20161006_data_release_notes

Overview of changes in the release of Oct 6, 2016

Please also see our RSS feed for information about accessing the data.

Overview of submissions: 2016

Date	Total Submissions
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

Content

Brief	Explanation
ENIGMA	ENIGMA provided 2024 novel variant interpretations and one update.
PreventionGenetics	PreventionGenetics submitted more than 15000 benign and likely benign variants.
Ambry Genetics	Ambry provided updates for more than 9000 cancer variants and submitted over 3300 cardiac variants.
UniProtKB	HGVS expressions based on UniProtKB sequences were added for more than 17,000 variants. On the web site, a link was added back to UniProtKB based on the UniProt's identifier for the altered protein. These identifiers are reported in variant_summary.txt (e.g. Q30201#VAR_008113). These additions are the result of a trial load; UniProtKB and ClinVar have not finalized a maintenance schedule.
modifications to variant_summary.txt	variant_summary.txtgz in the directory ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/tab_delimited/ was modified significantly in the October release. The scope is now limited to simple variants (AlleleID) to reduce redundancy; with some columns removed and columns added. We did not attempt to retain column numbering although header names were retained if the scope was not changed.
	 Removed from the report HGVS(c.) - now available more comprehensively in ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/tab_delimited/hgv s4variation.txt.gz HGVS(p.) - now available more comprehensively in ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/tab_delimited/hgvs 4variation.txt.gz VariationID - Relationship with VariationID now reported in ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/tab_delimit ed/variation_allele.txt.gz Added to the report HGNC_ID ClinSigSimple PhenotypeSimple Please refer to the README file (ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/README.txt) for more details.

Coming soon - ClinVar will adopt the new HGVS standard for variants that are intronic or outside the UTRs	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. http://varnomen.hgvs.org/recommendations/general/ http://varnomen.hgvs.org/bg-material/numbering/
Coming soon - all submissions through Submission Portal	Soon we will direct all submissions through the Submission Portal: https://submit.ncbi.nlm.nih.gov/clinvar/ If you submit to ClinVar, or plan to submit, please register your organization in the portal now so that we are prepared to accept your submissions through the portal.

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