

# L<sup>A</sup>T<sub>E</sub>X 项目模板

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# 第一章 General

Since references to web sites are not yet acknowledged as citations, please mention Den Dunnen et al. (2016) HGVS recommendations for the description of sequence variants: 2016 update. Hum.Mutat. 25: 37: 564-569 when referring to these pages. Note that although the examples on these pages mainly give examples for human (Homo sapiens), the recommendations can be applied to all species.

## 1.1 General recommendations

1. all variants should be described at the most basic level, **the DNA level**. Descriptions at the RNA and/or protein level may be given in addition.
  - descriptions should make clear whether the change was **experimentally determined or theoretically deduced** by giving predicted consequences in parentheses
  - descriptions at RNA/protein level should describe the changes observed on that level (RNA/protein) and not try to incorporate any knowledge regarding the change at DNA-level (see Questions below)
2. all variants should be described in relation to an **accepted reference sequence** (see Reference Sequences).
  - the reference sequence file used should be **public** and **clearly described**, e.g. NC\_000023.10, LRG\_199, NG\_012232.1, ENST00000357033, NM\_004006.2, NR\_002196.1, NP\_003997.1, etc.
    - when variants are not reported in relation to a genomic reference sequence from a recent genome build, the preferred reference sequence is a **Locus Reference Genomic sequence (LRG)**
    - when no LRG is available, one should be requested (see Reference Sequences).
    - the reference sequence used must contain the residue(s) described to be changed.
  - a letter prefix should be used to indicate the type of reference sequence used. Accepted prefixes are;
    - “g.” for a **genomic reference sequence**
    - “c.” for a **coding DNA reference sequence**
    - “n.” for a **non-coding DNA reference sequence**

- “r.” for an **RNA reference sequence (transcript)**
  - “p.” for a **protein reference sequence**
  - numbering of the residues (nucleotide or amino acid) in relation to the reference sequence used should follow the approved scheme (see Numbering)
3. 3’ rule: for all descriptions the most 3’ position possible of the reference sequence is arbitrarily assigned to have been changed
- the 3’ rule also applies for changes in single residue stretches and tandem repeats (nucleotide or amino acid)
  - the 3’ rule applies to ALL descriptions (genome, gene, transcript and protein) of a given variant
4. descriptions at DNA, RNA and protein level are clearly different:
- **DNA-level** 123456A>T (see Details): number(s) referring to the nucleotide(s) affected, nucleotides in **CAPITALS** using **IUPAC-IUBMB assigned nucleotide symbols**
  - **RNA-level** 76a>u (see Details): number(s) referring to the nucleotide(s) affected, nucleotides in **lower case** using **IUPAC-IUBMB assigned nucleotide symbols**
  - **protein level** Lys76Asn (see Details): the amino acid(s) affected in **3- or 1-letter** followed by a number IUPAC-IUBMB assigned amino acid symbols \* **three-letter amino acid code is preferred** (see Standards)
5. prioritisation: when a description is possible according to several types, the preferred description is: (1) deletion, (2) inversion, (3) duplication, (4) conversion, (5) insertion
- when a variant can be described as a duplication or an insertion, prioritisation determines it should be described as a duplication
6. only approved **HGNC gene symbols** should be used to describe genes or proteins

## 1.2 Characters Used

In HGVS nomenclature some characters have a specific meaning

- “+” (plus) is used in nucleotide numbering; c.123+45A>G
- “-” (minus) is used in nucleotide numbering; c.124-56C>T
- “\*” (asterisk) is used in nucleotide numbering and to **indicate a translation termination (stop) codon** (see Standards); c.\*32G>A and P.Trp41\*
- “\_” (underscore) is used to **indicate a range**; g.12345\_12678del
- “[ ]” (angled brackets) are used for **alleles** (see DNA, RNA, protein)

- “;” (semi colon) is used to separate variants and alleles; g.[123456A>G;345678G>C] or g.[123456A>G];[345678G>C]
- “,” (comma) is used to separate different transcripts/proteins derived from one allele; r.[123a>t, 122\_154del]
- “:” (colon) is used to separate the reference sequence file identifier (accession.version\_number) from the actual description of a variant; NC\_000011.9:g.12345611G>A
- “( )” (parentheses) are used to indicate uncertainties and predicted consequences; NC\_000023.9:g.(123456\_23456p.(Ser123Arg)

NOTE: the range of the uncertainty should be described as precisely as possible (see below)

- “?” (question mark) is used to indicate unknown positions (nucleotide or amino acid); g.(?\_234567)\_(345678\_?)
- “^” (caret) is used as “or”; c.(370A>C^372C>R) as back translation of p.Ser124Arg
- “>” (greater than) is used to describe substitution variants (DNA and RNA level); g.12345A>T, r.123a>u (see DNA, RNA)
- “{ }” (curly braces) suggested for the description of variants in otherwise perfect copy sequences (see Open Issues); g.24\_65dup{46G>T}
- “=” (equals) is used to indicate a sequence was tested but found unchanged; p.(Arg234=)
- “/” (forward slash) is used to indicate mosaicism (see Complex (HGVS/ISCN))
- “//” (double forward slash) is used to indicate chimerism (see Complex (HGVS/ISCN))





# 第一部分

## 附录



## 1.3 元素周期表

表 期 周 表 元

1	2.20	1s	H 氢	Hydrogen
3	0.98	2s	Li 锂	Lithium
4	1.57	2s	Be 铍	Beryllium
5	6.98–6.997	9.01231(5)		
11	0.93	3s	Na 钠	Sodium
12	1.31	3s	Mg 镁	Magnesium
13	22.8897692(8)(2)	24.3041–24.3007		
19	0.82	4s	Ca 钙	Calcium
20	1.00	4s		
37	0.82	5s	Sr 锶	Strontium
38	0.95	5s		
55	0.79	6s	Cs 铯	Cesium
56	0.89	6s	Ba 钡	Barium
57–71			镧系	Lanthanides
87	0.7	7s	Ra 镭	Radium
88	0.9	7s		
89–103			锕系	Actinides
104	6d	6d	Rf 𬬻	Rutherfordium
105	6d	6d	Db 𬬿	Dubnium
106	6d	6d	Sg 𬬰	Seaborgium
107	6d	6d	Bh 𬬱	Bohrium
108	6d	6d	Hs 𬬻	Hassium
109	6d	6d	Mt 𬬿	Meitnerium
110	6d	6d	Ds 𬬽	Darmstadtium
111	6d	6d	Rg 𬬾	Roentgenium
112	6d	6d	Cn 𬬼	Copernicium
113	6d	6d	Nh 𬬿	Nihonium
114	7p	7p	Fl 𫓯	Flerovium
115	7p	7p	Mc 𫓯	Moscovium
116	7p	7p	Lv 𫓯	Livermorium
117	7p	7p	Ts 𫓯	Tennessine
118	7p	7p	Og 𫓯	Oganesson
119	7p	7p		
120	7p	7p		
121	7p	7p		
122	7p	7p		
123	7p	7p		
124	7p	7p		
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190	7p	7p		
191	7p	7p		</

钼系

57	1.1	5d <sup>8</sup>	La 镧	Lanthanum	138.90547(7)	89	1.1	6d <sup>2</sup>	Ac 锕	Actinium	227.0277(1)	(227)
58	1.2	5f	Ce 铈	Cerium	140.116(1)	90	1.3	5f <sup>2</sup>	Th 钍	Thorium	232.0377(1)	(232)
59	1.3	4f <sup>2</sup>	Pr 镨	Praseodymium	140.90766(2)	91	1.5	5f <sup>3</sup>	Pa 镤	Protactinium	231.03688(2)	(231)
60	1.4	4f	Nd 钕	Neodymium	144.242(3)	92	1.38	5f <sup>4</sup>	U 铀	Uranium	238.02891(3)	(238)
61	1.3	4f	Pm 钷	Promethium	144.9126(1)	93	1.36	5f <sup>5</sup>	Np 镎	Neptunium	(237)	(237)
62	1.17	4f	Sm 钐	Samarium	150.36(2)	94	1.28	5f <sup>6</sup>	Pu 钷	Plutonium	(244)	(244)
63	1.2	4f	Eu 铕	Europtium	151.964(1)	95	1.13	5f <sup>7</sup>	Am 镅	Americium	(243)	(243)
64	1.2	4f <sup>6</sup>	Gd 钆	Gadolinium	157.25(3)	96	1.28	5f <sup>8</sup>	Cm 锔	Curium	(247)	(247)
65	1.1	4f <sup>6</sup>	Tb 铽	Terbium	158.925(3)	97	1.3	5f <sup>9</sup>	Bk 锫	Berkelium	(247)	(247)
66	1.22	4f	Dy 镝	Dysprosium	162.500(1)	98	1.3	5f <sup>9</sup>	Cf 锎	Californium	(251)	(251)
67	1.23	4f	Ho 钬	Holmium	164.93033(2)	99	1.3	5f <sup>9</sup>	Es 镱	Einsteinium	(252)	(252)
68	1.24	4f	Er 铒	Erbium	167.259(3)	100	1.3	5f <sup>9</sup>	Fm 镆	Fermium	(257)	(257)
69	1.25	4f	Tm 铥	Thulium	168.93422(2)	101	1.3	5f <sup>9</sup>	Md 钔	Mendelevium	(258)	(258)
70	1.1	4f	Yb 镱	Ytterbium	173.045(10)	102	1.3	5f <sup>9</sup>	No 镎	Nobelium	(259)	(259)
71	1.27	4f	Lu 镥	Lutetium	174.9668(1)	103	1.3	5f <sup>9</sup>	Lr 镈	Lawrencium	(260)	(260)

## 铜系

相对原子质量来源: (<http://ciaaw.org/atomic-weights.htm>). © 2017 张洋

An asterisk (\*) next to a subshell indicates an anomalous (Aufbau rule-breaking) ground state electron configuration.



### 1.3 元素周期表