20150702_data_release_notes

Overview of changes in the release of July 2, 2015

Note: for the week of July 2-9, 2015, an old version of the XML file was incorrectly posted to the ftp site. The correct file was added on July 9, 2015. If you downloaded ClinVar's July XML release before July 9, please download the new corrected file, which includes all the new values for ReviewStatus that depend on submission of Assertion Criteria (http://www.ncbi.nlm.nih.gov/clinvar/docs/assertion_criteria/).

Please also see our RSS feed for information about accessing the data, and our release notes for recent changes to ClinVar's web display.

Overview of submissions: 2015

Date	Total Submissions
Jan 01, 2015	149013
Feb 01, 2015	156999
March 1, 2015	162455
Apr 01, 2015	171408
May 1, 2015	172044
June 1, 2015	173236
July 1, 2015	184506

Content

Brief	Explanation
Assertion criteria and review status	ClinVar's definitions of review statuses have changed: www.ncbi.nlm.nih.gov/clinvar/docs/variation_report/#review_status Submitters are now asked to provide their assertion criteria used to classify variants. Submissions without assertion criteria will have the review status "no assertion criteria provided" and will not contribute to the calculation of gold stars on aggregate records. Submissions with assertion criteria will have the review status "criteria provided, single submitter" and will contribute to the number of stars. Documentation is available here: www.ncbi.nlm.nih.gov/clinvar/docs/assertion_criteria/ If you have assertion criteria to document for your submissions, it is not too late to contact us. You can also provide your assertion criteria when you submit an update to your records.
Children's Mercy Hospitals and Clinics submission	Children's Mercy Hospitals and Clinics submitted 23 MECP2 variants associated with developmental delay.
Pathway Genomics	Pathway Genomics submitted 49 interpretations of variants with respect to several types of cancers and related syndromes.

Emory Genetics Laboratory	Emory Genetics Laboratory submitted a complete update of their records, now totaling more than 16,000.
ClinSeq	The ClinSeq project at NHGRI submitted 1713 variants identified as secondary findings.
GeneDX	GeneDX submitted 14 PURA variants and one variant in EPG5.
Review status now aggregated by variant, not RCV accession	The review status that is reported in the VCF and variant_summary files is now aggregated by variant, rather than the RCV accession. This value is now consistent with the review status that is displayed on the corresponding variant record on the website.
Known gaps in the VCF file	In this release, the VCF file has known gaps due to a change in clinical significance terms. The clinical significance "Conflicting data from submitters" was changed to "Conflicting interpretations of pathogenicity"; RCVs with this clinical significance are missing from the VCF file. This will be corrected in the August release.
Coming soon - removal of large datasets without variant interpretation	In the following month, two large datasets of variants associated with a phenotype but without variant interpretation will be removed from ClinVar. All the variants remain available in dbSNP, and BioSample records have been created to represent the phenotypes associated with the variants.

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