
v	a or c or g; not t/u
h	a or c or t/u; not g
d	a or g or t/u; not c
b	c or g or t/u; not a
n	a or c or g or t/u; “unknown” or “other”

SECTION 2: LIST OF MODIFIED NUCLEOTIDES

The abbreviations listed in Table 2 are the only permitted values for the mod_base qualifier. Where a specific modified nucleotide is not present in the table below, then the abbreviation “OTHER” must be used as its value. If the abbreviation is “OTHER,” then the complete unabbreviated name of the modified base must be provided in a note qualifier. The abbreviations provided in Table 2 must not be used in the sequence itself.

Table 2: List of modified nucleotides

Abbreviation	Modified Nucleotide
ac4c	4-acetylcytidine
chm5u	5-(carboxyhydroxylmethyl)uridine
cm	2’-O-methylcytidine
cmnm5s2u	5-carboxymethylaminomethyl-2-thiouridine
cmnm5u	5-carboxymethylaminomethyluridine
~~d~~dhu	dihydrouridine
fm	2’-O-methylpseudouridine
gal q	beta-D-~~galactosylqueosine~~galactosylqueuosine
gm	2’-O-methylguanosine
i	inosine
i6a	N6-isopentenyladenosine
m1a	1-methyladenosine
m1f	1-methylpseudouridine
m1g	1-methylguanosine
m1i	1-methylinosine
m22g	2,2-dimethylguanosine
m2a	2-methyladenosine
m2g	2-methylguanosine
m3c	3-methylcytidine
m4c	N4-methylcytosine
m5c	5-methylcytidine
m6a	N6-methyladenosine

Abbreviation	Modified Nucleotide
m7g	7-methylguanosine
mam5u	5-methylaminomethyluridine
mam5s2u	5-~~methoxyaminomethyl~~methylaminomethyl-2-thiouridine
man q	beta-D-~~mannosylqueosine~~mannosylqueuosine
mcm5s2u	5-methoxycarbonylmethyl-2-thiouridine
mcm5u	5-methoxycarbonylmethyluridine
mo5u	5-methoxyuridine
ms2i6a	2-methylthio-N6-isopentenyladenosine
ms2t6a	N-((9-beta-D-ribofuranosyl-2-~~methyltiopurine~~methylthiopurine-6-
mt6a	N-((9-beta-D-ribofuranosylpurine-6-yl)N-methyl-carbamoyl)threonine
mv	uridine-5-~~oxyacetic~~oxoacetic acid-methylester
o5u	uridine-5-oxyacetic acid (v)
osyw	wybutoxosine
p	pseudouridine
q	~~queosine~~queuosine
s2c	2-thiocytidine
s2t	5-methyl-2-thiouridine
s2u	2-thiouridine
s4u	4-thiouridine
m5u	5-methyluridine
t6a	N-((9-beta-D-ribofuranosylpurine-6-yl)carbamoyl)threonine
tm	2'-O-methyl-5-methyluridine
um	2'-O-methyluridine
yw	wybutosine
x	3-(3-amino-3-carboxypropyl)uridine, (acp3)u
OTHER	(requires note qualifier)

SECTION 3: LIST OF AMINO ACIDS

The amino acid codes to be used in sequence ~~listings~~ are presented in Table 3. Where an ambiguity symbol (representing two or more amino acids in the alternative) is appropriate, the most restrictive symbol should be used. For example, if an amino acid in a given position could be aspartic acid or asparagine, the symbol "B" should be used, rather than "X". The symbol "X" will be construed as any one of "A", "R", "N", "D", "C", "Q", "E", "G", "H", "I", "L", "K", "M", "F", "P", "O", "S", "U", "T", "W", "Y", or "V", when it is used with no further description.

Table 3: List of amino acids

Symbol	Amino acid
A	Alanine
R	Arginine
N	Asparagine
D	Aspartic acid (Aspartate)
C	Cysteine
Q	Glutamine
E	Glutamic acid (Glutamate)
G	Glycine
H	Histidine
I	Isoleucine
L	Leucine
K	Lysine
M	Methionine
F	Phenylalanine
P	Proline
O	Pyrrolysine
S	Serine
U	Selenocysteine
T	Threonine
W	Tryptophan
Y	Tyrosine
V	Valine
B	Aspartic acid or Asparagine
Z	Glutamine or Glutamic acid
J	Leucine or Isoleucine
X	~~unknown or other~~A or R or N or D or C or Q or E or G or H or I or L or K or M or F or P or O or S or U or T or W or Y or V; "unknown" or "other"

SECTION 4: LIST OF MODIFIED AND UNUSUAL AMINO ACIDS

Table 4 lists the only permitted abbreviations for a modified or unusual amino acid in the mandatory qualifier "NOTE" for feature keys "MOD_RES" or "SITE". The value for the qualifier "NOTE" must be either an abbreviation from this table, where appropriate, or the complete, unabbreviated name of the modified amino acid. The abbreviations (or full names) provided in this table must not be used in the sequence itself.

Table 4: List of modified and unusual amino acids

Abbreviation	Modified or Unusual Amino acid
Aad	2-Aminoadipic acid
bAad	3-Aminoadipic acid
bAla	beta-Alanine, beta-Aminoproprionic acid
Abu	2-Aminobutyric acid
4Abu	4-Aminobutyric acid, piperidinic acid
Acp	6-Aminocaproic acid
Ahe	2-Aminoheptanoic acid
Aib	2-Aminoisobutyric acid
bAib	3-Aminoisobutyric acid
Apm	2-Aminopimelic acid
Dbu	2,4-Diaminobutyric acid
Des	Desmosine
Dpm	2,2'-Diaminopimelic acid
Dpr	2,3-Diaminoproprionic acid
EtGly	N-Ethylglycine
EtAsn	N-Ethylasparagine
Hyl	Hydroxylysine
aHyl	allo-Hydroxylysine
3Hyp	3-Hydroxyproline
4Hyp	4-Hydroxyproline
Ide	Isodesmosine
aIle	allo-Isoleucine
MeGly	N-Methylglycine, sarcosine
MeIle	N-Methylisoleucine
MeLys	6-N-Methyllysine
MeVal	N-Methylvaline
Nva	Norvaline
Nle	Norleucine
Orn	Ornithine

SECTION 5: FEATURE KEYS FOR NUCLEIC ~~ACID~~ SEQUENCES

This ~~paragraph~~section contains the list of allowed feature keys to be used for ~~nucleic acid~~nucleotide sequences, and lists mandatory and optional qualifiers. The feature keys are listed in alphabetic order. The feature keys can be used for either DNA or RNA unless otherwise indicated under "Molecule scope". ~~Some feature keys include a 'Parent Key' designation; when a parent key is indicated in the description of a feature key, it is mandatory that the designated parent key be used~~. Certain Feature Keys may be appropriate for use with artificial sequences in addition to the specified "organism scope".

Feature key names must be used in the XML instance of the sequence listing exactly as they appear following "Feature key" in the descriptions below, except for the feature keys 3'UTR and 5'UTR. See "Comment" in the description for the 3'UTR and 5'UTR feature keys.

~~5.1. Feature Key attenuator~~

~~Definition 1) region of DNA at which regulation of termination of transcription occurs, which controls the expression of some bacterial operons;~~
~~2) sequence segment located between the promoter and the first structural gene that causes partial termination of transcription~~

~~Optional qualifiers allele~~
~~gene~~
~~gene_synonym~~
~~map~~
~~note~~
~~operon~~
~~phenotype~~

~~Organism scope prokaryotes~~

~~Molecule scope DNA~~

5.1. Feature Key C_region

Definition constant region of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains; includes one or more exons depending on the particular chain

Optional qualifiers allele
gene
gene_synonym
map
note
product
pseudo
pseudogene
standard_name

~~Parent Key CDS~~

Organism scope eukaryotes

~~5.3. Feature Key CAAT_signal~~

~~Definition CAAT box; part of a conserved sequence located about 75 bp up-stream of the start point of eukaryotic transcription units which may be involved in RNA polymerase binding; consensus=GG(C or T)CAATCT [1,2]~~

~~Optional qualifiers allele~~
~~gene~~
~~gene_synonym~~
~~map~~
~~note~~

~~Organism scope eukaryotes and eukaryotic viruses~~

~~Molecule scope DNA~~

~~References [1] Efstratiadis, A. et al. Cell 21, 653-668 (1980)~~

~~[2] Nevins, J.R. "The pathway of eukaryotic mRNA formation" Ann Rev Biochem 52, 441-466 (1983)~~

5.2.	Feature Key	CDS
	Definition	coding sequence; sequence of nucleotides that corresponds with the sequence of amino acids in a protein (location includes stop codon); feature may include amino acid conceptual translation
	Optional qualifiers	allele ~~artificial_location~~ codon_start EC_number exception function gene gene_synonym map note number operon product protein_id pseudo pseudogene ribosomal_slippage standard_name translation transl_except transl_table trans_splicing
	Comment	codon_start qualifier has valid value of 1 or 2 or 3, indicating the offset at which the first complete codon of a coding feature can be found, relative to the first base of that feature; transl_table defines the genetic code table used if other than the Standard or universal genetic code table; genetic code exceptions outside the range of the specified tables are reported in transl_except qualifier; only one of the qualifiers translation ~~and~~, pseugogene or pseudo are permitted with a CDS feature key; when the translation qualifier is used, the protein_id qualifier is mandatory if the translation product contains four or more specifically defined amino acids
5.3.	Feature Key	centromere
	Definition	region of biological interest ~~indentified~~identified as a centromere and which has been experimentally characterized
	Optional qualifiers	note standard_name
	Comment	the centromere feature describes the interval of DNA that corresponds to a region where chromatids are held and a kinetochore is formed
5.4.	Feature Key	D-loop
	Definition	displacement loop; a region within mitochondrial DNA in which a short stretch of RNA is paired with one strand of DNA, displacing the original partner DNA strand in this region; also used to describe the displacement of a region of one strand of duplex DNA by a single stranded invader in the reaction catalyzed by RecA protein
	Optional qualifiers	allele gene gene_synonym map note
	Molecule scope	DNA

5.5.	Feature Key	D_segment
	Definition	Diversity segment of immunoglobulin heavy chain, and T-cell receptor beta chain
	Optional qualifiers	allele gene gene_synonym map note product pseudo pseudogene standard_name
	Organism scope	eukaryotes~~Parent Key CDS~~
	~~Organism scope~~	~~eukaryotes~~ ~~5.8. Feature Key enhancer~~ ~~Definition a cis-acting sequence that increases the utilization of (some) eukaryotic promoters, and can function in either orientation and in any location (upstream or downstream) relative to the promoter~~
	~~Optional qualifiers~~	~~allele~~ ~~bound_moiety~~ ~~gene~~ ~~gene_synonym~~ ~~map~~ ~~note~~ ~~standard_name~~
	~~Organism scope~~	~~eukaryotes and eukaryotic viruses~~

5.6.	Feature Key	exon
	Definition	region of genome that codes for portion of spliced mRNA,rRNA and tRNA; may contain 5’UTR, all CDSs and 3’ UTR
	Optional qualifiers	allele EC_number function gene gene_synonym map note number product pseudo pseudogene standard_name trans_splicing
~~5.10.~~	~~Feature Key~~	~~GC_signal~~
	~~Definition~~	~~GC box; a conserved GC-rich region located upstream of the start point of eukaryotic transcription units which may occur in multiple copies or in either orientation; consensus=GGGCGG~~
	~~Optional qualifiers~~	~~allele~~ ~~gene~~ ~~gene_synonym~~ ~~map~~ ~~note~~
	~~Organism scope~~	~~eukaryotes and eukaryotic viruses~~

5.7.	Feature Key	gene
	Definition	region of biological interest identified as a gene and for which a name has been assigned
	Optional qualifiers	allele function gene gene_synonym map note operon product pseudo pseudogene phenotype standard_name trans_splicing
	Comment	the gene feature describes the interval of DNA that corresponds to a genetic trait or phenotype; the feature is, by definition, not strictly bound to its positions at the ends; it is meant to represent a region where the gene is located.

5.8.	Feature Key	iDNA
	Definition	intervening DNA; DNA which is eliminated through any of several kinds of recombination
	Optional qualifiers	allele function gene gene_synonym map note number standard_name
	Molecule scope	DNA
	Comment	e.g., in the somatic processing of immunoglobulin genes.

5.9.	Feature Key	intron
	Definition	a segment of DNA that is transcribed, but removed from within the transcript by splicing together the sequences (exons) on either side of it
	Optional qualifiers	allele function gene gene_synonym map note number pseudo pseudogene standard_name trans_splicing

5.10.	Feature Key	J_segment
	Definition	joining segment of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains
	Optional qualifiers	allele gene gene_synonym map note product

		pseudo pseudogene standard_name
	Organism scope	eukaryotes~~Parent Key CDS~~
	~~Organism scope~~	~~eukaryotes~~
~~5.15.~~	~~Feature Key~~	~~LTR~~
	~~Definition~~	~~long terminal repeat, a sequence directly repeated at both ends of a defined sequence, of the sort typically found in retroviruses~~
	~~Optional qualifiers~~	~~allele~~ ~~function~~ ~~gene~~ ~~gene_synonym~~ ~~map~~ ~~note~~ ~~standard_name~~

5.11.	Feature Key	mat_peptide
	Definition	mature peptide or protein coding sequence; coding sequence for the mature or final peptide or protein product following post-translational modification; the location does not include the stop codon (unlike the corresponding CDS)
	Optional qualifiers	allele EC_number function gene gene_synonym map note product pseudo pseudogene standard_name

5.12.	Feature Key	misc_binding
	Definition	site in nucleic acid which covalently or non-covalently binds another moiety that cannot be described by any other binding key (primer_bind or protein_bind)
	Mandatory qualifiers	bound_moiety
	Optional qualifiers	allele function gene gene_synonym map note
	Comment	note that the regulatory feature key ~~RBS is~~and regulatory_class qualifier with the value "ribosome_binding_site" must be used for describing ribosome binding sites

5.13.	Feature Key	misc_difference
	Definition	featured sequence differs from the presented sequence at this location and cannot be described by any other Difference key (~~unsure~~, variation, or modified_base)
	Optional qualifiers	allele clone compare gene gene_synonym map note phenotype replace standard_name

	Comment	the misc_difference feature key ~~should~~must be used to describe variability introduced artificially, e.g. by genetic manipulation or by chemical synthesis; use the replace qualifier to annotate a deletion, insertion, or substitution. The variation feature key must be used to describe naturally occurring genetic variability.

5.14.	Feature Key	misc_feature
	Definition	region of biological interest which cannot be described by any other feature key; a new or rare feature
	Optional qualifiers	allele function gene gene_synonym map note number phenotype product pseudo pseudogene standard_name
	Comment	this key should not be used when the need is merely to mark a region in order to comment on it or to use it in another feature’s location

5.15.	Feature Key	misc_recomb
	Definition	site of any generalized, site-specific or replicative recombination event where there is a breakage and reunion of duplex DNA that cannot be described by other recombination keys or qualifiers of source key (proviral)
	Optional qualifiers	allele gene gene_synonym map note recombination_class standard_name
	Molecule scope	DNA

5.16.	Feature Key	misc_RNA
	Definition	any transcript or RNA product that cannot be defined by other RNA keys (prim_transcript, precursor_RNA, mRNA, 5’UTR, 3’UTR, exon, CDS, sig_peptide, transit_peptide, mat_peptide, intron, polyA_site, ncRNA, rRNA and tRNA)
	Optional qualifiers	allele function gene gene_synonym map note operon product pseudo pseudogene standard_name trans_splicing

~~5.22.~~	~~Feature Key~~	~~misc_signal~~
	~~Definition~~	~~any region containing a signal controlling or altering gene function or expression that cannot be described by other signal keys (promoter, CAAT_signal, TATA_signal,~~

		-35_signal, -10_signal, GC_signal, RBS, polyA_signal, enhancer, attenuator, terminator, and rep_origin)
	Optional qualifiers	allele function gene gene_synonym map note operon phenotype standard_name

5.17.	Feature Key	misc_structure
	Definition	any secondary or tertiary nucleotide structure or conformation that cannot be described by other Structure keys (stem_loop and D-loop)
	Optional qualifiers	allele function gene gene_synonym map note standard_name

5.18.	Feature Key	mobile_element
	Definition	region of genome containing mobile elements
	Mandatory qualifiers	mobile_element_type
	Optional qualifiers	allele function gene gene_synonym map note rpt_family rpt_type standard_name

5.19.	Feature Key	modified_base
	Definition	the indicated nucleotide is a modified nucleotide and should be substituted for by the indicated molecule (given in the mod_base qualifier value)
	Mandatory qualifiers	mod_base
	Optional qualifiers	allele frequency gene gene_synonym map note
	Comment	value for the mandatory mod_base qualifier is limited to the restricted vocabulary for modified base abbreviations in Section 2 of this Annex.

5.20.	Feature Key	mRNA
	Definition	messenger RNA; includes 5’ untranslated region (5’UTR), coding sequences (CDS, exon) and 3’ untranslated region (3’UTR)
	Optional qualifiers	allele ~~artificial_location~~ function gene gene_synonym map note operon product pseudo pseudogene standard_name trans_splicing

5.21.	.Feature Key	ncRNA
	Definition	a non-protein-coding gene, other than ribosomal RNA and transfer RNA, the functional molecule of which is the RNA transcript
	Mandatory qualifiers	ncRNA_class
	Optional qualifiers	allele function gene gene_synonym map note operon product pseudo pseudogene standard_name trans_splicing
	Comment	the ncRNA feature ~~is~~must not be used for ribosomal and transfer RNA annotation, for which the rRNA and tRNA feature keys ~~should~~must be used, respectively

5.22.	Feature Key	N_region
	Definition	extra nucleotides inserted between rearranged immunoglobulin segments
	Optional qualifiers	allele gene gene_synonym map note product pseudo pseudogene standard_name
	~~Parent Key~~	~~CDS~~
	~~Organism scope~~	~~eukaryotes~~

5.23.	Feature Key	operon
	Definition	region containing polycistronic transcript including a cluster of genes that are under the control of the same regulatory sequences/~~promotor~~promoter and in the same biological pathway
	Mandatory qualifiers	operon
	Optional qualifiers	allele function map note phenotype pseudo pseudogene standard_name

5.24.	Feature Key	oriT
	Definition	origin of transfer; region of a DNA molecule where transfer is initiated during the process of conjugation or mobilization
	Optional qualifiers	allele bound_moiety direction gene gene_synonym map note rpt_family rpt_type rpt_unit_range rpt_unit_seq standard_name
	Molecule Scope	DNA
	Comment	rep_origin ~~should~~must be used ~~for~~to describe origins of replication; direction qualifier has legal values ~~RIGHT, LEFT~~left, right, and ~~BOTH~~both, however only ~~RIGHT~~left and ~~LEFT~~right are valid when used in conjunction with the oriT feature; origins of transfer can be present in the chromosome; plasmids can contain multiple origins of transfer

~~5.31.~~	~~Feature Key~~	~~polyA_signal~~
	~~Definition~~	~~recognition region necessary for endonuclease cleavage of an RNA transcript that is followed by polyadenylation; consensus=AATAAA [1]~~
	~~Optional qualifiers~~	~~allele~~ ~~gene~~ ~~gene_synonym~~ ~~map~~ ~~note~~
	~~Organism scope~~	~~eukaryotes and eukaryotic viruses~~
	~~References~~	~~[1] Proudfoot, N. and Brownlee, G.G. Nature 263, 211-214 (1976)~~

~~5.32.~~

5.25.	Feature Key	polyA_site
	Definition	site on an RNA transcript to which will be added adenine residues by post-transcriptional polyadenylation
	Optional qualifiers	allele gene gene_synonym map note
	Organism scope	eukaryotes and eukaryotic viruses

5.26.	Feature Key	precursor_RNA
	Definition	any RNA species that is not yet the mature RNA product; may include ncRNA, rRNA, tRNA, 5’ untranslated region (5’UTR), coding sequences (CDS, exon), intervening sequences (intron) and 3’ untranslated region (3’UTR)
	Optional qualifiers	allele function gene gene_synonym map note operon product standard_name trans_splicing
	Comment	used for RNA which may be the result of post-transcriptional processing; if the RNA in question is known not to have been processed, use the prim_transcript key

5.27.	Feature Key	prim_transcript
	Definition	primary (initial, unprocessed) transcript; ~~includes~~may include ncRNA, rRNA, tRNA, 5’ untranslated region (5’UTR), coding sequences (CDS, exon), intervening sequences (intron) and 3’ untranslated region (3’UTR)
	Optional qualifiers	allele ~~function~~ ~~gene~~ ~~gene_synonym~~ ~~map~~ ~~note~~ operon standard_name

5.28.	Feature Key	primer_bind
	Definition	non-covalent primer binding site for initiation of replication, transcription, or reverse transcription; includes site(s) for synthetic e.g., PCR primer elements
	Optional qualifiers	allele gene gene_synonym map note standard_name ~~PCR_conditions~~
	Comment	used to annotate the site on a given sequence to which a primer molecule binds - not intended to represent the sequence of the primer molecule itself; ~~PCR components and reaction times may be stored under the PCR_conditions qualifier;~~ since PCR reactions most often involve pairs of primers, a single primer_bind key may use the order(location,location) operator with two locations, or a pair of primer_bind keys may be used

5.29.	Feature Key	~~promoter~~propeptide
	~~Definition~~	~~region on a DNA molecule involved in RNA polymerase binding to initiate transcription~~
	~~Optional qualifiers~~	~~allele~~
	Definition	propeptide coding sequence; coding sequence for the domain of a proprotein that is cleaved to form the mature protein product.
		~~bound_moiety~~
		function
		gene
		gene_synonym
		map
		note
		~~operon~~
		~~phenotype~~
		product
		pseudo
		pseudogene
		standard_name
	~~Molecule scope~~	~~DNA~~

5.30.	Feature Key	protein_bind
	Definition	non-covalent protein binding site on nucleic acid
	Mandatory qualifiers	bound_moiety
	Optional qualifiers	allele
		function
		gene
		gene_synonym
		map
		note
		operon
		standard_name
	Comment	note that ~~RBS is~~the regulatory feature key and regulatory_class qualifier with the value "ribosome_binding_site" must be used ~~for~~to describe ribosome binding sites

5.31.	Feature Key	~~RBS~~regulatory
	~~Definition~~	~~ribosome binding site~~
	~~Optional~~Definition	any region of a sequence that functions in the regulation of transcription, translation, replication or chromatin structure;
	Mandatory qualifiers	~~allele~~regulatory_class
		~~gene~~
		~~gene_synonym~~
		~~map~~
		~~note~~
		pseudo
		pseudogene
		standard_name
	~~References~~	~~[1] Shine, J. and Dalgarno, L. Proc Natl Acad Sci USA 71, 1342-1346 (1974)~~
		~~[2] Gold, L. et al. Ann Rev Microb 35, 365-403 (1981)~~
	~~Comment~~	~~in prokaryotes, known as the Shine-Dalgarno sequence: is located 5 to 9 bases upstream of the initiation codon; consensus GGAGGT [1,2]~~

5.32.	Feature Key	repeat_region
	Definition	region of genome containing repeating units
	Optional qualifiers	allele function gene gene_synonym map note rpt_family rpt_type rpt_unit_range rpt_unit_seq satellite standard_name ~~standard_name~~

5.33.	Feature Key	rep_origin
	Definition	origin of replication; starting site for duplication of nucleic acid to give two identical copies
	Optional Qualifiers	allele direction ~~gene~~ ~~gene_synonym~~ ~~map~~ ~~note~~ standard_name
	Comment	direction qualifier has valid values: ~~RIGHT, LEFT~~left, right, or ~~BOTH~~both

5.34.	Feature Key	rRNA
	Definition	mature ribosomal RNA; RNA component of the ribonucleoprotein particle (ribosome) which assembles amino acids into proteins
	Optional qualifiers	allele function gene gene_synonym map note operon product pseudo pseudogene standard_name
	Comment	rRNA sizes should be annotated with the product qualifier

5.35.	Feature Key	S_region
	Definition	switch region of immunoglobulin heavy chains; involved in the rearrangement of heavy chain DNA leading to the expression of a different immunoglobulin class from the same B-cell
	Optional qualifiers	allele gene gene_synonym map note product pseudo pseudogene standard_name
	~~Parent Key~~	~~misc_signal~~

	~~Organism scope~~	~~eukaryotes~~

5.36.	Feature Key	sig_peptide
	Definition	signal peptide coding sequence; coding sequence for an N-terminal domain of a secreted protein; this domain is involved in attaching nascent polypeptide to the membrane leader sequence
	Optional qualifiers	allele function gene gene_synonym map note product pseudo pseudogene standard_name

5.37.	Feature Key	source
	Definition	identifies the source of the sequence; this key is mandatory; every sequence will have a single source key spanning the entire sequence
	Mandatory qualifiers	organism mol_type
	Optional qualifiers	cell_line cell_type chromosome clone clone_lib collected_by collection_date cultivar dev_stage ecotype environmental_sample germline haplogroup haplotype host identified_by isolate isolation_source lab_host lat_lon macronuclear map mating_type note organelle PCR_primers plasmid pop_variant proviral rearranged segment serotype serovar sex strain sub_clone sub_species sub_strain tissue_lib tissue_type variety
	Molecule scope	any

5.38.	Feature Key	stem_loop
	Definition	hairpin; a double-helical region formed by base-pairing between adjacent (inverted) complementary sequences in a single strand of RNA or DNA
	Optional qualifiers	allele function gene gene_synonym map note operon standard_name

5.39.	Feature Key	STS
	Definition	sequence tagged site; short, single-copy DNA sequence that characterizes a mapping landmark on the genome and can be detected by PCR; a region of the genome can be mapped by determining the order of a series of STSs
	Optional qualifiers	allele gene gene_synonym map note standard_name
	Molecule scope	DNA
	~~Parent key~~	~~misc_binding~~
	Comment	STS location to include primer(s) in primer_bind key or primers

~~5.47.~~	~~Feature Key~~	~~TATA_signal~~
	~~Definition~~	~~TATA box; Goldberg-Hogness box; a conserved AT-rich septamer found about 25 bp before the start point of each eukaryotic RNA polymerase II transcript unit which may be involved in positioning the enzyme for correct initiation; consensus=TATA(A or T)A(A or T) [1,2]~~
	~~Optional qualifiers~~	~~allele~~ ~~gene~~ ~~gene_synonym~~ ~~map~~ ~~note~~
	~~Organism scope~~	~~eukaryotes and eukaryotic viruses~~
	~~Molecule scope~~	~~DNA~~
	~~References~~	~~[1] Efstratiadis, A. et al. Cell 21, 653-668 (1980)~~ ~~[2] Corden, J., et al. "Promoter sequences of eukaryotic protein-encoding genes" Science 209, 1406-1414 (1980)~~

5.40.	Feature Key	telomere
	Definition	region of biological interest identified as a telomere and which has been experimentally characterized
	Optional qualifiers	note rpt_type rpt_unit_range rpt_unit_seq standard_name
	Comment	the telomere feature describes the interval of DNA that corresponds to a specific structure at the end of the linear eukaryotic chromosome which is required for the integrity and maintenance of the end; this region is unique compared to the rest of the chromosome and represents the physical end of the chromosome

~~5.49.~~	~~Feature Key~~	~~terminator~~
	~~Definition~~	~~sequence of DNA located either at the end of the transcript that causes RNA polymerase to terminate transcription~~
	~~Optional qualifiers~~	~~allele~~ ~~gene~~ ~~gene_synonym~~ ~~map~~ ~~note~~ ~~operon~~ ~~standard_name~~
	~~Molecule scope~~	~~DNA~~

5.41.	Feature Key	tmRNA
	Definition	transfer messenger RNA; tmRNA acts as a tRNA first, and then as an mRNA that encodes a peptide tag; the ribosome translates this mRNA region of tmRNA and attaches the encoded peptide tag to the C-terminus of the unfinished protein; this attached tag targets the protein for destruction or proteolysis
	Optional qualifiers	allele function gene gene_synonym map note product pseudo pseudogene standard_name tag_peptide

5.42.	Feature Key	transit_peptide
	Definition	transit peptide coding sequence; coding sequence for an N-terminal domain of a nuclear-encoded organellar protein; this domain is involved in post-translational import of the protein into the organelle
	Optional qualifiers	allele function gene gene_synonym map note product pseudo pseudogene standard_name

5.43.	Feature Key	tRNA
	Definition	mature transfer RNA, a small RNA molecule (75-85 bases long) that mediates the translation of a nucleic acid sequence into an amino acid sequence
	Optional qualifiers	allele anticodon function gene gene_synonym map note product pseudo pseudogene standard_name trans_splicing

5.44.	Feature Key	unsure
	~~Definition~~	~~author is unsure of exact sequence in this region~~
	Definition	a small region of sequenced bases, generally 10 or fewer in its length, which could not be confidently identified. Such a region might contain called bases (a, t, g, or c), or a mixture of called-bases and uncalled-bases ('n').
	Optional qualifiers	allele compare gene gene_synonym map note replace
	Comment	use the replace qualifier to annotate a deletion, insertion, or substitution.

5.45.	Feature Key	V_region
	Definition	variable region of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains; codes for the variable amino terminal portion; can be composed of V_segments, D_segments, N_regions, and J_segments
	Optional qualifiers	allele gene gene_synonym map note product pseudo pseudogene standard_name
	~~Parent Key~~	~~CDS~~
	Organism scope	eukaryotes

5.46.	Feature Key	V_segment
	Definition	variable segment of immunoglobulin light and heavy chains, and T-cell receptor alpha, beta, and gamma chains; codes for most of the variable region (V_region) and the last few amino acids of the leader peptide
	Optional qualifiers	allele gene gene_synonym map note product pseudo

		pseudogene standard_name
	~~Parent Key~~	~~CDS~~
	~~Organism scope~~	~~eukaryotes~~

5.47.	Feature Key	variation
	Definition	a related strain contains stable mutations from the same gene (e.g., RFLPs, polymorphisms, etc.) which differ from the presented sequence at this location (and possibly others)
	Optional qualifiers	allele compare frequency gene gene_synonym map note phenotype product replace standard_name
	Comment	used to describe alleles, RFLP's, and other naturally occurring mutations and polymorphisms; use the replace qualifier to annotate a deletion, insertion, or substitution; variability arising as a result of genetic manipulation (e.g. site directed mutagenesis) ~~should~~must be described with the misc_difference feature~~; use the replace qualifier to annotate a deletion, insertion, or substitution~~

5.48.	Feature Key	3'UTR
	Definition	1) region at the 3' end of a mature transcript (following the stop codon) that is not translated into a protein; 2) region at the 3' end of an RNA virus (following the last stop codon) that is not translated into a protein;
	Optional qualifiers	allele function gene gene_synonym map note standard_name trans_splicing
	Comment	The apostrophe character has special meaning in XML, and must be substituted with "'" in the value of an element. Thus "3'UTR" must be represented as "3'UTR" in the XML file, i.e., <INSDFeature_key>3'UTR</INSDFeature_key>.

5.49.	Feature Key	5'UTR
	Definition	1) region at the 5' end of a mature transcript (preceding the initiation codon) that is not translated into a protein; 2) region at the 5' end of an RNA virus (preceding the first initiation codon) that is not translated into a protein;
	Optional qualifiers	allele function gene gene_synonym map note standard_name trans_splicing
	Comment	The apostrophe character has special meaning in XML, and must be substituted with "'" in the value of an element. Thus "5'UTR" must be represented as

“5'UTR” in the XML file, i.e., <INSDFeature_key>5'UTR</INSDFeature_key>.

5.59. Feature Key	-10_signal
Definition	Pribnow box; a conserved region about 10 bp upstream of the start-point of bacterial transcription units which may be involved in binding RNA polymerase; consensus=TAtAaT [1,2,3,4]
Optional qualifiers	allele gene gene_synonym map note operon standard_name
Organism scope	prokaryotes
Molecule scope	DNA
References	[1] Schaller, H., Gray, C., and Hermann, K. Proc Natl Acad Sci USA 72, 737-741 (1974) [2] Pribnow, D. Proc Natl Acad Sci USA 72, 784-788 (1974) [3] Hawley, D.K. and McClure, W.R. "Compilation and analysis of Escherichia coli promoter DNA sequences" Nucl Acid Res 11, 2237-2255 (1983) [4] Rosenberg, M. and Court, D. "Regulatory sequences involved in the promotion and termination of RNA transcription" Ann Rev Genet 13, 319-353 (1979)

5.60. Feature Key	-35_signal
Definition	a conserved hexamer about 35 bp upstream of the start.point of bacterial transcription units; consensus=TTGACa or TGTTGACA
Optional qualifiers	allele gene gene_synonym map note operon standard_name
Organism scope	prokaryotes
Molecule scope	DNA
References	[1] Takanami, M., et al. Nature 260, 297-302 (1976) [2] Moran, C.P., Jr., et al. Molec Gen Genet 186, 339-346 (1982) [3] Maniatis, T., et al. Cell 5, 109-113 (1975)

SECTION 6: ~~DESCRIPTION OF~~ QUALIFIERS FOR NUCLEIC ~~ACID~~ SEQUENCES

This section contains the list of qualifiers to be used for features in ~~nucleic acid~~nucleotide sequences. The qualifiers are listed in alphabetic order.

Where a Value format of “none” is indicated in the description of a qualifier (e.g. germline), the `INSDQualifier_value` element must not be used.

PLEASE NOTE: Any qualifier value provided for a qualifier with a “free text” value format may require translation for National/Regional procedures.

6.1.	Qualifier	allele
	Definition	name of the allele for the given gene
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>adh1-1</INSDQualifier_value>
	Comment	all gene-related features (exon, CDS etc) for a given gene should share the same allele qualifier value; the allele qualifier value must, by definition, be different from the gene qualifier value; when used with the variation feature key, the allele qualifier value should be that of the variant.

6.2.	Qualifier	anticodon
	Definition	location of the anticodon of tRNA and the amino acid for which it codes
	Value format	(pos:<location>,aa:<amino_acid>,seq~~=~~:<text>) where <location> is the position of the anticodon and <amino_acid> is the three letter abbreviation for the amino acid encoded and ~~seq~~<text> is the sequence of the anticodon
	Example	<INSDQualifier_value>(pos:34..36,aa:Phe,seq:aaa)</INSDQualifier_value> <INSDQualifier_value>(pos:join(5,495..496),aa:Leu,seq:taa)</INSDQualifier_value> <INSDQualifier_value>(pos:complement(4156..4158),aa:Glu,seq:ttg)</INSDQualifier_value>

6.3.	Qualifier	bound_moiety
	Definition	name of the molecule/complex that may bind to the given feature
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>GAL4</INSDQualifier_value>
	Comment	~~Multiple bound_moiety qualifiers are legal on "promoter" and "enhancer" features~~. A single bound_moiety qualifier is legal on the "misc_binding", "oriT" and "protein_bind" features.

6.4.	Qualifier	cell_line
	Definition	cell line from which the sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>MCF7</INSDQualifier_value>

6.5.	Qualifier	cell_type
	Definition	cell type from which the sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>leukocyte</INSDQualifier_value>

6.6.	Qualifier	chromosome
	Definition	chromosome (e.g. Chromosome number) from which the sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>1</INSDQualifier_value> <INSDQualifier_value>X</INSDQualifier_value>

6.7.	Qualifier	clone
	Definition	clone from which the sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>lambda-hIL7.3</INSDQualifier_value>
	Comment	a source feature must not contain more than one clone ~~should be specified for a given source feature~~qualifier; where the sequence was obtained from multiple clones it may be further described in the feature table using the feature key misc_feature and a note qualifier to specify the multiple clones.

6.8.	Qualifier	clone_lib
	Definition	clone library from which the sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>lambda-hIL7</INSDQualifier_value>

6.9.	Qualifier	codon_start
	Definition	indicates the offset at which the first complete codon of a coding feature can be found, relative to the first base of that feature.
	Value format	1 or 2 or 3
	Example	<INSDQualifier_value>2</INSDQualifier_value>

6.10.	Qualifier	collected_by
	Definition	name of persons or institute who collected the specimen
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>Dan Janzen</INSDQualifier_value>

6.11.	Qualifier	collection_date
	Definition	date that the specimen was collected.
	Value format	~~DD-Mmm-~~YYYY~~, Mmm~~-MM-DD, YYYY-MM or YYYY
	Example	<INSDQualifier_value>~~21-Oct-~~1952-10-21</INSDQualifier_value> <INSDQualifier_value>~~Oct-~~1952-10</INSDQualifier_value> <INSDQualifier_value>1952</INSDQualifier_value>
	~~Comment~~	~~full date format DD-Mmm-YYYY is preferred; where day and/or month of collection is not known either "Mmm-YYYY" or "YYYY" can be used; three-letter month abbreviation can be one of the following: Jan, Feb, Mar, Apr, May, Jun, Jul, Aug, Sep, Oct, Nov, Dec.~~
	~~6.12.~~	Comment 'YYYY' is a four-digit value representing the year. 'MM' is a two-digit value representing the month. 'DD' is a two-digit value representing the day of the month.

6.12.	Qualifier	compare
	Definition	Reference details of an existing public INSD entry to which a comparison is made
	Value format	[accession-number.sequence-version]
	Example	<INSDQualifier_value>AJ634337.1</INSDQualifier_value>
	Comment	This qualifier may be used on the following features: misc_difference, unsure, and variation. Multiple compare qualifiers with different contents are allowed within a single feature. This qualifier is not intended for large-scale annotation of variations, such as SNPs.

6.13.	Qualifier	cultivar
	Definition	cultivar (cultivated variety) of plant from which sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>Nipponbare</INSDQualifier_value> <INSDQualifier_value>Tenuifolius</INSDQualifier_value> <INSDQualifier_value>Candy Cane</INSDQualifier_value> <INSDQualifier_value>IR36</INSDQualifier_value>
	Comment	'cultivar' is applied solely to products of artificial selection; use the variety qualifier for natural, named plant and fungal varieties.

6.14.	Qualifier	dev_stage
	Definition	if the sequence was obtained from an organism in a specific developmental stage, it is specified with this qualifier
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>fourth instar larva</INSDQualifier_value>

6.15.	Qualifier	direction
	Definition	direction of DNA replication
	Value format	left, right, or both where left indicates toward the 5′ end of the sequence (as presented) and right indicates toward the 3′ end
	Example	<INSDQualifier_value>~~LEFT~~left</INSDQualifier_value>
	Comment	The values left, right, and both are permitted when the direction qualifier is used to annotate a rep_origin feature key. However, only left and right values are permitted when the direction qualifier is used to annotate an oriT feature key. ~~The values are case-insensitive, i.e. both "RIGHT" and "right" are valid.~~
6.16.	Qualifier	EC_number
	Definition	Enzyme Commission number for enzyme product of sequence
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>1.1.2.4</INSDQualifier_value> <INSDQualifier_value>1.1.2.-</INSDQualifier_value> <INSDQualifier_value>1.1.2.n</INSDQualifier_value>
	Comment	valid values for EC numbers are defined in the list prepared by the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (NC-IUBMB) (published in Enzyme Nomenclature 1992, Academic Press, San Diego, or a more recent revision thereof).The format represents a string of four numbers separated by full stops; up to three numbers starting from the end of the string ~~can~~may be replaced by dash ~~"."~~"-" to indicate uncertain assignment. Symbol "n" ~~can~~may be used in the last position instead of a number where the EC number is awaiting assignment. Please note that such incomplete EC numbers are not approved by NC-IUBMB.
6.17.	Qualifier	ecotype
	Definition	a population within a given species displaying genetically based, phenotypic traits that reflect adaptation to a local habitat
	Value Format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>Columbia</INSDQualifier_value>
	Comment	an example of such a population is one that has adapted hairier than normal leaves as a response to an especially sunny habitat. 'Ecotype' is often applied to standard genetic stocks of Arabidopsis thaliana, but it can be applied to any sessile organism.
6.18.	Qualifier	environmental_sample
	Definition	identifies sequences derived by direct molecular isolation from a bulk environmental DNA sample (by PCR with or without subsequent cloning of the product, DGGE, or other anonymous methods) with no reliable identification of the source organism. Environmental samples include clinical samples, gut contents, and other sequences from anonymous organisms that may be associated with a particular host. They do not include endosymbionts that can be reliably recovered from a particular host, organisms from a readily identifiable but uncultured field sample (e.g., many cyanobacteria), or phytoplasmas that can be reliably recovered from diseased plants (even though these cannot be grown in axenic culture)
	Value format	none
	Comment	used only with the source feature key; source feature keys containing the environmental_sample qualifier should also contain the isolation_source qualifier. ~~Sequences~~; a source feature including the environmental_sample qualifier must not

		include the strain qualifier.
6.19.	Qualifier	exception
	Definition	indicates that the coding region cannot be translated using standard biological rules
	Value format	One of the following controlled vocabulary phrases: RNA editing rearrangement required for product annotated by transcript or proteomic data
	Example	<INSDQualifier_value>RNA editing</INSDQualifier_value> <INSDQualifier_value>rearrangement required for product</INSDQualifier_value>
	Comment	only to be used to describe biological mechanisms such as RNA editing; protein translation of a CDS with an exception qualifier will be different from the ~~according~~corresponding conceptual translation; must not be used where transl_except qualifier would be adequate, e.g. in case of stop codon completion use.
6.20.	Qualifier	frequency
	Definition	frequency of the occurrence of a feature
	Value format	free text representing the proportion of a population carrying the feature expressed as a fraction (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>23/108</INSDQualifier_value> <INSDQualifier_value>1 in 12</INSDQualifier_value> <INSDQualifier_value>0.85</INSDQualifier_value>
6.21.	Qualifier	function
	Definition	function attributed to a sequence
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>essential for recognition of cofactor </INSDQualifier_value>
	Comment	The function qualifier is used when the gene name and/or product name do not convey the function attributable to a sequence.
6.22.	Qualifier	gene
	Definition	symbol of the gene corresponding to a sequence region
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>ilvE</INSDQualifier_value>
	Comment	Use gene qualifier to provide the gene symbol; use standard_name qualifier to provide the full gene name.

6.23.	Qualifier	gene_synonym
	Definition	synonymous, replaced, obsolete or former gene symbol
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>Hox-3.3</INSDQualifier_value> in a feature where the gene qualifier value is Hoxc6
	Comment	used where it is helpful to indicate a gene symbol synonym; when the gene synonym qualifier is used, a primary gene symbol must always be indicated in a gene qualifier
6.24.	Qualifier	germline
	Definition	the sequence presented has not undergone somatic rearrangement as part of an adaptive immune response; it is the unrearranged sequence that was inherited from the parental germline
	Value format	none
	Comment	germline qualifier ~~should~~must not be used to indicate that the source of the sequence is a gamete or germ cell; germline and rearranged qualifiers ~~cannot~~must not be used in the same source feature; germline and rearranged qualifiers ~~should~~must only be used for molecules that can undergo somatic rearrangements as part of an adaptive immune response; these are the T-cell receptor (TCR) and immunoglobulin loci in the jawed vertebrates, and the unrelated variable lymphocyte receptor (VLR) locus in the jawless fish (lampreys and hagfish); germline and rearranged qualifiers should not be used outside of the Craniata (taxid=89593)
6.25.	Qualifier	haplogroup
	Definition	name for a group of similar haplotypes that share some sequence variation. Haplogroups are often used to track migration of population groups.
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>H*</INSDQualifier_value>
6.26.	Qualifier	haplotype
	Definition	name for a specific set of alleles that are linked together on the same physical chromosome. In the absence of recombination, each haplotype is inherited as a unit, and may be used to track gene flow in populations.
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>Dw3 B5 Cw1 A1</INSDQualifier_value>
6.27.	Qualifier	host
	Definition	natural (as opposed to laboratory) host to the organism from which sequenced molecule was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>Homo sapiens</INSDQualifier_value> <INSDQualifier_value>Homo sapiens 12 year old girl</INSDQualifier_value> <INSDQualifier_value>Rhizobium NGR234</INSDQualifier_value>

6.28.	Qualifier	identified_by
	Definition	name of the expert who identified the specimen taxonomically
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>John Burns</INSDQualifier_value>

6.29.	Qualifier	isolate
	Definition	individual isolate from which the sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>Patient #152</INSDQualifier_value> <INSDQualifier_value>DGGE band PSBAC-13</INSDQualifier_value>

6.30.	Qualifier	isolation_source
	Definition	describes the physical, environmental and/or local geographical source of the biological sample from which the sequence was derived
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Examples	<INSDQualifier_value>rumen isolates from standard Pelleted ration-fed steer #67</INSDQualifier_value> <INSDQualifier_value>permanent Antarctic sea ice</INSDQualifier_value> <INSDQualifier_value>denitrifying activated sludge from carbon_limited continuous reactor</INSDQualifier_value>
	Comment	used only with the source feature key; source feature keys containing an environmental_sample qualifier should also contain an isolation_source qualifier

6.31.	Qualifier	lab_host
	Definition	scientific name of the laboratory host used to propagate the source organism from which the sequenced molecule was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>Gallus gallus</INSDQualifier_value> <INSDQualifier_value>Gallus gallus embryo</INSDQualifier_value> <INSDQualifier_value>Escherichia coli strain DH5 alpha</INSDQualifier_value> <INSDQualifier_value>Homo sapiens HeLa cells</INSDQualifier_value>
	Comment	the full binomial scientific name of the host organism should be used when known; extra conditional information relating to the host may also be included

6.32.	Qualifier	lat_lon
	Definition	geographical coordinates of the location where the specimen was collected
	Value format	free text - degrees latitude and longitude in format "d[d.dddd] N|S d[dd.dddd] W|E" (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>47.94 N 28.12 W</INSDQualifier_value> <INSDQualifier_value>45.0123 S 4.1234 E</INSDQualifier_value>

6.33.	Qualifier	macronuclear
	Definition	if the sequence shown is DNA and from an organism which undergoes chromosomal differentiation between macronuclear and micronuclear stages, this qualifier is used to denote that the sequence is from macronuclear DNA
	Value format	none

6.34.	Qualifier	map
	Definition	genomic map position of feature
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>8q12-~~13~~q13</INSDQualifier_value>

6.35.	Qualifier	mating_type
	Definition	mating type of the organism from which the sequence was obtained; mating type is used for prokaryotes, and for eukaryotes that undergo meiosis without sexually dimorphic gametes
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Examples	<INSDQualifier_value>MAT-1</INSDQualifier_value> <INSDQualifier_value>plus</INSDQualifier_value> <INSDQualifier_value>-</INSDQualifier_value> <INSDQualifier_value>odd</INSDQualifier_value> <INSDQualifier_value>even</INSDQualifier_value>"
	Comment	mating_type qualifier values male and female are valid in the prokaryotes, but not in the eukaryotes; for more information, see the entry for the sex qualifier.

6.36.	Qualifier	mobile_element_type
	Definition	type and name or identifier of the mobile element which is described by the parent feature
	Value format	<mobile_element_type>[:<mobile_element_name>] where <mobile_element_type> is one of the following: transposon retrotransposon integron insertion sequence non-LTR retrotransposon SINE MITE LINE other
	Example	<INSDQualifier_value>transposon:Tnp9</INSDQualifier_value>
	Comment	mobile_element_type is legal on mobile_element feature key only. Mobile element should be used to represent both elements which are currently mobile, and those which were mobile in the past. Value "other" for <mobile_element_type> requires a <mobile_element_name>

6.37.	Qualifier	mod_base
	Definition	abbreviation for a modified nucleotide base
	Value format	modified base abbreviation chosen from this Annex, ~~Table~~Section 2
	Example	<INSDQualifier_value>m5c</INSDQualifier_value> <INSDQualifier_value>OTHER</INSDQualifier_value>
	Comment	specific modified nucleotides not found in Section 2 of this Annex are annotated by entering OTHER as the value for the mod_base qualifier and including a note qualifier with the full name of the modified base as its value

6.38.	Qualifier	mol_type
	Definition	molecule type of sequence
	Value format	One chosen from the following: genomic DNA genomic RNA mRNA tRNA rRNA other RNA other DNA transcribed RNA viral cRNA unassigned DNA unassigned RNA
	Example	<INSDQualifier_value>genomic DNA</INSDQualifier_value> <INSDQualifier_value>other RNA</INSDQualifier_value>
	Comment	mol_type qualifier is mandatory on the source feature key; the value "genomic DNA" does not imply that the molecule is nuclear (e.g. organelle and plasmid DNA ~~should~~must be described using "genomic DNA"); ribosomal RNA genes ~~should~~must be described using "genomic DNA"; "rRNA" ~~should~~must only be used if the ribosomal RNA molecule itself has been sequenced; values "other RNA" and "other DNA" ~~should~~must be applied to synthetic molecules, values "unassigned DNA", "unassigned RNA" ~~should~~must be applied where in vivo molecule is unknown.

6.39.	Qualifier	ncRNA_class
	Definition	a structured description of the classification of the non-coding RNA described by the ncRNA parent key
	Value format	TYPE where TYPE is one of the following controlled vocabulary terms or phrases: antisense_RNA autocatalytically_spliced_intron ribozyme hammerhead_ribozyme lncRNA RNase_P_RNA RNase_MRP_RNA telomerase_RNA guide_RNA rasiRNA scRNA siRNA miRNA piRNA snoRNA snRNA SRP_RNA vault_RNA Y_RNA other
	Example	<INSDQualifier_value>autocatalytically_spliced_intron </INSDQualifier_value>

		<INSDQualifier_value>siRNA</INSDQualifier_value> <INSDQualifier_value>scRNA</INSDQualifier_value> <INSDQualifier_value>other</INSDQualifier_value>
	Comment	specific ncRNA types not yet in the ncRNA_class controlled vocabulary ~~can~~must be annotated by entering "other" as the ncRNA_class qualifier value, and providing a brief explanation of novel ncRNA_class in a note qualifier
6.40.	Qualifier	note
	Definition	any comment or additional information
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>A comment about the feature</INSDQualifier_value>
6.41.	Qualifier	number
	Definition	a number to indicate the order of genetic elements (e.g. exons or introns) in the 5’ to 3’ direction
	Value format	free text (with no whitespace characters) (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>4</INSDQualifier_value> <INSDQualifier_value>6B</INSDQualifier_value>
	Comment	text limited to integers, letters or combination of integers and/or letters represented as a data value that contains no whitespace characters; any additional terms should be included in a standard_name qualifier. Example: a number qualifier with a value of 2A and a standard_name qualifier with a value of “long”
6.42.	Qualifier	operon
	Definition	name of the group of contiguous genes transcribed into a single transcript to which that feature belongs
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>lac</INSDQualifier_value>
	~~Comment~~	~~valid only on Prokaryota-specific features~~
6.43.	6.43.	Qualifier organelle
	Definition	type of membrane-bound intracellular structure from which the sequence was obtained
	Value format	One of the following controlled vocabulary terms and phrases: chromatophore hyrogenosome mitochondrion nucleomorph plastid mitochondrion:kinetoplast plastid:chloroplast plastid:apicoplast plastid:chromoplast plastid:cyanelle plastid:leucoplast plastid:proplastid
	Examples	<INSDQualifier_value>chromatophore</INSDQualifier_value> <INSDQualifier_value>hydrogenosome</INSDQualifier_value> <INSDQualifier_value>mitochondrion</INSDQualifier_value> <INSDQualifier_value>nucleomorph</INSDQualifier_value>

<INSDQualifier_value>plastid</INSDQualifier_value>
<INSDQualifier_value>mitochondrion:kinetoplast</INSDQualifier_value>
<INSDQualifier_value>plastid:chloroplast</INSDQualifier_value>
<INSDQualifier_value>plastid:apicoplast</INSDQualifier_value>
<INSDQualifier_value>plastid:chromoplast</INSDQualifier_value>
<INSDQualifier_value>plastid:cyanelle</INSDQualifier_value>
<INSDQualifier_value>plastid:leucoplast</INSDQualifier_value>
<INSDQualifier_value>plastid:proplastid</INSDQualifier_value>

6.44.	Qualifier	organism
	Definition	scientific name of the organism that provided the sequenced genetic material, if known, or the available taxonomic information if the organism is unclassified; or an indication that the sequence is a synthetic construct
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>Homo sapiens</INSDQualifier_value>

6.45.	Qualifier	PCR_primers
	Definition	PCR primers that were used to amplify the sequence. A single PCR_primers qualifier should contain all the primers used for a single PCR reaction. If multiple forward or reverse primers are present in a single PCR reaction, multiple sets of fwd_name/fwd_seq or rev_name/rev_seq values will be present
	Value format	[fwd_name: XXX1,]fwd_seq: xxxxx1,[fwd_name: XXX2,]fwd_seq: xxxxx2, [rev_name: YYY1,]rev_seq: yyyyy1,[rev_name: YYY2,]rev_seq: yyyyy2~~</INSDQualifier_value>~~
	Example	<INSDQualifier_value>fwd_name: CO1P1, fwd_seq: ttgatttttggtcayccwgaagt,rev_name: CO1R4, rev_seq: ccwvytardcctarraartgttg</INSDQualifier_value> <INSDQualifier_value>fwd_name: hoge1, fwd_seq: cgkgtgtatcttact, rev_name: hoge2, rev_seq: cg<i>gtgtatcttact</INSDQualifier_value> <INSDQualifier_value>fwd_name: CO1P1, fwd_seq: ttgatttttggtcayccwgaagt, fwd_name: CO1P2, fwd_seq: gatacacaggtcayccwgaagt, rev_name: CO1R4, rev_seq: ccwvytardcctarraartgttg</INSDQualifier_value>
	Comment	fwd_seq and rev_seq are both mandatory; fwd_name and rev_name are both optional. Both sequences ~~should~~must be presented in 5'>3' order. The sequences ~~should~~must be given in the symbols from Section 1 of this Annex, except for the modified bases~~;~~ ~~those~~, which must be enclosed within angle brackets < >. In XML, the angle brackets < and > must be substituted with < and > since they are reserved characters in XML.

6.46.	Qualifier	phenotype
	Definition	phenotype conferred by the feature, where phenotype is defined as a physical, biochemical or behavioural characteristic or set of characteristics
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>erythromycin resistance</INSDQualifier_value>

6.47.	Qualifier	plasmid
	Definition	name of naturally occurring plasmid from which the sequence was obtained, where plasmid is defined as an independently replicating genetic unit that cannot be described by chromosome or segment qualifiers
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>pC589</INSDQualifier_value>

6.48.	Qualifier	pop_variant
	Definition	name of subpopulation or phenotype of the sample from which the sequence was derived
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>pop1</INSDQualifier_value> <INSDQualifier_value>Bear Paw</INSDQualifier_value>
6.49.	Qualifier	product
	Definition	name of the product associated with the feature, e.g. the mRNA of an mRNA feature, the polypeptide of a CDS, the mature peptide of a mat_peptide, etc.
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>trypsinogen</INSDQualifier_value> (when qualifier appears in CDS feature) <INSDQualifier_value>trypsin</INSDQualifier_value> (when qualifier appears in mat_peptide feature) <INSDQualifier_value>XYZ neural-specific transcript</INSDQualifier_value> (when qualifier appears in mRNA feature)
6.50.	Qualifier	protein_id
	Definition	protein sequence identification number, an integer used in a sequence listing to designate the protein sequence encoded by the coding sequence identified in the corresponding CDS feature key and translation qualifier
	Value format	an integer greater than zero
	Example	<INSDQualifier_value>89</INSDQualifier_value>
6.51.	Qualifier	proviral
	Definition	this qualifier is used to flag sequence obtained from a virus or phage that is integrated into the genome of another organism
	Value format	none
6.52.	Qualifier	pseudo
	Definition	indicates that this feature is a non-functional version of the element named by the feature key
	Value format	none
	Comment	The qualifier pseudo should be used to describe non-functional genes that are not formally described as pseudogenes, e.g. CDS has no translation due to other reasons than ~~pseudogenisation~~pseudogenization events. Other reasons may include sequencing or assembly errors. In order to annotate pseudogenes the qualifier pseudogene must be used, indicating the TYPE of pseudogene.

6.53.	Qualifier	pseudogene
	Definition	indicates that this feature is a pseudogene of the element named by the feature key
	Value format	TYPE where TYPE is one of the following controlled vocabulary terms or phrases: processed unprocessed unitary allelic unknown
	Example	<INSDQualifier_value>processed</INSDQualifier_value> <INSDQualifier_value>unprocessed</INSDQualifier_value> <INSDQualifier_value>unitary</INSDQualifier_value> <INSDQualifier_value>allelic</INSDQualifier_value> <INSDQualifier_value>unknown</INSDQualifier_value>
	Comment	Definitions of TYPE values: processed - the pseudogene has arisen by reverse transcription of a mRNA into cDNA, followed by reintegration into the genome. Therefore, it has lost any intron/exon structure, and it might have a pseudo-polyA-tail. unprocessed - the pseudogene has arisen from a copy of the parent gene by duplication followed by accumulation of random ~~mutation~~mutations. The changes, compared to their functional homolog, include insertions, deletions, premature stop codons, frameshifts and a higher proportion of non-synonymous versus synonymous substitutions. unitary - the pseudogene has no parent. It is the original gene, which is functional is some species but disrupted in some way (indels, mutation, recombination) in another species or strain. allelic - a (unitary) pseudogene that is stable in the population but importantly it has a functional alternative allele also in the population. i.e., one strain may have the gene, another strain may have the pseudogene. MHC haplotypes have allelic pseudogenes. unknown - the submitter does not know the method of ~~pseudogenisation~~pseudogenization.

6.54.	Qualifier	rearranged
	Definition	the sequence presented in the entry has undergone somatic rearrangement as part of an adaptive immune response; it is not the unrearranged sequence that was inherited from the parental germline
	Value format	none
	Comment	The rearranged qualifier ~~should~~must not be used to annotate chromosome rearrangements that are not involved in an adaptive immune response; germline and rearranged qualifiers ~~cannot~~must not be used in the same source feature; germline and rearranged qualifiers ~~should~~must only be used for molecules that can undergo somatic rearrangements as part of an adaptive immune response; these are the T-cell receptor (TCR) and immunoglobulin loci in the jawed vertebrates, and the unrelated variable lymphocyte receptor (VLR) locus in the jawless fish (lampreys and hagfish); germline and rearranged qualifiers should not be used outside of the Craniata (taxid=89593)

6.55.	Qualifier	recombination_class
	Definition	a structured description of the classification of recombination hotspot region within a sequence
	Value format	TYPE where TYPE is one of the following controlled vocabulary terms or phrases: mitotic recombination non allelic homologous recombination region chromosome_breakpoint
	Example	<INSDQualifier value>meiotic recombination</INSDQualifier value> <INSDQualifier value>chromosome breakpoint</INSDQualifier value>
	Comment	specific recombination classes not yet in the recombination_class controlled vocabulary must be annotated by entering “other” as the recombination_class qualifier value and providing a brief explanation of the novel recombination class in a note qualifier

6.56.	Qualifier	regulatory_class
	Definition	a structured description of the classification of transcriptional, translational, replicational and chromatin structure related regulatory elements in a sequence
	Value format	TYPE where TYPE is one of the following controlled vocabulary terms or phrases: DNase_I_hypersensitive_site enhancer_blocking_element imprinting_control_region insulator locus_control_region matrix_attachment_region minus_35_signal minus_10_signal recoding_stimulatory_region replication regulatory region response_element polyA_signal_sequence ribosome_binding_site riboswitch silencer TATA_box ~~6.55.~~ transcriptional_cis_regulatory_region other
	Example	<INSDQualifier_value>promoter</INSDQualifier_value> <INSDQualifier_value>enhancer</INSDQualifier_value> <INSDQualifier_value>ribosome_binding_site</INSDQualifier_value>
	Comment	specific regulatory classes not yet in the regulatory class controlled vocabulary must be annotated by entering “other” as the regulatory class qualifier value and providing a brief explanation of the novel regulatory_class in a note qualifier

6.57.	Qualifier	replace
	Definition	indicates that the sequence identified in a feature's location is replaced by the sequence shown in the qualifier's value; if no sequence (i.e., no value) is contained within the qualifier, this indicates a deletion
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>a</INSDQualifier_value> <INSDQualifier_value></INSDQualifier_value> - for a deletion
6.58.	Qualifier	ribosomal_slippage
	Definition	during protein translation, certain sequences can program ribosomes to change to an alternative reading frame by a mechanism known as ribosomal slippage
	Value format	none
	Comment	a join operator, e.g.: [join(486..1784,1787..4810)] ~~should~~must be used in the CDS ~~spans~~feature location to indicate the location of ribosomal_slippage
6.59.	Qualifier	rpt_family
	Definition	type of repeated sequence; "Alu" or "Kpn", for example
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>Alu</INSDQualifier_value>
6.60.	Qualifier	rpt_type
	Definition	~~organization~~structure and distribution of repeated sequence
	Value format	One of the following controlled vocabulary terms or phrases: tandem direct inverted flanking ~~terminal~~ nested dispersed long_terminal_repeat non_ltr_retrotransposon_polymeric_tract centromeric_repeat telomeric_repeat x_element_combinatorial_repeat y_prime_element other
	Example	<INSDQualifier_value>~~INVERTED~~inverted</INSDQualifier_value> <INSDQualifier_value>long_terminal_repeat</INSDQualifier_value>
	~~Comment~~	~~the values are case-insensitive, i.e. both "INVERTED" and "inverted" are valid;~~ Comment Definitions of the values: tandem - a repeat that exists adjacent to another in the same orientation; direct - a repeat that exists not always adjacent but is in the same orientation; inverted ~~- a repeat which occurs as part of as set (normally -~~ a ~~part)~~ ~~organized~~repeat pair occurring in ~~the~~ reverse orientation to one another on the same molecule; flanking - a repeat lying outside the sequence for which it has functional significance (eg. transposon insertion target sites); nested - a repeat that is disrupted by the insertion of another element; dispersed - a repeat that is found dispersed throughout the genome; terminal - a repeat at the ends of and within the sequence for which it has functional significance (eg. transposon LTRs); long_terminal_repeat - a sequence directly repeated at both ends of a defined

sequence, of the sort typically found in retroviruses;
non ltr retrotransposon polymeric tract - a polymeric tract, such as poly(dA), within a non LTR retrotransposon;
centromeric_repeat - a repeat region found within the modular centromere;
telomeric repeat - a repeat region found within the telomere;
x element combinatorial repeat - a repeat region located between the X element and the telomere or adjacent Y' element;
y_prime_element - a repeat region located adjacent to telomeric repeats or X element combinatorial repeats, either as a single copy or tandem repeat of two to four copies;
other - a repeat exhibiting important attributes that cannot be described by other values.

6.61.	Qualifier	rpt_unit_range
	Definition	location ~~(range)~~ of a repeating unit expressed as a range
	Value format	<base_range> - where <base_range> is the first and last base (separated by two dots) of a repeating unit
	Example	<INSDQualifier_value>202..245</INSDQualifier_value>
	Comment	used to indicate the base range of the sequence that constitutes a repeating unit within the region specified by the feature keys oriT and repeat_region.
6.62.	Qualifier	rpt_unit_seq
	Definition	identity of a repeat sequence
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>aagggc</INSDQualifier_value> <INSDQualifier_value>ag(5)tg(8)</INSDQualifier_value> <INSDQualifier_value>(AAAGA)6(AAAA)1(AAAGA)12</INSDQualifier_value>
	Comment	used to indicate the literal sequence that constitutes a repeating unit within the region specified by the feature keys oriT and repeat_region
6.63.	Qualifier	satellite
	Definition	identifier for a satellite DNA marker, compose of many tandem repeats (identical or related) of a short basic repeated unit
	Value format	<satellite_type>[:<class>][<identifier>] - where <satellite_type> is one of the following: satellite; microsatellite; minisatellite
	Example	<INSDQualifier_value>satellite: S1a</INSDQualifier_value> <INSDQualifier_value>satellite: alpha</INSDQualifier_value> <INSDQualifier_value>satellite: gamma III</INSDQualifier_value> <INSDQualifier_value>microsatellite: DC130</INSDQualifier_value>
	Comment	many satellites have base composition or other properties that differ from those of the rest of the genome that allows them to be identified.
6.64.	Qualifier	segment
	Definition	name of viral or phage segment sequenced
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>6</INSDQualifier_value>

6.65.	Qualifier	serotype
	Definition	serological variety of a species characterized by its antigenic properties
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>B1</INSDQualifier_value>
	Comment	used only with the source feature key; the Bacteriological Code recommends the use of the term 'serovar' instead of 'serotype' for the prokaryotes; see the International Code of Nomenclature of Bacteria (1990 Revision) Appendix 10.B "Infraspecific Terms".

6.66.	Qualifier	serovar
	Definition	serological variety of a species (usually a prokaryote) characterized by its antigenic properties
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>O157:H7</INSDQualifier_value>
	Comment	used only with the source feature key; the Bacteriological Code recommends the use of the term 'serovar' instead of 'serotype' for prokaryotes; see the International Code of Nomenclature of Bacteria (1990 Revision) Appendix 10.B "Infraspecific Terms".

6.67.	Qualifier	sex
	Definition	sex of the organism from which the sequence was obtained; sex is used for eukaryotic organisms that undergo meiosis and have sexually dimorphic gametes
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Examples	<INSDQualifier_value>female</INSDQualifier_value> <INSDQualifier_value>male</INSDQualifier_value> <INSDQualifier_value>hermaphrodite</INSDQualifier_value> <INSDQualifier_value>unisexual</INSDQualifier_value> <INSDQualifier_value>bisexual</INSDQualifier_value> <INSDQualifier_value>asexual</INSDQualifier_value> <INSDQualifier_value>monoecious</INSDQualifier_value> [or monecious] <INSDQualifier_value>dioecious</INSDQualifier_value> [or diecious]
	Comment	The sex qualifier should be used (instead of mating_type qualifier) in the Metazoa, Embryophyta, Rhodophyta & Phaeophyceae; mating_type qualifier should be used (instead of sex qualifier) in the Bacteria, Archaea & Fungi; neither sex nor mating_type qualifiers should be used in the viruses; outside of the taxa listed above, mating_type qualifier should be used unless the value of the qualifier is taken from the vocabulary given in the examples above

6.68.	Qualifier	standard_name
	Definition	accepted standard name for this feature
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>dotted</INSDQualifier_value>
	Comment	use standard_name qualifier to give full gene name, but use gene qualifier to give gene symbol (in the above example gene qualifier value is Dt).

6.69.	Qualifier	strain
	Definition	strain from which sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>BALB/c</INSDQualifier_value>
	Comment	feature entries including a strain qualifier must not include the environmental_sample qualifier

6.70.	Qualifier	sub_clone
	Definition	sub-clone from which sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>lambda-hIL7.20g</INSDQualifier_value>
	Comment	a source feature must not contain more than one sub_clone ~~should be specified for a given source feature~~qualifier; to indicate that the sequence was obtained from multiple sub_clones, multiple ~~source features should be given~~sources may be further described using the feature key “misc_feature” and the qualifier “note”

6.71.	Qualifier	sub_species
	Definition	name of sub-species of organism from which sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>lactis</INSDQualifier_value>

6.72.	Qualifier	sub_strain
	Definition	name or identifier of a genetically or otherwise modified strain from which sequence was obtained, derived from a parental strain (which should be annotated in the strain qualifier). sub_strain from which sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>abis</INSDQualifier_value>
	Comment	~~If~~must be accompanied by a strain qualifier in a source feature; if the parental strain is not given, ~~this~~the modified strain should be annotated in the strain qualifier instead of sub_strain. For example, either a strain qualifier with the value K-12 and a substrain qualifier with the value MG1655 or a strain qualifier with the value MG1655

6.73.	Qualifier	tag_peptide
	Definition	base location encoding the polypeptide for proteolysis tag of tmRNA and its termination codon
	Value format	<base_range> - where <base_range> provides the first and last base (separated by two dots) of the location for the proteolysis tag
	Example	<INSDQualifier_value>90..122</INSDQualifier_value>
	Comment	it is recommended that the amino acid sequence corresponding to the tag_peptide be annotated by describing a 5’ partial CDS feature; e.g. CDS with a location of <90..122

6.74.	Qualifier	tissue_lib
	Definition	tissue library from which sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>tissue library 772</INSDQualifier_value>

6.75.	Qualifier	tissue_type
	Definition	tissue type from which the sequence was obtained
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>liver</INSDQualifier_value>

6.76.	Qualifier	transl_except
	Definition	translational exception: single codon the translation of which does not conform to genetic code defined by organism or transl_table.
	Value format	(pos:location,aa:<amino_acid>) where <amino_acid> is the three letter abbreviation for the amino acid coded by the codon at the base_range position
	Example	<INSDQualifier_value>(pos:213..215,aa:Trp) </INSDQualifier_value> <INSDQualifier_value>(pos:462..464,aa:OTHER) </INSDQualifier_value> <INSDQualifier_value>(pos:1017,aa:TERM) </INSDQualifier_value> <INSDQualifier_value>(pos:2000..2001,aa:TERM) </INSDQualifier_value> ~~<INSDQualifier_value>(pos:X22222:15..17,aa:Ala) </INSDQualifier_value>~~
	Comment	if the amino acid is not one of the specific amino acids listed in Section 3 of this Annex, use OTHER as <amino_acid> and provide the name of the unusual amino acid in a note qualifier; for modified amino-acid selenocysteine use three letter ~~code 'Sec' (one letter code 'U'~~abbreviation 'Sec' (one letter symbol 'U' in amino-acid sequence) for <amino acid>; for modified amino-acid pyrrolysine use three letter abbreviation 'Pyl' (one letter symbol 'O' in amino-acid sequence) for <amino_acid>; for partial termination codons where TAA stop codon is completed by the addition of 3' A residues to the mRNA either a single base_position or a base_range is used for the location, see the third and fourth examples above, in conjunction with a note qualifier indicating 'stop codon completed by the addition of 3' A residues to the mRNA'.

6.77.	Qualifier	transl_table
	Definition	definition of genetic code table used if other than universal or standard genetic code table. Tables used are described in this Annex
	Value format	<integer> where <integer> is the number assigned to the genetic code table
	Example	<INSDQualifier_value>3</INSDQualifier_value> - example where the yeast mitochondrial code is to be used
	Comment	if the transl_table qualifier is not used to further annotate a CDS feature key, then the CDS is translated using the Standard Code (i.e. Universal Genetic Code). Genetic code exceptions outside the range of specified tables are reported in transl_except qualifiers.

6.78.	Qualifier	trans_splicing
	Definition	indicates that exons from two RNA molecules are ligated in intermolecular reaction to form mature RNA
	Value format	none
	Comment	should be used on features such as CDS, mRNA and other features that are produced as a result of a trans-splicing event. This qualifier ~~should~~must be used only when the splice event is indicated in the "join" operator, e.g. join(complement(69611..69724),139856..140087) in the feature location

6.79.	Qualifier	translation
	Definition	one-letter abbreviated amino acid sequence derived from either the standard (or universal) genetic code or the table as specified in a transl_table qualifier and as determined by an exception in the transl_except qualifier
	Value format	contiguous string of one-letter amino acid abbreviations from Section 3 of this Annex, "X" is to be used for AA exceptions.
	Example	<INSDQualifier_value>MASTFPPWYRGCASTPSLKGLIMCTW</INSDQualifier_value>
	Comment	to be used with CDS feature only; must be accompanied by protein_id qualifier when the translation product contains four or more specifically defined amino acids; see transl_table for definition and location of genetic code Tables; only one of the qualifiers translation, pseudo and pseudogene are permitted to further annotate a CDS feature.

6.80.	Qualifier	variety
	Definition	variety (= varietas, a formal Linnaean rank) of organism from which sequence was derived.
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>insularis</INSDQualifier_value>
	Comment	use the cultivar qualifier for cultivated plant varieties, i.e., products of artificial selection; varieties other than plant and fungal variatas should be annotated via a note qualifier, e.g. with the value <INSDQualifier_value>breed:Cukorova</INSDQualifier_value>

SECTION 7: FEATURE KEYS FOR AMINO ACID SEQUENCES

This section contains the list of allowed feature keys to be used for amino acid sequences. The feature keys are listed in alphabetic order.

7.1.	Feature Key	ACT_SITE
	Definition	Amino acid(s) involved in the activity of an enzyme
	Optional qualifiers	NOTE
	Comment	Each amino acid ~~residue~~residue of the active site ~~should~~must be annotated separately with the ACT_SITE feature key. The corresponding amino acid residue number ~~should~~must be provided as the location descriptor in the feature location element.

7.2.	Feature Key	BINDING
	Definition	Binding site for any chemical group (co-enzyme, prosthetic group, etc.). The chemical nature of the group is indicated in the NOTE qualifier
	Mandatory qualifiers	NOTE
	Comment	Examples of values for the “NOTE” qualifier: “Heme (covalent)” and “Chloride.” Where appropriate, the features keys CA_BIND, DNA_BIND, METAL,and NP_BIND should be used rather than BINDING.

7.3.	Feature Key	CA_BIND
	Definition	Extent of a calcium-binding region
	Optional qualifiers	NOTE

7.4.	Feature Key	CARBOHYD
	Definition	Glycosylation site
	Mandatory qualifiers	NOTE
	Comment	This key describes the occurrence of the attachment of a glycan (mono- or polysaccharide) to a residue of the protein. The type of linkage (C-, N- or O-linked) to the protein is indicated in the “NOTE” qualifier. If the nature of the reducing terminal sugar is known, its abbreviation is shown between parentheses. If three dots ’...’ follow the abbreviation this indicates an extension of the carbohydrate chain. Conversely no dots means that a monosaccharide is linked. Examples of values used in the “NOTE” qualifier: N-linked (GlcNAc...); O-linked (GlcNAc); O-linked (Glc...); C-linked (Man~~); N-linked (GlcNAc...); and~~) partial; O-linked (~~Glc~~Ara...).

7.5.	Feature Key	CHAIN
	Definition	Extent of a polypeptide chain in the mature protein
	Optional qualifiers	NOTE

7.6.	Feature Key	COILED
	Definition	Extent of a coiled-coil region
	Optional qualifiers	NOTE

7.7.	Feature Key	COMPBIAS
	Definition	Extent of a compositionally biased region
	Optional qualifiers	NOTE

7.8.	Feature Key	CONFLICT
	Definition	Different sources report differing sequences
	Optional qualifiers	NOTE
	Comment	Examples of values for the “NOTE” qualifier: Missing; K -> Q; GSDSE -> RIRLR; V -> A.

7.9.	Feature Key	CROSSLNK
	Definition	Post translationally formed amino acid bonds
	Mandatory qualifiers	NOTE
	Comment	Covalent linkages of various types formed between two proteins (interchain cross-links) or between two parts of the same protein (intrachain cross-links); except for cross-links formed by disulfide bonds, for which the “DISULFID” feature key is to be used. For an interchain cross-link, the location descriptor in the feature location element is the residue number of the amino acid cross-linked to the other protein. For an intrachain cross-link, the location descriptors in the feature location element are the residue numbers of the cross-linked amino acids in conjunction with the “join” location operator, e.g. “join(42,50).” The NOTE qualifier indicates the nature of the cross-link; at least specifying the name of the conjugate and the identity of the two amino acids involved. Examples of values for the “NOTE” qualifier: “Isoglutamyl cysteine thioester (Cys-Gln);” “Beta-methyllanthionine (Cys-Thr);” and “Glycyl lysine isopeptide (Lys-Gly) (interchain with G-Cter in ubiquitin)”

7.10.	Feature Key	DISULFID
	Definition	Disulfide bond
	Optional qualifiers	NOTE
	Comment	For an interchain disulfide bond, the location descriptor in the feature location element is the residue number of the cysteine linked to the other protein. For an intrachain cross-link, the location descriptors in the feature location element are the residue numbers of the linked cysteines in conjunction with the “join” location operator, e.g. “join(42,50)”. For interchain disulfide bonds, the NOTE qualifier indicates the nature of the cross-link, by identifying the other protein, for example, “Interchain (between A and B chains)”

7.11.	Feature Key	DNA_BIND
	Definition	Extent of a DNA-binding region
	Mandatory qualifiers	NOTE
	Comment	The nature of the DNA-binding region is given in the NOTE qualifier. Examples of values for the “NOTE” qualifier: “Homeobox” and “Myb 2”

7.12.	Feature Key	DOMAIN
	Definition	Extent of a domain, which is defined as a specific combination of secondary structures organized into a characteristic three-dimensional structure or fold
	Mandatory qualifiers	NOTE
	Comment	The domain type is given in the NOTE qualifier. Where several copies of a domain are present, the domains are numbered. Examples of values for the “NOTE” qualifier: “Ras-GAP” and “Cadherin 1”

7.13.	Feature Key	HELIX
	Definition	Secondary structure: Helices, for example, Alpha-helix; 3(10) helix; or Pi-helix
	Optional qualifiers	NOTE
	Comment	This feature is used only for proteins whose tertiary structure is known. Only three types of secondary structure are specified: helices (key HELIX), beta-strands (key STRAND) and turns (key TURN). Residues not specified in one of these classes are in a ’loop’ or ’random-coil’ structure.

7.14.	Feature Key	INIT_MET
	Definition	Initiator methionine
	Optional qualifiers	NOTE
	Comment	The location descriptor in the feature location element is “1”. This feature key indicates the N-terminal methionine is cleaved off. This feature is not used when the initiator methionine is not cleaved off.

7.15.	Feature Key	INTRAMEM
	Definition	Extent of a region located in a membrane without crossing it
	Optional qualifiers	NOTE

7.16.	Feature Key	LIPID
	Definition	Covalent binding of a lipid moiety
	Mandatory qualifiers	NOTE
	Comment	The chemical nature of the bound lipid moiety is given in the NOTE qualifier, indicating at least the name of the lipidated amino acid. Examples of values for the “NOTE” qualifier: “N-myristoyl glycine”; “GPI-anchor amidated serine” and “S-diacylglycerol cysteine.”

7.17.	Feature Key	METAL
	Definition	Binding site for a metal ion.
	Mandatory qualifiers	NOTE
	Comment	The NOTE qualifier indicates the nature of the metal. Examples of values for the “NOTE” qualifier: “Iron (heme axial ligand)” and “Copper”.

7.18.	Feature Key	MOD_RES
	Definition	Posttranslational modification of a residue
	Mandatory qualifiers	NOTE
	Comment	The chemical nature of the modified residue is given in the NOTE qualifier, indicating at least the name of the post-translationally modified amino acid. If the modified amino acid is listed in ~~Table~~Section 4 of this Annex, the abbreviation may be used in place of the the full name. Examples of values for the “NOTE” qualifier: “N-acetylalanine”; “3-Hyp”; and “MeLys” or “N-6-methyllysine"

7.19.	Feature Key	MOTIF
	Definition	Short (up to 20 amino acids) sequence motif of biological interest
	Optional qualifiers	NOTE

7.20.	Feature Key	MUTAGEN
	Definition	Site which has been experimentally altered by mutagenesis
	Optional qualifiers	NOTE

7.21.	Feature Key	NON_STD
	Definition	Non-standard amino acid
	Optional qualifiers	NOTE
	Comment	This key describes the occurrence of non-standard amino acids selenocysteine (U) and pyrrolysine (O) in the amino acid sequence.

7.22.	Feature Key	NON_TER
	Definition	The residue at an extremity of the sequence is not the terminal residue
	Optional qualifiers	NOTE
	Comment	If applied to position 1, this means that the first position is not the N-terminus of the complete molecule. If applied to the last position, it means that this position is not the C-terminus of the complete molecule.

7.23.	Feature Key	NP_BIND
	Definition	Extent of a nucleotide phosphate-binding region
	Mandatory qualifiers	NOTE
	Comment	The nature of the nucleotide phosphate is indicated in the NOTE qualifier. Examples of values for the “NOTE” qualifier: “ATP” and “FAD”.

7.24.	Feature Key	PEPTIDE
	Definition	Extent of a released active peptide
	Optional qualifiers	NOTE

7.25.	Feature Key	PROPEP
	Definition	Extent of a propeptide
	Optional qualifiers	NOTE

7.26.	Feature Key	REGION
	Definition	Extent of a region of interest in the sequence
	Optional qualifiers	NOTE

7.27.	Feature Key	REPEAT
	Definition	Extent of an internal sequence repetition
	Optional qualifiers	NOTE

7.28.	Feature Key	SIGNAL
	Definition	Extent of a signal sequence (prepeptide)
	Optional qualifiers	NOTE

7.29.	Feature Key	SITE
	Definition	Any interesting single amino-acid site on the sequence that is not defined by another feature key. It can also apply to an amino acid bond which is represented by the positions of the two flanking amino acids
	Mandatory qualifier	NOTE
	Comment	When SITE is used to annotate a modified amino acid the value for the qualifier “NOTE” must either be an abbreviation set forth in Section 4 of this Annex, ~~Table 4,~~ or the complete, unabbreviated name of the modified amino acid.

7.30.	Feature Key	SOURCE
	Definition	Identifies the source of the sequence; this key is mandatory; every sequence will have a single SOURCE feature spanning the entire sequence
	Mandatory qualifiers	MOL_TYPE ORGANISM
	Optional qualifiers	NOTE

7.31.	Feature Key	STRAND
	Definition	Secondary structure: Beta-strand; for example Hydrogen bonded beta-strand or residue in an isolated beta-bridge
	Optional qualifiers	NOTE
	Comment	This feature is used only for proteins whose tertiary structure is known. Only three types of secondary structure are specified: helices (key HELIX), beta-strands (key STRAND) and turns (key TURN). Residues not specified in one of these classes are in a ’loop’ or ’random-coil’ structure.

7.32.	Feature Key	TOPO_DOM
	Definition	Topological domain
	Optional qualifiers	NOTE

7.33.	Feature Key	TRANSMEM
	Definition	Extent of a transmembrane region
	Optional qualifiers	NOTE

7.34.	Feature Key	TRANSIT
	Definition	Extent of a transit peptide (mitochondrion, chloroplast, thylakoid, cyanelle, peroxisome etc.)
	Optional qualifiers	NOTE

7.35.	Feature Key	TURN
	Definition	Secondary structure Turns, for example, H-bonded turn (3-turn, 4-turn or 5-turn)
	Optional qualifiers	NOTE
	Comment	This feature is used only for proteins whose tertiary structure is known. Only three types of secondary structure are specified: helices (key HELIX), beta-strands (key STRAND) and turns (key TURN). Residues not specified in one of these classes are in a ’loop’ or ’random-coil’ structure.

7.36.	Feature Key	UNSURE
	Definition	Uncertainties in the ~~amino acid~~ sequence
	Optional qualifiers	NOTE
	Comment	Used to describe region(s) of an amino acid sequence for which the authors are unsure about the sequence presentation.

7.37.	Feature Key	VARIANT
	Definition	Authors report that sequence variants exist
	Optional qualifiers	NOTE

7.38.	Feature Key	VAR_SEQ
	Definition	Description of sequence variants produced by alternative splicing, alternative promoter usage, alternative initiation and ribosomal frameshifting
	Optional qualifiers	NOTE

7.39.	Feature Key	ZN_FING
	Definition	Extent of a zinc finger region
	Mandatory qualifiers	NOTE
	Comment	The type of zinc finger is indicated in the NOTE qualifier. For example: “GATA-type” and “NR C4-type”

SECTION 8: QUALIFIERS FOR AMINO ACID SEQUENCES

This section contains the list of allowed qualifiers to be used for amino acid sequences.

PLEASE NOTE: Any qualifier value provided for a qualifier with a “free text” value format may require translation for National/Regional procedures.

8.1.	Qualifier	MOL_TYPE
	Definition	In vivo molecule type of sequence
	Value format	protein
	Example	<INSDQualifier_value>protein</INSDQualifier_value>
	Comment	The "MOL_TYPE" qualifier is mandatory on the SOURCE feature key.

8.2.	Qualifier	NOTE
	Definition	Any comment or additional information
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>Heme (covalent)</INSDQualifier_value>
	Comment	The “NOTE” qualifier is mandatory for the feature keys: BINDING; CARBOHYD; CROSSLNK; DISULFID; DNA_BIND; DOMAIN; LIPID; METAL; MOD_RES; NP_BIND and ZN_FING

8.3.	Qualifier	ORGANISM
	Definition	Scientific name of the organism that provided the peptide
	Value format	free text (NOTE: this value may require translation for National/Regional procedures)
	Example	<INSDQualifier_value>Homo sapiens</INSDQualifier_value>
	Comment	The “ORGANISM” qualifier is mandatory for the SOURCE feature key.

~~SECTION 9: GENETIC CODE TABLES~~

Table 5 reproduces ~~genetic code tables~~Genetic Code Tables to be used for translating coding sequences. The value for the trans_table qualifier is the number assigned to the corresponding genetic code table. Where a CDS feature is described with a translation qualifier but not a transl_table qualifier, the 1 - Standard Code is used by default for translation. (Note: Genetic code tables 7, 8, 15, and 17 to 20 do not exist, therefore these numbers do not appear in Table 5.)

Table 5: Genetic Code Tables

1 - Standard Code

```
  AAs  = FFLLSSSSYY**CC*WLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts = ---M---------------M---------------M----------------------------
Base1  = TTTTTTTTTTTTTTTTCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGG
Base2  = TTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGG
Base3  = TCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG
```

2 - Vertebrate Mitochondrial Code

```
  AAs  = FFLLSSSSYY**CCWWLLLLPPPPHHQQRRRRIIMMTTTTNNKKSS**VVVVAAAADDEEGGGG
Starts = --------------------------------MMMM---------------M------------
Base1  = TTTTTTTTTTTTTTTTCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGG
Base2  = TTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGG
Base3  = TCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG
```

3 - Yeast Mitochondrial Code

```
  AAs  = FFLLSSSSYY**CCWWTTTTPPPPHHQQRRRRIIMMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts = ----------------------------------MM----------------------------
Base1  = TTTTTTTTTTTTTTTTCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGG
Base2  = TTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGG
Base3  = TCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG
```

4 - Mold, Protozoan, Coelenterate Mitochondrial Code & Mycoplasma/Spiroplasma Code

```
  AAs  = FFLLSSSSYY**CCWWLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts = --MM---------------M------------MMMM---------------M------------
Base1  = TTTTTTTTTTTTTTTTCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGG
Base2  = TTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGG
Base3  = TCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG
```

5 - Invertebrate Mitochondrial Code

```
  AAs  = FFLLSSSSYY**CCWWLLLLPPPPHHQQRRRRIIMMTTTTNNKKSSSSVVVVAAAADDEEGGGG
Starts = ---M----------------------------MMMM---------------M------------
Base1  = TTTTTTTTTTTTTTTTCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGG
Base2  = TTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGG
Base3  = TCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG
```

6 - Ciliate, Dasycladacean and Hexamita Nuclear Code

```
  AAs  = FFLLSSSSYYQQCC*WLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts = ----------------------------------M----------------------------
Base1  = TTTTTTTTTTTTTTTTCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGG
Base2  = TTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGG
Base3  = TCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG
```

9 - Echinoderm and Flatworm Mitochondrial Code

```
  AAs  = FFLLSSSSYY**CCWWLLLLPPPPHHQQRRRRIIIMTTTTNNNKSSSSVVVVAAAADDEEGGGG
Starts = ----------------------------------M---------------M------------
Base1  = TTTTTTTTTTTTTTTTCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGG
Base2  = TTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGG
Base3  = TCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG
```

10 - Euplotid Nuclear Code

```
  AAs  =  FFLLSSSSYY**CCCWLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  ----------------------------------M----------------------------
Base1  =  ttttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaagggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

11 - Bacterial and Plant Plastid Code

```
  AAs  =  FFLLSSSSYY**CC*WLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  ---M---------------M------------MMMM---------------M------------
Base1  =  ttttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaagggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

12 - Alternative Yeast Nuclear Code

```
  AAs  =  FFLLSSSSYY**CC*WLLLSPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  --------------------M---------------M----------------------------
Base1  =  ttttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaagggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

13- Ascidian Mitochondrial Code

```
  AAs  =  FFLLSSSSYY**CCWWLLLLPPPPHHQQRRRRIIMMTTTTNNKKSSGGVVVVAAAADDEEGGGG
Starts =  ---M------------------------------MM---------------M------------
Base1  =  ttttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaagggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

14 - Alternative Flatworm Mitochondrial Code

```
  AAs  =  FFLLSSSSYYY*CCWWLLLLPPPPHHQQRRRRIIIMTTTTNNNKSSSSVVVVAAAADDEEGGGG
Starts =  ----------------------------------M----------------------------
Base1  =  ttttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaagggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
Starts =  ----------------------------------M----------------------------
Base1  =  ttttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaagggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

~~**15 - Blepharisma Nuclear Code**~~

~~```~~
~~ AAs = FFLLSSSSYY*QCC*WLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG~~
~~Starts = ----------------------------------M----------------------------~~
~~Base1 = ttttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggggg~~
~~Base2 = ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaagggg~~
~~Base3 = tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag~~
~~```~~

16 - Chlorophycean Mitochondrial Code

```
  AAs  =  FFLLSSSSYY*LCC*WLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  ----------------------------------M----------------------------
Base1  =  ttttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaagggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

21 - Trematode Mitochondrial Code

```
  AAs  =  FFLLSSSSYY**CCWWLLLLPPPPHHQQRRRRIIMMTTTTNNNKSSSSVVVVAAAADDEEGGGG
Starts =  ----------------------------------M---------------M------------
Base1  =  ttttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaagggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

22 - Scenedesmus obliquus Mitochondrial Code

```
  AAs  =  FFLLSS*SYY*LCC*WLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  ----------------------------------M----------------------------
Base1  =  tttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaaggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

23 - Thraustochytrium Mitochondrial Code

```
  AAs  =  FF*LSSSSYY**CC*WLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  --------------------------------M--M---------------M------------
Base1  =  tttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaaggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

24 - Pterobranchia Mitochondrial Code

```
  AAs  =  FFLLSSSSYY**CCWWLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSSKVVVVAAAADDEEGGGG
Starts =  ---M---------------M---------------M---------------M------------
Base1  =  tttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaaggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

25 - Candidate Division SR1 and Gracilibacteria Code

```
  AAs  =  FFLLSSSSYY**CCGWLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  ---M---------------M---------------M----------------------------
Base1  =  tttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaaggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

26 - Pachysolen tannophilus Nuclear Code

```
  AAs  =  FFLLSSSSYY**CC*WLLLAPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  --------------------M---------------M----------------------------
Base1  =  tttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaaggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

27 - Karyorelict Nuclear

```
  AAs  =  FFLLSSSSYYQQCCWWLLLAPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  ---------------*--------------------M----------------------------
Base1  =  tttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaaggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

28 - Condylostoma Nuclear

```
  AAs  =  FFLLSSSSYYQQCCWWLLLAPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  ----------**--*--------------------M----------------------------
Base1  =  tttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaaggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

29 - Mesodinium Nuclear

```
  AAs  =  FFLLSSSSYYYYCC*WLLLAPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  ----------------------------------M----------------------------
Base1  =  tttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaaggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

30 - Peritrich Nuclear

```
  AAs  =  FFLLSSSSYYEECC*WLLLAPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  ----------------------------------M----------------------------
Base1  =  tttttttttttttttcccccccccccccccaaaaaaaaaaaaaaaaggggggggggggggg
Base2  =  ttttccccaaaaggggttttccccaaaaggggttttccccaaaaggggttttccccaaaaggg
Base3  =  tcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag
```

31 - Blastocrithidia Nuclear

```
  AAs  =  FFLLSSSSYYEECCWWLLLLPPPPHHQQRRRRIIIMTTTTNNKKSSRRVVVVAAAADDEEGGGG
Starts =  ----------**--------------------------M----------------------------
Base1  =  TTTTTTTTTTTTTTTTCCCCCCCCCCCCCCCCAAAAAAAAAAAAAAAAGGGGGGGGGGGGGGGG
Base2  =  TTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGGTTTTCCCCAAAAGGGG
Base3  =  TCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAG
```

[Annex II to ST.26 follows]

ST.26 - ANNEX II

DOCUMENT TYPE DEFINITION FOR SEQUENCE LISTING (DTD)

Final Draft

Proposal presented by the SEQL Task Force for consideration and adoption at the CWS/5

```
<?xml version="1.0" encoding="UTF-8"?>
<!--Annex II of WIPO Standard ST.26, Document Type Definition (DTD) for Sequence Listing

This entity may be identified by the PUBLIC identifier:
************************************************************************************
****
PUBLIC "-//WIPO//DTD SEQUENCE LISTING 1.01//EN" "ST26SequenceListing_V1_01.dtd"
************************************************************************************
****
* PUBLIC DTD URL

* http://www.wipo.int/standards/DTD/ST26SequenceListing_V1_01.dtd
************************************************************************

WIPO Standard ST.26, version 1.0, Recommended Standard for the presentation of
nucleotide and amino acid sequence listings using XML (eXtensible Markup Language),
adopted by the Committee on WIPO Standards (CWS) at its reconvened fourth session on
March 24, 2016
Revision of Annex II to WIPO Standard ST.26 is submitted for approval by the Committee
on WIPO Standards (CWS) at its fifth session.

************************************************************************
* CONTACTS
************************************************************************
xml.standards@wipo.int


************************************************************************
* NOTES
************************************************************************
The sequence data part is a subset of the complete INSDC DTD V.1.5 that only covers
the requirements of WIPO Standard ST.26.

************************************************************************
* REVISION HISTORY
************************************************************************
2017-06-02: Version 1.1 (if it is approved by the CWS)
Changes:
Comments added to <INSDSeq_length>, <INSDSeq_division> and <INSDSeq_sequence> to clarify
the reason of the differences between the INSDC DTD v.1.5 and ST26 Sequence Listing DTD
V1_1.
************************************************************************
2016-03-24: Version 1.0 adopted by the CWS/4Bis
2014-03-11: Final draft for adoption.
************************************************************************

ST26SequenceListing
************************************************************************
* ROOT ELEMENT
************************************************************************
-->
<!ELEMENT ST26SequenceListing  ((ApplicantFileReference | (
               ApplicationIdentification,ApplicantFileReference?)),
               EarliestPriorityApplicationIdentification?,(ApplicantName,
               ApplicantNameLatin?)?,(InventorName,InventorNameLatin?)?,
               InventionTitle+,SequenceTotalQuantity,SequenceData+) >

<!--The elements ApplicantName and InventorName are optional in this DTD to facilitate
the conversion between various encoding schemes-->
```

```
<!ATTLIST ST26SequenceListing
               dtdVersion  CDATA    #REQUIRED
               fileName  CDATA    #IMPLIED
               softwareName  CDATA    #IMPLIED
               softwareVersion  CDATA    #IMPLIED
               productionDate  CDATA    #IMPLIED  >

<!--ApplicantFileReference
Applicant's or agent's file reference, mandatory if application identification not
provided.
-->
<!ELEMENT ApplicantFileReference  (#PCDATA) >

<!--ApplicationIdentification
Application identification for which the sequence listing is submitted, when available.
-->
<!ELEMENT ApplicationIdentification  (IPOfficeCode,ApplicationNumberText,
               FilingDate?) >

<!--EarliestPriorityApplicationIdentification
Application identification of the earliest claimed priority, which contains
IPOfficeCode, ApplicationNumberText and FilingDate elements.
For details, please see ApplicationIdentification.
-->
<!ELEMENT EarliestPriorityApplicationIdentification  (IPOfficeCode,
               ApplicationNumberText,FilingDate?) >

<!--ApplicantName
The name of the first mentioned applicant in characters set forth in paragraph 40 (a) of
the ST.26 main body document.
-->
<!--languageCode: Appropriate language code from ISO 639-1 – Codes for the
representation of names of languages - Part 1: Alpha-2
-->
<!ELEMENT ApplicantName  (#PCDATA) >
<!ATTLIST ApplicantName
               languageCode  CDATA    #REQUIRED  >

<!--ApplicantNameLatin
Where ApplicantName is typed in characters other than those as set forth in paragraph 40
(b), a translation or transliteration of the name of the first mentioned applicant must
also be typed in characters as set forth in paragraph 40 (b) of the ST.26 main body
document.
-->
<!ELEMENT ApplicantNameLatin  (#PCDATA) >

<!--InventorName
Name of the first mentioned inventor typed in the characters as set forth in paragraph
40 (a).-->
<!--languageCode: Appropriate language code from ISO 639-1 – Codes for the
representation of names of languages - Part 1: Alpha-2
-->
<!ELEMENT InventorName  (#PCDATA) >
<!ATTLIST InventorName
               languageCode  CDATA    #REQUIRED  >

<!--InventorNameLatin
Where InventorName is typed in characters other than those as set forth in paragraph 40
(b), a translation or transliteration of the first mentioned inventor may also be typed
in characters as set forth in paragraph 40 (b).
-->
<!ELEMENT InventorNameLatin  (#PCDATA) >

<!--InventionTitle
Title of the invention typed in the characters as set forth in paragraph 40 (a) in the
language of filing. A translation of the title of the invention into additional
languages may be typed in the characters as set forth in paragraph 40 (a) using
additional InventionTitle elements. Preferably two to seven words.
-->
<!--languageCode: Appropriate language code from ISO 639-1 - Codes
for the representation of names of languages - Part 1: Alpha-2
```

```
-->
<!ELEMENT InventionTitle  (#PCDATA) >
<!ATTLIST InventionTitle
               languageCode  CDATA    #REQUIRED  >

<!--SequenceTotalQuantity
Indicates the total number of sequences in the document.
Its purpose is to be quickly accessible for automatic processing.
-->
<!ELEMENT SequenceTotalQuantity  (#PCDATA) >

<!--SequenceData
Data for individual Sequence.
For intentionally skipped sequences see the ST.26 main body document.
-->
<!ELEMENT SequenceData  (INSDSeq) >
<!ATTLIST SequenceData
               sequenceIDNumber  CDATA    #REQUIRED  >

<!--IPOfficeCode
ST.3 code. For example, if the application identification is PCT/IB2013/099999, then
IPOfficeCode value will be International Bureau of WIPO.
-->
<!ELEMENT IPOfficeCode  (#PCDATA) >

<!--ApplicationNumberText
The application identification as provided by the office of filing (e.g.
PCT/IB2013/099999)
-->
<!ELEMENT ApplicationNumberText  (#PCDATA) >

<!--FilingDate
The date of filing of the patent application for which the sequence listing is submitted
in ST.2 format "CCYY-MM-DD", using a 4-digit calendar year, a 2-digit calendar month and
a 2-digit day within the calendar month, e.g., 2015-01-31. For details, please see
paragraphs 7 (a) and 11 of WIPO Standard ST.2.
-->
<!ELEMENT FilingDate  (#PCDATA) >

<!--************************************************************************
* INSD Part
*************************************************************************

The purpose of the INSD part of this DTD is to define a customized DTD for sequence
listings to support the work of IP offices while facilitating the data exchange with the
public repositories.

The INSD part is subset of the INSD DTD v1.45 and as such can only be used to generate
an XML instance as it will not support the complete INSD structure.

This part is based on:

The International Nucleotide Sequence Database (INSD) collaboration.

INSDSeq provides the elements of a sequence as presented in the GenBank/EMBL/DDBJ-style
flatfile formats. Not all elements are used here.
-->

<!--INSDSeq
Sequence data. Changed INSD V1.5 DTD elements, INSDSeq_division and INSDSeq_sequence
from optional to mandatory per business requirements.
-->
<!ELEMENT INSDSeq  (INSDSeq_length,INSDSeq_moltype,INSDSeq_division,
               INSDSeq_other-seqids?,INSDSeq_feature-table?,INSDSeq_sequence) >

<!--INSDSeq_length
The length of the sequence. INSDSeq_length allows only integer.
-->
<!ELEMENT INSDSeq_length  (#PCDATA) >

<!--INSDSeq_moltype
```

```
Admissible values: DNA, RNA, AA
-->
<!ELEMENT INSDSeq_moltype  (#PCDATA) >

<!--INSDSeq_division
Indication that a sequence is related to a patent application. Must be populated with
the value PAT.
-->
<!ELEMENT INSDSeq_division  (#PCDATA) >

<!--INSDSeq_other-seqids
In the context of data exchange with database providers, the Patent Offices should
populate for each sequence the element INSDSeq_other-seqids with one INSDSeqid
containing a reference to the corresponding published patent and the sequence
identification.
-->
<!ELEMENT INSDSeq_other-seqids  (INSDSeqid?) >

<!--INSDSeq_feature-table
Information on the location and roles of various regions within a particular sequence.
Whenever the element INSDSeq_feature-table is used, it must contain at least one
feature.
-->
<!ELEMENT INSDSeq_feature-table  (INSDFeature+) >

<!--INSDSeq_sequence
The residues of the sequence. The sequence must not contain numbers, punctuation or
whitespace characters.
-->
<!ELEMENT INSDSeq_sequence  (#PCDATA) >

<!--INSDSeqid
Intended for the use of Patent Offices in data exchange only.

Format:
pat|{office code}|{publication number}|{document kind code}|{Sequence identification
number}

where office code is the code of the IP office publishing the patent document,
publication number is the publication number of the application or patent, document kind
code is the letter codes to distinguish patent documents as defined in ST.16 and
Sequence identification number is the number of the sequence in that application or
patent

Example:
pat|WO|2013999999|A1|123456

This represents the 123456th sequence from WO patent publication No. 2013999999 (A1)
-->
<!ELEMENT INSDSeqid  (#PCDATA) >

<!--INSDFeature
Description of one feature.
-->
<!ELEMENT INSDFeature  (INSDFeature_key,INSDFeature_location,INSDFeature_quals?) >

<!--INSDFeature_key
A word or abbreviation indicating a feature.
-->
<!ELEMENT INSDFeature_key  (#PCDATA) >

<!--INSDFeature_location
Region of the presented sequence which corresponds to the feature.
-->
<!ELEMENT INSDFeature_location  (#PCDATA) >

<!--INSDFeature_quals
List of qualifiers containing auxiliary information about a feature.
-->
<!ELEMENT INSDFeature_quals  (INSDQualifier*) >
```

```
<!--INSDQualifier
Additional information about a feature.
For coding sequences and variants see the ST.26 main body document.
-->
<!ELEMENT INSDQualifier  (INSDQualifier_name,INSDQualifier_value?) >

<!--INSDQualifier_name
Name of the qualifier.
-->
<!ELEMENT INSDQualifier_name  (#PCDATA) >

<!--INSDQualifier_value
Value of the qualifier.
-->
<!ELEMENT INSDQualifier_value  (#PCDATA) >
```

[Annex VI to ST.26 follows]

ST.26 - ANNEX VI

GUIDANCE DOCUMENT

Final Draft

Proposal presented by the SEQL Task Force for consideration and adoption at the CWS/5

Introduction

This Standard indicates as one of its purposes, to "allow applicants to draw up a single sequence listing in a patent application acceptable for the purposes of both international and national or regional procedures." The purpose of this Guidance Document is to ensure that all applicants and Intellectual Property Offices (IPOs) understand and agree on the requirements for inclusion and representation of sequence disclosures, such that this purpose is realized.

This guidance document consists of this introduction, an example index, examples of sequence disclosures, and an appendix containing a sequence listing in XML with sequences from the examples. This introduction explains certain concepts and terminology used in the remainder of this document. The examples illustrate the requirements of specific paragraphs of the standard and each example has been designated with the most relevant paragraph number. Some examples further illustrate other paragraphs and appropriate cross-references are indicated at the end of each example. The index provides page numbers for the examples and any indicated cross-references. Each sequence in an example that either must or may be included in a sequence listing has been assigned a sequence identification number (SEQ ID NO) and appears in XML format in the Appendix to this document.

For each example, any explanatory information presented with a sequence is intended to be considered as the entirety of the disclosure concerning that sequence. The given answers take into account only the information explicitly presented in the example.

The guidance provided in this document is directed to the preparation of a sequence listing for provision **on the filing date** of a patent application. Preparation of a sequence listing for provision **subsequent to the filing date** of a patent application must take into account whether the information provided could be considered by an IPO to add subject matter to the original disclosure. Therefore, it is possible that the guidance provided in this document may not be applicable to a sequence listing provided subsequent to the filing date of a patent application.

Preparation of a sequence listing

Sequence listing preparation for a patent application requires consideration of the following questions:

1. Does ST.26 paragraph 7 require inclusion of a particular disclosed sequence?

2. If inclusion of a particular disclosed sequence is not required, is inclusion of that sequence permitted by ST.26?

3. If inclusion of a particular disclosed sequence is required or permitted by ST.26, how should that sequence be represented in the sequence listing?

Regarding the first question, ST.26 paragraph 7 (with certain restrictions) requires inclusion of a sequence disclosed in a patent application by **enumeration of its residues**, where the sequence contains ten or more **specifically defined** nucleotides or four or more **specifically defined** amino acids.

Regarding the second question, ST.26 paragraph 8 prohibits inclusion of any sequences having fewer than ten **specifically defined** nucleotides or four **specifically defined** amino acids.

A clear understanding of "enumeration of its residues" and "specifically defined" is necessary to answer these two questions.

Regarding the third question, this document provides sequence disclosures which exemplify a variety of scenarios together with a complete discussion of the preferred means of representation of each sequence, or where a sequence contains multiple variations - the **"most encompassing sequence",** in accordance with this Standard. Since it is impossible to address every possible unusual sequence scenario, this guidance document attempts to set forth the reasoning behind the approach to each example and the manner in which ST.26 provisions are applied, such that the same reasoning can be applied to other sequence scenarios not exemplified.

“Enumeration of its residues”

ST.26 paragraph 3(c) defines “**enumeration of its residues”** as disclosure of a sequence in a patent application by listing, in order, each residue of the sequence, wherein (i) the residue is represented by a name, abbreviation, symbol, or structure; or (ii) multiple residues are represented by a shorthand formula. A sequence should be disclosed in a patent application by “enumeration of its residues” using **conventional symbols**, which are the nucleotide symbols set forth in Section 1, Table 1 of ST.26 Annex 1 (i.e. the lower case symbols or their upper case equivalents[1]) and the amino acid symbols set forth in Section 3, Table 3 of ST.26 Annex 1 (i.e. the upper case symbols or their lower case equivalents[1]). Symbols other than those set forth in these tables are “**nonconventional”**.

A sequence is sometimes disclosed in a non-preferred manner by “enumeration of its residues” using **conventional abbreviations** or **full names** (as opposed to conventional symbols) as set forth in Tables A and B below, conventional symbols or abbreviations used in a nonconventional manner, nonconventional symbols or abbreviations, chemical formulas/structures, or shorthand formulas. Care should be taken to disclose sequences in the preferred manner; however, where sequences are disclosed in a non-preferred manner, consultation of the explanation of the sequence in the disclosure may be necessary to determine the meaning of the non-preferred symbol or abbreviation.

Where a conventional symbol or abbreviation is used, the explanation of the sequence in the disclosure must still be consulted to confirm that the symbol is used in a conventional manner. Otherwise, if the symbol is used in a nonconventional manner, the explanation is necessary to determine whether ST.26 paragraph 7 requires inclusion in the sequence listing or whether paragraph 8 prohibits inclusion.

Where a nonconventional symbol or abbreviation is disclosed as equivalent to a conventional symbol or abbreviation (e.g., “Z_1” means “A”), or to a specific sequence of conventional symbols (e.g., “Z_1” means “agga”), then the sequence is interpreted as though it were disclosed using the equivalent conventional symbol(s) or abbreviation(s), to determine whether ST.26 paragraph 7 requires inclusion in the sequence listing or whether paragraph 8 prohibits inclusion. Where a nonconventional nucleotide symbol is used as an ambiguity symbol (e.g., X1 = inosine or pseudouridine), but is not equivalent to one of the conventional ambiguity symbols in Section 1, Table 1 (i.e., “m”, “r”, “w”, “s”, “y”, “k”, “v”, “h”, “d”, “b”, or “n”), then the residue is interpreted as an “n” residue to determine whether ST.26 Paragraph 7 requires inclusion of the sequence in the sequence listing or whether ST.26 Paragraph 8 prohibits inclusion. Similarly, where a nonconventional amino acid symbol is used as an ambiguity symbol (e.g., “Z_1” means “A”, “G”, “S” or “T”), but is not equivalent to one of the conventional ambiguity symbols in Section 3, Table 3 (i.e., B, Z, J, or X), then the residue is interpreted as an “X” residue to determine whether ST.26 paragraph 7 requires inclusion of the sequence in the sequence listing or whether ST.26 paragraph 8 prohibits inclusion.

“Specifically defined”

ST.26 paragraph 3(k) defines “**specifically defined**” as any nucleotide other than those represented by the symbol “n” and any amino acid other than those represented by the symbol “X”, listed in Annex I, wherein “n” and “X” are used in a conventional manner as described in Section 1, Table 1 (i.e., “a or c or g or t/u; ‘unknown’ or ‘other’”) and Section 3, Table 3 (i.e., A or R or N or D or C or Q or E or G or H or I or L or K or M or F or P or O or S or U or T or W or Y or V, ‘unknown’ or ‘other’”), respectively. The discussion above concerning conventional symbols or nonconventional symbols or abbreviations and their use in a conventional or nonconventional manner will be taken into account to determine whether a nucleotide or an amino acid is “specifically defined”.

“Most encompassing sequence”

Where a sequence that meets the requirements of paragraph 7 is disclosed by enumeration of its residues only once in an application, but is described differently in multiple embodiments, e.g. in one embodiment “X” in one or more locations could be any amino acid, but in further embodiments, “X” could be only a limited number of amino acids, ST.26 requires inclusion in a sequence listing of only the single sequence that has been enumerated by its residues. As per paragraphs 15 and 27, where such a sequence contains multiple “n” or “X” ambiguity symbols, “n” or “X” is construed to represent any nucleotide or amino acid, respectively, in the absence of further annotation. Consequently, the single sequence required to be included is the most encompassing sequence disclosed. The **most encompassing sequence** is the single sequence having variant residues which are represented by the most restrictive ambiguity symbols that include the most disclosed embodiments. However, inclusion of additional specific sequences is *strongly* encouraged where practical, e.g. which represent additional embodiments that are a key part of the invention. Inclusion of the additional sequences allows for a more thorough search and provides public notice of the subject matter for which a patent is sought.

1 NOTE: While an application disclosure may represent nucleotides or amino acids with either lower case or upper case symbols, for a sequence included in a sequence listing, only lower case letters must be used for representation of a nucleotide sequence (see ST.26 paragraph 13) and only upper case letters must be used for representation of an amino acid sequence (see ST.26 paragraph 26).

Proper Usage of the Ambiguity Symbol "n" in a Sequence Listing

The symbol "n"

a. must not be used to represent anything other than a single nucleotide;

b. will be construed as any one of "a", "c", "g", or "t/u" except where it is used with a further description;

c. should be used to represent any of the following nucleotides together with a further description:

i. modified nucleotide, e.g., natural, synthetic, or non-naturally occurring, that cannot otherwise be represented by any other symbol in Annex I (see Section 1, Table 1);

ii. "unknown" nucleotide, i.e., not determined, not disclosed, or unsure;

iii. an abasic site; or

d. may be used to represent a sequence variant, i.e., alternatives, deletions, insertions, or substitutions, where "n" is the most restrictive ambiguity symbol.

Proper Usage of the Ambiguity Symbol "X" in a Sequence Listing

The symbol "X"

a. must not be used to represent anything other than a single amino acid;

b. will be construed as any one of "A", "R", "N", "D", "C", "Q", "E", "G", "H", "I", "L", "K", "M", "F", "P", "O", "S", "U", "T", "W", "Y", or "V", except where it is used with a further description;

c. should be used to represent any of the following amino acids together with a further description:

i. modified amino acid, e.g., natural, synthetic, or non-naturally occurring, that cannot otherwise be represented by any other symbol in Annex I (see Section 3, Table 3);

ii. "unknown" amino acid, i.e., not determined, not disclosed, or unsure; or

d. may be used to represent a sequence variant, i.e., alternatives, deletions, insertions, or substitutions, where "X" is the most restrictive ambiguity symbol.

Table A – Conventional Nucleotide Symbols, Abbreviations, and Names

Symbol	Abbreviation	Nucleotide Name
a		Adenine
c		Cytosine
g		Guanine
t		Thymine in DNA Uracil in RNA (t/u)
m	a or c	
r	a or g	
w	a or t/u	
s	c or g	
y	c or t/u	
k	g or t/u	
v	a or c or g; not t/u	
h	a or c or t/u; not g	
d	a or g or t/u; not c	
b	c or g or t/u; not a	
n	a or c or g or t/u; "unknown" or "other"	

Table B – Conventional Amino Acid Symbols, Abbreviations, and Names

Symbol	3-Letter Abbreviation	Amino Acid Name
A	Ala	Alanine
R	Arg	Arginine
N	Asn	Asparagine
D	Asp	Aspartic Acid (Aspartate)
C	Cys	Cysteine
E	Glu	Glutamic Acid (Glutamate)
Q	Gln	Glutamine
G	Gly	Glycine
H	His	Histidine
I	Ile	Isoleucine
L	Leu	Leucine
K	Lys	Lysine
M	Met	Methionine
F	Phe	Phenylalanine
P	Pro	Proline
O	Pyl	Pyrrolysine
S	Ser	Serine
U	Sec	Selenocysteine
T	Thr	Threonine
W	Trp	Tryptophan
Y	Tyr	Tyrosine
V	Val	Valine
B	Asx	Aspartic acid or Asparagine
Z	Glx	Glutamine or Glutamic Acid
J	Xle	Leucine or Isoleucine
X	Xaa	A or R or N or D or C or Q or E or G or H or I or L or K or M or F or P or O or S or U or T or W or Y or V, “unknown” or “other”

Example Index

Page

Paragraph 7(a) – Nucleotide sequences required in a sequence listing

Cross-referenced examples

Paragraph 7(b) – Amino acid sequences required in a sequence listing

Cross-referenced examples

Examples

Paragraph 3(a) Definition of "amino acid"

Example 3(a)-1: D amino acids

A patent application describes the following sequence:

Cyclo (D-Ala-D-Glu-Lys-Nle-Gly-D-Met-D-Nle)

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

Paragraph 3(a) of the Standard defines "amino acid" as including "D-amino acids" and amino acids containing modified or synthetic side chains. Based on this definition, the enumerated peptide contains five amino acids that are specifically defined (D-Ala, D-Glu, Lys, Gly, and D-Met). Therefore, the sequence must be included in a sequence listing as required by ST.26 paragraph 7(b).

Question 3: How should the sequence(s) be represented in the sequence listing?

Paragraph 29 requires that D-amino acids should be represented in the sequence as the corresponding unmodified L-amino acid. Further, any modified amino acid that cannot be represented by any other symbol in Annex I, Section 3, Table 3, must be represented by the symbol "X".

In this example, the sequence contains three D-amino acids that can be represented by an unmodified L-amino acid in Annex I, Section 3, Table 3, one L-amino acid (Nle), and one D-amino acid (D-Nle) that must be represented by the symbol "X".

Paragraph 25 indicates that when amino acid sequences are circular in configuration, applicant must choose the amino acid in residue position number 1. Accordingly, the sequence may be represented as:

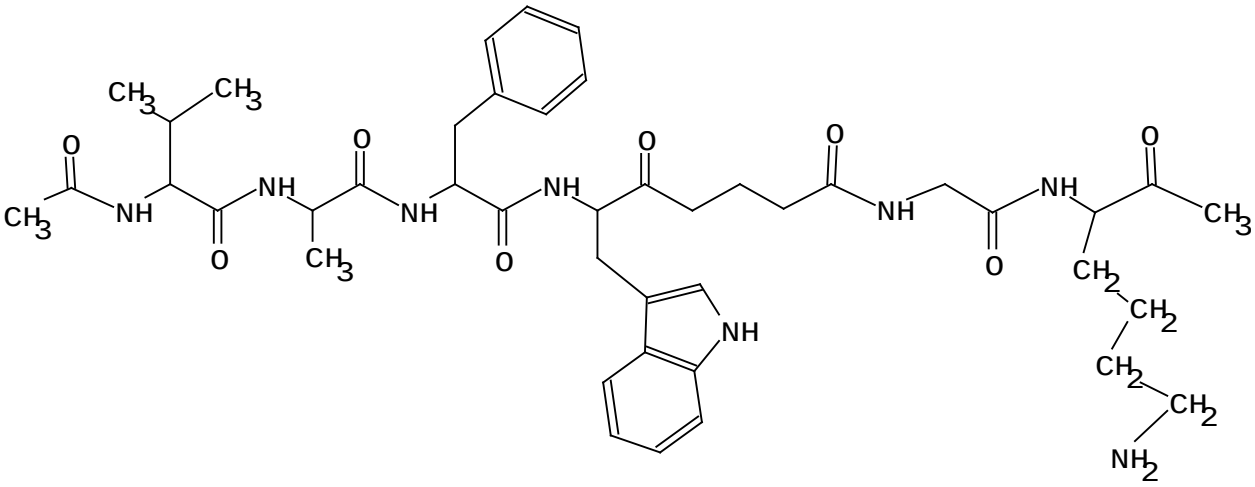
AEKXGMX (SEQ ID NO: 1)

or otherwise, with any other amino acid in the sequence in residue position number 1. A feature key "SITE" and a qualifier "NOTE" must be provided for each D-amino acid with the complete, unabbreviated name of the D-amino acid as the qualifier value, e.g., D-Alanine and D-Norleucine. Further, a feature key "SITE" and a qualifier "NOTE" must be provided with the abbreviation for L-norleucine as the qualifier value, i.e. "Nle", as set forth in Annex I, Section 4, Table 4. Finally, a feature key "REGION" and a qualifier "NOTE" should be provided to indicate that the peptide is circular.

Relevant ST.26 paragraphs: Paragraphs **3(a)**, 7(b), 25, 26, 29, 30, and 31

Paragraph 3(c) – Definition of "enumeration of its residues"

Example 3(c)-1: Enumeration of amino acids by chemical structure



Question 1: Does ST.26 require inclusion of the sequence(s)?

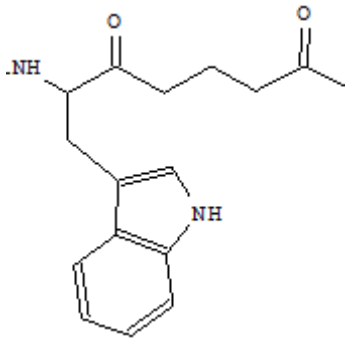
YES

The enumerated peptide, illustrated as a structure, contains at least four specifically defined amino acids. Therefore, the sequence must be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence may be represented as:

VAFXGK (SEQ ID NO: 2)



wherein "X" represents an "other" modified amino acid: , which requires a feature key "SITE" together with the qualifier "NOTE". The qualifier "NOTE" provides the complete, unabbreviated name of the modified tryptophan in position 4 of the enumerated peptide, e.g., "6-amino-7-(1H-indol-3-yl)-5-oxoheptanoic acid". Further, additional feature keys "SITE" and qualifier "NOTE" are required to indicate the acetylation of the N-terminus and the methylation of the C-terminus.

Alternatively, the sequence may be represented as:

VAFW (SEQ ID NO: 3)

A feature key "SITE" and qualifier "NOTE" are required to indicate modification of tryptophan in position 4 of the enumerated peptide with the value: "C-terminus linked via a glutaraldehyde bridge to dipeptide GK". Further, an additional feature key "SITE" at location 1 and qualifier "NOTE" is required to indicate the acetylation of the N-terminus.

Relevant ST.26 paragraph(s): Paragraphs **3(c)**, 7(b), 29, 30, and 31

Example 3(c)-2: Shorthand formula for an amino acid sequence

$(G_4z)_n$

Where G= Glycine, z = any amino acid and variable n can be any whole integer.

Question 1: Does ST.26 require inclusion of the sequence(s)?

Yes

The disclosure indicates that “n” can be “any whole integer”; therefore, the most encompassing embodiment of “n” is indeterminate. Since “n” is indeterminate, the peptide of the formula cannot be expanded to a definite length, and therefore, the unexpanded formula must be considered.

The enumerated peptide in the unexpanded formula (“n” = 1) provides four specifically defined amino acids, each of which is Gly, and the symbol “z”. Conventionally “Z” is the symbol for “glutamine or glutamic acid”; however, the example defines “z” as “any amino acid”. Under ST.26, an amino acid that is not specifically defined is represented by “X”. Based on this analysis, the enumerated peptide, i.e. GGGGX, contains four glycine residues that are enumerated and specifically defined. Thus, ST.26 paragraph 7(b) requires inclusion of the sequence in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence uses a nonconventional symbol “z”, the definition of which must be determined from the disclosure (*see* Introduction to this document). Since “z” is defined as any amino acid, the conventional symbol used to represent this amino acid is “X.” Therefore, the sequence must be represented as a single sequence:

GGGGX (SEQ ID NO: 4)

preferably annotated with the feature key REGION, feature location “>5” (corresponds to >5), with a NOTE qualifier with the value “The entire sequence of amino acids 1-5 can be repeated one or more times.”

CAUTION: The preferred representation of the sequence indicated above is directed to the provision of a sequence listing on the filing date of a patent application. The same representation may not be applicable to a sequence listing provided subsequent to the filing date of a patent application, since consideration must be given to whether the information provided could be considered by an IPO to add subject matter to the original disclosure.

Relevant ST.26 paragraph(s): Paragraph **3(c)** and 7(b)

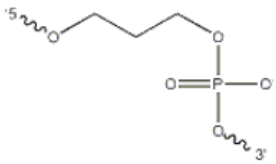
Paragraph 3(g) Definition of "nucleotide"

Example 3(g)-1: Nucleotide sequence interrupted by a C3 spacer

A patent application describes the following sequence:

atgcatgcatgcncggcatgcatgc

where n = a C3 spacer with the following structure:



Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The enumerated sequence contains two segments of specifically defined nucleotides separated by a C3 spacer.

The C3 spacer is not a nucleotide according to paragraph 3(g); the conventional symbol "n" is being used in a nonconventional manner (*see* Introduction to this document). Consequently, each segment is a separate nucleotide sequence. Since each segment contains more than 10 specifically defined nucleotides, both must be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

Each segment must be included in a sequence listing as a separate sequence, each with their own sequence identification number:

atgcatgcatgc (SEQ ID NO: 5)

cggcatgcatgc (SEQ ID NO: 6)

The cytosine in each segment that is attached to the C3 spacer should be further described in a feature table using the feature key "misc_feature" and the qualifier "note". The "note" qualifier value, which is "free text", should indicate the presence of the spacer, which is joined to another nucleic acid.

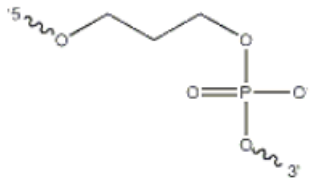
Relevant ST.26 paragraphs: Paragraphs **3(g)**, 7(a), and 15

Example 3(g)-2: Nucleotide sequence with residue alternatives, including a C3 spacer

A patent application describes the following sequence:

atgcatgcatgcncggcatgcatgc

where n = c, a, g, or a C3 spacer with the following structure:



Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

There are 24 specifically defined residues in the enumerated sequence interrupted by the variable "n." The explanation of the sequence in the disclosure must be consulted to determine if the "n" is used in a conventional or nonconventional manner (*see* Introduction to this document).

The disclosure indicates that n = c, a, g, or a C3 spacer. The "n" is a conventional symbol used in a nonconventional manner, since it is described as including a C3 spacer, which does not meet the definition of a nucleotide. The symbol "n" is also described as including "c", "a", or "g"; therefore, ST.26 requires inclusion of the 25 nucleotide sequence in a sequence listing. Since two segments separated by the C3 spacer are distinct sequences from the 25 nucleotide sequence, the two 12 nucleotide sequences may also be included.

Question 3: How should the sequence(s) be represented in the sequence listing?

The example indicates that "n = c, a, g, or a C3 spacer". As discussed above, a C3 spacer is not a nucleotide. According to paragraph 15, the symbol "n" must not be used to represent anything other than a nucleotide; therefore, the symbol "n" cannot represent a C3 spacer in a sequence listing.

Paragraph 15 also states that where an ambiguity symbol is appropriate, the most restrictive symbol should be used. The symbol "v" represents "a or c or g" according to Annex I, Section 1, Table 1, which is more restrictive than "n".

Where variable "n" in the example is c, a, or g, the single sequence enumerated by its residues that includes the most disclosed embodiments, and is therefore, the most encompassing sequence (*see* Introduction to this document) that must be included in a sequence listing is:

atgcatgcatgcvcggcatgcatgc (SEQ ID NO: 7)

Inclusion of any additional sequences essential to the disclosure or claims of the invention is strongly encouraged, as discussed in the introduction to this document.

Where variable "n" in the example is a C3 spacer, the sequence can be considered two separate segments of specifically defined nucleotides on either side of the variable "n", i.e. atgcatgcatgc (SEQ ID NO: 8); and cggcatgcatgc (SEQ ID NO: 9). If essential to the disclosure or claims, these two sequences should also be included in the sequence listing, each with their own sequence identification number.

The cytosine in each segment that is attached to the C3 spacer should be further described in a feature table using the feature key "misc_feature" and the qualifier "note". The "note" qualifier value, which is "free text", should indicate the presence of the spacer, which is joined to another nucleic acid and identify the spacer by either its complete unabbreviated chemical name, or by its common name, e.g. C3 spacer.

CAUTION: The preferred representation of the sequence indicated above is directed to the provision of a sequence listing on the filing date of a patent application. The same representation may not be applicable to a sequence listing provided subsequent to the filing date of a patent application, since consideration must be given to whether the information provided could be considered by an IPO to add subject matter to the original disclosure.

Relevant ST.26 paragraphs: Paragraphs **3(g)**, 7(a), and 15

Example 3(g)-3: Abasic site

A patent application describes the following sequence:

gagcattgac-AP-taaggct

Wherein AP is an abasic site

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The specifically defined residues of the enumerated sequence are interrupted by an abasic site. The 5' side of the abasic site contains 10 nucleotides and the 3' side of the abasic site contains 7 nucleotides. Paragraph 3(g)(ii)(2) defines an abasic site as a "nucleotide" when it is part of a nucleotide sequence. Consequently, the abasic site in this example is considered a "nucleotide" for the purposes of determining if and how the sequence is required to be included in a sequence listing. Accordingly, the residues on each side of the abasic site are part of a single enumerated sequence containing 18 nucleotides total, 17 of which are specifically defined. Therefore, the sequence must be included as a single sequence in a sequence listing as required by ST.26 paragraph (7)(b).

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence must be included in a sequence listing as:

gagcattgacntaaggct (SEQ ID NO: 10)

The abasic site must be represented by an "n" and must be further described in a feature table. The preferred means of annotation is the feature key "modified_base" and the mandatory qualifier "mod_base" with the value "OTHER". A "note" qualifier must be included that describes the modified base as an abasic site.

Relevant ST.26 paragraphs: Paragraphs **3(g)**, 7(a), and 17

Example 3(g)-4: Nucleic Acid Analogues

A patent application discloses the following glycol nucleic acid (GNA) sequence:

PO_4-tagttcattgactaaggctccccattgact-OH

Wherein the left end of the sequence mimics the 5' end of a DNA sequence.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES – The individual residues that comprise a GNA sequence are considered nucleotides according to ST.26 paragraph 3(g)(i)(2). Accordingly, the sequence has more than ten enumerated and "specifically defined" nucleotides and is required to be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

GNA sequences do not have a 5'-end and a 3'-end, but rather, a 3'-end and a 2'-end. The 3'-end, which is routinely depicted as having a terminal phosphate group, corresponds to the 5'-end of DNA or RNA. (Note that other nucleic acid analogues may correspond differently to the 5'-end and 3'-end of DNA and RNA.) According to paragraph 10, it must be included in a sequence listing "in the direction from left to right that mimics the 5'-end to 3'-end direction." Therefore, it must be included in a sequence listing as:

tagttcattgactaaggctccccattgact (SEQ ID NO: 11)

The sequence must be described in a feature table using the feature key "modified_base" and the mandatory qualifier "mod_base" with the abbreviation "OTHER". A "note" qualifier must be included with the complete unabbreviated name of the modified nucleotides, such as "glycol nucleic acids" or "2,3-dihydroxypropyl nucleosides". A single INSDFeature element can be used to describe the entire sequence as a GNA where the INSDFeature_location has the range "1..30".

Relevant ST.26 paragraphs: Paragraphs 3(d), **3(g)**, 7(a), 11, 16, 18, 65, and 66

Paragraph 3(k) Definition of "specifically defined"

Example 3(k)-1: Nucleotide ambiguity symbols

5' NNG KNG KNG K 3'

N and K are IUPAC-IUB ambiguity codes

Question 1: Does ST.26 require inclusion of the sequence(s)?

NO

IUPAC-IUB ambiguity codes correspond to the list of nucleotide symbols defined in Annex I, Section 1, Table 1. According to paragraph 3(k), a specifically defined nucleotide is any nucleotide other than those represented by the symbol "n" listed in Annex I. Therefore, "K" and "G" are specifically defined nucleotides and "N" is not a specifically defined nucleotide.

The enumerated sequence does not have ten or more specifically defined nucleotides and therefore is not required by ST.26 paragraph 7(a) to be included in a sequence listing.

Question 2: Does ST.26 permit inclusion of the sequence(s)?

NO

According to paragraph 8, "A sequence listing must not include any sequences having fewer than ten specifically defined nucleotides…." The enumerated sequence does not have ten or more specifically defined nucleotides; therefore, it must not be included in a sequence listing.

Relevant ST.26 paragraphs: Paragraphs **3(k)**, 7(a), 8, and 13

Example 3(k)-2: Ambiguity symbol "n" used in both a conventional and nonconventional manner

An application discloses the artificial sequence: 5'-AATGCCGGAN-3'. The disclosure further states:

(i) in one embodiment, N is any nucleotide;

(ii) in one embodiment, N is optional but is preferably G;

(iii) in one embodiment, N is K;

(iv) in one embodiment, N is C.

Question 1: Does ST.26 require inclusion of the sequence(s)?

NO

The enumerated sequence contains 9 specifically defined nucleotides and an "N." The explanation of the sequence in the disclosure must be consulted to determine if the symbol "N" is used in a conventional manner (*see* Introduction to this document).

Consideration of disclosed embodiments (i) through (iv) of the enumerated sequence reveals that the most encompassing embodiment of "N" is "any nucleotide". In the most encompassing embodiment, "N" in the enumerated sequence is used in a conventional manner.

In certain embodiments "N" is described as specifically defined residues (i.e., "N is C" in part (iv)). However, only the most encompassing embodiment (i.e., "N is any nucleotide") is considered when determining if a sequence must be included in a sequence listing. Thus, the enumerated sequence that must be evaluated is 5'-AATGCCGGAN-3'.

Based on this analysis, the enumerated sequence, i.e. AATGCCGGAN, does not contain ten specifically defined nucleotides. Therefore, ST.26 paragraph 7(a) does not require inclusion of the sequence in a sequence listing, despite the fact that "n" is also defined as specific nucleotides in some embodiments.

Question 2: Does ST.26 permit inclusion of the sequence(s)?

NO

The sequence "AATGCCGGAN" must not be included in a sequence listing.

However, a described alternative sequence may be included in a sequence listing if the "N" is replaced with a specifically defined nucleotide.

Question 3: How should the sequence(s) be represented in the sequence listing?

Inclusion of sequences which represent embodiments that are a key part of the invention is **strongly** encouraged. Inclusion of these sequences allows for a more thorough search and provides public notice of the subject matter for which a patent is sought.

For the above example, it is highly recommended that the following three additional sequences are included in the sequence listing, each with their own sequence identification number:

aatgccggag (SEQ ID NO: 12)

aatgccggak (SEQ ID NO: 13)

aatgccggac (SEQ ID NO: 14)

If less than all three of the above sequences are included, the nucleotide that replaces the "n" should be annotated to describe the alternatives. For example, if only SEQ ID NO: 12 above is included in the sequence listing, the feature key "misc_difference" with feature location "10" should be used together with two "replace" qualifiers where the value for one would be "g" and the second would be "c".

CAUTION: The preferred representation of the sequence indicated above is directed to the provision of a sequence listing on the filing date of a patent application. The same representation may not be applicable to a sequence listing provided subsequent to the filing date of a patent application, since consideration must be given to whether the information provided could be considered by an IPO to add subject matter to the original disclosure.

Relevant ST.26 paragraphs: Paragraphs **3(k)**, 7(a), 8, and 13

Example 3(k)-3: Ambiguity symbol "n" used in a nonconventional manner

An application discloses the sequence: 5'-aatgttggan-3'

Wherein n is c

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

According to paragraph 3(k), a "specifically defined" nucleotide is any nucleotide other than those represented by the symbol "n" listed in Annex I, Section 1,Table 1.

In this example "n" is used in a nonconventional manner to represent only "c". The disclosure does not indicate that "n" is used in the conventional manner to represent "any nucleotide". Therefore, the sequence must be interpreted as if the equivalent conventional symbol, i.e. "c", had been used in the sequence (*see* Introduction to this document). Accordingly, the enumerated sequence that must be considered is:

5'-aatgttggac-3'

This sequence has ten specifically defined nucleotides and is required by ST.26 paragraph 7(a) to be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence must be included in a sequence listing as: aatgttggac (SEQ ID NO: 15)

Relevant ST.26 paragraphs: Paragraphs **3(k)** and 7(a)

Example 3(k)-4: Ambiguity symbols other than "n" are "specifically defined"

A patent application describes the following sequence:

5' NNG KNG KNG KAG VCR 3'

wherein N, K, V, and R are IUPAC-IUB ambiguity codes

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

IUPAC-IUB ambiguity codes correspond to the list of nucleotide symbols defined in Annex I, Section 1, Table 1. According to paragraph 3(k), a "specifically defined" nucleotide is any nucleotide other than those represented by the symbol "n" listed in Annex I, Section 1, Table 1. Therefore, "K", "V", and "R" are "specifically defined" nucleotides.

The sequence has eleven enumerated and "specifically defined" nucleotides and is required by ST.26 paragraph 7(a) to be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence must be included in a sequence listing as:

nngkngkngkagvcr (SEQ ID NO: 16)

Relevant ST.26 paragraphs: Paragraphs **3(k)**, 7(a) and 15

Example 3(k)-5: Ambiguity abbreviation "Xaa" used in a nonconventional manner

A patent application describes the following sequence:

Xaa-Tyr-Glu-Xaa-Xaa-Xaa-Leu

Wherein Xaa in position 1 is any amino acid, Xaa in position 4 is Lys, Xaa in position 5 is Gly and Xaa in position 6 is Leucine or Isoleucine.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The enumerated peptide in the formula provides three specifically defined amino acids in positions 2, 3 and 7. The first amino acid is represented by a conventional abbreviation, i.e., Xaa, representing any amino acid. However, the 4^{th}, 5^{th} and 6^{th} amino acids are represented by a conventional abbreviation used in a nonconventional manner (*see* Introduction to this document). Therefore, the explanation of the sequence in the disclosure is consulted to determine the definition of "Xaa" in these positions. Since "Xaa" in positions 4-6 are indicated as a specific amino acid, the sequence must be interpreted as if the equivalent conventional abbreviations had been used in the sequence, i.e. Lys, Gly, and (Leu or Ile). Consequently, the sequence contains four or more specifically defined amino acids and must be included in a sequence listing as required by ST.26 paragraph 7(b).

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence uses a conventional abbreviation "Xaa" in a nonconventional manner. Therefore, the explanation of the sequence in the disclosure must be consulted to determine the definition of "Xaa" in positions 4, 5 and 6. The explanation defines "Xaa" as a lysine in position 4, a glycine in position 5 and a leucine or isoleucine in position 6. The conventional symbols for these amino acids are K, G, and J respectively. Therefore, the sequence should be represented as in the sequence listing as:

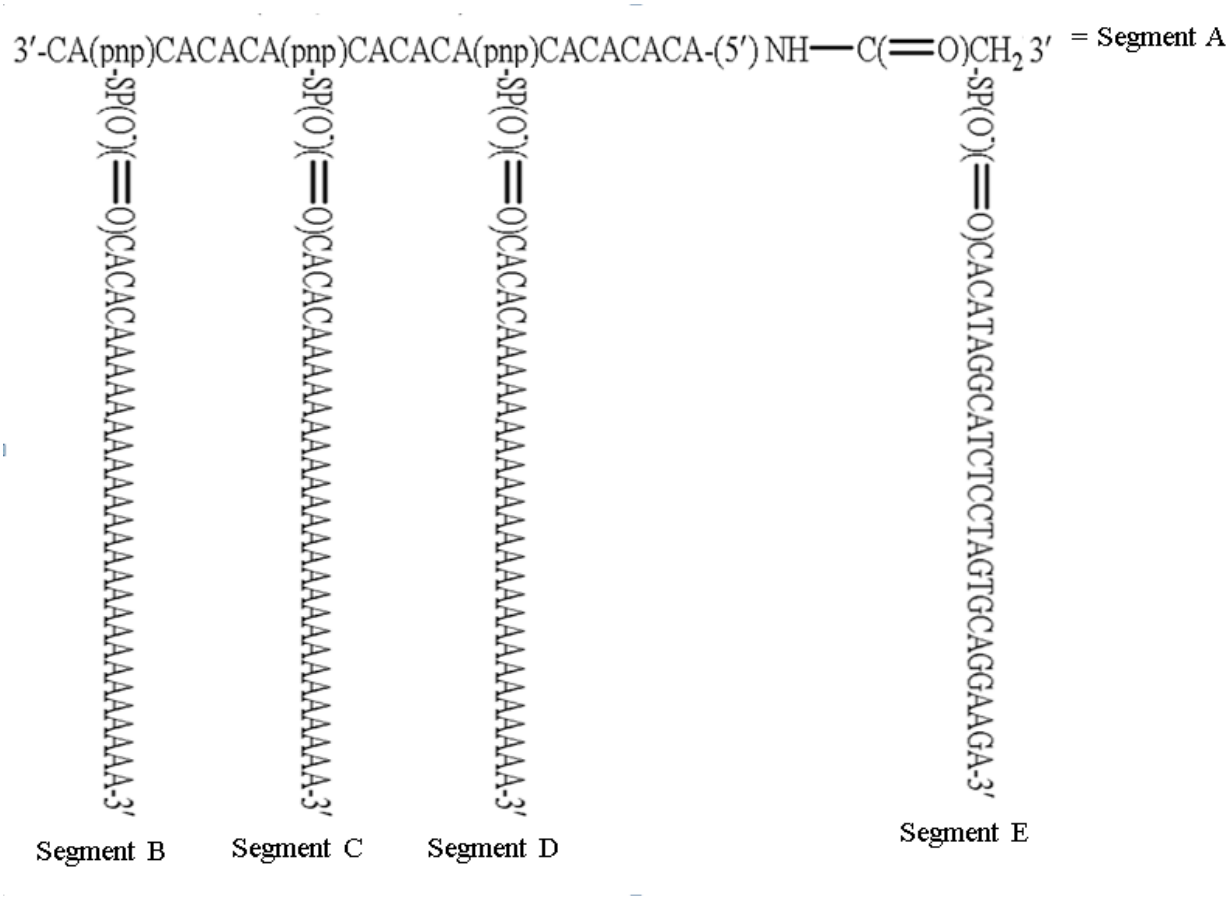
XYEKGJL (SEQ ID NO: 17)

Relevant ST.26 paragraphs: Paragraphs **3(k)**, 7(b), 26, and 27

Paragraph 7(a) – Nucleotide sequences required in a sequence listing

Example 7(a)-1: Branched nucleotide sequence

The description discloses the following branched nucleotide sequence:



wherein "pnp" is a linkage or monomer containing an bromoacetylamino functionality;

3’-CA(pnp)CACACA(pnp)CACACA(pnp)CACACACA-(5’)NH—C(=O)CH_2 3’ is segment A;

SP(O^-)(=O)CACACAAAAAAAAAAAAAAAAAAAAA 3’ is segments B, C, and D; and

SP(O^-)(=O)CACATAGGCATCTCCTAGTGCAGGAAGA 3’ is segment E.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES – the four vertical segments B-E must be included in a sequence listing

NO – the horizontal segment A must not be included in a sequence listing

The above figure is an example of a “comb-type” branched nucleic acid sequence containing five linear segments: the horizontal segment A and the four vertical segments B-E.

According to paragraph 7(a), the linear portions of branched nucleotide sequences containing ten or more specifically defined nucleotides, wherein adjacent nucleotides are joined 3’ to 5’, must be included in a sequence listing.

The four vertical segments B-E each contain more than ten specifically defined nucleotides, wherein adjacent nucleotides are joined 3’ to 5’, and therefore each is required to be included in a sequence listing.

In horizontal segment A, the linear portions of the nucleotide sequence are linked by the non-nucleotide moiety "pnp" and each of these linked linear portions contains fewer than ten specifically defined nucleotides. Therefore, since no portion of segment A contains ten or more specifically defined nucleotides wherein adjacent nucleotides are joined 3' to 5', they are not required ST.26 paragraph 7(a) to be included in a sequence listing.

Question 2: Does ST.26 permit inclusion of the sequence(s)?

According to paragraph 8, "A sequence listing must not include any sequences having fewer than ten specifically defined nucleotides…."

No portion of Segment A contains ten or more specifically defined nucleotides wherein adjacent nucleotides are joined 3' to 5'; therefore, it must not be included in a sequence listing as a separate sequence with its own sequence identification number.

However, segments B, C, D, and E may be annotated to indicate that they are linked to segment A.

Question 3: How should the sequence(s) be represented in the sequence listing?

Segments B, C, and D are identical and must be included in a sequence listing as a single sequence:

cacacaaaaaaaaaaaaaaaaaaaaaaaa. (SEQ ID NO: 18)

The first "c" in the sequence should be further described as a modified nucleotide using the feature key "misc_feature" and the qualifier "note" with the value e.g., "This sequence is one of four branches of a branched polynucleotide.".

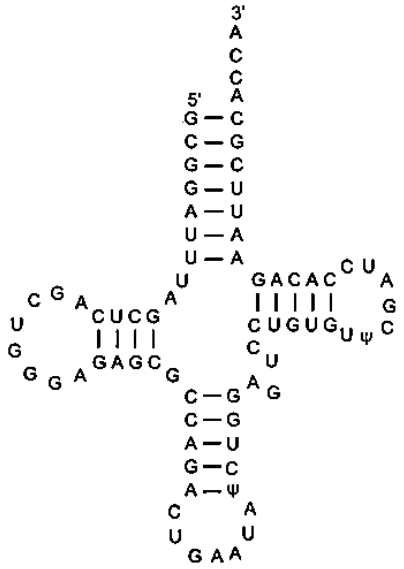
Segment E must be included in a sequence listing as a single sequence:

cacataggcatctcctagtgcaggaaga. (SEQ ID NO: 19)

The first "c" in the sequence should be further described as a modified nucleotide using the feature key "misc_feature" and the qualifier "note" with the value e.g., "This sequence is one of four branches of a branched polynucleotide."

Relevant ST.26 paragraph(s): Paragraphs **7(a)**, 8, 11, 13, and 17

Example 7(a)-2: Linear nucleotide sequence having a secondary structure



Wherein Ψ is pseudouridine.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The nucleotide sequence contains seventy-three enumerated and specifically defined nucleotides. Thus, the example has ten or more "specifically defined" nucleotides, and as required by ST.26 paragraph (7)(a), must be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

Consultation of the disclosure indicates that "Ψ" is equivalent to pseudouridine. The only conventional symbol that can be used to represent pseudouridine is "n"; therefore, the "Ψ" is a nonconventional symbol used to represent the conventional symbol "n" (*see* Introduction to this document). Accordingly, the sequence must be interpreted to have two "n" symbols in place of the two "Ψ" symbols.

The symbol "u" must not be used to represent uracil in an RNA molecule in the sequence listing. According to paragraph 14, the symbol "t" will be construed as uracil in RNA. The sequence must be included as:

gcggatttagctcagctgggagagcgccagactgaatanctggagtcctgtgtncgatccacagaattcgcacca (SEQ ID NO: 20)

The value of the mandatory "mol_type" qualifier of the mandatory "source" feature key is "tRNA". Additional information may be provided with feature key "tRNA" and any appropriate qualifier(s).

The "n" residues must be further described in a feature table using the feature key "modified_base" and the mandatory qualifier "mod_base" with the abbreviation "p" for pseudouridine as the qualifier value (see Annex 1, Table 2).

Relevant ST.26 paragraph(s): Paragraphs **7(a)**, 11, 13, 14, 62, 84 and Annex I, sections 2 and 5, feature key 5.43

Example 7(a)-3: Nucleotide ambiguity symbols used in a nonconventional manner

A patent application describes the following sequence:

5' GATC-MDR-MDR-MDR-MDR-GTAC 3'

The explanation of the sequence in the disclosure further indicates: "A "DR Element" consists of the sequence 5' ATCAGCCAT 3'. A mutant DR Element, or MDR, is a DR element wherein the middle 5 nucleotides, CAGCC, are mutated to TTTTT."

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The enumerated sequence uses the symbol "MDR". Where it is unclear if a symbol used in a sequence is intended to be a conventional symbol, i.e., a symbol set forth in Annex 1,Section 3, Table 3, or a nonconventional symbol, the explanation of the sequence in the disclosure must be consulted to make a determination (*see* Introduction to this document). According to Table 3, "MDR" could be interpreted as three conventional symbols (m = a or c, d = a or g or t/u, r = g or a) or as an abbreviation that is short-hand notation for some other structure.

Consultation of the disclosure indicates that an MDR element is equivalent to 5' ATTTTTTAT 3'. The letters "MDR" are considered conventional symbols used in a nonconventional manner; therefore, the sequence must be interpreted as though it were disclosed using the equivalent conventional symbols. Accordingly, the enumerated sequence that is considered for inclusion in a sequence listing is:

5' GATC ATTTTTTAT ATTTTTTAT ATTTTTTAT ATTTTTTAT GTAC 3'

The enumerated sequence has 44 specifically defined nucleotides and is required by ST.26 paragraph 7(a) to be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence must be included in a sequence listing as:

gatcatttttttatatttttttatatttttttatatttttttatgtac (SEQ ID NO: 21)

Relevant ST.26 paragraphs: Paragraph **7(a) and 13**

Example 7(a)-4: Nucleotide ambiguity symbols used in a nonconventional manner

A patent application describes the following sequence:

5' ATTC-N-N-N-N-GTAC 3'

The explanation of the sequence in the disclosure further indicates that "N" consists of the sequence 5' ATACGCACT 3'.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The enumerated sequence uses the symbol "N". The explanation of the sequence in the disclosure must be consulted to determine if the "N" is used in a conventional or nonconventional manner (*see* Introduction to this document).

Consultation of the disclosure indicates that "N" is equivalent to 5' ATACGCACT 3'. Thus, the "N" is a conventional symbol used in a nonconventional manner. Accordingly, the sequence must be interpreted as though it were disclosed using the equivalent conventional symbols:

5' ATTC-ATACGCACT-ATACGCACT-ATACGCACT-ATACGCACT-GTAC 3'

The enumerated sequence has 44 specifically defined nucleotides and is required by ST.26 paragraph 7(a) to be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence must be included in a sequence listing as:

attcatacgcactatacgcactatacgcactatacgcactgtac (SEQ ID NO: 22)

Relevant ST.26 paragraphs: Paragraph **7(a) and 13**

Example 7(a)-5: Nonconventional nucleotide symbols

A patent application describes the following sequence:

5' GATC-β-β-β-β-GTAC 3'

The explanation of the sequence in the disclosure further indicates that "β" consists of the sequence 5' ATACGCACT 3'.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The enumerated sequence uses the nonconventional symbol "β". The explanation of the sequence in the disclosure must be consulted to determine the meaning of "β" (*see* Introduction to this document).

Consultation of the disclosure indicates that "β" is equivalent to 5' ATACGCACT 3'. Thus, the "β" is a nonconventional symbol used to represent a sequence of nine specifically defined, conventional symbols. Accordingly, the sequence must be interpreted as though it were disclosed using the equivalent conventional symbols:

5' GATC-ATACGCACT-ATACGCACT-ATACGCACT-ATACGCACT-GTAC 3'

The enumerated sequence has 44 specifically defined nucleotides and is required by ST.26 paragraph 7(a) to be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence must be included in a sequence listing as:

gatcatacgcactatacgcactatacgcactatacgcactgtac (SEQ ID NO: 23)

Relevant ST.26 paragraphs: Paragraph **7(a) and 13**

Example 7(a)-6: Nonconventional nucleotide symbols

A patent application describes the following sequence:

5' GATC-β-β-β-β-GTAC 3'

The explanation of the sequence in the disclosure further indicates that "β" is equal to adenine, inosine, or pseudouridine.

Question 1: Does ST.26 require inclusion of the sequence(s)?

NO

The enumerated sequence uses the nonconventional symbol "β". The explanation of the sequence in the disclosure must be consulted to determine the meaning of "β" (*see* Introduction to this document).

Consultation of the disclosure indicates that "β" is equivalent to adenine, inosine, or pseudouridine. The only conventional symbol that can be used to represent "adenine, inosine, or pseudouridine" is "n"; therefore, the "β" is a nonconventional symbol used to represent the conventional symbol "n". Accordingly, the sequence must be interpreted to have four "n" symbols in place of the four "β" symbols:

5' GATC-N-N-N-N-GTAC 3'

The enumerated sequence has only eight specifically defined nucleotides and is not required by ST.26 paragraph 7(a) to be included in a sequence listing.

Question 2: Does ST.26 permit inclusion of the sequence(s)?

NO

The enumerated sequence, 5' GATC-N-N-N-N-GTAC 3' must not be included in a sequence listing.

However, a disclosed alternative sequence may be included in a sequence listing if at least 2 of the "n" symbols are replaced by adenine, resulting in a sequence with at least 10 or more specifically defined nucleotides.

Question 3: How should the sequence(s) be represented in the sequence listing?

One possible permitted representation is:

gatcaaaagtac (SEQ ID NO: 24)

In the above example, the four adenine nucleotides that replace the β symbols should be annotated to note that these positions could be substituted with inosine or pseudouridine.

The feature key "misc_difference" should be used with a feature location 5-8 and a qualifier "note" with the value, e.g., "A nucleotide in any of positions 5-8 may be replaced with inosine or pseudouridine". Since these alternatives are modified nucleotides, then the feature key "modified_base" together with the qualifier "mod_base" would be required. The value for the "mod_base" qualifier can be "OTHER" with a "note" qualifier and the value of "i or p".

Other permutations are possible.

CAUTION: The preferred representation of the sequence indicated above is directed to the provision of a sequence listing on the filing date of a patent application. The same representation may not be applicable to a sequence listing provided subsequent to the filing date of a patent application, since consideration must be given to whether the information provided could be considered by an IPO to add subject matter to the original disclosure.

Relevant ST.26 paragraphs: Paragraph **7(a)**, 8, 13, and 17

Paragraph 7(b) – Amino Acid sequences required in a sequence listing

Example 7(b)-1: Four or more specifically defined amino acids

XXXXXXXXDXXXXXXXXXXFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXGXXXXX

Where X = any amino acid

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The enumerated peptide contains four specifically defined amino acids. The symbol "X" is used conventionally to represent the remaining amino acids as any amino acid (*see* Introduction to this document).

Because there are four specifically defined amino acids, i.e., Asp, Phe, Ala and Gly, ST.26 paragraph 7(b) requires that the sequence be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence must be represented as:

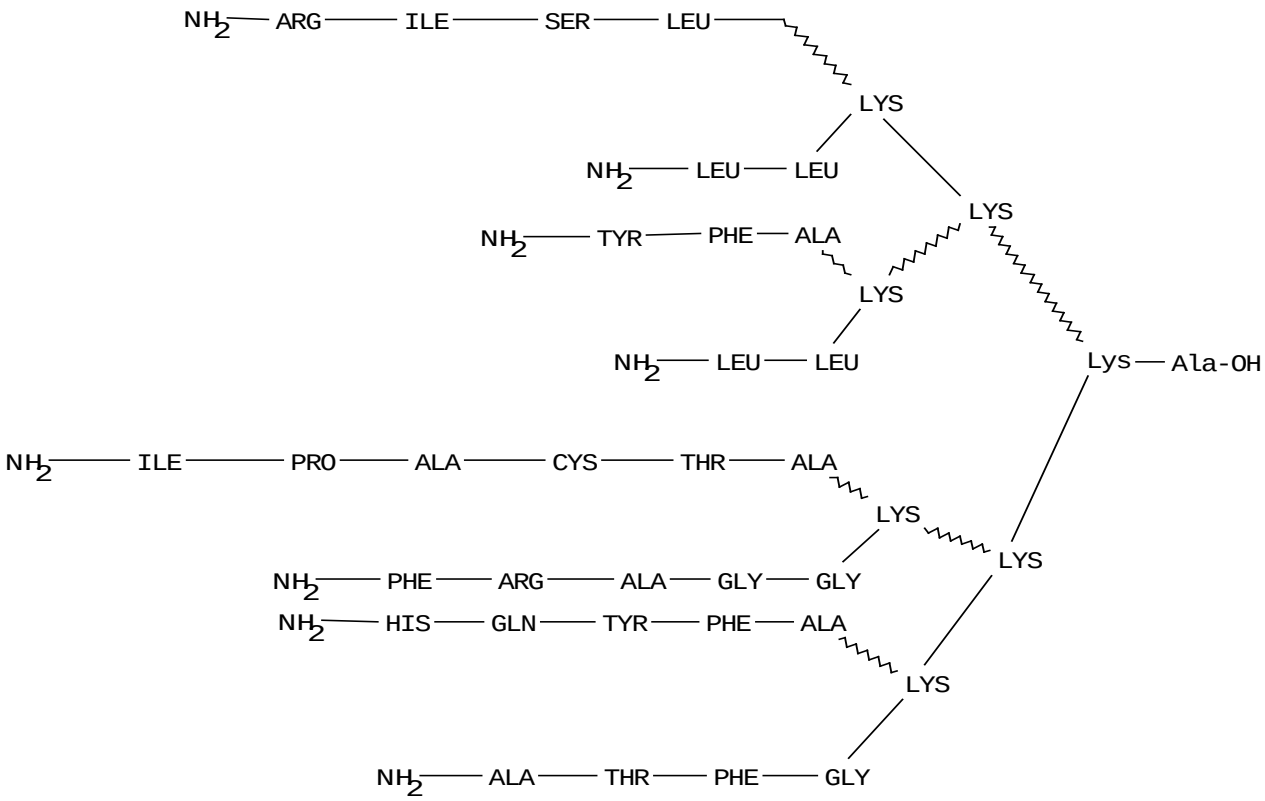
XXXXXXXXDXXXXXXXXXXFXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXAXXXXXXXXXXXXXXXXXXXXGXXXXX (SEQ ID NO: 25)

Since "X" can be any amino acid, annotation of the "X" residues is not required under paragraph 27.

Relevant ST.26 paragraph(s): Paragraphs **7(b)**, 8 and 27

Example 7(b)-2: Branched amino acid sequence

The application describes a branched sequence where the Lysine residues are used as a scaffolding core to form eight branches to which multiple linear peptide chains are attached. Lysine is a dibasic amino acid, providing it with two sites for peptide-bonding. The peptide is illustrated as follows:

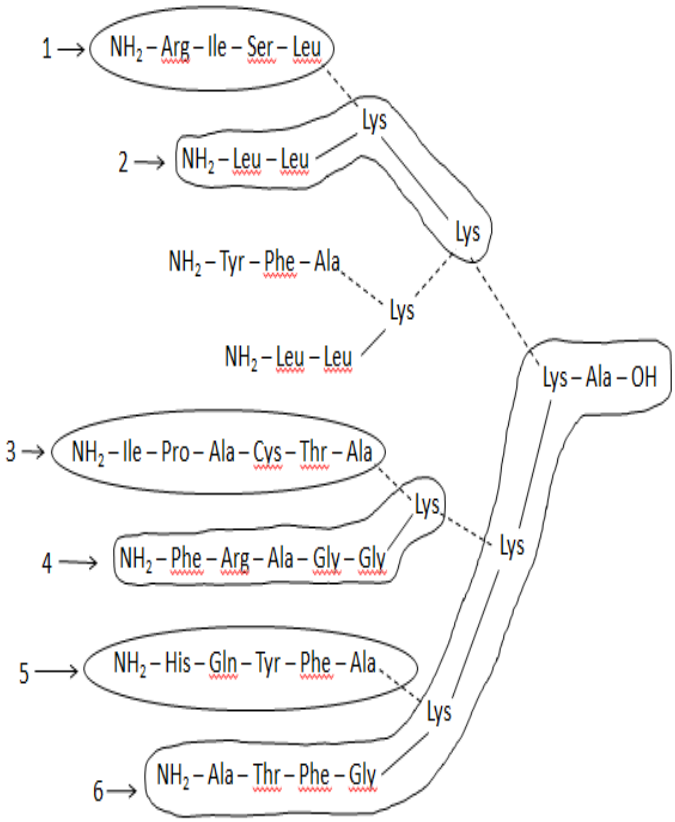


In the above branched peptide, the bonds depicted by ——— represent an amide linkage between the terminal amine of the Lysine and the carboxyl end of the bonded amino acid. The bonds depicted by ∿∿∿ represent an amide linkage between the side chain amine of the Lysine and the carboxyl end the bonded amino acid.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The example discloses a branched sequence where the lysine residues are used as a scaffolding. Paragraph 7(b) requires that the unbranched or linear portion of the sequence, containing four or more specifically defined amino acids, be included in a sequence listing. In the above example, the linear portions of the branched peptide that have four or more specifically defined amino acids are encircled:



ST.26 paragraph 7(b) requires inclusion of peptides 1-6 above in a sequence listing.

Peptides which are not required, and in fact are prohibited, from inclusion in the sequence listing are:

YFA

LLK

Question 3: How should the sequence(s) be represented in the sequence listing?

Peptides 1-6 must be represented with separate sequence identifiers:

RISL (SEQ ID NO: 26)

LLKK (SEQ ID NO: 27)

IPACTA (SEQ ID NO: 28)

FRAGGK (SEQ ID NO: 29)

HQYFA (SEQ ID NO: 30)

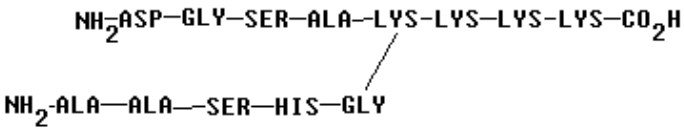
ATFGKKKA (SEQ ID NO: 31)

The cross linkage is preferably noted using the feature key “SITE” and the mandatory qualifier “NOTE” with the value e.g., “This sequence is one part of a branched peptide”.

Relevant ST.26 paragraph(s): Paragraphs **7(b)**, 26, 30, and 31

Example 7(b)-3: Branched amino acid sequence

Peptide of the following sequence:

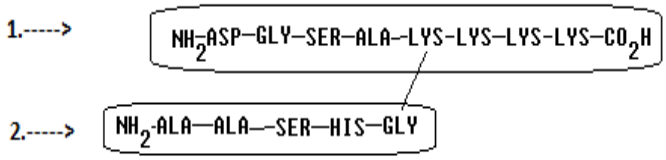


The linkage between the terminal Glycine residue in the lower sequence and the Lysine in the upper sequence is through an amide bond between the carboxy terminus of the Glycine and the amino terminal side chain of the Lysine.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The unbranched or linear portion of a sequence, containing four or more specifically defined amino acids, must be included in a sequence listing. In the above example, the linear portions of the branched peptide that have more than four amino acids are:



ST.26 paragraph 7(b) requires inclusion of peptides 1 and 2 in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

Peptides 1 and 2 must be represented with separate sequence identifiers:

DGSAKKK (SEQ ID NO: 32)

AASHG (SEQ ID NO: 33)

Preferably the sequence DSAKKKK should include an annotation to indicate that the 5th lysine is a modified amino acid using the feature key “SITE” together with the qualifier “NOTE” describing that lysine links the peptide AASHG. Preferably the sequence AASHG should include an annotation to indicate that the 5th glycine is linked to DGSAKKK using the feature key “SITE” together with the qualifier “NOTE”.

Relevant ST.26 paragraph(s): Paragraphs **7(b)**, 26, 30, and 31

Paragraph 11(a) – Double-stranded nucleotide sequence – fully complementary

Example 11(a)-1: Double-stranded nucleotide sequence – same lengths

A patent application describes the following double-stranded DNA sequence:

3′-CCGGTTAACGCTA-5′

5′-GGCCAATTGCGAT-3′

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

Each enumerated nucleotide sequence has more than 10 specifically defined nucleotides. At least one strand must be included in the sequence listing, because the two strands of this double-stranded nucleotide sequence are fully complementary to each other.

Question 2: Does ST.26 permit inclusion of the sequence(s)?

While the sequence of only one strand must be included in the sequence listing, the sequences of both strands may be included, each with its own sequence identification number.

Question 3: How should the sequence(s) be represented in the sequence listing?

The double-stranded DNA sequence must be represented either as a single sequence or as two separate sequences. Each sequence included in the sequence listing must be represented in the 5' to 3' direction and assigned its own sequence identification number.

atcgcaattggcc (top strand) (SEQ ID NO: 34)

and/or

ggccaattgcgat (bottom strand) (SEQ ID NO: 35)

Relevant ST.26 paragraphs: Paragraphs 7(a), **11(a)**, and 13

Paragraph 11(b) – Double-stranded nucleotide sequence - not fully complementary

Example 11(b)-1: Double-stranded nucleotide sequence – different lengths

A patent application contains the following drawing and caption:

```
5′-tagttcattgactaaggctccccattgactaaggcgactagcattgactaaggcaagc-3′

                      ||||||||||||||||

                      gggtaactgantccgc
```

The human gene ABC1 promoter region (top strand) bound by a PNA probe (bottom strand). Where "n" in the PNA probe is a universal PNA base selected from the group consisting of 5-nitroindole and 3-nitroindole.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES – the ABC1 promoter region (top strand)

The top strand has more than ten enumerated and "specifically defined" nucleotides and is required to be included in a sequence listing.

YES – the PNA probe (bottom strand)

The bottom strand must also be included in the sequence listing, with its own sequence identification number, because the two strands are not fully complementary to each other. The individual residues that comprise a PNA or "peptide nucleic acid" are considered nucleotides according to ST.26 paragraph 3(g). Therefore, the bottom strand has more than 10 enumerated and "specifically defined" nucleotides and is required to be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The top strand must be included in a sequence listing as:

tagttcattgactaaggctccccattgactaaggcgactagcattgactaaggcaagc (SEQ ID NO: 36)

The bottom strand is a peptide nucleic acid and therefore does not have a 3' and 5' end. According to paragraph 11, it must be included in a sequence listing "in the direction from left to right that mimics the 5'–end to 3'-end direction." Therefore, it must be included in a sequence listing as:

cgcctnagtcaatggg (SEQ ID NO: 37)

The "organism" qualifier of the feature key "source" must have the value "synthetic construct" and the mandatory qualifier "mol_type" with the value "other DNA". The bottom strand must be described in a feature table using the feature key "modified_base" and the mandatory qualifier "mod_base" with the abbreviation "OTHER". A "note" qualifier must be included with the complete unabbreviated name of the modified nucleotides, such as "N-(2-aminoethyl) glycine nucleosides".

The "n" residue must be further described in a feature table using the feature key "modified_base" and the mandatory qualifier "mod_base" with the abbreviation "OTHER". A "note" qualifier must be included with the complete unabbreviated name of the modified nucleotide: "N-(2-aminoethyl) glycine 5-nitroindole or N-(2-aminoethyl) glycine 3-nitroindole".

Relevant ST.26 paragraphs: Paragraphs 3(g), 7(a), **11(b)**, 17, and 18

Example 11(b)-2: Double-stranded nucleotide sequence – no base-pairing segment

A patent application describes the following double-stranded DNA sequence:

3'-CCGGTTAGCTTATACGCTAGGGCTA-5'

||||||| ||||||||||||

5'-GGCCAATATGGCTTGCGATCCCGAT-3'

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

Each strand of the enumerated, double-stranded nucleotide sequence has more than 10 specifically defined nucleotides. Both strands must be included in the sequence listing, each with its own sequence identification number, because the two strands are not fully complementary to each other.

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence of each strand must be represented in the 5' to 3' direction and assigned its own sequence identification number:

atcgggatcgcatattcgattggcc (top strand) (SEQ ID NO: 38)

and

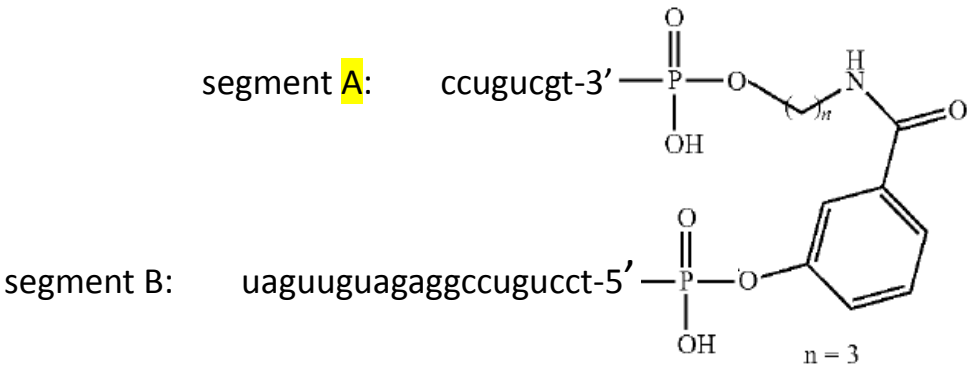
ggccaatatggcttgcgatcccgat (bottom strand) (SEQ ID NO: 39)

Relevant ST.26 paragraphs: Paragraphs 7(a), **11(b)**, and 13

<u>Paragraph 14 – Symbol "t" construed as uracil in RNA</u>

Example 14-1: The symbol "t" represents uracil in RNA

A patent application describes the following compound:



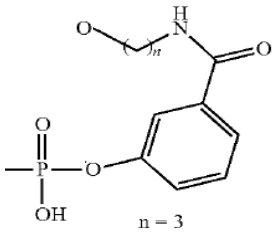
Wherein segment A and segment B are RNA sequences.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES – segment B

NO – segment A

The enumerated sequence contains two segments of specifically defined nucleotides separated by the following "linker" structure:



The linker structure is not a nucleotide according to paragraph 3(g); therefore, each segment must be considered a separate sequence. Segment B contains more than 10 specifically defined nucleotides and ST.26 paragraph 7(a) requires inclusion in a sequence listing. Segment A contains only 8 specifically defined nucleotides and therefore is not required to be included in a sequence listing.

Question 2: Does ST.26 permit inclusion of the sequence(s)?

Segment A contains fewer than 10 specifically defined nucleotides, and therefore it must not be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

Segment B is an RNA molecule; therefore, the element "INSDSeq_moltype" must be "RNA." The symbol "u" must not be used to represent uracil in an RNA molecule in a sequence listing. According to paragraph 14, the symbol "t" will be construed as uracil in RNA. Accordingly, segment B must be included in the sequence listing as:

tcctgtccggagatgttgat (SEQ ID NO: 40)

Thymine in RNA is considered a modified nucleotide, i.e. modified uracil, and must be represented in the sequence as "t" and be further described in a feature table. Accordingly, the thymine in position 1 must be further described using the feature key "modified_base", the qualifier "mod_base" with "OTHER" as the qualifier value, and a qualifier "note" with "thymine" as the qualifier value.

The thymine, i.e. modified uracil, in position 1 should also be further described in a feature table using the feature key "misc_feature" and a qualifier "note" with the value e.g., "ccugucgt (Segment A) is attached at its 3'-end to a linker which is attached to the 5' oxygen of the thymidine. The linker is (4-(3-hydroxybenzamido)butyl) phosphinic acid."

Relevant ST.26 paragraphs: Paragraphs 3(g), 7(a), 8, 13, **14**, 19, and 54

Paragraph 27 – The most restrictive ambiguity symbol should be used

Example 27-1: Shorthand formula for a nucleotide sequence

$(GGGz)_2$

Where z is any amino acid.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The sequence is disclosed as a formula. $(GGGz)_2$ is simply a shorthand way of representing the sequence GGGzGGGz. Conventionally, a sequence is expanded first, and the definition of any variable, i.e. "z", is determined thereafter.

The sequence uses the nonconventional symbol "z". The definition of "z" must be determined from the explanation of the sequence in the disclosure, which defines this symbol as any amino acid (*see* Introduction to this document). The example does not provide any constraint on "z", e.g., that it is the same in each occurrence.

Therefore, "z" is equivalent to the conventional symbol "X", and the peptide in the example has eight enumerated amino acids, six of which are specifically defined glycine residues. ST.26 paragraph 7(b) requires inclusion of the sequence in a sequence listing as a single sequence with a single sequence identification number.

Note that the sequence is still encompassed by Paragraph 7(b) despite the fact that the enumerated and specifically defined residues are not contiguous.

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence uses the nonconventional symbol "z", which according to the disclosure is any amino acid. The conventional symbol used to represent "any amino acid" is "X". Therefore, the sequence must be represented as the single expanded sequence:

GGGXGGGX (SEQ ID NO: 41)

Further, the example does not disclose that "z" is the same amino acid in both positions in the expanded sequence. However, if "z" is disclosed as the same amino acid in both positions, then a feature key "VARIANT" and a qualifier "NOTE" should be provided stating that "X" in position 4 and 8 can be any amino acid, as long as they are the same in both positions.

Relevant ST.26 paragraph(s): Paragraphs 3(c), 7(b) and **27**

Example 27-2: Shorthand formula - less than four specifically defined amino acids

A peptide of the formula $(Gly\text{-}Gly\text{-}Gly\text{-}z)_n$

The disclosure further states, that z is any amino acid and

(i) variable n is any length; or

(ii) variable n is 2-100, preferably 3

Question 1: Does ST.26 require inclusion of the sequence(s)?

NO

Consideration of both disclosed embodiments (i) and (ii) of the enumerated peptide of the formula reveals that "n" can be "any length"; therefore, the most encompassing embodiment of "n" is indeterminate. Since "n" is indeterminate, the peptide of the formula cannot be expanded to a definite length, and therefore, the unexpanded formula must be considered.

The enumerated peptide in the unexpanded formula ("n" = 1) provides three specifically defined amino acids, each of which is Gly, and the symbol "z". Conventionally "Z" is the symbol for "glutamine or glutamic acid"; however, the example defines "z" as "any amino acid" (*see* Introduction to this document). Under ST.26, an amino acid that is not specifically defined is represented by "X". Based on this analysis, the enumerated peptide, i.e. GGGX, does not

contain four specifically defined amino acids. Therefore, ST.26 paragraph 7(b) does not require inclusion, despite the fact that "n" is also defined as specific numerical values in some embodiments.

Question 2: Does ST.26 permit inclusion of the sequence(s)?

YES

The example provides a specific numerical value for variable "n," i.e., a lower limit of 2, an upper limit of 100, and an exact value 3. Any sequence containing at least four specifically defined amino acids may be included in the sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

A sequence containing 100 copies of GGGX is preferred (SEQ ID NO: 42). A further annotation should indicate that up to 98 copies of GGGX could be deleted. Inclusion of further specific embodiments that are a key part of the invention is strongly encouraged.

CAUTION: The preferred representation of the sequence indicated above is directed to the provision of a sequence listing on the filing date of a patent application. The same representation may not be applicable to a sequence listing provided subsequent to the filing date of a patent application, since consideration must be given to whether the information provided could be considered by an IPO to add subject matter to the original disclosure.

Relevant ST.26 paragraph(s): Paragraphs 3(c), 7(b), 26, and **27**

Example 27-3: Shorthand formula - four or more specifically defined amino acids

A peptide of the formula $(Gly\text{-}Gly\text{-}Gly\text{-}z)_n$

Where z is any amino acid and variable n is 2-100, preferably 3.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The enumerated peptide of the formula provides three specifically defined amino acids, each of which is Gly, and the symbol "z". Conventionally, "Z" is the symbol for "glutamine or glutamic acid"; however, the description in this example defines "z" as "any amino acid" (*see* Introduction to this document). Under ST.26, an amino acid that is not specifically defined is represented by "X". Based on this analysis, the enumerated repeat peptide does not contain four specifically defined amino acids. However, the description provides a specific numerical value for variable "n," i.e., a lower limit of 2 and an upper limit of 100. Therefore, the example discloses a peptide having at least six specifically defined amino acids in the sequence GGGzGGGz, which is required by ST.26 to be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

Since "z" represents any amino acid, the conventional symbol used to represent the fourth and eighth amino acids is "X."

ST.26 requires inclusion in a sequence listing of only the single sequence that has been enumerated by its residues. Therefore, at least one sequence containing any of 2, 3, or 100 copies of GGGX must be included in the sequence listing; however, the most encompassing sequence containing 100 copies of GGGX is preferred (SEQ ID NO: 42) (*see* Introduction to this document). In the latter case, a further annotation could indicate that up to 98 copies of GGGX could be deleted. Inclusion of two additional sequences containing 2 and 3 copies of GGGX, respectively (SEQ ID NO: 44-45), is strongly encouraged.

Further, the example does not disclose that the "z" variable is the same in each of the two occurrences in the expanded sequence. However, if "z" is disclosed as the same amino acid in all locations, then a feature Key VARIANT and a Qualifier NOTE should indicate that "X" in all positions can be any amino acid, as long as they are the same in all locations.

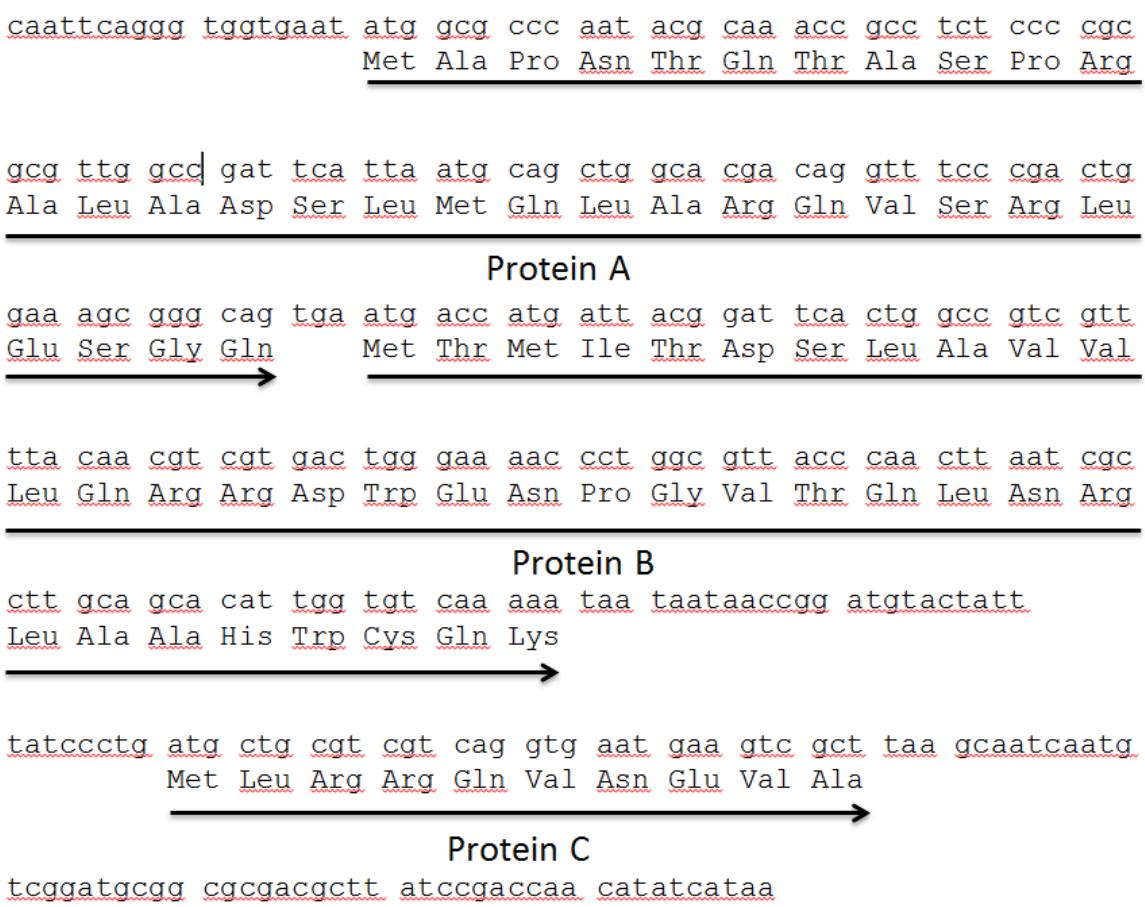
CAUTION: The preferred representation of the sequence indicated above is directed to the provision of a sequence listing on the filing date of a patent application. The same representation may not be applicable to a sequence listing provided subsequent to the filing date of a patent application, since consideration must be given to whether the information provided could be considered by an IPO to add subject matter to the original disclosure.

Relevant ST.26 paragraph(s): Paragraphs 3(c), 7(b), 26, and **27**

Paragraph 28 – Amino acid sequences separated by internal terminator symbols

Example 28-1: Encoding nucleotide sequence and encoded amino acid sequence

A patent application describes the following sequences:



Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The application describes a nucleotide sequence, containing termination codons, which encodes three distinct amino acids sequences.

The enumerated nucleotide sequence contains more than 10 specifically defined nucleotides and must be included in a sequence listing as a single sequence.

Regarding the encoded amino acid sequences, paragraph 28 requires that amino acid sequences separated by an internal terminator symbol such as a blank space, must be included as separate sequences. Since each of "Protein A", "Protein B", and "Protein C" contain four or more specifically defined amino acids, ST.26 paragraph 7(b) requires that each must be included in a sequence listing and must be assigned its own sequence identification number.

Question 3: How should the sequence(s) be represented in the sequence listing?

The nucleotide sequence must be included in a sequence listing as:

caattcagggtggtgaatatggcgcccaatacgcaaaccgcctctccccgcgcgttggccgattcattaatggaaagcgggcagtgaatgaccatgattacggat
tcactggccgtcgttttacaacgtcgtgactgggaaaaccctggcgttacccaacttaatcgccttgcagcacattggtgtcaaaaataataataaccggatgtacta

tttatccctgatgctgcgtcgtcaggtgaatgaagtcgcttaagcaatcaatgtcggatgcggcgcgacgcttatccgaccaacatatcataa. (SEQ ID NO: 46)

The nucleotide sequence should further be described using a "CDS" feature key for each of the three proteins and the element INSDFeature_location should identify the location of each coding sequence, including the stop codon. In addition, for each "CDS" feature key, the "translation" qualifier should be included with the amino acid sequence of the protein as the qualifier value. The application does not disclose the genetic code table that applies to the translation (see Annex 1, Section 9, Table 5). If the Standard Code table applies, then the qualifier "transl_table" is not necessary; however, if a different genetic code table applies, then the appropriate qualifier value from Table 5 must be indicated for the qualifier "transl_table". Finally, the qualifier "protein _id" must be included with the qualifier value indicating the sequence identification number of each of the translated amino acid sequences.

The amino acid sequences must be included as separate sequences, each assigned its own sequence identification number:

MAPNTQTASPRALADSLMQLARQVSRLESGQ (SEQ ID NO: 47)

MTMITDSLAVVLQRRDWENPGVTQLNRLAAHWCQK (SEQ ID NO: 48)

MLRRQVNEVA (SEQ ID NO: 49)

NOTE: See "Example 90-1 Amino acid sequence encoded by a coding sequence with introns" for an illustration of a translated amino acid sequence represented as a single sequence.

Relevant ST.26 paragraphs: Paragraphs 7, 26, **28**, 57, 87-90

Paragraph 29 – Representation of an "other" amino acid

Example 29-1: Most restrictive ambiguity symbol for an "other" amino acid

A patent application describes the following sequence:

Ala-Hse-X_1-X_2-X_3-X_4-Tyr-Leu-Gly-Ser

Wherein, X_1= Ala or Gly,

X_2= Ala or Gly,

X_3= Ala or Gly,

X_4= Ala or Gly, and

Hse = Homoserine

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The enumerated peptide contains five specifically defined amino acids. The symbol "X" is used conventionally to represent two amino acids in the alternative (*see* Introduction to this document).

Because there are five specifically defined amino acids, i.e., Ala, Tyr, Leu, Gly and Ser, ST.26 paragraph 7(b) requires that the sequence must be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

Paragraph 29 requires any "other" amino acid must be represented by the symbol "X". In the example, the sequence contains the amino acid Hse in position 2 which is not found in Annex I, Section 3, Table 3. Accordingly, Hse is an "other" amino acid and must be represented by the symbol "X".

X_1-X_4 are variant positions, each of which can be A or G. The most restrictive ambiguity symbol for alternatives A or G is "X". Therefore, the sequence may be represented as:

AXXXXXYLGS (SEQ ID NO: 50)

Inclusion of any specific sequences essential to the disclosure or claims of the invention is strongly encouraged, as discussed in the introduction to this document.

Since amino acid Hse is not found in Annex I, Section 4, Table 4, a feature key “SITE” and a qualifier “NOTE” must be provided with the complete, unabbreviated name of Homoserine.

According to paragraph 27, because X_1-X_4 represent an alternative of only 2 amino acids, then further description is required. Paragraph 94 indicates that the feature key “VARIANT” should be used with the qualifier “NOTE” and qualifier value “A or G”. According to ST.26 paragraph 34, since these positions are adjacent and have the same description, they may be jointly described using the syntax “3..6” as the location descriptor in the element INSDFeature_location.

Relevant ST.26 paragraphs: Paragraphs 3(a), 7(b), 25-27, **29**, 34, 66, 70, 71, and 94-95

Paragraph 30 – Annotation of a modified amino acid

Example 30-1 – Feature key “CARBOHYD”

A patent application describes a polypeptide with a specifically modified amino acid, containing a glycosylated side chain, characterized in that Cys corresponding to positions 4 and 15 of the polypeptide forms a disulfide bond, according to the following sequence:

Leu-Glu-Tyr-Cys-Leu-Lys-Arg-Trp-Asn(asialyloligosaccharide)-Glu-Thr-Ile-Ser-His-Cys-Ala-Trp

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The enumerated peptide provides 17 specifically defined amino acids. There are 16 natural amino acids, wherein the ninth (asparagine) is glycosylated. Therefore, the sequence must be included in a sequence listing as required by ST.26 paragraph (7)(b).

Question 3: How should the sequence(s) be represented in the sequence listing?

According to ST.26 paragraph 29, a modified amino acid should be represented in the sequence as the corresponding unmodified amino acid whenever possible.

Therefore the sequence must be included in a sequence listing as:

LEYCLKRWNETISHCAW (SEQ ID NO: 51)

A further description of the modified amino acid is required. The feature key “CARBOHYD” together with the (mandatory) qualifier “NOTE” should be used to indicate the occurrence of the attachment of a sugar chain (asialyloligosaccharide) to asparagine in position 9. The qualifier “NOTE” describes the type of linkage, e.g. N-linked. The location descriptor in the feature location element is the residue position number of the modified asparagine.

In addition, there is a disulfide bond between the two Cys residues. Therefore the feature key “DISULFID” is used to describe an intrachain crosslink. The location descriptors in the feature location element are the residue position numbers of the linked Cys residues in conjunction with the “join” location operator, “join(4,15)”. The qualifier NOTE is not mandatory.

Relevant ST.26 paragraph(s): Paragraphs 3(a), 7(b), 26, 29, **30**, and Annex I, section 7, feature key 7.4

Paragraph 36 – Sequences containing regions of an exact number of contiguous "n" or "X" residues

Example 36-1: Sequence with a region of a known number of "X" residues represented as a single sequence

LL-100-KYMR

Where the "-100-"between amino acids Leucine and Lysine reflects a 100 amino acid region in the sequence.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

ST.26 paragraph 36 requires inclusion of a sequence that contains at least four specifically defined amino acids separated by one or more regions of a defined number of "X" residues.

The disclosed sequence uses a nonconventional symbol, i.e. "-100-." The definition of "-100-" must be determined from the explanation of the sequence in the disclosure, which defines this symbol as 100 amino acids between leucine and lysine (*see* Introduction to this document). Therefore, "-100-" is a defined region of "X" residues. Since six of the 106 amino acids in the sequence are specifically defined, ST.26 paragraph 7(b) requires that the sequence must be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The nonconventional symbol "-100-" is represented as 100 "X" residues (since any symbol used to represent an amino acid is equivalent to only one residue). Therefore, a single sequence of 106 amino acids in length, containing 100 "X" residues between LL and KYMR, must be included in a sequence listing (SEQ ID NO: 52).

Relevant ST.26 paragraph(s): Paragraphs 7(b), 26, 27, and **36**

Example 36-2: Sequence with multiple regions of a known number or range of "X" residues represented as a single sequence

Lys-z_2-Lys-z_m-Lys-z_3-Lys-z_n-Lys-z_2-Lys

Where z is any amino acid, m=20, n=19-20, z_2 means that the pairs of Lysines are separated by any two amino acids, and z_3 means the pairs of Lysines are separated by any three amino acids.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The disclosed sequence uses a nonconventional symbol, i.e. "z." Therefore, the disclosure must be consulted to determine the definition; "z" is defined as any amino acid (*see* Introduction to this document). The conventional symbol used to represent any amino acid is "X". Considering the presence of "X" variables, the peptide contains six lysine residues that are enumerated and specifically defined, which is required to be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence uses a nonconventional symbol "z", the definition of which must be determined from the disclosure. Since "z" is defined as any amino acid, the conventional symbol is "X."

The preferred and most encompassing means of representation is (*see* Introduction to this document):

KXXKXXXXXXXXXXXXXXXXXXXXKXXXKXXXXXXXXXXXXXXXXXXXXXXXKXXK (SEQ ID NO: 53)

Wherein z_n is equal to 20 "X's", with a further description that the "X" variable corresponding to position 30 can be deleted.

Alternatively, or in addition to the above, the sequence may be represented as:

KXXKXXXXXXXXXXXXXXXXXXXXKXXXKXXXXXXXXXXXXXXXXXXXXXXXKXXK (SEQ ID NO: 54)

Wherein z_n is equal to 19 "X's", with a further description that an "X" variable between position numbers 29 and 30 can be inserted.

Relevant ST.26 paragraph(s): Paragraphs 26, 27, and **36**

Example 36-3: Sequence with multiple regions of a known number or range of "X" residues represented as a single sequence

K-z_2-K-z_m-K-z_3-K-z_n-K-z_2-K

Where z is any amino acid , where m=15-25, preferably 20-22, n=15-25, preferably 19-20, z_2 means that the pairs of Lysines are separated by any two amino acids, and z_3 means the pairs of Lysines are separated by any three amino acids.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The sequence in the example uses a nonconventional symbol, i.e. "z." Therefore, the surrounding disclosure is consulted to determine the definition of "z" (*see* Introduction to this document). The disclosure defines this symbol as any amino acid. The conventional symbol used to represent this amino acid is "X." After considering the presence of "X" variables, the peptide contains 6 lysine residues that are enumerated and specifically defined, which is required in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The sequence uses a nonconventional symbol "z", the definition of which must be determined from the disclosure. Since "z" is defined as any amino acid, the conventional symbol is "X". The preferred and most encompassing means of representation is:

KXXKXXXXXXXXXXXXXXXXXXXXXXXXXKXXXKXXXXXXXXXXXXXXXXXXXXXXXXXKXXK (SEQ ID NO: 55)

(where m=25 and n=25), with a further description that up to 10 "X" residues in each of the "z_m" or "z_n" regions may be deleted.

Inclusion of any specific sequences essential to the disclosure or claims of the invention is strongly encouraged, as discussed in the introduction to this document.

Alternatively, the sequence may be represented as:

KXXKXXXXXXXXXXXXXXKXXXKXXXXXXXXXXXXXXXXKXXK (SEQ ID NO: 56)

(where m=15 and n=15), with a further description that up to 10 "X" residues in each of the "z_m" or "z_n" regions may be inserted.

As further alternatives, any or all possible variations may be included.

CAUTION: The preferred representation of the sequence indicated above is directed to the provision of a sequence listing on the filing date of a patent application. The same representation may not be applicable to a sequence listing provided subsequent to the filing date of a patent application, since consideration must be given to whether the information provided could be considered by an IPO to add subject matter to the original disclosure.

Relevant ST.26 paragraph(s): Paragraphs 27 and **36**

Paragraph 37 – Sequences containing regions of an unknown number of "n" or "X" residues

Example 37-1: Sequence with regions of an unknown number of "X" residues must not be represented as a single sequence

Gly-Gly----Gly-Gly-Xaa-Xaa

where the symbol ---- is an undefined gap within the sequence, where Xaa is any amino acid, and the Glycine and Xaa residues are connected to one another through peptide bonds.

Question 1: Does ST.26 require inclusion of the sequence(s)?

NO

ST.26 paragraph 37 prohibits the inclusion of any sequence that contains an undefined gap; therefore, inclusion of the entire sequence is not required.

ST.26 paragraph 37 does require inclusion of any portion of a sequence adjacent to an undefined gap that contains four or more specifically defined amino acids. In the example above, inclusion of either portion adjacent to the undefined gap is not required, since each portion contains only two specifically defined amino acids.

Question 2: Does ST.26 permit inclusion of the sequence(s)?

NO – not the entire sequence

NO – not any portion of the sequence

ST.26 paragraph 37 does not permit inclusion of the entire sequence.

ST.26 paragraph 8 does not permit inclusion of either portion adjacent to the undefined gap, since each portion contains only two specifically defined amino acids.

Relevant ST.26 paragraphs: Paragraphs 7(b), 8, 26, and **37**

Example 37-2: Sequence with regions of an unknown number of "X" residues must not be represented as a single sequence

Gly-Gly----Gly-Gly-Ala-Gly-Xaa-Xaa

wherein the symbol ---- is an undefined gap within the sequence, where Xaa is any amino acid, and the Glycine and Xaa residues are connected to one another through peptide bonds.

Question 1: Does ST.26 require inclusion of the sequence(s)?

NO – not the entire sequence

YES – a portion of the sequence

ST.26 paragraph 37 prohibits the inclusion of any sequence that contains an undefined gap, but requires inclusion of any portion of a sequence adjacent to an undefined gap that contains four or more specifically defined amino acids.

In the example above, ST.26 does not require (and prohibits) inclusion of both the entire sequence, which contains an undefined gap, and the Gly-Gly portion adjacent to the undefined gap, which contains only two specifically defined amino acids. However, ST.26 requires inclusion of the Gly-Gly-Ala-Gly- Xaa-Xaa portion adjacent to the undefined gap, since it contains at least four specifically defined amino acids.

Question 2: Does ST.26 permit inclusion of the sequence(s)?

NO – not the entire sequence and not the Gly-Gly portion

Question 3: How should the sequence(s) be represented in the sequence listing?

The portion of the sequence adjacent to the undefined gap that contains four specifically defined amino acids must be represented as:

GGAGXX (SEQ ID NO: 57)

Preferably, the sequence should be annotated to indicate that the represented sequence is part of a larger sequence that contains an undefined gap by using the feature key “SITE”, the feature location “1” and the qualifier “NOTE” with the value, e.g., “This residue is linked N-terminally to a peptide having an N-terminal Gly-Gly and a gap of undefined length.”.

Relevant ST.26 paragraph(s): Paragraphs 7(b), 8, 26, and **37**

Paragraph 87 – “CDS” Feature key

Example 87-1: Encoding nucleotide sequence and encoded amino acid sequence

A patent application describes the following nucleotide sequence and its translation:

```
atg acc gga aat aaa cct gaa acc gat gtt tac gaa att tta tga

Met Thr Gly Asn Lys Pro Glu Thr Asp Val Tyr Glu Ile Leu STOP
```

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES – **the nucleotide sequence.** The enumerated nucleotide sequence has more than ten specifically defined nucleotides.

YES – **the peptide sequence.** The enumerated peptide sequence has more than four specifically defined amino acids.

Question 3: How should the sequence(s) be represented in the sequence listing?

The nucleotide sequence must be presented as:

atgaccggaaataaacctgaaaccgatgtttacgaaattttatga (SEQ ID NO: 58)

The nucleotide sequence should further be described using the “CDS” feature key and the element INSDFeature_location should identify the entire sequence, including the stop codon (i.e., position 1 through 45). In addition, the “translation” qualifier should be included with the qualifier value “MTGNKPETDVYEIL”. The application does not disclose the genetic code table that applies to the translation (see Annex 1, Section 9, Table 5). If the Standard Code table applies, then the qualifier “transl_table” is not necessary; however, if a different genetic code table applies, then the appropriate qualifier value from Table 5 must be indicated for the qualifier “transl_table”. Finally, the qualifier “protein _id” must be included with the qualifier value indicating the sequence identification number of the translated peptide.

The peptide sequence must be separately presented with its own sequence identification number using single letter codes as follows:

MTGNKPETDVYEIL (SEQ ID NO: 59)

The STOP following the enumerated peptide sequence must not be included in the peptide sequence in the sequence listing.

CAUTION: The preferred representation of the sequence indicated above is directed to the provision of a sequence listing on the filing date of a patent application. The same representation may not be applicable to a sequence listing provided subsequent to the filing date of a patent application, since consideration must be given to whether the information provided could be considered by an IPO to add subject matter to the original disclosure.

Relevant ST.26 paragraphs: Paragraphs 7(a), 7(b), 26, 28, **87**, 88, and 90

Paragraph 90 – Amino acid sequence encoded by a coding sequence

Example 90-1: Amino acid sequence encoded by a coding sequence with introns

A patent application contains the following figure disclosing a coding sequence and its translation:

```
atg aag act ttc gca gcc ttg ctt tcc gct gtc act ctc gcg ctc tcg
Met Lys Thr Phe Ala Ala Leu Leu Ser Ala Val Thr Leu Ala Leu Ser

gtg cgc gcc cag gcg gct gtc tgg agt caa t gtaagtgccg ctgcttttca
Val Arg Ala Gln Ala Ala Val Trp Ser Gln

ttgatacgag actctacgcc gagctgacgt gctaccgtat ag gt  ggc ggt aca
                                               Cys Gly Gly Thr

ccg ggt tgg acg ggc gag acc act tgc gtt gct ggt tcg gtt tgt acc
Pro Gly Trp Thr Gly Glu Thr Thr Cys Val Ala Gly Ser Val Cys Thr

tcc ttg agc tca gtgagcgact ttcaatccgt cgtcattgct cctcatgtat
Ser Leu Ser Ser

tgacgattgg ccttcatag tca tac tct caa tgc gtt ccg ggc tcc gca acg
                    Ser Tyr Ser Gln Cys Val Pro Gly Ser Ala Thr

tcc agc gct ccg gcg gcc ccc tca gcg aca act tca ggc ccc gca cct
Ser Ser Ala Pro Ala Ala Pro Ser Ala Thr Thr Ser Gly Pro Ala Pro

acg gac gga acg tgc tcg gcc agc ggg gca tgg ccg cca ttg acc tga
Thr Asp Gly Thr Cys Ser Ala Ser Gly Ala Trp Pro Pro Leu Thr Ter
```

Figure 1 – nucleotides shown in bold-face are intron regions.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The application discloses a nucleotide sequence and its amino acid translation. The enumerated nucleotide sequence contains more than 10 specifically defined nucleotides and must be included in a sequence listing as a single sequence.

The nucleotide sequence contains coding sequence (exons) separated by noncoding sequence (introns). The figure depicts the translation of the nucleotide sequence as three non-contiguous amino acid sequences. According to the figure caption, the bolded regions of nucleotides are intron sequences that will be spliced out of an RNA transcript before translation into a protein. Accordingly, the three amino acid sequences are actually a single, contiguous, enumerated sequence, which contains more than four specifically defined amino acids and must be included in a sequence listing as a single sequence.

Question 3: How should the sequence(s) be represented in the sequence listing?

The nucleotide sequence must be included in a sequence listing as:

atgaagactttcgcagccttgctttccgctgtcactctcgcgctctcggtgcgcgcccaggcggctgtctggagtcaatgtaagtgccgctgcttttcattgatacgaga ctctacgccgagctgacgtgctaccgtataggtggcggtacaccgggttggacgggcgagaccacttgcgttgctggttcggtttgtacctccttgagctcagtgag cgactttcaatccgtcgtcattgctcctcatgtattgacgattggccttcatagtcatactctcaatgcgttccgggctccgcaacgtccagcgctccggcggccccctc agcgacaacttcaggccccgcacctacggacggaacgtgctcggccagcggggcatggccgccattgacctga (SEQ ID NO: 74)

The nucleotide sequence should further be described using a "CDS" feature key and the element INSDFeature_location should identify the location of the coding sequence, including the stop codon indicated by "Ter". In addition, the "translation" qualifier should be included, with the amino acid sequence of the protein as the qualifier value. (Note that the terminator symbol "Ter" in the last position of the sequence must not be included in the amino acid sequence.) The application does not disclose the genetic code table that applies to the translation (see Annex 1, Section 9, Table 5). If the "Standard Code" table applies, then the qualifier "transl_table" is not necessary; however, if a different genetic code table applies, then the appropriate qualifier value from Table 5 must be indicated for the qualifier "transl_table". Finally, the qualifier "protein _id" must be included with the qualifier value indicating the sequence identification number of the translated amino acid sequence.

The amino acid sequence must be included as a single sequence:

MKTFAALLSAVTLALSVRAQAAVWSQCGGTPGWTGETTCVAGSVCTSLSSSYSQCVPGSATSSAPAAPSATTSG PAPTDGTCSASGAWPPLT (SEQ ID NO: 75)

Relevant ST.26 paragraphs: Paragraphs 7, 26, 28, 57, 87-**90**

Paragraph 91 – Primary sequence and a variant, each enumerated by its residues

Example 91-1: Representation of enumerated variants

The description includes the following sequence alignment.

```
D. melanogaster      ACATTGAATCTCATACCACTTT

D. virilis           ...-..G...C..-.-G.....

D. simulans          GT..G.CG..GT..SGT.G...
```

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

It is common in the art to include "dots" in a sequence alignment to indicate "this position is the same as the position above it." Therefore, the "dots" in species 2 and 3 are considered enumerated and specifically defined nucleotides, as they are simply a short-hand way of indicating that a given position is the same nucleotide as in species 1. In addition, sequence alignments frequently display the symbol "-" to indicate the absence of a residue in order to maximize the alignment.

Accordingly, the nucleotide sequences of species 1 and 3 contain twenty-two enumerated and specifically defined nucleotides, whereas the nucleotide sequences of species 2 contains nineteen. Thus, each sequence is required by ST.26 paragraph 7(a) to be included in a sequence listing with separate sequence identification numbers.

Question 3: How should the sequence(s) be represented in the sequence listing?

Drosophila melanogaster sequence must be included in a sequence listing as:

acattgaatctcataccacttt (SEQ ID NO: 60)

Drosophila virilis sequence must be included in a sequence listing as:

acatggatcccacgacttt (SEQ ID NO: 61)

Drosophila simulans sequence must be included in a sequence listing as:

gtatggcgtcgtatsgtagttt (SEQ ID NO: 62)

Relevant ST.26 paragraphs: Paragraphs 7(a), 13, and **91**

Example 91-2: Representation of enumerated variants

The description includes the following table of a peptide and functional variants thereof. A blank space in the table below indicates that an amino acid in the variant is the same as the corresponding amino acid in the "Sequence" and a "-" indicates deletion of the corresponding amino acid in the "Sequence".

Position	1	2	3	4	5	6	7	8	9
Sequence	A	V	L	T	Y	L	R	G	E
Variant 1									A
Variant 2			P			P			
Variant 3			A	I	G	Y			
Variant 4							-		

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

As indicated, a blank space in this table indicates that an amino acid in the variant is the same as the corresponding amino acid in the "Sequence". Therefore, the amino acids of the variant sequences are enumerated and specifically defined.

Since the four variant sequences each contain more than four enumerated and specifically defined amino acids, each sequence is required by ST.26 paragraph 7(a) to be included in a sequence listing with separate sequence identification numbers.

Question 3: How should the sequence(s) be represented in the sequence listing?

AVLTYLRGE (SEQ ID NO: 76)

AVLTYLRGA (SEQ ID NO: 77)

AVPTYPRGE (SEQ ID NO: 78)

AVAIGYRGE (SEQ ID NO: 79)

AVLTYLGE (SEQ ID NO: 80)

Relevant ST.26 paragraphs: Paragraphs 7(b), 26, and **91**

Example 91-3: Representation of a consensus sequence

A patent application includes Figure 1 with the following multiple sequence alignment.

Consensus *LEG**n**EQFINA**ak**IIRHP**k**Y**nrk**T**ln**NDI**m**LIK*

Homo sapiens LEG**N**EQFINA**AK**IIRHP**Q**Y**DRK**T**LN**NDI**M**LIK

Pongo abelii LEG**N**EQFINA**AK**IIRHP**Q**Y**DRK**T**VN**NDI**M**LIK

Papio anubis LEG**T**EQFINA**AK**IIRHP**D**Y**DRK**T**LN**NDI**L**LIK

Rhinopithecus roxellana LEG**T**EQFINA**AK**IIRHP**N**Y**NRI**T**LD**NDI**L**LIK

Pan paniscus LEG**N**EQFINA**AK**IIRHP**K**Y**NRI**T**LN**NDI**M**LIK

Rhinopithecus bieti LEG**N**EQFINA**TK**IIRHP**K**Y**NGN**T**LN**NDI**M**LIK

Rhinopithecus roxellana LEG**N**EQFINA**TQ**IIRHP**K**Y**NGN**T**LN**NDI**M**LIK

The consensus sequence includes upper case letters to represent conserved amino acid residues, while the lower case letters “n”, “a”, “k”, “r”, “l” and “m” represent the predominant amino acid residues among the aligned sequences.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The lower case letters in the consensus sequence each represent a single amino acid residue. Consequently, the consensus sequence, as well as each of the remaining seven sequences in Figure 1, includes at least four specifically defined amino acids. ST.26 paragraph 7(b) requires inclusion of all eight sequences in the sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The lower case letters in the consensus sequence are being used as ambiguity symbols to represent the predominant amino acid among the possible variants for a specific position. Therefore, the lower case letters “n”, “a”, “k”, “r”, “l” and “m” are conventional symbols used in a nonconventional manner and the consensus sequence must be represented using an ambiguity symbol in place of each of the lower case letters.

The most restrictive ambiguity symbol should be used. For most positions in the consensus sequence, “X” is the most restrictive ambiguity symbol; however, the most restrictive ambiguity symbol for “D” or “N” in positions 20 and 25 is “B”. The consensus sequence should be included in the sequence listing as:

LEGXEQFINAXXIIRHPXYBXXTXBNDIXLIK (SEQ ID NO: 81)

According to paragraph 27, the symbol “X” will be construed as any one of “A”, “R”, “N”, “D”, “C”, “Q”, “E”, “G”, “H”, “I”, “L”, “K”, “M”, “F”, “P”, “O”, “S”, “U”, “T”, “W”, “Y”, or “V”, except where it is used with a further description in the feature table. Therefore, each “X” in the consensus sequence must be further described in a feature table using the feature key “VARIANT” and the qualifier “NOTE” to indicate the possible variants for each position.

The remaining seven sequences must be included in the sequence listing as:

LEGNEQFINAAKIIRHPQYDRKTLNNDIMLIK (SEQ ID NO: 82)

LEGNEQFINAAKIIRHPQYDRKTVNNDIMLIK (SEQ ID NO: 83)

LEGTEQFINAAKIIRHPDYDRKTLNNDILLIK (SEQ ID NO: 84)

LEGTEQFINAAKIIRHPNYNRITLDNDILLIK (SEQ ID NO: 85)

LEGNEQFINAAKIIRHPKYNRITLNNDIMLIK (SEQ ID NO: 86)

LEGNEQFINATKIIRHPKYNGNTLNNDIMLIK (SEQ ID NO: 87)

LEGNEQFINATQIIRHPKYNGNTLNNDIMLIK (SEQ ID NO: 88)

CAUTION: The preferred representation of the sequence indicated above is directed to the provision of a sequence listing on the filing date of a patent application. The same representation may not be applicable to a sequence listing provided subsequent to the filing date of a patent application, since consideration must be given to whether the information provided could be considered by an IPO to add subject matter to the original disclosure.

Relevant ST.26 paragraphs: Paragraphs 7(b), 26, 27, **91**, and 95

Paragraph 92 – Variant sequence disclosed as a single sequence with enumerated alternative residues

Example 92-1: Representation of single sequence with enumerated alternative amino acids

A patent application claims a peptide of the sequence:

(i) Gly-Gly-Gly-[Leu or Ile]-Ala-Thr-[Ser or Thr]

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The sequence provides four specifically defined amino acids and ST.26 paragraph 7(b) requires inclusion of the sequence in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

Table 3 of Annex I, Section 3 defines the ambiguity symbol "J" as isoleucine or leucine. Therefore, the preferred representation of the sequence is:

GGGJATX (SEQ ID NO: 63)

which requires a further description in a feature table using the feature key "VARIANT" and the qualifier "NOTE" to indicate that the "X" is Serine or Threonine.

Alternatively, the sequence may be represented, for example, as:

GGGLATS (SEQ ID NO: 64)

which requires a further description in a feature table using the feature key "VARIANT" and the qualifier "NOTE" to indicate that L can be replaced by I, and S can be replaced by T.

CAUTION: The preferred representation of the sequence indicated above is directed to the provision of a sequence listing on the filing date of a patent application. The same representation may not be applicable to a sequence listing provided subsequent to the filing date of a patent application, since consideration must be given to whether the information provided could be considered by an IPO to add subject matter to the original disclosure.

Relevant ST.26 paragraph(s): Paragraphs 7(b), 8, 26, 27, **92**, and 95

Paragraph 93(a) – A variant sequence disclosed only by reference to a primary sequence with multiple independent variations

Example 93(a)-1: Representation of a variant sequence by annotation of the primary sequence

An application contains the following disclosure:

"Peptide fragment 1 is Gly-Leu-Pro-Xaa-Arg-Ile-Cys wherein Xaa can be any amino acid….

In another embodiment, peptide fragment 1 is Gly-Leu-Pro-Xaa-Arg-Ile-Cys wherein Xaa can be Val, Thr, or Asp….

In another embodiment, peptide fragment 1 is Gly-Leu-Pro-Xaa-Arg-Ile-Cys wherein Xaa can be Val."

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

"Peptide fragment 1" in each of the three disclosed embodiments provides at least six specifically defined amino acids; therefore, the sequence must be included in a sequence listing as required by ST.26 paragraph 7(b).

Question 3: How should the sequence(s) be represented in the sequence listing?

In this example, the enumerated sequence of "Peptide fragment 1" is disclosed three times, as three different embodiments, each with an alternative description of Xaa. In this example, "X" is the most restrictive ambiguity symbol for the Xaa position.

ST.26 requires inclusion of the disclosed enumerated sequence only once. In the most encompassing of the three embodiments, Xaa is any amino acid (*see* Introduction to this document). Therefore, the sequence that must be included in the sequence listing is:

GLPXRIC (SEQ ID NO: 65)

Inclusion of any additional sequences essential to the disclosure or claims of the invention is strongly encouraged, as discussed in the introduction to this document.

For the above example, it is strongly encouraged that the following additional three sequences are included in the sequence listing, each with their own sequence identification number:

GLPVRIC (SEQ ID NO: 66)

GLPTRIC (SEQ ID NO: 67)

GLPDRIC (SEQ ID NO: 68)

CAUTION: The preferred representation of the sequence indicated above is directed to the provision of a sequence listing on the filing date of a patent application. The same representation may not be applicable to a sequence listing provided subsequent to the filing date of a patent application, since consideration must be given to whether the information provided could be considered by an IPO to add subject matter to the original disclosure.

Relevant ST.26 paragraph(s): Paragraphs 7(b), 26, 27, and **93(a)**

Paragraph 93(b) – A variant sequence disclosed only by reference to a primary sequence with multiple interdependent variations

Example 93(b)-1: Representation of individual variant sequences with multiple interdependent variations

A patent application describes the following consensus sequence:

cgaatg**n**$_1$cccactacgaatg**n**$_2$cacgaatg**n**$_3$cccaca

wherein n_1, n_2, and n_3 can be a, t, g, or c.

Several variant sequences are disclosed as follows:

if n_1 is a, then n2 and n3 are t, g, or c;

if n_1 is t, then n2 and n3 are a, g, or c;

if n_1 is g, then n2 and n3 are t, a, or c;

if n_1 is c, then n2 and n3 are t, g, or a.

Question 1: Does ST.26 require inclusion of the sequence(s)?

YES

The sequence has more than ten enumerated and "specifically defined" nucleotides and is required by ST.26 paragraph 7(a) to be included in a sequence listing.

Question 3: How should the sequence(s) be represented in the sequence listing?

The enumerated sequence contains more than ten specifically defined nucleotides and three "n" residues. ST.26 requires inclusion of the disclosed enumerated sequence and where an ambiguity symbol is appropriate, the most restrictive symbol should be used. In this example, n_1, n_2, and n_3 can be a, t, g, or c, so "n" is the most restrictive ambiguity symbol. Therefore, the sequence that must be included in the sequence listing is:

cgaatgncccactacgaatgncacgaatgncccaca (SEQ ID NO: 69)

The enumerated sequence contains variations at three distinct locations and the occurrence of the variations is interdependent. Inclusion of additional sequences which represent additional embodiments that are a key part of the invention is **strongly** encouraged, as discussed in the introduction to this document. Therefore, according to ST.26 paragraph 93(b), the additional embodiments should be included in a sequence listing as four separate sequences, each with its own sequence identification number:

cgaatgacccactacgaatgbcacgaatgbcccaca (SEQ ID NO: 70)

cgaatgtcccactacgaatgvcacgaatgvcccaca (SEQ ID NO: 71)

cgaatggcccactacgaatghcacgaatghcccaca (SEQ ID NO: 72)

cgaatgccccactacgaatgdcacgaatgdcccaca (SEQ ID NO: 73)

(Note that b = t, g, or c; v = a, g, or c; h = t, a, or c; and d = t, g, or a; see Annex I, Section 1, Table 1)

According to ST.26 paragraph 15, the most restrictive symbol must be used to represent variable positions. Consequently, n2 and n3 must not be represented by "n" in the sequence.

CAUTION: The preferred representation of the sequence indicated above is directed to the provision of a sequence listing on the filing date of a patent application. The same representation may not be applicable to a sequence listing provided subsequent to the filing date of a patent application, since consideration must be given to whether the information provided could be considered by an IPO to add subject matter to the original disclosure.

Relevant ST.26 paragraphs: Paragraphs 7(a), 15, and **93(b)**

Appendix

GUIDANCE DOCUMENT SEQUENCES IN XML

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[End of Annex VI to ST.26 and of Standard]

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