20141204_data_release_notes

Overview of changes in the release of December 4, 2014

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

Content

Brief	Explanation
ISCA update	Some of the data from ClinGen Structural Variant Working Group (formerly the International Standards for Cytogenomic Arrays Consortium, or ISCA), namely that represented in dbVar as nstd101, has been updated in ClinVar. These records can be retrieved using nstd101 as the query term.
new GeneDx submission	GeneDx submitted 143 assertions for developmental delay.

new report of conflicting data	The ftp site now includes a tab-delimited report (summary_of_conflicting_data.txt) based on variants in ClinVar, for which information has been provided by more than one submitter, and for which there is inconsistency in reporting phenotype or interpretation. The file includes some basic information about the variant, and then describes what each submitter said for which a discrepancy was noted. Although generated primarily for the submitter, or groups reviewing evidence supporting variant assessments, this file may be of interest to others as well. See the README file for more information about this report: ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/tab_delimited/README
January 2015 release	The first release of 2015 will be January 8, 2015 instead of January 1, 2015.
Coming soon	ClinVar will alter the representation of some types of HGVS expressions: Novel submissions may already be reported according to this standard, but the comprehensive revision will not be reported until the January release. • HGVS expressions without an accession and version will be reported as "HGVS, incomplete" rather than as "nucleotide change" • protein HGVS expressions based on legacy numbering systems are curated as "HGVS, legacy"
Coming soon	ClinVar will update its sequence location data to include representation of position according to the VCF standard, rather than HGVS only. This data is represented as "Genomic location" on the website and SequenceLocation in the XML. These updates will happen incrementally, according to variant type.

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