

20170202_data_release_notes

Overview of changes in the release of Feb 2, 2017

Please also see our [RSS feed](#) for information about accessing the data.

Overview of submissions: 2017

Date	Total Submissions
Jan 01, 2017	396005
Feb 01, 2016	405182

Content

Brief	Explanation
Counsyl	Counsyl provided 5013 novel variant interpretations.
Knight Diagnostic Laboratories, Oregon Health and Sciences University	Knight Diagnostic Laboratories, part of the CSER consortium, submitted 116 novel variant interpretations.
HudsonAlpha	HudsonAlpha, part of the CSER consortium, provided 5 novel variant interpretations.
Correction to the ClinVar VCF files	The VCF files posted on 2/2/17 contain some errors in the alt allele column. We will provide corrected files shortly.
"beta" version of new ClinVar VCF file	We have developed a new version of the ClinVar VCF file. It will be available on the ftp site shortly for review and comment; a README explaining the differences versus the current VCF will be made available also. Note that we will continue to provide the current version of the VCF file for a few months. We will announce when the current version will no longer be provided.
Coming soon - possible retirement of Variation Reporter	<p>NCBI is considering whether to retire Variation Reporter: https://www.ncbi.nlm.nih.gov/variation/tools/reporter</p> <p>We have developed a set of stand-alone variation services that would replace some of the functions of Variation Reporter, but not all. You can try the new services here: https://api.ncbi.nlm.nih.gov/variation/v0/</p> <p>To help us in guiding the decision, if you are a user of Variation Reporter, let us know for what specific purpose you access it by emailing tkr-varhd@ncbi.nlm.nih.gov.</p> <p>Note that on March 1, 2017 there will be a one-day shutdown of Variation Reporter to alert API users of its possible retirement.</p>
Coming soon - ClinVar will adopt the new HGVS standard for variants that are intronic or outside the UTRs	<p>HGVS standard states that "the reference sequence used must contain the residue(s) described to be changed." Therefore "a coding DNA reference sequence does not contain intron or 5' and 3' gene flanking sequences and can therefore not be used as a reference to describe variants in introns and up/down-stream of the gene." ClinVar is working to adopt this standard so we encourage our submitters and users to start describing these variants on genomic sequence instead.</p> <p>http://varnomen.hgvs.org/recommendations/general/</p> <p>http://varnomen.hgvs.org/bg-material/numbering/</p>

Overview of submissions: 2016

Date	Total Submissions
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Jan 01, 2016	172867
Feb 01, 2016	176710
Mar 01, 2016	178032
Apr 01, 2016	180549
May 01, 2016	181155
Jun 01, 2016	192617
Jul 01, 2016	204415
Aug 01, 2016	209842
Sep 01, 2016	210200
Oct 01, 2016	213499
Nov 01, 2016	236420
Dec 01, 2016	240042

Overview of submissions: 2015

Date	Total Submissions
Jan 01, 2015	149013
Feb 01, 2015	156999
Mar 01, 2015	162455
Apr 01, 2015	171408
May 01, 2015	172044
Jun 01, 2015	173236
Jul 01, 2015	184506
Aug 01, 2015	154686
Sep 01, 2015	158580
Oct 01, 2015	160538
Nov 01, 2015	170931
Dec 01, 2015	172006

Overview of submissions: 2014

Date	Total Submissions
Jan 01, 2014	68204
Feb 01, 2014	73492
Mar 01, 2014	83343
Apr 01, 2014	111501
May 01, 2014	112349
Jun 01, 2014	117209

Jul 01, 2014	127132
Aug 01, 2014	127557
Sep 1, 2014	143114
Oct 1, 2014	143601
Nov 1, 2014	144117
Dec 1, 2014	148008

Overview of Submissions: 2013

Date	Total Submissions
Apr 05, 2013	30333
May 01, 2013	30386
Jun 01, 2013	39047
Jul 01, 2013	39170
Aug 01, 2013	45901
Sep 01, 2013	50263
Oct 01, 2013	52047
Nov 01, 2013	64750
Dec 01, 2013	64881