

# Hepatitis B Virus (HBV) amino acid alignments and genotype-specific consensus sequences

**Philippa C. Matthews**

Wellcome Trust Clinical Research Fellow, Nuffield Department of Medicine, University of Oxford,  
Peter Medawar Building for Pathogen Research, South Parks Road, Oxford OX1 3SY, UK  
Honorary Consultant in Microbiology and Infectious Diseases, Oxford University Hospitals NHS Foundation Trust, John  
Radcliffe Hospital, Headington, Oxford OX3 9DU, UK  
Email: [p.matthews@doctors.org.uk](mailto:p.matthews@doctors.org.uk)

## Background:

Hepatitis B Virus (HBV) is the prototype human hepadnavirus. Unified reference sequences are important for informing phylogenetic analysis, studying diversity within and between hosts, identifying sequence changes (sites of polymorphisms / insertions / deletions) and providing standardised sequence numbering. We have developed a database of HLA Class I epitopes within HBV, 'hepitoes', (on-line at <http://www.expmedndm.ox.ac.uk/hepitoes>), for which we required a unified approach to HBV sequence numbering in order to provide a reference by which epitopes can be located. This work provides aligned and numbered HBV sequences, subdivided by genotype where possible, in the form of a pdf file and an xls spreadsheet.

## Methods:

1. Recently published HBV reference sequences<sup>1</sup> were used as a baseline. The sequences were retrieved from Genbank (<https://www.ncbi.nlm.nih.gov/>) where they can be found under the following accession numbers:
  - Pol: AJW31599
  - Large HBs: AJW31600
  - HBx: AJW31597
  - Pre-core: AJW31591 (first 29 residues only, as remainder of sequence is Core protein)
  - Core: AJW31598
2. Amino acid sequences were downloaded from The Hepatitis B Virus Database (<https://hbvdb.ibcp.fr>) for large HBs, HBx, Core and Pol, for all proteins for which >100 sequences were available. (Download dates 30-Sept to 18-Oct 2016; see Table for numbers of sequences).
3. Downloaded sequences were converted to fasta format using [https://hcv.lanl.gov/cgi-bin/FORMAT\\_CONVERSION/convert.cgi](https://hcv.lanl.gov/cgi-bin/FORMAT_CONVERSION/convert.cgi)
4. Sequences were aligned using clustal omega (up to a maximum of 2000 sequences per alignment) at <http://www.ebi.ac.uk/Tools/msa/clustalo/>
5. A consensus sequence and entropy data was generated from each alignment using tools available on-line at the Los Alamos website [https://www.hiv.lanl.gov/content/sequence/ENTROPY/entropy\\_one.html](https://www.hiv.lanl.gov/content/sequence/ENTROPY/entropy_one.html)
6. Alignments for sequences for Genotype E Pol and the first 29 residues of genotype D pre-core protein failed to align, so these are not represented in the consensus sequences.

**Table:** Number of sequences informing consensus for each HBV protein / genotype

Protein	Geno A	Geno B	Geno C	Geno D	Geno E	Geno F
Pol	1020	1403	1869	982	272	229
Large surface	1271	1799	1897	1167	292	237
HBx	862	1224	2000	1058	288	340
Pre-core	984	1149	1738	768	313	219
Core	1371	1500	1991	1433	453	252

## References:

1. Liu WC, Lin CP, Cheng CP, Ho CH, Lan KL, Cheng JH, et al. Aligning to the sample-specific reference sequence to optimize the accuracy of next-generation sequencing analysis for hepatitis B virus. Hepatol Int. 2016 Jan;10(1):147-57.



HBV Pol Amino Acid Alignment (page 2/5)

Reference sequence is from Liu WC, et al., *Hepatal. Int.* 2016;10:147-57.

Consensus sequences are derived from all available sequences at (<https://hbvdb.ibcp.fr>); see methods (page 1).

'-' designates a residue the same as that within the reference sequence.

'.' designates missing data

Residues that differ from the reference sequence are specified.

The sequence is numbered consecutively from 1 and divided into blocks of ten residues (dashed lines) for ease of navigation.

Terminal protein     Spacer     Reverse transcriptase     RNase H

Position	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250
Reference	S	P	G	I	L	R	G	S	S	V	G	P	S	I	Q	S	Q	L	R	K	S	R	L	G	P	Q	P	A	Q	G	Q	L	A	G	R	Q	Q	G	S	G	S	I	R	A	R	V	H	P	S	
Geno A	P	S	-	-	S	R	-	-	-	-	-	C	-	R	-	-	-	K	Q	-	-	-	-	L	-	H	-	-	P	-	-	S	S	Q	P	-	R	-	-	-	-	-	-	A	-	-	-	-		
Geno B	-	-	-	-	P	R	-	-	-	-	-	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
Geno C	-	S	-	-	S	R	-	P	-	-	-	C	V	R	-	-	-	K	Q	-	-	-	-	L	-	Q	-	-	S	-	-	R	G	K	S	-	R	-	-	-	-	-	-	-	-	-	T	-	-	
Geno D	-	S	-	-	S	R	P	P	-	-	S	-	L	-	-	K	H	-	-	-	-	-	-	L	-	S	Q	-	-	H	-	-	R	-	-	-	-	R	-	W	-	-	-	G	I	-	-	T	-	-
Geno F	-	S	-	-	S	R	P	-	A	-	S	-	-	-	G	K	F	Q	Q	-	-	-	-	L	-	Q	K	-	-	-	-	N	G	K	-	-	R	-	-	R	L	-	S	-	-	-	T	P	-	-

Position	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300
Reference	P	W	G	T	V	G	V	E	P	S	G	S	G	Q	T	H	N	C	A	S	S	S	S	S	C	L	H	Q	S	A	V	R	K	A	A	Y	S	L	I	S	T	S	K	G	H	S	S	G	H	
Geno A	T	R	R	Y	F	-	-	-	-	-	-	-	-	H	I	D	H	S	V	N	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	H	L	-	-	-	-	R	Q	-	-	-	-	
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	P	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
Geno C	T	R	R	S	F	-	-	-	-	-	-	-	-	H	I	D	-	S	-	-	T	-	-	-	-	-	-	-	-	-	-	-	-	T	-	-	-	H	L	-	-	-	-	R	Q	-	-	-	-	
Geno D	A	R	R	P	F	-	-	-	-	-	-	-	-	H	T	T	-	L	-	-	K	-	A	-	-	-	Y	-	-	P	-	-	-	-	-	-	-	P	A	V	-	-	F	E	K	-	-	-	-	
Geno F	T	R	W	P	-	-	-	-	-	-	-	T	-	C	A	N	-	L	-	-	R	-	A	-	-	F	-	-	-	-	-	-	E	K	-	N	P	S	L	-	-	-	R	-	T	-	T	-		

Position	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	
Reference	A	V	E	L	H	H	F	P	P	N	S	S	R	S	Q	S	P	G	P	V	P	S	C	W	W	L	Q	F	R	N	S	E	P	C	S	E	Y	C	L	C	H	I	V	N	L	I	D	D	W	G	
Geno A	-	-	-	F	-	C	L	-	-	S	-	A	G	-	-	Q	-	S	-	F	-	-	-	-	-	-	-	-	-	-	-	K	-	-	-	-	-	S	-	L	-	-	-	R	-	-	-	-			
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Q	-	-	-	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
Geno C	-	-	-	-	-	N	I	-	-	S	-	A	-	-	-	E	-	-	I	L	-	-	-	-	-	-	-	-	-	-	-	K	-	-	-	D	-	-	T	-	-	-	-	L	-	-	-	-			
Geno D	-	-	-	-	-	N	L	-	-	-	-	A	-	-	-	-	E	R	-	-	F	P	-	-	-	-	-	-	-	-	-	-	K	-	-	-	D	-	-	S	-	-	-	-	L	-	-	-	-		
Geno F	-	-	-	-	N	S	V	-	-	G	-	V	-	-	E	G	K	-	S	-	F	-	-	-	-	-	-	-	-	-	-	D	T	-	-	-	-	D	-	-	S	-	-	I	-	-	L	-	-	-	-

Position	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400
Reference	P	C	T	E	H	G	E	H	L	I	R	T	P	R	T	P	A	R	V	T	G	G	V	F	L	V	D	K	N	P	H	N	T	T	E	S	R	L	V	V	D	F	S	Q	F	S	R	G	N	T
Geno A	-	-	D	-	-	-	-	H	-	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	I	-		
Geno B	-	-	-	-	-	-	-	R	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno C	-	-	-	-	-	-	-	N	-	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	
Geno D	-	-	A	-	-	-	-	H	-	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Y		
Geno F	-	-	Y	-	-	Q	-	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	

➔ continues on next page

Consensus sequences are derived from all available sequences at (<https://hbvdb.ibcp.fr>); see methods (page 1).

‘.’ designates missing data

Residues that differ from the reference sequence are specified.

The sequence is numbered consecutively from 1 and divided into blocks of ten residues (dashed lines) for ease of navigation. YMDD motif is marked with a box (residues 549-552 in this alignment).

Terminal protein    Spacer    Reverse transcriptase    RNase H

[illegible]

Position	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500
Reference	S	S	G	L	S	R	Y	V	A	P	L	S	S	N	S	R	I	N	N	Q	H	R	T	M	Q	N	L	H	D	S	C	S	R	N	L	Y	V	S	L	M	L	Y	Q	T	Y	G	R	K		
Geno A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	-	-	Y	G	-	-	-	-	-	-	-	-	-	-	-	-	Q	-	-	-	-	-	-	-	-	-	K	-	-	W	-		
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	-	-	-	-	-	
Geno C	-	-	-	P	-	-	-	-	-	-	-	-	-	T	-	-	N	-	Y	-	G	-	-	-	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	-	-	-	K	-	F	-	-	-
Geno D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	F	-	H	-	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	-	-	-	-	F	-	-	-	-
Geno F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	-	-	H	D	H	-	G	-	-	-	-	-	-	N	-	-	-	-	-	-	-	-	-	L	-	-	F	-	-	L	-	-	-	-	-

[illegible]

Position	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600
Reference	D	D	V	V	L	G	A	K	S	V	Q	H	L	E	S	L	Y	A	A	V	T	N	F	L	L	S	L	G	I	H	L	N	P	H	K	T	K	R	W	G	Y	S	L	N	F	M	G	Y	V	I
Geno A	-	-	-	-	-	-	-	-	-	-	-	R	-	-	-	-	-	T	-	-	-	-	-	-	-	-	L	-	-	-	-	-	-	N	-	-	-	-	-	-	-	-	-	-	-	-	-	I	-	
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	F	T	S	I	-	-	-	-	-	-	L	-	-	-	-	-	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	F	T	-	-	-	-	-	-	-	-	L	-	-	-	-	N	-	-	-	-	-	-	-	-	-	-	H	-	-	-	-	-
Geno F	-	-	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	S	-	-	-	-	-	-	T	-	H	-	-	-	-	-	-

➔ continues on next page

HBV Pol Amino Acid Alignment (page 4/5)

Reference sequence is from Liu WC, et al., *Hepatol. Int.* 2016;10:147-57.

Consensus sequences are derived from all available sequences at (<https://hbvdb.ibcp.fr>); see methods (page 1).

'-' designates a residue the same as that within the reference sequence.

'.' designates missing data

Residues that differ from the reference sequence are specified.

The sequence is numbered consecutively from 1 and divided into blocks of ten residues (dashed lines) for ease of navigation.

Terminal protein     Spacer     Reverse transcriptase     RNase H

Position	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650
Reference	G	S	W	G	T	L	P	Q	E	H	I	V	Q	K	I	K	M	C	F	R	K	L	P	V	N	R	P	I	D	W	K	V	C	Q	R	I	V	G	L	L	G	F	A	A	P	F	T	Q	C	G
Geno A	-	-	-	-	-	-	-	D	-	-	-	-	-	-	-	H	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno C	-	-	-	-	-	-	-	-	-	-	-	-	L	-	-	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno D	-	C	Y	-	S	-	-	D	-	-	I	-	-	-	-	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno F	-	-	-	S	-	-	D	-	-	-	H	-	-	-	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Position	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700
Reference	Y	P	A	L	M	P	L	Y	A	C	I	Q	A	K	Q	A	F	T	F	S	P	T	Y	K	A	F	L	S	K	Q	Y	L	N	L	P	V	A	R	Q	R	P	G	L	C	Q	V	F	A	D	
Geno A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno C	-	-	-	-	-	-	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno D	-	-	-	-	-	-	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno F	-	-	-	-	-	-	-	-	-	-	-	T	-	-	-	-	V	-	-	-	-	-	-	-	-	-	-	-	C	-	-	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	

Position	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750
Reference	A	T	P	T	G	W	G	L	A	I	G	H	Q	R	L	R	G	T	F	V	S	P	L	P	I	H	T	A	E	L	L	A	A	C	F	A	R	S	R	S	G	A	K	L	I	G	T	D	N	S
Geno A	-	-	-	-	-	-	-	-	-	I	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno B	-	-	-	-	-	-	-	-	-	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno C	-	-	-	-	-	-	-	-	-	I	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno D	-	-	-	-	-	-	-	-	V	M	-	-	-	-	-	-	-	-	-	L	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	N	I	L	-	-	-	-	-	
Geno F	-	-	-	-	-	-	-	-	I	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Position	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800
Reference	V	V	L	S	R	K	Y	T	S	F	P	W	L	L	G	C	A	A	N	W	I	L	R	G	T	S	F	V	Y	V	P	S	A	L	N	P	A	D	D	P	S	R	G	R	L	G	L	Y	R	P
Geno A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	-	
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	-	
Geno F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

➔ continues on next page

HBV Pol Amino Acid Alignment (page 5/5)

Reference sequence is from Liu WC, et al., *Hepatol. Int.* 2016;10:147-57.

Consensus sequences are derived from all available sequences at (<https://hbvdb.ibcp.fr>); see methods (page 1).

'-' designates a residue the same as that within the reference sequence.

'.' designates missing data

Residues that differ from the reference sequence are specified.

The sequence is numbered consecutively from 1 and divided into blocks of ten residues (dashed lines) for ease of navigation.

	Terminal protein	Spacer	Reverse transcriptase	RNAse H																																								
Position	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	
Reference	L	L	R	L	L	Y	R	P	T	T	G	R	T	S	L	Y	A	D	S	P	S	V	P	S	H	L	P	D	R	V	H	F	A	S	P	L	H	V	A	W	K	P	P	
Geno A	-	-	-	-	P	F	Q	-	-	-	-	-	-	-	-	-	V	-	-	-	-	-	-	-	-	-	-	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno C	-	-	H	-	P	F	-	-	-	-	-	-	-	-	-	-	-	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno D	-	-	-	-	P	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno F	-	-	-	-	P	F	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

HBV Large S Protein Amino Acid Alignment (page 1/2)

Reference sequence is from Liu WC, et al., *Hepatol. Int.* 2016;10:147-57.

Consensus sequences are derived from all available sequences at (<https://hbvdb.ibcp.fr>); see methods (page 1).

'-' designates a residue the same as that within the reference sequence.

'.' designates missing data

Residues that differ from the reference sequence are specified.

The sequence is numbered consecutively from 1 and divided into blocks of ten residues (dashed lines) for ease of navigation.

 Pre-S2       Surface antigen

Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50		
Reference	M	G	G	W	S	S	K	P	R	K	G	M	G	T	N	L	S	V	P	N	P	L	G	F	F	G	D	H	Q	L	D	P	L	F	R	A	N	S	E	N	P	D	W	D	L	N	P	H	K	D		
Geno A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
Geno C	-	-	-	-	-	-	-	-	-	-	Q	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
Geno D	-	-	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno E	-	-	.	L	-	W	T	V	P	L	E	W	-	K	-	H	-	T	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno F	-	-	A	P	L	S	T	T	-	R	-	-	-	Q	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Position	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
Reference	N	W	P	D	A	N	K	V	G	V	G	A	F	G	P	G	F	T	P	P	H	G	G	L	L	G	W	S	P	Q	A	Q	G	R	L	T	T	V	P	A	A	P	P	P	A	S	T	N	R	Q	
Geno A	H	-	-	A	-	-	Q	-	-	-	-	-	-	-	-	-	L	-	-	-	-	-	-	I	-	-	-	-	-	-	-	-	I	-	-	-	-	-	S	T	I	-	-	-	-	-	-	-	-	-	
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno C	H	-	-	E	-	-	Q	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno D	T	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	-	Q	-	L	-	-	N	-	-	-	-	-	-	-	-	
Geno E	H	-	T	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	M	-	K	-	L	-	-	D	-	-	-	-	-	-	-	-	
Geno F	-	-	-	M	-	-	-	-	-	-	-	G	Y	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	-	-	-	L	-	-	D	-	-	-	-	-	-	-	-	R

Position	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	
Reference	S	G	R	Q	P	T	P	L	S	P	P	L	R	D	T	H	P	Q	A	M	Q	W	N	S	T	T	F	H	Q	T	L	Q	D	P	R	V	R	A	L	Y	L	P	A	G	G	S	S	S	G	I	
Geno A	-	-	-	-	-	-	-	I	-	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	-	A	-	-	-	A	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno C	-	-	-	-	-	-	-	I	-	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	-	L	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-	
Geno D	-	-	-	-	-	-	-	-	-	-	-	-	-	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	
Geno E	-	-	-	-	-	-	-	I	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	G	-	-	-	-	-	-	-	-	-	-	-	-
Geno F	-	-	-	K	-	-	-	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Q	-	-	A	-	L	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	E

Position	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200			
Reference	V	S	P	A	Q	N	T	V	S	A	I	S	S	I	L	S	T	T	G	D	P	V	P	N	M	E	N	I	S	S	G	L	L	G	P	L	L	V	L	Q	A	G	F	F	L	L	T	K	I	L			
Geno A	-	N	-	-	P	-	I	A	-	H	-	-	-	-	S	A	R	-	-	-	-	-	T	-	-	-	-	T	-	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
Geno C	-	N	-	V	P	T	-	A	-	P	-	-	-	-	F	-	R	-	-	-	-	A	-	-	-	-	T	T	-	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno D	-	N	-	V	P	T	-	A	-	P	-	-	-	-	F	-	R	I	-	-	-	A	L	-	-	-	-	T	-	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno E	-	N	-	V	P	T	-	A	-	L	-	-	-	-	F	-	R	I	-	-	-	A	-	-	-	-	S	-	T	-	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno F	Q	N	-	-	P	T	I	A	-	L	T	-	-	-	F	-	K	-	-	G	-	A	M	-	-	D	-	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-



HBV X Protein Amino Acid Alignment

Reference sequence is from Liu WC, et al., *Hepatol. Int.* 2016;10:147-57.  
Consensus sequences are derived from all available sequences at (<https://hbvdb.ibcp.fr>); see methods (page 1).  
'-' designates a residue the same as that within the reference sequence.  
'.' designates missing data  
Residues that differ from the reference sequence are specified.  
The sequence is numbered consecutively from 1 and divided into blocks of ten residues (dashed lines) for ease of navigation.

Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
Reference	M	A	A	R	L	C	C	Q	L	D	P	A	R	D	V	L	R	L	R	P	V	G	A	E	S	R	G	R	P	L	P	G	P	L	G	A	L	P	P	A	S	P	P	V	V	P	T	D	H	G
Geno A	-	-	-	-	-	Y	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	-	-	-	-	T	-	S	S	P	-	-	S	A	-	-	A	-	-	
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
Geno C	-	-	-	-	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	S	-	-	F	-	T	-	-	S	P	-	-	S	A	-	-	A	-	-		
Geno D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	F	S	-	-	-	-	T	-	S	S	P	-	-	S	A	-	-	S	-	-		
Geno E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	-	-	C	-	-	V	S	-	S	-	-	D	-	S	S	P	-	-	S	A	-	-	A	-	-		
Geno F	-	-	-	-	-	-	-	-	-	-	-	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	-	S	-	S	-	-	V	-	-	P	-	-	S	A	-	-	A	-	D		

Position	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
Reference	A	H	L	S	L	R	G	L	P	V	C	A	F	S	S	A	G	P	C	A	L	R	F	T	S	A	R	R	M	E	T	T	V	N	A	H	R	N	L	P	K	V	L	H	K	R	T	L	G	L
Geno A	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	-	-	-	-	-	-	-	Q	I	-	-	-	-	-	-	-	-	-	-	-		
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Geno C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Q	V	-	-	-	-	-	-	-	-	-	-		
Geno D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Q	F	-	-	-	-	-	-	-	-	-	-	-	
Geno E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Q	I	-	-	-	-	-	-	-	-	-	-	-	
Geno F	S	-	-	-	-	-	-	-	-	-	S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	S	-	T	-	-	-	-	-	-	-	-	-	

Position	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
Reference	S	A	M	S	T	T	D	L	E	A	Y	F	K	D	C	V	F	T	E	W	E	E	L	G	E	E	I	R	L	M	I	F	V	L	G	G	C	R	H	K	L	V	R	S	P	A	P	C	N	F
Geno A	P	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	D	-	-	-	-	-	-	-	-	-	K	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	K	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno D	-	V	-	-	-	-	-	-	-	-	-	-	-	-	-	L	-	K	D	-	-	-	-	-	-	-	-	-	-	-	K	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	L	-	K	D	-	-	-	-	-	-	-	-	-	-	-	K	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno F	-	G	R	-	M	-	W	I	-	E	-	I	-	-	-	-	-	K	D	-	-	-	-	-	-	-	-	-	-	-	K	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Position	151	152	153	154
Reference	F	T	S	A
Geno A	-	-	-	-
Geno B	-	-	-	-
Geno C	-	-	-	-
Geno D	-	-	-	-
Geno E	-	-	-	-
Geno F	-	-	-	-

**HBV Pre-Core Protein Amino Acid Alignment (first 29 residues only)**

The remaining residues (30 onwards) are represented in the alignment for core sequence (see page 11)

Reference sequence is from Liu WC, et al., *Hepatol. Int.* 2016;10:147-57.

Consensus sequences are derived from all available sequences at (<https://hbvdb.ibcp.fr>); see methods (page 1).

'-' designates a residue the same as that within the reference sequence.

'.' designates missing data

Residues that differ from the reference sequence are specified.

The sequence is numbered consecutively from 1 and divided into blocks of ten residues (dashed lines) for ease of navigation.

Position	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29
Reference	M	Q	L	F	H	L	C	L	I	I	S	C	S	C	P	T	V	Q	A	S	K	L	C	L	G	W	L	W	G
Geno A	-	-	-	-	-	-	-	-	-	-	-	-	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno F	-	-	-	-	-	-	-	-	-	-	F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

### HBV Core Protein Amino Acid Alignment

The pre-core protein incorporates an additional 29 residues upstream of this sequence (see sequences represented on page 10).

Reference sequence is from Liu WC, et al., *Hepatol. Int.* 2016;10:147-57.

Consensus sequences are derived from all available sequences at (<https://hbvdb.ibcp.fr>); see methods (page 1).

' ' designates a residue the same as that within the reference sequence.

‘.’ designates missing data

Residues that differ from the reference sequence are specified.

The sequence is numbered consecutively from 1 and divided into blocks of ten residues (dashed lines) for ease of navigation.

[illegible][illegible][illegible]

Position	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183
Reference	R	R	G	R	S	P	R	R	R	T	P	S	P	R	R	R	R	S	Q	S	P	R	R	R	R	S	Q	S	R	E	S	K	C
Geno A	-	-	D	.	R	G	-	.	.	.	.	-	-	-	-	-	T	P	.	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno B	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno C	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Geno E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	A	-	-	-
Geno F	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	A	-	-	-