

Nucleotide

COVID-19 is an emerging, rapidly evolving situation.

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Get the latest research from NIH: <https://www.nih.gov/coronavirus>.

Find NCBI SARS-CoV-2 literature, sequence, and clinical content: <https://www.ncbi.nlm.nih.gov/s>

GenBank

Due to the large size of this record, sequence and annotated features are not shown. Use the "Customize view" panel to c

Homo sapiens chromosome 8, GRCh38.p13 Primary Assembly

NCBI Reference Sequence: NC_000008.11

[FASTA](#) [Graphics](#)

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LOCUS NC_000008 18 bp DNA linear CON 17-AUG-2020

DEFINITION Homo sapiens chromosome 8, GRCh38.p13 Primary Assembly.

ACCESSION [NC_000008](#) REGION: 63648346..63648363

VERSION NC_000008.11

DBLINK BioProject: [PRJNA168](#)
Assembly: [GCF_000001405.39](#)

KEYWORDS RefSeq.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 18)

AUTHORS Nusbaum,C., Mikkelsen,T.S., Zody,M.C., Asakawa,S., Taudien,S.,
Garber,M., Kodira,C.D., Schueler,M.G., Shimizu,A., Whittaker,C.A.,
Chang,J.L., Cuomo,C.A., Dewar,K., FitzGerald,M.G., Yang,X.,
Allen,N.R., Anderson,S., Asakawa,T., Blechschmidt,K., Bloom,T.,
Borowsky,M.L., Butler,J., Cook,A., Corum,B., DeArellano,K.,
DeCaprio,D., Dooley,K.T., Dorris,L. III, Engels,R., Glockner,G.,
Hafez,N., Hagopian,D.S., Hall,J.L., Ishikawa,S.K., Jaffe,D.B.,
Kamat,A., Kudoh,J., Lehmann,R., Lokitsang,T., Macdonald,P.,
Major,J.E., Matthews,C.D., Mauceli,E., Menzel,U., Mihalev,A.H.,
Minoshima,S., Murayama,Y., Naylor,J.W., Nicol,R., Nguyen,C.,
O'Leary,S.B., O'Neill,K., Parker,S.C., Polley,A., Raymond,C.K.,
Reichwald,K., Rodriguez,J., Sasaki,T., Schilhabel,M., Siddiqui,R.,
Smith,C.L., Sneddon,T.P., Talamas,J.A., Tenzin,P., Topham,K.,
Venkataraman,V., Wen,G., Yamazaki,S., Young,S.K., Zeng,Q.,
Zimmer,A.R., Rosenthal,A., Birren,B.W., Platzer,M., Shimizu,N. and
Lander,E.S.

TITLE DNA sequence and analysis of human chromosome 8

JOURNAL Nature 439 (7074), 331-335 (2006)

PUBMED [16421571](#)

REFERENCE 2 (bases 1 to 18)

CONSRM International Human Genome Sequencing Consortium

TITLE Finishing the euchromatic sequence of the human genome

JOURNAL Nature 431 (7011), 931-945 (2004)
 PUBMED [15496913](https://pubmed.ncbi.nlm.nih.gov/15496913/)
 REFERENCE 3 (bases 1 to 18)
 AUTHORS Lander,E.S., Linton,L.M., Birren,B., Nusbaum,C., Zody,M.C., Baldwin,J., Devon,K., Dewar,K., Doyle,M., FitzHugh,W., Funke,R., Gage,D., Harris,K., Heaford,A., Howland,J., Kann,L., Lehoczky,J., LeVine,R., McEwan,P., McKernan,K., Meldrim,J., Mesirov,J.P., Miranda,C., Morris,W., Naylor,J., Raymond,C., Rosetti,M., Santos,R., Sheridan,A., Sougnez,C., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Wyman,D., Rogers,J., Sulston,J., Ainscough,R., Beck,S., Bentley,D., Burton,J., Clee,C., Carter,N., Coulson,A., Deadman,R., Deloukas,P., Dunham,A., Dunham,I., Durbin,R., French,L., Grafham,D., Gregory,S., Hubbard,T., Humphray,S., Hunt,A., Jones,M., Lloyd,C., McMurray,A., Matthews,L., Mercer,S., Milne,S., Mullikin,J.C., Mungall,A., Plumb,R., Ross,M., Shownkeen,R., Sims,S., Waterston,R.H., Wilson,R.K., Hillier,L.W., McPherson,J.D., Marra,M.A., Mardis,E.R., Fulton,L.A., Chinwalla,A.T., Pepin,K.H., Gish,W.R., Chissoe,S.L., Wendl,M.C., Delehaunty,K.D., Miner,T.L., Delehaunty,A., Kramer,J.B., Cook,L.L., Fulton,R.S., Johnson,D.L., Minx,P.J., Clifton,S.W., Hawkins,T., Branscomb,E., Predki,P., Richardson,P., Wenning,S., Slezak,T., Doggett,N., Cheng,J.F., Olsen,A., Lucas,S., Elkin,C., Uberbacher,E., Frazier,M., Gibbs,R.A., Muzny,D.M., Scherer,S.E., Bouck,J.B., Sodergren,E.J., Worley,K.C., Rives,C.M., Gorrell,J.H., Metzker,M.L., Naylor,S.L., Kucherlapati,R.S., Nelson,D.L., Weinstock,G.M., Sakaki,Y., Fujiyama,A., Hattori,M., Yada,T., Toyoda,A., Itoh,T., Kawagoe,C., Watanabe,H., Totoki,Y., Taylor,T., Weissenbach,J., Heilig,R., Saurin,W., Artiguenave,F., Brottier,P., Bruls,T., Pelletier,E., Robert,C., Wincker,P., Smith,D.R., Doucette-Stamm,L., Rubenfield,M., Weinstock,K., Lee,H.M., Dubois,J., Rosenthal,A., Platzer,M., Nyakatura,G., Taudien,S., Rump,A., Yang,H., Yu,J., Wang,J., Huang,G., Gu,J., Hood,L., Rowen,L., Madan,A., Qin,S., Davis,R.W., Federspiel,N.A., Abola,A.P., Proctor,M.J., Myers,R.M., Schmutz,J., Dickson,M., Grimwood,J., Cox,D.R., Olson,M.V., Kaul,R., Raymond,C., Shimizu,N., Kawasaki,K., Minoshima,S., Evans,G.A., Athanasiou,M., Schultz,R., Roe,B.A., Chen,F., Pan,H., Ramser,J., Lehrach,H., Reinhardt,R., McCombie,W.R., de la Bastide,M., Dedhia,N., Blocker,H., Hornischer,K., Nordsiek,G., Agarwala,R., Aravind,L., Bailey,J.A., Bateman,A., Batzoglou,S., Birney,E., Bork,P., Brown,D.G., Burge,C.B., Cerutti,L., Chen,H.C., Church,D., Clamp,M., Copley,R.R., Doerks,T., Eddy,S.R., Eichler,E.E., Furey,T.S., Galagan,J., Gilbert,J.G., Harmon,C., Hayashizaki,Y., Haussler,D., Hermjakob,H., Hokamp,K., Jang,W., Johnson,L.S., Jones,T.A., Kasif,S., Kasprzyk,A., Kennedy,S., Kent,W.J., Kitts,P., Koonin,E.V., Korf,I., Kulp,D., Lancet,D., Lowe,T.M., McLysaght,A., Mikkelsen,T., Moran,J.V., Mulder,N., Pollara,V.J., Ponting,C.P., Schuler,G., Schultz,J., Slater,G., Smit,A.F., Stupka,E., Szustakowski,J., Thierry-Mieg,D., Thierry-Mieg,J., Wagner,L., Wallis,J., Wheeler,R., Williams,A., Wolf,Y.I., Wolfe,K.H., Yang,S.P., Yeh,R.F., Collins,F., Guyer,M.S., Peterson,J., Felsenfeld,A., Wetterstrand,K.A., Patrinos,A., Morgan,M.J., de Jong,P., Catanese,J.J., Osoegawa,K., Shizuya,H., Choi,S. and Chen,Y.J.

CONSRM International Human Genome Sequencing Consortium
 TITLE Initial sequencing and analysis of the human genome

JOURNAL Nature 409 (6822), 860-921 (2001)
 PUBMED [11237011](#)
 REMARK Erratum:[Nature 2001 Aug 2;412(6846):565]
 COMMENT [REFSEQ INFORMATION](#): The reference sequence is identical to [CM000670.2](#).
 On Feb 3, 2014 this sequence version replaced [NC_000008.10](#).
 Assembly Name: GRCh38.p13 Primary Assembly
 The DNA sequence is composed of genomic sequence, primarily finished clones that were sequenced as part of the Human Genome Project. PCR products and WGS shotgun sequence have been added where necessary to fill gaps or correct errors. All such additions are manually curated by GRC staff. For more information see: <https://genomereference.org>.

##Genome-Annotation-Data-START##

Annotation Provider :: NCBI
 Annotation Status :: Updated annotation
 Annotation Name :: [Homo sapiens Updated Annotation Release 109.20200815](#)
 Annotation Version :: 109.20200815
 Annotation Pipeline :: NCBI eukaryotic genome annotation pipeline
 Annotation Software Version :: [8.5](#)
 Annotation Method :: Best-placed RefSeq; propagated RefSeq model
 Features Annotated :: Gene; mRNA; CDS; ncRNA

##Genome-Annotation-Data-END##

FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:[9606](#)"
 /chromosome="8"

ORIGIN

1 ctccctttgt tgtgttgt

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