20160901_data_release_notes

Overview of changes in the release of Sep 1, 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

Content

Brief	Explanation
Invitae	Invitae provided 12423 variant interpretations, both novel and updates.
GeneDx	GeneDx submitted 5984 variant interpretations, both novel and updates.
CHOP	Children's Hospital of Philadelphia provided 604 variant interpretations, both novel and updates.
UW Clinical Cytogenomics Laboratory	UW Clinical Cytogenomics Laboratory submitted 18 novel copy number variant interpretations.
HudsonAlpha	HudsonAlpha, part of the CSER consortium, provided 13 interpreted variants, both novel and updates.
CHEO	Children's Hospital of Eastern Ontario updated three variant interpretations.
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.

Coming soon: modifications to variant_summary.txt	variant_summary.txt..gz in the directory ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/tab_delimited/ will be modified significantly in the October release. The scope will be limited to simple variants (AlleleID) to reduce redundancy; some columns will be removed and columns added. **We will not attempt to retain column numbering although header names will be retained if the scope was not changed.**
	• To be removed from the report
	  • HGVS(c.) - now available more comprehensively in ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/tab_delimited/hgvs4variation.txt.gz
	  • HGVS(p.) - now available more comprehensively in ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/tab_delimited/hgvs4variation.txt.gz
	  • VariationID - Relationship with VariationID now reported in ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/tab_delimited/variation_allele.txt.gz
	• To be added to the report
	  • HGNC_ID
	  • ClinSigSimple
	  • PhenotypeSimple

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